

Sjors H W Scheres

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2615968/publications.pdf>

Version: 2024-02-01

116
papers

34,802
citations

12322

69
h-index

23514

111
g-index

170
all docs

170
docs citations

170
times ranked

27905
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM structures of amyloid- β 42 filaments from human brains. <i>Science</i> , 2022, 375, 167-172.	6.0	228
2	Age-dependent formation of TMEM106B amyloid filaments in human brains. <i>Nature</i> , 2022, 605, 310-314.	13.7	88
3	Assembly of recombinant tau into filaments identical to those of Alzheimer's disease and chronic traumatic encephalopathy. <i>ELife</i> , 2022, 11, .	2.8	121
4	Exploiting prior knowledge about biological macromolecules in cryo-EM structure determination. <i>IUCr</i> , 2021, 8, 60-75.	1.0	14
5	Seeded assembly <i>in vitro</i> does not replicate the structures of β -synuclein filaments from multiple system atrophy. <i>FEBS Open Bio</i> , 2021, 11, 999-1013.	1.0	95
6	Cryo-EM structures of tau filaments from Alzheimer's disease with PET ligand APN-1607. <i>Acta Neuropathologica</i> , 2021, 141, 697-708.	3.9	99
7	Structure-based classification of tauopathies. <i>Nature</i> , 2021, 598, 359-363.	13.7	409
8	Tau Protein and Frontotemporal Dementias. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1281, 177-199.	0.8	8
9	Multi-body Refinement of Cryo-EM Images in RELION. <i>Methods in Molecular Biology</i> , 2021, 2215, 145-160.	0.4	39
10	New tools for automated cryo-EM single-particle analysis in RELION-4.0. <i>Biochemical Journal</i> , 2021, 478, 4169-4185.	1.7	396
11	Single-particle cryo-EM at atomic resolution. <i>Nature</i> , 2020, 587, 152-156.	13.7	572
12	Revealing the structures of megadalton-scale DNA complexes with nucleotide resolution. <i>Nature Communications</i> , 2020, 11, 6229.	5.8	43
13	A thermostable, closed SARS-CoV-2 spike protein trimer. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 934-941.	3.6	261
14	Structures and distributions of SARS-CoV-2 spike proteins on intact virions. <i>Nature</i> , 2020, 588, 498-502.	13.7	918
15	Structures of β -synuclein filaments from multiple system atrophy. <i>Nature</i> , 2020, 585, 464-469.	13.7	446
16	Novel tau filament fold in corticobasal degeneration. <i>Nature</i> , 2020, 580, 283-287.	13.7	381
17	Cryo-EM structure of a neuronal functional amyloid implicated in memory persistence in <i>Drosophila</i> . <i>Science</i> , 2020, 367, 1230-1234.	6.0	140
18	Cryo-EM structures of tau filaments. <i>Current Opinion in Structural Biology</i> , 2020, 64, 17-25.	2.6	165

#	ARTICLE	IF	CITATIONS
19	Estimation of high-order aberrations and anisotropic magnification from cryo-EM data sets in RELION-3.1. IUCr, 2020, 7, 253-267.	1.0	574
20	Amyloid structure determination in RELION-3.1. Acta Crystallographica Section D: Structural Biology, 2020, 76, 94-101.	1.1	161
21	Heparin-induced tau filaments are polymorphic and differ from those in Alzheimer's and Pick's diseases. ELife, 2019, 8, .	2.8	309
22	Novel tau filament fold in chronic traumatic encephalopathy encloses hydrophobic molecules. Nature, 2019, 568, 420-423.	13.7	528
23	Structure of the Fanconi anaemia monoubiquitin ligase complex. Nature, 2019, 575, 234-237.	13.7	80
24	A Bayesian approach to beam-induced motion correction in cryo-EM single-particle analysis. IUCr, 2019, 6, 5-17.	1.0	696
25	Cryo-EM of dynein microtubule-binding domains shows how an axonemal dynein distorts the microtubule. ELife, 2019, 8, .	2.8	56
26	Atomic Structure of Type VI Contractile Sheath from Pseudomonas aeruginosa. Structure, 2018, 26, 329-336.e3.	1.6	29
27	Distinct Conformers of Assembled Tau in Alzheimer's and Pick's Diseases. Cold Spring Harbor Symposia on Quantitative Biology, 2018, 83, 163-171.	2.0	53
28	Tau filaments from multiple cases of sporadic and inherited Alzheimer's disease adopt a common fold. Acta Neuropathologica, 2018, 136, 699-708.	3.9	252
29	Structures of filaments from Pick's disease reveal a novel tau protein fold. Nature, 2018, 561, 137-140.	13.7	625
30	Characterisation of molecular motions in cryo-EM single-particle data by multi-body refinement in RELION. ELife, 2018, 7, .	2.8	434
31	New tools for automated high-resolution cryo-EM structure determination in RELION-3. ELife, 2018, 7, .	2.8	3,965
32	Self-correcting mismatches during high-fidelity DNA replication. Nature Structural and Molecular Biology, 2017, 24, 140-143.	3.6	42
33	Mechanistic insights into caspase-9 activation by the structure of the apoptosome holoenzyme. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1542-1547.	3.3	95
34	Cryo-EM structure of a metazoan separase-securin complex at near-atomic resolution. Nature Structural and Molecular Biology, 2017, 24, 414-418.	3.6	65
35	Structure of the MacAB-TolC ABC-type tripartite multidrug efflux pump. Nature Microbiology, 2017, 2, 17070.	5.9	140
36	Mefloquine targets the Plasmodium falciparum 80S ribosome to inhibit protein synthesis. Nature Microbiology, 2017, 2, 17031.	5.9	128

#	ARTICLE	IF	CITATIONS
37	Helical reconstruction in RELION. <i>Journal of Structural Biology</i> , 2017, 198, 163-176.	1.3	438
38	CryoEM structure of MxB reveals a novel oligomerization interface critical for HIV restriction. <i>Science Advances</i> , 2017, 3, e1701264.	4.7	47
39	CryoEM structures of spliceosomal complexes reveal the molecular mechanism of pre-mRNA splicing. <i>Current Opinion in Structural Biology</i> , 2017, 46, 130-139.	2.6	22
40	[E0302]: CRYOEM STRUCTURES OF TAU FILAMENTS FROM ALZHEIMER'S DISEASE BRAIN. <i>Alzheimer's and Dementia</i> , 2017, 13, P892.	0.4	3
41	The structural basis of proton driven zinc transport by ZntB. <i>Nature Communications</i> , 2017, 8, 1313.	5.8	27
42	Cryo-EM structures of tau filaments from Alzheimer's disease. <i>Nature</i> , 2017, 547, 185-190.	13.7	1,502
43	A pipeline approach to single-particle processing in RELION. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 496-502.	1.1	262
44	CryoEM structure of dynamin-like MxB in assembly. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a54-a54.	0.0	0
45	Accelerated cryo-EM structure determination with parallelisation using GPUs in RELION-2. <i>ELife</i> , 2016, 5, .	2.8	919
46	Sub-tomogram Averaging in RELION. <i>Microscopy and Microanalysis</i> , 2016, 22, 1124-1125.	0.2	1
47	E0102: Structure of Î³-secretases and Implications for Drug Development. <i>Alzheimer's and Dementia</i> , 2016, 12, P161.	0.4	0
48	Resolving macromolecular structures from electron cryo-tomography data using subtomogram averaging in RELION. <i>Nature Protocols</i> , 2016, 11, 2054-2065.	5.5	216
49	Processing of Structurally Heterogeneous Cryo-EM Data in RELION. <i>Methods in Enzymology</i> , 2016, 579, 125-157.	0.4	502
50	Unravelling biological macromolecules with cryo-electron microscopy. <i>Nature</i> , 2016, 537, 339-346.	13.7	352
51	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.	3.3	24
52	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.	3.3	93
53	Cryo-EM structure of the yeast U4/U6.U5 tri-snRNP at 3.7 Å... resolution. <i>Nature</i> , 2016, 530, 298-302.	13.7	184
54	Sampling the conformational space of the catalytic subunit of human Î³-secretase. <i>ELife</i> , 2015, 4, .	2.8	556

#	ARTICLE	IF	CITATIONS
55	Cryo-EM: A Unique Tool for the Visualization of Macromolecular Complexity. <i>Molecular Cell</i> , 2015, 58, 677-689.	4.5	300
56	Semi-automated selection of cryo-EM particles in RELION-1.3. <i>Journal of Structural Biology</i> , 2015, 189, 114-122.	1.3	346
57	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.	2.7	55
58	Collaborative Computational Project for Electron cryo-Microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 123-126.	2.5	84
59	The architecture of the spliceosomal U4/U6.U5 tri-snRNP. <i>Nature</i> , 2015, 523, 47-52.	13.7	195
60	The structure of the human mitochondrial ribosome. <i>Science</i> , 2015, 348, 95-98.	6.0	432
61	An atomic structure of human $\hat{\text{I}}^3$ -secretase. <i>Nature</i> , 2015, 525, 212-217.	13.7	490
62	Advances in Single-Particle Electron Cryomicroscopy Structure Determination applied to Sub-tomogram Averaging. <i>Structure</i> , 2015, 23, 1743-1753.	1.6	189
63	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.	2.7	201
64	Structure of the rabbit ryanodine receptor RyR1 at near-atomic resolution. <i>Nature</i> , 2015, 517, 50-55.	13.7	391
65	How cryo-EM is revolutionizing structural biology. <i>Trends in Biochemical Sciences</i> , 2015, 40, 49-57.	3.7	709
66	cryo-EM structures of the <i>E. coli</i> replicative DNA polymerase reveal its dynamic interactions with the DNA sliding clamp, exonuclease and $\hat{\text{I}}^3$. <i>ELife</i> , 2015, 4, .	2.8	75
67	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Science</i> , 2014, 343, 1485-1489.	6.0	521
68	Initiation of Translation by Cricket Paralysis Virus IRES Requires Its Translocation in the Ribosome. <i>Cell</i> , 2014, 157, 823-831.	13.5	211
69	Structure of the large ribosomal subunit from human mitochondria. <i>Science</i> , 2014, 346, 718-722.	6.0	260
70	Three-dimensional structure of human $\hat{\text{I}}^3$ -secretase. <i>Nature</i> , 2014, 512, 166-170.	13.7	317
71	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.	2.0	24
72	Structure of the Mammalian Ribosome-Sec61 Complex to 3.4Å... Resolution. <i>Cell</i> , 2014, 157, 1632-1643.	13.5	302

#	ARTICLE	IF	CITATIONS
73	Beam-induced motion correction for sub-megadalton cryo-EM particles. <i>ELife</i> , 2014, 3, e03665.	2.8	298
74	Cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to the anti-protozoan drug emetine. <i>ELife</i> , 2014, 3, .	2.8	274
75	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Microscopy and Microanalysis</i> , 2014, 20, 1252-1253.	0.2	1
76	Molecular Architecture of a Eukaryotic Translational Initiation Complex. <i>Science</i> , 2013, 342, 1240585.	6.0	120
77	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.	0.8	843
78	Structure of active dimeric human telomerase. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 454-460.	3.6	115
79	Ribosome structures to near-atomic resolution from thirty thousand cryo-EM particles. <i>ELife</i> , 2013, 2, e00461.	2.8	378
80	A Bayesian view on cryo-EM structure determination. , 2012, , .		1
81	Prevention of overfitting in cryo-EM structure determination. <i>Nature Methods</i> , 2012, 9, 853-854.	9.0	1,104
82	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	3.6	49
83	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.	3.3	219
84	RELION: Implementation of a Bayesian approach to cryo-EM structure determination. <i>Journal of Structural Biology</i> , 2012, 180, 519-530.	1.3	4,715
85	A Bayesian View on Cryo-EM Structure Determination. <i>Journal of Molecular Biology</i> , 2012, 415, 406-418.	2.0	765
86	Maximum likelihood based classification of electron tomographic data. <i>Journal of Structural Biology</i> , 2011, 173, 77-85.	1.3	56
87	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.	3.3	65
88	Structure of hibernating ribosomes studied by cryoelectron tomography in vitro and in situ. <i>Journal of Cell Biology</i> , 2010, 190, 613-621.	2.3	83
89	Classification of Structural Heterogeneity by Maximum-Likelihood Methods. <i>Methods in Enzymology</i> , 2010, 482, 295-320.	0.4	84
90	An Introduction to Maximum-Likelihood Methods in Cryo-EM. <i>Methods in Enzymology</i> , 2010, 482, 263-294.	0.4	65

#	ARTICLE	IF	CITATIONS
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.	1.3	34
92	Conformational Rearrangements of SV40 Large T Antigen during Early Replication Events. <i>Journal of Molecular Biology</i> , 2010, 397, 1276-1286.	2.0	40
93	Visualizing molecular machines in action. <i>Advances in Protein Chemistry and Structural Biology</i> , 2010, 81, 89-119.	1.0	8
94	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.	3.3	116
95	Averaging of Electron Subtomograms and Random Conical Tilt Reconstructions through Likelihood Optimization. <i>Structure</i> , 2009, 17, 1563-1572.	1.6	112
96	Electron microscopy of Xrcc4 and the DNA ligase IV-Xrcc4 DNA repair complex. <i>DNA Repair</i> , 2009, 8, 1380-1389.	1.3	24
97	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
98	Maximum likelihood refinement of electron microscopy data with normalization errors. <i>Journal of Structural Biology</i> , 2009, 166, 234-240.	1.3	33
99	Structure and Uncoating of Immature Adenovirus. <i>Journal of Molecular Biology</i> , 2009, 392, 547-557.	2.0	64
100	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.	3.6	85
101	Image processing for electron microscopy single-particle analysis using XMIPP. <i>Nature Protocols</i> , 2008, 3, 977-990.	5.5	310
102	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.	3.3	161
103	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. <i>Nature Methods</i> , 2007, 4, 27-29.	9.0	387
104	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.	1.6	54
105	Modeling Experimental Image Formation for Likelihood-Based Classification of Electron Microscopy Data. <i>Structure</i> , 2007, 15, 1167-1177.	1.6	68
106	Optimization problems in electron microscopy of single particles. <i>Annals of Operations Research</i> , 2006, 148, 133-165.	2.6	12
107	Fast maximum-likelihood refinement of electron microscopy images. <i>Bioinformatics</i> , 2005, 21, ii243-ii244.	1.8	54
108	SPI-EM: Towards a Tool For Predicting CATH Superfamilies in 3D-EM Maps. <i>Journal of Molecular Biology</i> , 2005, 345, 759-771.	2.0	25

#	ARTICLE	IF	CITATIONS
109	Maximum-likelihood Multi-reference Refinement for Electron Microscopy Images. <i>Journal of Molecular Biology</i> , 2005, 348, 139-149.	2.0	239
110	Classification of single-projection reconstructions for cryo-electron microscopy data of icosahedral viruses. <i>Journal of Structural Biology</i> , 2005, 151, 79-91.	1.3	20
111	The potentials of conditional optimization in phasing and model building of protein crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2202-2209.	2.5	2
112	XMIPP: a new generation of an open-source image processing package for electron microscopy. <i>Journal of Structural Biology</i> , 2004, 148, 194-204.	1.3	434
113	Development of a force field for conditional optimization of protein structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 438-446.	2.5	1
114	Conditional optimization: a new formalism for protein structure refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1820-1828.	2.5	1
115	Ab initio structure determination of low-molecular-weight compounds using synchrotron radiation Laue diffraction. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 19-28.	1.0	4
116	Grid Computing in 3D-EM Image Processing Using Xmipp. , 0, , .		3