

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	Automated molecular microscopy: The new Legion system. <i>Journal of Structural Biology</i> , 2005, 151, 41-60.	2.8	1,608
2	Appion: An integrated, database-driven pipeline to facilitate EM image processing. <i>Journal of Structural Biology</i> , 2009, 166, 95-102.	2.8	848
3	Structure of the Sec13/31 COPII coat cage. <i>Nature</i> , 2006, 439, 234-238.	27.8	286
4	Study of the Structural Dynamics of the E. coli 70S Ribosome Using Real-Space Refinement. <i>Cell</i> , 2003, 113, 789-801.	28.9	273
5	Structural Basis for Cargo Regulation of COPII Coat Assembly. <i>Cell</i> , 2008, 134, 474-484.	28.9	242
6	The COPII cage: unifying principles of vesicle coat assembly. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 727-738.	37.0	197
7	ATP-Triggered Conformational Changes Delineate Substrate-Binding and -Folding Mechanics of the GroEL Chaperonin. <i>Cell</i> , 2012, 149, 113-123.	28.9	160
8	Modeling a Minimal Ribosome Based on Comparative Sequence Analysis. <i>Journal of Molecular Biology</i> , 2002, 321, 215-234.	4.2	139
9	Structure of an RNA Silencing Complex of the CRISPR-Cas Immune System. <i>Molecular Cell</i> , 2013, 52, 146-152.	9.7	117
10	<scp>TFG</scp> clusters <scp>COPII</scp>-coated transport carriers and promotes early secretory pathway organization. <i>EMBO Journal</i> , 2015, 34, 811-827.	7.8	92
11	Automated cryoEM data acquisition and analysis of 284742 particles of GroEL. <i>Journal of Structural Biology</i> , 2006, 155, 470-481.	2.8	84
12	Structure of adeno-associated virus-2 in complex with neutralizing monoclonal antibody A20. <i>Virology</i> , 2012, 431, 40-49.	2.4	77
13	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
14	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
15	Automated batch fiducial-less tilt-series alignment in Appion using Protomo. <i>Journal of Structural Biology</i> , 2015, 192, 270-278.	2.8	64
16	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
17	Structure of the gene therapy vector, adeno-associated virus with its cell receptor, AAVR. <i>ELife</i> , 2019, 8, .	6.0	60
18	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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19	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
20	New Insights into the Structural Mechanisms of the COPII Coat. <i>Traffic</i> , 2010, 11, 303-310.	2.7	55
21	The structures of natively assembled clathrin-coated vesicles. <i>Science Advances</i> , 2020, 6, eaba8397.	10.3	45
22	Ca ²⁺ -induced Conformational Transition in the Inhibitory and Regulatory Regions of Cardiac Troponin I. <i>Journal of Biological Chemistry</i> , 2003, 278, 8686-8692.	3.4	43
23	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
24	A Structural Model for the Assembly of the 30S Subunit of the Ribosome. <i>Journal of Molecular Biology</i> , 2003, 328, 49-61.	4.2	35
25	A test-bed for optimizing high-resolution single particle reconstructions. <i>Journal of Structural Biology</i> , 2008, 163, 29-39.	2.8	33
26	Multiple States of a Nucleotide-Bound Group 2 Chaperonin. <i>Structure</i> , 2008, 16, 528-534.	3.3	32
27	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
28	The Structure of the Sec13/31 COPII Cage Bound to Sec23. <i>Journal of Molecular Biology</i> , 2012, 420, 324-334.	4.2	30
29	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
30	The 2.8Å Electron Microscopy Structure of Adeno-Associated Virus-DJ Bound by a Heparinoid Pentasaccharide. <i>Molecular Therapy - Methods and Clinical Development</i> , 2017, 5, 1-12.	4.1	30
31	Structural Studies of the tRNA Domain of tmRNA. <i>Journal of Molecular Biology</i> , 2001, 309, 727-735.	4.2	28
32	Throughput and resolution with a next-generation direct electron detector. <i>IUCr</i> , 2019, 6, 1007-1013.	2.2	28
33	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
34	Out-of-Register Parallel β -Sheets and Antiparallel β -Sheets Coexist in 150-kDa Oligomers Formed by Amyloid- β (1-42). <i>Journal of Molecular Biology</i> , 2020, 432, 4388-4407.	4.2	27
35	Pathogenic TFG Mutations Underlying Hereditary Spastic Paraplegia Impair Secretory Protein Trafficking and Axon Fasciculation. <i>Cell Reports</i> , 2018, 24, 2248-2260.	6.4	24
36	Pih1p-Tah1p Puts a Lid on Hexameric AAA+ ATPases Rvb1/2p. <i>Structure</i> , 2017, 25, 1519-1529.e4.	3.3	22

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37	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
38	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
39	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
40	The structure of a COPII tubule. <i>Journal of Structural Biology</i> , 2011, 173, 358-364.	2.8	17
41	The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018, 204, 291-300.	2.8	17
42	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
43	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
44	Cryo-electron Microscopy of Adeno-associated Virus. <i>Chemical Reviews</i> , 2022, 122, 14018-14054.	47.7	15
45	Three-Dimensional Interfacial Structure Determination of Hollow Gold Nanosphere Aggregates. <i>Journal of Physical Chemistry Letters</i> , 2011, 2, 2946-2950.	4.6	13
46	Cleavage and Structural Transitions during Maturation of <i>Staphylococcus aureus</i> Bacteriophage 80 \pm and SaPI1 Capsids. <i>Viruses</i> , 2017, 9, 384.	3.3	13
47	Creating an infrastructure for high-throughput high-resolution cryogenic electron microscopy. <i>Journal of Structural Biology</i> , 2012, 180, 254-258.	2.8	10
48	Quantification of Protein-Induced Membrane Remodeling Kinetics In Vitro with Lipid Multilayer Gratings. <i>Small</i> , 2016, 12, 506-515.	10.0	10
49	Assessing the quality of single particle reconstructions by atomic model building. <i>Journal of Structural Biology</i> , 2018, 204, 276-282.	2.8	8
50	Flexibility of the Sec13/31 cage is influenced by the Sec31 C-terminal disordered domain. <i>Journal of Structural Biology</i> , 2018, 204, 250-260.	2.8	8
51	Probing intracellular vesicle trafficking and membrane remodelling by cryo-EM. <i>Journal of Structural Biology</i> , 2022, 214, 107836.	2.8	8
52	Interfacing Microfluidics with Negative Stain Transmission Electron Microscopy. <i>Analytical Chemistry</i> , 2016, 88, 629-634.	6.5	7
53	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
54	Exploring the Flexibility of Ribosome Recycling Factor Using Molecular Dynamics. <i>Biophysical Journal</i> , 2005, 89, 2659-2666.	0.5	6

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55	Yeast R2TP Interacts with Extended Termini of Client Protein Nop58p. <i>Scientific Reports</i> , 2019, 9, 20228.	3.3	5
56	Problems with the transorientation hypothesis. <i>Rna</i> , 2002, 8, 1093-1094.	3.5	4
57	Processing apoferritin with the Appion pipeline. <i>Journal of Structural Biology</i> , 2018, 204, 85-89.	2.8	3
58	The Past, Present, and Future of Sample Preparation for CryoEM \hat{t} . , 2018, , .		2
59	FTIP: an accurate and efficient method for global protein surface comparison. <i>Bioinformatics</i> , 2020, 36, 3056-3063.	4.1	2
60	COPI gets a fancy new coat. <i>Science</i> , 2015, 349, 142-143.	12.6	1
61	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
62	Modeling Large RNA Assemblies using a Reduced Representation. , 0, , 546-559.		0
63	The Structure and Heterogeneity of the COPII Coat. <i>Biophysical Journal</i> , 2011, 100, 411a.	0.5	0
64	Structure and Heterogeneity of the COPII Coat. <i>Microscopy and Microanalysis</i> , 2012, 18, 46-47.	0.4	0
65	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
66	ResLog Plots: A New Metric for the Quality of Cryo-EM Reconstructions. <i>Microscopy and Microanalysis</i> , 2014, 20, 1254-1255.	0.4	0
67	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
68	Navigating the Job Market for Careers Inside and Outside of Academia.. <i>Microscopy and Microanalysis</i> , 2016, 22, 2076-2077.	0.4	0
69	478. An Essential and Ubiquitous Protein Receptor for AAV; Glycans as Attachment Receptors. <i>Molecular Therapy</i> , 2016, 24, S189.	8.2	0
70	Structure of the Sar1 Lattice and its Role in COPII Vesicle Formation and Scission. <i>Biophysical Journal</i> , 2017, 112, 479a.	0.5	0
71	Cryo-EM Structure Determination of Truncated SEC13/31 Proteins in COPII Vertices. <i>Biophysical Journal</i> , 2017, 112, 577a.	0.5	0
72	Pros and Cons of Integrating Versus Counting with a Direct Electron Detecting Camera. <i>Microscopy and Microanalysis</i> , 2018, 24, 888-889.	0.4	0

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73	Reconstruction of Average Subtracted Tubular Regions (RASTR). Biophysical Journal, 2019, 116, 576a.	0.5	0
74	Investigating the Structural Mechanism of the Stalled Bacterial Ribosome Bound to a Drug that Targets Trans-Translation. Biophysical Journal, 2019, 116, 573a-574a.	0.5	0
75	Characterization of the DE64 Direct Electron Detector. Biophysical Journal, 2019, 116, 574a.	0.5	0
76	Throughput and Resolution with a Next Generation Direct Detector. Biophysical Journal, 2019, 116, 11a.	0.5	0
77	Cryo-EM of Intact Clathrin-Coated Vesicles Reveals Adaptor Distribution and Novel Interactions Between Subunits. Biophysical Journal, 2020, 118, 487a.	0.5	0
78	FTIP - An Accurate and Efficient Method for Global Protein Surface Comparison. Biophysical Journal, 2020, 118, 501a.	0.5	0
79	The Influence of Detector Quality and Throughput for Cryo-EM of Challenging Proteins. Microscopy and Microanalysis, 2020, 26, 2318-2320.	0.4	0
80	Structure and function of a snoRNP maturation complex. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a306-a306.	0.1	0
81	Quality <i>versus</i> resolution in cryo-EM maps. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a410-a410.	0.1	0