

Sjors H W Scheres

List of Publications by Year in descending order

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116
papers

34,802
citations

12330

69
h-index

23533

111
g-index

170
all docs

170
docs citations

170
times ranked

27905
citing authors

#	ARTICLE	IF	CITATIONS
1	RELION: Implementation of a Bayesian approach to cryo-EM structure determination. <i>Journal of Structural Biology</i> , 2012, 180, 519-530.	2.8	4,715
2	New tools for automated high-resolution cryo-EM structure determination in RELION-3. <i>ELife</i> , 2018, 7, .	6.0	3,965
3	Cryo-EM structures of tau filaments from Alzheimer's disease. <i>Nature</i> , 2017, 547, 185-190.	27.8	1,502
4	Prevention of overfitting in cryo-EM structure determination. <i>Nature Methods</i> , 2012, 9, 853-854.	19.0	1,104
5	Accelerated cryo-EM structure determination with parallelisation using GPUs in RELION-2. <i>ELife</i> , 2016, 5, .	6.0	919
6	Structures and distributions of SARS-CoV-2 spike proteins on intact virions. <i>Nature</i> , 2020, 588, 498-502.	27.8	918
7	High-resolution noise substitution to measure overfitting and validate resolution in 3D structure determination by single particle electron cryomicroscopy. <i>Ultramicroscopy</i> , 2013, 135, 24-35.	1.9	843
8	A Bayesian View on Cryo-EM Structure Determination. <i>Journal of Molecular Biology</i> , 2012, 415, 406-418.	4.2	765
9	How cryo-EM is revolutionizing structural biology. <i>Trends in Biochemical Sciences</i> , 2015, 40, 49-57.	7.5	709
10	A Bayesian approach to beam-induced motion correction in cryo-EM single-particle analysis. <i>IUCr</i> , 2019, 6, 5-17.	2.2	696
11	Structures of filaments from Pick's disease reveal a novel tau protein fold. <i>Nature</i> , 2018, 561, 137-140.	27.8	625
12	Estimation of high-order aberrations and anisotropic magnification from cryo-EM data sets in RELION-3.1. <i>IUCr</i> , 2020, 7, 253-267.	2.2	574
13	Single-particle cryo-EM at atomic resolution. <i>Nature</i> , 2020, 587, 152-156.	27.8	572
14	Sampling the conformational space of the catalytic subunit of human β -secretase. <i>ELife</i> , 2015, 4, .	6.0	556
15	Novel tau filament fold in chronic traumatic encephalopathy encloses hydrophobic molecules. <i>Nature</i> , 2019, 568, 420-423.	27.8	528
16	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Science</i> , 2014, 343, 1485-1489.	12.6	521
17	Processing of Structurally Heterogeneous Cryo-EM Data in RELION. <i>Methods in Enzymology</i> , 2016, 579, 125-157.	1.0	502
18	An atomic structure of human β -secretase. <i>Nature</i> , 2015, 525, 212-217.	27.8	490

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19	Structures of τ -synuclein filaments from multiple system atrophy. <i>Nature</i> , 2020, 585, 464-469.	27.8	446
20	Helical reconstruction in RELION. <i>Journal of Structural Biology</i> , 2017, 198, 163-176.	2.8	438
21	XMIPP: a new generation of an open-source image processing package for electron microscopy. <i>Journal of Structural Biology</i> , 2004, 148, 194-204.	2.8	434
22	Characterisation of molecular motions in cryo-EM single-particle data by multi-body refinement in RELION. <i>ELife</i> , 2018, 7, .	6.0	434
23	The structure of the human mitochondrial ribosome. <i>Science</i> , 2015, 348, 95-98.	12.6	432
24	Structure-based classification of tauopathies. <i>Nature</i> , 2021, 598, 359-363.	27.8	409
25	New tools for automated cryo-EM single-particle analysis in RELION-4.0. <i>Biochemical Journal</i> , 2021, 478, 4169-4185.	3.7	396
26	Structure of the rabbit ryanodine receptor RyR1 at near-atomic resolution. <i>Nature</i> , 2015, 517, 50-55.	27.8	391
27	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. <i>Nature Methods</i> , 2007, 4, 27-29.	19.0	387
28	Novel tau filament fold in corticobasal degeneration. <i>Nature</i> , 2020, 580, 283-287.	27.8	381
29	Ribosome structures to near-atomic resolution from thirty thousand cryo-EM particles. <i>ELife</i> , 2013, 2, e00461.	6.0	378
30	Unravelling biological macromolecules with cryo-electron microscopy. <i>Nature</i> , 2016, 537, 339-346.	27.8	352
31	Semi-automated selection of cryo-EM particles in RELION-1.3. <i>Journal of Structural Biology</i> , 2015, 189, 114-122.	2.8	346
32	Three-dimensional structure of human β -secretase. <i>Nature</i> , 2014, 512, 166-170.	27.8	317
33	Image processing for electron microscopy single-particle analysis using XMIPP. <i>Nature Protocols</i> , 2008, 3, 977-990.	12.0	310
34	Heparin-induced tau filaments are polymorphic and differ from those in Alzheimer's and Pick's diseases. <i>ELife</i> , 2019, 8, .	6.0	309
35	Structure of the Mammalian Ribosome-Sec61 Complex to 3.4Å... Resolution. <i>Cell</i> , 2014, 157, 1632-1643.	28.9	302
36	Cryo-EM: A Unique Tool for the Visualization of Macromolecular Complexity. <i>Molecular Cell</i> , 2015, 58, 677-689.	9.7	300

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37	Beam-induced motion correction for sub-megadalton cryo-EM particles. <i>ELife</i> , 2014, 3, e03665.	6.0	298
38	Cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to the anti-protozoan drug emetine. <i>ELife</i> , 2014, 3, .	6.0	274
39	A pipeline approach to single-particle processing in <i>RELION</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 496-502.	2.3	262
40	A thermostable, closed SARS-CoV-2 spike protein trimer. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 934-941.	8.2	261
41	Structure of the large ribosomal subunit from human mitochondria. <i>Science</i> , 2014, 346, 718-722.	12.6	260
42	Tau filaments from multiple cases of sporadic and inherited Alzheimer's disease adopt a common fold. <i>Acta Neuropathologica</i> , 2018, 136, 699-708.	7.7	252
43	Maximum-likelihood Multi-reference Refinement for Electron Microscopy Images. <i>Journal of Molecular Biology</i> , 2005, 348, 139-149.	4.2	239
44	Cryo-EM structures of amyloid- β 42 filaments from human brains. <i>Science</i> , 2022, 375, 167-172.	12.6	228
45	Cryo-EM structure of a 3D DNA-origami object. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20012-20017.	7.1	219
46	Resolving macromolecular structures from electron cryo-tomography data using subtomogram averaging in RELION. <i>Nature Protocols</i> , 2016, 11, 2054-2065.	12.0	216
47	Initiation of Translation by Cricket Paralysis Virus IRES Requires Its Translocation in the Ribosome. <i>Cell</i> , 2014, 157, 823-831.	28.9	211
48	Atomic structure of the apoptosome: mechanism of cytochrome <i>c</i> and dATP-mediated activation of Apaf-1. <i>Genes and Development</i> , 2015, 29, 2349-2361.	5.9	201
49	The architecture of the spliceosomal U4/U6.U5 tri-snRNP. <i>Nature</i> , 2015, 523, 47-52.	27.8	195
50	Advances in Single-Particle Electron Cryomicroscopy Structure Determination applied to Sub-tomogram Averaging. <i>Structure</i> , 2015, 23, 1743-1753.	3.3	189
51	Cryo-EM structure of the yeast U4/U6.U5 tri-snRNP at 3.7 Å... resolution. <i>Nature</i> , 2016, 530, 298-302.	27.8	184
52	Cryo-EM structures of tau filaments. <i>Current Opinion in Structural Biology</i> , 2020, 64, 17-25.	5.7	165
53	Structure of ratcheted ribosomes with tRNAs in hybrid states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16924-16927.	7.1	161
54	Amyloid structure determination in <i>RELION</i> -3.1. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 94-101.	2.3	161

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55	Structure of the MacAB–TolC ABC-type tripartite multidrug efflux pump. <i>Nature Microbiology</i> , 2017, 2, 17070.	13.3	140
56	Cryo-EM structure of a neuronal functional amyloid implicated in memory persistence in <i>Drosophila</i> . <i>Science</i> , 2020, 367, 1230-1234.	12.6	140
57	Mefloquine targets the <i>Plasmodium falciparum</i> 80S ribosome to inhibit protein synthesis. <i>Nature Microbiology</i> , 2017, 2, 17031.	13.3	128
58	Assembly of recombinant tau into filaments identical to those of Alzheimer’s disease and chronic traumatic encephalopathy. <i>ELife</i> , 2022, 11, .	6.0	121
59	Molecular Architecture of a Eukaryotic Translational Initiation Complex. <i>Science</i> , 2013, 342, 1240585.	12.6	120
60	Insights into the molecular architecture of the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11943-11947.	7.1	116
61	Structure of active dimeric human telomerase. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 454-460.	8.2	115
62	Averaging of Electron Subtomograms and Random Conical Tilt Reconstructions through Likelihood Optimization. <i>Structure</i> , 2009, 17, 1563-1572.	3.3	112
63	Cryo-EM structures of tau filaments from Alzheimer’s disease with PET ligand APN-1607. <i>Acta Neuropathologica</i> , 2021, 141, 697-708.	7.7	99
64	Mechanistic insights into caspase-9 activation by the structure of the apoptosome holoenzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1542-1547.	7.1	95
65	Seeded assembly <i>in vitro</i> does not replicate the structures of τ synuclein filaments from multiple system atrophy. <i>FEBS Open Bio</i> , 2021, 11, 999-1013.	2.3	95
66	Design of a molecular support for cryo-EM structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7456-E7463.	7.1	93
67	Age-dependent formation of TMEM106B amyloid filaments in human brains. <i>Nature</i> , 2022, 605, 310-314.	27.8	88
68	The structure of CCT–Hsc70NBD suggests a mechanism for Hsp70 delivery of substrates to the chaperonin. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 858-864.	8.2	85
69	Classification of Structural Heterogeneity by Maximum-Likelihood Methods. <i>Methods in Enzymology</i> , 2010, 482, 295-320.	1.0	84
70	Collaborative Computational Project for Electron cryo-Microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 123-126.	2.5	84
71	Structure of hibernating ribosomes studied by cryoelectron tomography <i>in vitro</i> and <i>in situ</i> . <i>Journal of Cell Biology</i> , 2010, 190, 613-621.	5.2	83
72	Structure of the Fanconi anaemia monoubiquitin ligase complex. <i>Nature</i> , 2019, 575, 234-237.	27.8	80

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73	cryo-EM structures of the E. coli replicative DNA polymerase reveal its dynamic interactions with the DNA sliding clamp, exonuclease and γ . <i>ELife</i> , 2015, 4, .	6.0	75
74	Modeling Experimental Image Formation for Likelihood-Based Classification of Electron Microscopy Data. <i>Structure</i> , 2007, 15, 1167-1177.	3.3	68
75	An Introduction to Maximum-Likelihood Methods in Cryo-EM. <i>Methods in Enzymology</i> , 2010, 482, 263-294.	1.0	65
76	Electron microscopy studies on the quaternary structure of p53 reveal different binding modes for p53 tetramers in complex with DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 557-562.	7.1	65
77	Cryo-EM structure of a metazoan separase-securin complex at near-atomic resolution. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 414-418.	8.2	65
78	Structure and Uncoating of Immature Adenovirus. <i>Journal of Molecular Biology</i> , 2009, 392, 547-557.	4.2	64
79	Maximum likelihood based classification of electron tomographic data. <i>Journal of Structural Biology</i> , 2011, 173, 77-85.	2.8	56
80	Cryo-EM of dynein microtubule-binding domains shows how an axonemal dynein distorts the microtubule. <i>ELife</i> , 2019, 8, .	6.0	56
81	Structure of the apoptosome: mechanistic insights into activation of an initiator caspase from <i>Drosophila</i> . <i>Genes and Development</i> , 2015, 29, 277-287.	5.9	55
82	Fast maximum-likelihood refinement of electron microscopy images. <i>Bioinformatics</i> , 2005, 21, ii243-ii244.	4.1	54
83	Quasi-Atomic Model of Bacteriophage T7 Procapsid Shell: Insights into the Structure and Evolution of a Basic Fold. <i>Structure</i> , 2007, 15, 461-472.	3.3	54
84	Distinct Conformers of Assembled Tau in Alzheimer's and Pick's Diseases. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2018, 83, 163-171.	1.1	53
85	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	8.2	49
86	CryoEM structure of MxB reveals a novel oligomerization interface critical for HIV restriction. <i>Science Advances</i> , 2017, 3, e1701264.	10.3	47
87	Revealing the structures of megadalton-scale DNA complexes with nucleotide resolution. <i>Nature Communications</i> , 2020, 11, 6229.	12.8	43
88	Self-correcting mismatches during high-fidelity DNA replication. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 140-143.	8.2	42
89	Conformational Rearrangements of SV40 Large T Antigen during Early Replication Events. <i>Journal of Molecular Biology</i> , 2010, 397, 1276-1286.	4.2	40
90	Multi-body Refinement of Cryo-EM Images in RELION. <i>Methods in Molecular Biology</i> , 2021, 2215, 145-160.	0.9	39

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91	tmRNA-SmpB complex mimics native aminoacyl-tRNAs in the A site of stalled ribosomes. <i>Journal of Structural Biology</i> , 2010, 169, 342-348.	2.8	34
92	Maximum likelihood refinement of electron microscopy data with normalization errors. <i>Journal of Structural Biology</i> , 2009, 166, 234-240.	2.8	33
93	Atomic Structure of Type VI Contractile Sheath from <i>Pseudomonas aeruginosa</i> . <i>Structure</i> , 2018, 26, 329-336.e3.	3.3	29
94	The structural basis of proton driven zinc transport by ZntB. <i>Nature Communications</i> , 2017, 8, 1313.	12.8	27
95	SPI-EM: Towards a Tool For Predicting CATH Superfamilies in 3D-EM Maps. <i>Journal of Molecular Biology</i> , 2005, 345, 759-771.	4.2	25
96	Electron microscopy of Xrcc4 and the DNA ligase IV-Xrcc4 DNA repair complex. <i>DNA Repair</i> , 2009, 8, 1380-1389.	2.8	24
97	Subunit Positioning and Stator Filament Stiffness in Regulation and Power Transmission in the V1 Motor of the <i>Manduca sexta</i> V-ATPase. <i>Journal of Molecular Biology</i> , 2014, 426, 286-300.	4.2	24
98	X-ray and cryo-EM structures of monomeric and filamentous actin-like protein MamK reveal changes associated with polymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13396-13401.	7.1	24
99	CryoEM structures of spliceosomal complexes reveal the molecular mechanism of pre-mRNA splicing. <i>Current Opinion in Structural Biology</i> , 2017, 46, 130-139.	5.7	22
100	Classification of single-projection reconstructions for cryo-electron microscopy data of icosahedral viruses. <i>Journal of Structural Biology</i> , 2005, 151, 79-91.	2.8	20
101	Exploiting prior knowledge about biological macromolecules in cryo-EM structure determination. <i>IUCr</i> , 2021, 8, 60-75.	2.2	14
102	Optimization problems in electron microscopy of single particles. <i>Annals of Operations Research</i> , 2006, 148, 133-165.	4.1	12
103	Visualizing molecular machines in action. <i>Advances in Protein Chemistry and Structural Biology</i> , 2010, 81, 89-119.	2.3	8
104	Tau Protein and Frontotemporal Dementias. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1281, 177-199.	1.6	8
105	Introducing robustness to maximum-likelihood refinement of electron-microscopy data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 672-678.	2.5	6
106	Ab initio structure determination of low-molecular-weight compounds using synchrotron radiation Laue diffraction. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 19-28.	2.4	4
107	Grid Computing in 3D-EM Image Processing Using Xmipp. , 0, , .		3
108	[E3A02]: CRYO-EM STRUCTURES OF TAU FILAMENTS FROM ALZHEIMER'S DISEASE BRAIN. <i>Alzheimer's and Dementia</i> , 2017, 13, P892.	0.8	3

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109	The potentials of conditional optimization in phasing and model building of protein crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2202-2209.	2.5	2
110	Conditional optimization: a new formalism for protein structure refinement. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1820-1828.	2.5	1
111	Development of a force field for conditional optimization of protein structures. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 438-446.	2.5	1
112	A Bayesian view on cryo-EM structure determination. , 2012, , .		1
113	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. Microscopy and Microanalysis, 2014, 20, 1252-1253.	0.4	1
114	Sub-tomogram Averaging in RELION. Microscopy and Microanalysis, 2016, 22, 1124-1125.	0.4	1
115	ECâ€01â€02: Structure of Î“â€05 Secretases and Implications for Drug Development. Alzheimer's and Dementia, 2016, 12, P161.	0.8	0
116	CryoEM structure of dynamin-like MxB in assembly. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a54-a54.	0.1	0