

# Scott M Stagg

## List of Publications by Year in descending order

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Version: 2024-02-01

81  
papers

5,408  
citations

186265

28  
h-index

118850

62  
g-index

87  
all docs

87  
docs citations

87  
times ranked

6854  
citing authors

#	ARTICLE	IF	CITATIONS
1	Probing intracellular vesicle trafficking and membrane remodelling by cryo-EM. <i>Journal of Structural Biology</i> , 2022, 214, 107836.	2.8	8
2	Cryo-electron Microscopy of Adeno-associated Virus. <i>Chemical Reviews</i> , 2022, 122, 14018-14054.	47.7	15
3	Adeno-Associated Virus Receptor-Binding: Flexible Domains and Alternative Conformations through Cryo-Electron Tomography of Adeno-Associated Virus 2 (AAV2) and AAV5 Complexes. <i>Journal of Virology</i> , 2022, 96, .	3.4	7
4	Olfactory bulb-targeted quantum dot (QD) bioconjugate and Kv1.3 blocking peptide improve metabolic health in obese male mice. <i>Journal of Neurochemistry</i> , 2021, 157, 1876-1896.	3.9	15
5	trans-Translation inhibitors bind to a novel site on the ribosome and clear <i>Neisseria gonorrhoeae</i> in vivo. <i>Nature Communications</i> , 2021, 12, 1799.	12.8	20
6	Cryo-EM of Intact Clathrin-Coated Vesicles Reveals Adaptor Distribution and Novel Interactions Between Subunits. <i>Biophysical Journal</i> , 2020, 118, 487a.	0.5	0
7	The structures of natively assembled clathrin-coated vesicles. <i>Science Advances</i> , 2020, 6, eaba8397.	10.3	45
8	FTIP - An Accurate and Efficient Method for Global Protein Surface Comparison. <i>Biophysical Journal</i> , 2020, 118, 501a.	0.5	0
9	The Influence of Detector Quality and Throughput for Cryo-EM of Challenging Proteins. <i>Microscopy and Microanalysis</i> , 2020, 26, 2318-2320.	0.4	0
10	Out-of-Register Parallel $\beta$ -Sheets and Antiparallel $\beta$ -Sheets Coexist in 150-kDa Oligomers Formed by Amyloid- $\beta$ (1-42). <i>Journal of Molecular Biology</i> , 2020, 432, 4388-4407.	4.2	27
11	Reconstruction of Average Subtracted Tubular Regions (RASTR) enables structure determination of tubular filaments by cryo-EM. <i>Journal of Structural Biology: X</i> , 2020, 4, 100023.	1.3	1
12	FTIP: an accurate and efficient method for global protein surface comparison. <i>Bioinformatics</i> , 2020, 36, 3056-3063.	4.1	2
13	Reconstruction of Average Subtracted Tubular Regions (RASTR). <i>Biophysical Journal</i> , 2019, 116, 576a.	0.5	0
14	Functionally critical residues in the aminoglycoside resistance-associated methyltransferase RmtC play distinct roles in 30S substrate recognition. <i>Journal of Biological Chemistry</i> , 2019, 294, 17642-17653.	3.4	32
15	Investigating the Structural Mechanism of the Stalled Bacterial Ribosome Bound to a Drug that Targets Trans-Translation. <i>Biophysical Journal</i> , 2019, 116, 573a-574a.	0.5	0
16	Characterization of the DE64 Direct Electron Detector. <i>Biophysical Journal</i> , 2019, 116, 574a.	0.5	0
17	Throughput and Resolution with a Next Generation Direct Detector. <i>Biophysical Journal</i> , 2019, 116, 11a.	0.5	0
18	Yeast R2TP Interacts with Extended Termini of Client Protein Nop58p. <i>Scientific Reports</i> , 2019, 9, 20228.	3.3	5

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19	Throughput and resolution with a next-generation direct electron detector. IUCr, 2019, 6, 1007-1013.	2.2	28
20	Structure of the gene therapy vector, adeno-associated virus with its cell receptor, AAVR. ELife, 2019, 8, .	6.0	60
21	Quality <i>versus</i> resolution in cryo-EM maps. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a410-a410.	0.1	0
22	Pros and Cons of Integrating Versus Counting with a Direct Electron Detecting Camera. Microscopy and Microanalysis, 2018, 24, 888-889.	0.4	0
23	Assessing the quality of single particle reconstructions by atomic model building. Journal of Structural Biology, 2018, 204, 276-282.	2.8	8
24	Flexibility of the Sec13/31 cage is influenced by the Sec31 C-terminal disordered domain. Journal of Structural Biology, 2018, 204, 250-260.	2.8	8
25	Pathogenic TFG Mutations Underlying Hereditary Spastic Paraplegia Impair Secretory Protein Trafficking and Axon Fasciculation. Cell Reports, 2018, 24, 2248-2260.	6.4	24
26	The Past, Present, and Future of Sample Preparation for CryoEM $\hat{t}$ . , 2018, , .		2
27	Processing apoferritin with the Appion pipeline. Journal of Structural Biology, 2018, 204, 85-89.	2.8	3
28	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	2.8	17
29	Structure of the Sar1 Lattice and its Role in COPII Vesicle Formation and Scission. Biophysical Journal, 2017, 112, 479a.	0.5	0
30	Cryo-EM Structure Determination of Truncated SEC13/31 Proteins in COPII Vertices. Biophysical Journal, 2017, 112, 577a.	0.5	0
31	The 2.8Å... Electron Microscopy Structure of Adeno-Associated Virus-DJ Bound by a Heparinoid Pentasaccharide. Molecular Therapy - Methods and Clinical Development, 2017, 5, 1-12.	4.1	30
32	Pih1p-Tah1p Puts a Lid on Hexameric AAA+ ATPases Rvb1/2p. Structure, 2017, 25, 1519-1529.e4.	3.3	22
33	Cleavage and Structural Transitions during Maturation of Staphylococcus aureus Bacteriophage 80 $\hat{t}$ and SaPI1 Capsids. Viruses, 2017, 9, 384.	3.3	13
34	Structure and function of a snoRNP maturation complex. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a306-a306.	0.1	0
35	Navigating the Job Market for Careers Inside and Outside of Academia.. Microscopy and Microanalysis, 2016, 22, 2076-2077.	0.4	0
36	Quantification of Protein-Induced Membrane Remodeling Kinetics In Vitro with Lipid Multilayer Gratings. Small, 2016, 12, 506-515.	10.0	10

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37	478. An Essential and Ubiquitous Protein Receptor for AAV; Glycans as Attachment Receptors. <i>Molecular Therapy</i> , 2016, 24, S189.	8.2	0
38	Interfacing Microfluidics with Negative Stain Transmission Electron Microscopy. <i>Analytical Chemistry</i> , 2016, 88, 629-634.	6.5	7
39	Sar1 Forms Ordered Arrays That Can Facilitate Vesicle Scission in the COPII Pathway. <i>Microscopy and Microanalysis</i> , 2015, 21, 57-58.	0.4	0
40	Automated batch fiducial-less tilt-series alignment in Appion using Protomo. <i>Journal of Structural Biology</i> , 2015, 192, 270-278.	2.8	64
41	Kv1.3 contains an alternative C-terminal ER exit motif and is recruited into COPII vesicles by Sec24a. <i>BMC Biochemistry</i> , 2015, 16, 16.	4.4	18
42	The influence of frame alignment with dose compensation on the quality of single particle reconstructions. <i>Journal of Structural Biology</i> , 2015, 192, 196-203.	2.8	30
43	<sc>TFG</sc> clusters <sc>COPII</sc>-coated transport carriers and promotes early secretory pathway organization. <i>EMBO Journal</i> , 2015, 34, 811-827.	7.8	92
44	Host endoplasmic reticulum COPII proteins control cell-to-cell spread of the bacterial pathogen <i>Listeria monocytogenes</i> . <i>Cellular Microbiology</i> , 2015, 17, 876-892.	2.1	20
45	COPII gets a fancy new coat. <i>Science</i> , 2015, 349, 142-143.	12.6	1
46	Essential Structural and Functional Roles of the Cmr4 Subunit in RNA Cleavage by the Cmr CRISPR-Cas Complex. <i>Cell Reports</i> , 2014, 9, 1610-1617.	6.4	57
47	Insights into the Mechanisms of Membrane Curvature and Vesicle Scission by the Small GTPase Sar1 in the Early Secretory Pathway. <i>Journal of Molecular Biology</i> , 2014, 426, 3811-3826.	4.2	40
48	ResLog plots as an empirical metric of the quality of cryo-EM reconstructions. <i>Journal of Structural Biology</i> , 2014, 185, 418-426.	2.8	72
49	Cryo-EM Structures of the Actin:Tropomyosin Filament Reveal the Mechanism for the Transition from C- to M-State. <i>Biophysical Journal</i> , 2014, 106, 454a.	0.5	0
50	ResLog Plots: A New Metric for the Quality of Cryo-EM Reconstructions. <i>Microscopy and Microanalysis</i> , 2014, 20, 1254-1255.	0.4	0
51	Cryo-EM Structures of the Actin:Tropomyosin Filament Reveal the Mechanism for the Transition from C- to M-State. <i>Journal of Molecular Biology</i> , 2013, 425, 4544-4555.	4.2	27
52	Electron microscopy analysis of a disaccharide analog complex reveals receptor interactions of adeno-associated virus. <i>Journal of Structural Biology</i> , 2013, 184, 129-135.	2.8	15
53	Structure of an RNA Silencing Complex of the CRISPR-Cas Immune System. <i>Molecular Cell</i> , 2013, 52, 146-152.	9.7	117
54	A pseudoatomic model of the COPII cage obtained from cryo-electron microscopy and mass spectrometry. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 167-173.	8.2	57

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55	Structure and Heterogeneity of the COPII Coat. <i>Microscopy and Microanalysis</i> , 2012, 18, 46-47.	0.4	0
56	Creating an infrastructure for high-throughput high-resolution cryogenic electron microscopy. <i>Journal of Structural Biology</i> , 2012, 180, 254-258.	2.8	10
57	The Structure of the Sec13/31 COPII Cage Bound to Sec23. <i>Journal of Molecular Biology</i> , 2012, 420, 324-334.	4.2	30
58	ATP-Triggered Conformational Changes Delineate Substrate-Binding and -Folding Mechanics of the GroEL Chaperonin. <i>Cell</i> , 2012, 149, 113-123.	28.9	160
59	Structure of AAV-DJ, a Retargeted Gene Therapy Vector: Cryo-Electron Microscopy at 4.5Å... Resolution. <i>Structure</i> , 2012, 20, 1310-1320.	3.3	63
60	Structure of adeno-associated virus-2 in complex with neutralizing monoclonal antibody A20. <i>Virology</i> , 2012, 431, 40-49.	2.4	77
61	Three-Dimensional Interfacial Structure Determination of Hollow Gold Nanosphere Aggregates. <i>Journal of Physical Chemistry Letters</i> , 2011, 2, 2946-2950.	4.6	13
62	The Structure and Heterogeneity of the COPII Coat. <i>Biophysical Journal</i> , 2011, 100, 411a.	0.5	0
63	The structure of a COPII tubule. <i>Journal of Structural Biology</i> , 2011, 173, 358-364.	2.8	17
64	New Insights into the Structural Mechanisms of the COPII Coat. <i>Traffic</i> , 2010, 11, 303-310.	2.7	55
65	Appion: An integrated, database-driven pipeline to facilitate EM image processing. <i>Journal of Structural Biology</i> , 2009, 166, 95-102.	2.8	848
66	Multiple States of a Nucleotide-Bound Group 2 Chaperonin. <i>Structure</i> , 2008, 16, 528-534.	3.3	32
67	A test-bed for optimizing high-resolution single particle reconstructions. <i>Journal of Structural Biology</i> , 2008, 163, 29-39.	2.8	33
68	Structural Basis for Cargo Regulation of COPII Coat Assembly. <i>Cell</i> , 2008, 134, 474-484.	28.9	242
69	Structural design of cage and coat scaffolds that direct membrane traffic. <i>Current Opinion in Structural Biology</i> , 2007, 17, 221-228.	5.7	69
70	Automated cryoEM data acquisition and analysis of 284742 particles of GroEL. <i>Journal of Structural Biology</i> , 2006, 155, 470-481.	2.8	84
71	The COPII cage: unifying principles of vesicle coat assembly. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 727-738.	37.0	197
72	Structure of the Sec13/31 COPII coat cage. <i>Nature</i> , 2006, 439, 234-238.	27.8	286

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73	Automated molecular microscopy: The new Legion system. Journal of Structural Biology, 2005, 151, 41-60.	2.8	1,608
74	Exploring the Flexibility of Ribosome Recycling Factor Using Molecular Dynamics. Biophysical Journal, 2005, 89, 2659-2666.	0.5	6
75	A Structural Model for the Assembly of the 30S Subunit of the Ribosome. Journal of Molecular Biology, 2003, 328, 49-61.	4.2	35
76	Study of the Structural Dynamics of the E. coli 70S Ribosome Using Real-Space Refinement. Cell, 2003, 113, 789-801.	28.9	273
77	Ca <sup>2+</sup> -induced Conformational Transition in the Inhibitory and Regulatory Regions of Cardiac Troponin I. Journal of Biological Chemistry, 2003, 278, 8686-8692.	3.4	43
78	Modeling a Minimal Ribosome Based on Comparative Sequence Analysis. Journal of Molecular Biology, 2002, 321, 215-234.	4.2	139
79	Problems with the transorientation hypothesis. Rna, 2002, 8, 1093-1094.	3.5	4
80	Structural Studies of the tRNA Domain of tmRNA. Journal of Molecular Biology, 2001, 309, 727-735.	4.2	28
81	Modeling Large RNA Assemblies using a Reduced Representation. , 0, , 546-559.		0