

John A G Briggs

List of Publications by Year in descending order

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119
papers

14,985
citations

20797

60
h-index

23514

111
g-index

137
all docs

137
docs citations

137
times ranked

16396
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures and distributions of SARS-CoV-2 spike proteins on intact virions. <i>Nature</i> , 2020, 588, 498-502.	13.7	918
2	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021, 592, 277-282.	13.7	802
3	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. <i>Nature</i> , 2022, 603, 706-714.	13.7	756
4	Implementation of a cryo-electron tomography tilt-scheme optimized for high resolution subtomogram averaging. <i>Journal of Structural Biology</i> , 2017, 197, 191-198.	1.3	556
5	The stoichiometry of Gag protein in HIV-1. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 672-675.	3.6	462
6	Correlated fluorescence and 3D electron microscopy with high sensitivity and spatial precision. <i>Journal of Cell Biology</i> , 2011, 192, 111-119.	2.3	408
7	Nuclear Pore Scaffold Structure Analyzed by Super-Resolution Microscopy and Particle Averaging. <i>Science</i> , 2013, 341, 655-658.	6.0	401
8	Structural organization of authentic, mature HIV-1 virions and cores. <i>EMBO Journal</i> , 2003, 22, 1707-1715.	3.5	390
9	The Neuronal Gene Arc Encodes a Repurposed Retrotransposon Gag Protein that Mediates Intercellular RNA Transfer. <i>Cell</i> , 2018, 172, 275-288.e18.	13.5	382
10	An atomic model of HIV-1 capsid-SP1 reveals structures regulating assembly and maturation. <i>Science</i> , 2016, 353, 506-508.	6.0	375
11	Pathogenic bacteria attach to human fibronectin through a tandem β -zipper. <i>Nature</i> , 2003, 423, 177-181.	13.7	326
12	Plasma Membrane Reshaping during Endocytosis Is Revealed by Time-Resolved Electron Tomography. <i>Cell</i> , 2012, 150, 508-520.	13.5	320
13	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , 2016, 352, 363-365.	6.0	284
14	Structure of the immature HIV-1 capsid in intact virus particles at 8.8 Å... resolution. <i>Nature</i> , 2015, 517, 505-508.	13.7	277
15	A thermostable, closed SARS-CoV-2 spike protein trimer. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 934-941.	3.6	261
16	Minimal Tags for Rapid Dual-Color Live-Cell Labeling and Super-Resolution Microscopy. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 2245-2249.	7.2	254
17	The structure and flexibility of conical HIV-1 capsids determined within intact virions. <i>Science</i> , 2016, 354, 1434-1437.	6.0	229
18	Efficient 3D-CTF correction for cryo-electron tomography using NovaCTF improves subtomogram averaging resolution to 3.4 Å... <i>Journal of Structural Biology</i> , 2017, 199, 187-195.	1.3	219

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19	Structural biology in situ—the potential of subtomogram averaging. <i>Current Opinion in Structural Biology</i> , 2013, 23, 261-267.	2.6	218
20	Endocytic sites mature by continuous bending and remodeling of the clathrin coat. <i>Science</i> , 2015, 348, 1369-1372.	6.0	216
21	Structural dissection of Ebola virus and its assembly determinants using cryo-electron tomography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4275-4280.	3.3	210
22	A saposin-lipoprotein nanoparticle system for membrane proteins. <i>Nature Methods</i> , 2016, 13, 345-351.	9.0	209
23	Three-Dimensional Analysis of Budding Sites and Released Virus Suggests a Revised Model for HIV-1 Morphogenesis. <i>Cell Host and Microbe</i> , 2008, 4, 592-599.	5.1	208
24	Cryo-Electron Tomographic Structure of an Immunodeficiency Virus Envelope Complex In Situ. <i>PLoS Pathogens</i> , 2006, 2, e83.	2.1	205
25	The Mechanism of HIV-1 Core Assembly: Insights from Three-Dimensional Reconstructions of Authentic Virions. <i>Structure</i> , 2006, 14, 15-20.	1.6	188
26	Structure and assembly of the Ebola virus nucleocapsid. <i>Nature</i> , 2017, 551, 394-397.	13.7	185
27	Virological Synapse-Mediated Spread of Human Immunodeficiency Virus Type 1 between T Cells Is Sensitive to Entry Inhibition. <i>Journal of Virology</i> , 2010, 84, 3516-3527.	1.5	177
28	Structure of the membrane-assembled retromer coat determined by cryo-electron tomography. <i>Nature</i> , 2018, 561, 561-564.	13.7	169
29	The Molecular Architecture of HIV. <i>Journal of Molecular Biology</i> , 2011, 410, 491-500.	2.0	164
30	A structure of the COPI coat and the role of coat proteins in membrane vesicle assembly. <i>Science</i> , 2015, 349, 195-198.	6.0	159
31	Vesicle coats: structure, function, and general principles of assembly. <i>Trends in Cell Biology</i> , 2013, 23, 279-288.	3.6	157
32	Structure of the immature retroviral capsid at 8Å resolution by cryo-electron microscopy. <i>Nature</i> , 2012, 487, 385-389.	13.7	152
33	The structure of the COPI coat determined within the cell. <i>ELife</i> , 2017, 6, .	2.8	152
34	Computational Model of Membrane Fission Catalyzed by ESCRT-III. <i>PLoS Computational Biology</i> , 2009, 5, e1000575.	1.5	141
35	Deciphering the Origin and Evolution of Hepatitis B Viruses by Means of a Family of Non-enveloped Fish Viruses. <i>Cell Host and Microbe</i> , 2017, 22, 387-399.e6.	5.1	134
36	Precise, Correlated Fluorescence Microscopy and Electron Tomography of Lowicryl Sections Using Fluorescent Fiducial Markers. <i>Methods in Cell Biology</i> , 2012, 111, 235-257.	0.5	130

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37	Cryo-Electron Tomography of Marburg Virus Particles and Their Morphogenesis within Infected Cells. PLoS Biology, 2011, 9, e1001196.	2.6	125
38	Double-labelled HIV-1 particles for study of virus-cell interaction. Virology, 2007, 360, 92-104.	1.1	121
39	Cryo Electron Tomography of Native HIV-1 Budding Sites. PLoS Pathogens, 2010, 6, e1001173.	2.1	119
40	Correlated cryo-fluorescence and cryo-electron microscopy with high spatial precision and improved sensitivity. Ultramicroscopy, 2014, 143, 24-32.	0.8	116
41	Do lipid rafts mediate virus assembly and pseudotyping?. Journal of General Virology, 2003, 84, 757-768.	1.3	114
42	The structure of the COPII transport-vesicle coat assembled on membranes. ELife, 2013, 2, e00951.	2.8	112
43	New hardware and workflows for semi-automated correlative cryo-fluorescence and cryo-electron microscopy/tomography. Journal of Structural Biology, 2017, 197, 83-93.	1.3	107
44	9Å... structure of the COPI coat reveals that the Arf1 GTPase occupies two contrasting molecular environments. ELife, 2017, 6, .	2.8	103
45	Cryo-electron microscopy of tubular arrays of HIV-1 Gag resolves structures essential for immature virus assembly. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8233-8238.	3.3	98
46	Structural Analysis of HIV-1 Maturation Using Cryo-Electron Tomography. PLoS Pathogens, 2010, 6, e1001215.	2.1	96
47	Phosphatidylinositol 4,5-Bisphosphate (PI(4,5)P2)-dependent Oligomerization of Fibroblast Growth Factor 2 (FGF2) Triggers the Formation of a Lipidic Membrane Pore Implicated in Unconventional Secretion. Journal of Biological Chemistry, 2012, 287, 27659-27669.	1.6	96
48	Structure and architecture of immature and mature murine leukemia virus capsids. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11751-E11760.	3.3	92
49	Cryo-electron Microscopy Reveals Conserved and Divergent Features of Gag Packing in Immature Particles of Rous Sarcoma Virus and Human Immunodeficiency Virus. Journal of Molecular Biology, 2006, 355, 157-168.	2.0	87
50	Multibudded tubules formed by COPII on artificial liposomes. Scientific Reports, 2011, 1, 17.	1.6	86
51	Tubular endocytosis drives remodelling of the apical surface during epithelial morphogenesis in Drosophila. Nature Communications, 2013, 4, 2244.	5.8	86
52	Immature HIV-1 lattice assembly dynamics are regulated by scaffolding from nucleic acid and the plasma membrane. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10056-E10065.	3.3	86
53	Complexin arrests a pool of docked vesicles for fast Ca ²⁺ -dependent release. EMBO Journal, 2012, 31, 3270-3281.	3.5	85
54	Determination of protein structure at 8.5 Å... resolution using cryo-electron tomography and sub-tomogram averaging. Journal of Structural Biology, 2013, 184, 394-400.	1.3	85

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55	Structure of the hexagonal surface layer on <i>Caulobacter crescentus</i> cells. <i>Nature Microbiology</i> , 2017, 2, 17059.	5.9	85
56	Structural Analysis of the Roles of Influenza A Virus Membrane-Associated Proteins in Assembly and Morphology. <i>Journal of Virology</i> , 2015, 89, 8957-8966.	1.5	78
57	Contrast transfer function correction applied to cryo-electron tomography and sub-tomogram averaging. <i>Journal of Structural Biology</i> , 2009, 168, 305-312.	1.3	77
58	An Organized Co-assembly of Clathrin Adaptors Is Essential for Endocytosis. <i>Developmental Cell</i> , 2015, 33, 150-162.	3.1	75
59	Architecture of the AP2/clathrin coat on the membranes of clathrin-coated vesicles. <i>Science Advances</i> , 2020, 6, eaba8381.	4.7	75
60	The Structures of COPI-Coated Vesicles Reveal Alternate Coatomer Conformations and Interactions. <i>Science</i> , 2012, 336, 1451-1454.	6.0	71
61	Correlative light and electron microscopy methods for the study of virus-cell interactions. <i>FEBS Letters</i> , 2016, 590, 1877-1895.	1.3	71
62	Coatomer and dimeric ADP ribosylation factor 1 promote distinct steps in membrane scission. <i>Journal of Cell Biology</i> , 2011, 194, 765-777.	2.3	70
63	Electron Tomography Reveals the Steps in Filovirus Budding. <i>PLoS Pathogens</i> , 2010, 6, e1000875.	2.1	65
64	High-resolution structures of HIV-1 Gag cleavage mutants determine structural switch for virus maturation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9401-E9410.	3.3	65
65	Retrovirus maturation—an extraordinary structural transformation. <i>Current Opinion in Virology</i> , 2016, 18, 27-35.	2.6	64
66	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> , 2015, 89, 10294-10302.	1.5	61
67	Combined Point-of-Care Nucleic Acid and Antibody Testing for SARS-CoV-2 following Emergence of D614G Spike Variant. <i>Cell Reports Medicine</i> , 2020, 1, 100099.	3.3	61
68	Maturation of the matrix and viral membrane of HIV-1. <i>Science</i> , 2021, 373, 700-704.	6.0	60
69	The native structure of the assembled matrix protein 1 of influenza A virus. <i>Nature</i> , 2020, 587, 495-498.	13.7	53
70	Conserved and Variable Features of Gag Structure and Arrangement in Immature Retrovirus Particles. <i>Journal of Virology</i> , 2010, 84, 11729-11736.	1.5	52
71	The contributions of the actin machinery to endocytic membrane bending and vesicle formation. <i>Molecular Biology of the Cell</i> , 2018, 29, 1346-1358.	0.9	52
72	Schnelle, zweifarbige Proteinmarkierung an lebenden Zellen für die hochauflösende Mikroskopie. <i>Angewandte Chemie</i> , 2014, 126, 2278-2282.	1.6	51

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73	Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. <i>Nature Communications</i> , 2021, 12, 1564.	5.8	50
74	<scp>SNARE</scp> and regulatory proteins induce local membrane protrusions to prime docked vesicles for fast calcium-triggered fusion. <i>EMBO Reports</i> , 2014, 15, 308-314.	2.0	46
75	Structures of virus-like capsids formed by the <i>Drosophila</i> neuronal Arc proteins. <i>Nature Neuroscience</i> , 2020, 23, 172-175.	7.1	46
76	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly. <i>PLoS Pathogens</i> , 2020, 16, e1008277.	2.1	44
77	A stable immature lattice packages IP₆ for HIV capsid maturation. <i>Science Advances</i> , 2021, 7, .	4.7	44
78	Architecture and mechanism of metazoan retromer:SNX3 tubular coat assembly. <i>Science Advances</i> , 2021, 7, .	4.7	44
79	Multiple site-specific infrared dichroism of CD3-Î¶, a transmembrane helix bundle. <i>Journal of Molecular Biology</i> , 2002, 316, 365-374.	2.0	42
80	Ebola and Marburg virus matrix layers are locally ordered assemblies of VP40 dimers. <i>ELife</i> , 2020, 9, .	2.8	41
81	Immature HIV-1 assembles from Gag dimers leaving partial hexamers at lattice edges as potential substrates for proteolytic maturation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	40
82	Structure of the Ty3/Gypsy retrotransposon capsid and the evolution of retroviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10048-10057.	3.3	39
83	Role of the SP2 Domain and Its Proteolytic Cleavage in HIV-1 Structural Maturation and Infectivity. <i>Journal of Virology</i> , 2012, 86, 13708-13716.	1.5	37
84	Convergence of experimental, computational and evolutionary approaches predicts the presence of a tetrameric form for CD3-Î¶. <i>Journal of Molecular Biology</i> , 2002, 316, 375-384.	2.0	35
85	SARS-CoV-2 Spike Protein Stabilized in the Closed State Induces Potent Neutralizing Responses. <i>Journal of Virology</i> , 2021, 95, e0020321.	1.5	35
86	Classification and three-dimensional reconstruction of unevenly distributed or symmetry mismatched features of icosahedral particles. <i>Journal of Structural Biology</i> , 2005, 150, 332-339.	1.3	34
87	Complexin Suppresses Spontaneous Exocytosis by Capturing the Membrane-Proximal Regions of VAMP2 and SNAP25. <i>Cell Reports</i> , 2020, 32, 107926.	2.9	33
88	HIV-1 cellular interactions analyzed by single virus tracing. <i>European Biophysics Journal</i> , 2008, 37, 1291-1301.	1.2	30
89	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core. <i>Nature Communications</i> , 2022, 13, 1002.	5.8	30
90	Induced Maturation of Human Immunodeficiency Virus. <i>Journal of Virology</i> , 2014, 88, 13722-13731.	1.5	29

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91	Higher-order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , 2016, 17, 1044-1060.	2.0	26
92	The HIV Mutation Browser: A Resource for Human Immunodeficiency Virus Mutagenesis and Polymorphism Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003951.	1.5	25
93	Contribution of Energy Values to the Analysis of Global Searching Molecular Dynamics Simulations of Transmembrane Helical Bundles. <i>Biophysical Journal</i> , 2002, 82, 3063-3071.	0.2	24
94	<i>In Vitro</i> Assembly of Virus-Like Particles of a Gammaretrovirus, the Murine Leukemia Virus XMRV. <i>Journal of Virology</i> , 2012, 86, 1297-1306.	1.5	24
95	The Nucleocapsid Domain of Gag Is Dispensable for Actin Incorporation into HIV-1 and for Association of Viral Budding Sites with Cortical F-Actin. <i>Journal of Virology</i> , 2014, 88, 7893-7903.	1.5	23
96	Cryoelectron Microscopy of Mouse Mammary Tumor Virus. <i>Journal of Virology</i> , 2004, 78, 2606-2608.	1.5	21
97	Strain and rupture of HIV-1 capsids during uncoating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2117781119.	3.3	21
98	High-throughput ultrastructure screening using electron microscopy and fluorescent barcoding. <i>Journal of Cell Biology</i> , 2019, 218, 2797-2811.	2.3	18
99	RNA and Nucleocapsid Are Dispensable for Mature HIV-1 Capsid Assembly. <i>Journal of Virology</i> , 2015, 89, 9739-9747.	1.5	17
100	FCHO controls AP2's initiating role in endocytosis through a PtdIns(4,5)P ₂ -dependent switch. <i>Science Advances</i> , 2022, 8, eabn2018.	4.7	14
101	Insights from reconstitution reactions of COPII vesicle formation using pure components and low mechanical perturbation. <i>Biological Chemistry</i> , 2014, 395, 801-812.	1.2	13
102	Nucleic Acid Binding by Mason-Pfizer Monkey Virus CA Promotes Virus Assembly and Genome Packaging. <i>Journal of Virology</i> , 2016, 90, 4593-4603.	1.5	13
103	Fluorescence-Based Detection of Membrane Fusion State on a Cryo-EM Grid using Correlated Cryo-Fluorescence and Cryo-Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2019, 25, 942-949.	0.2	11
104	Variable Internal Flexibility Characterizes the Helical Capsid Formed by <i>Agrobacterium</i> VirE2 Protein on Single-Stranded DNA. <i>Structure</i> , 2013, 21, 1158-1167.	1.6	8
105	Arrangements of proteins at reconstituted synaptic vesicle fusion sites depend on membrane separation. <i>FEBS Letters</i> , 2020, 594, 3450-3463.	1.3	8
106	Computational Identification of Novel Amino-Acid Interactions in HIV Gag via Correlated Evolution. <i>PLoS ONE</i> , 2012, 7, e42468.	1.1	7
107	New structural insights into the multifunctional influenza A matrix protein 1. <i>FEBS Letters</i> , 2021, 595, 2535-2543.	1.3	6
108	Imaging cellular structure across scales with correlated light, superresolution, and electron microscopy. <i>Molecular Biology of the Cell</i> , 2012, 23, 979-980.	0.9	5

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109	Critical Care Workers Have Lower Seroprevalence of SARS-CoV-2 IgG Compared with Non-patient Facing Staff in First Wave of COVID19. The Journal of Critical Care Medicine, 2021, 7, 199-210.	0.3	4
110	Directing Traffic into the Future. Developmental Cell, 2013, 27, 480-484.	3.1	2
111	Structural Biology of HIV Assembly. , 2013, , 1-22.		1
112	Automated cryo electron tomography and sub-tomogram averaging with the FEI Volta phase plate. Microscopy and Microanalysis, 2015, 21, 1833-1834.	0.2	0
113	Determining the Patchwork Lattice of Ebola and Marburg Virus Matrix Layers Using Cryo-Electron Tomography. Microscopy and Microanalysis, 2021, 27, 1884-1884.	0.2	0
114	Bridging length-scales from molecules to tissues using mouse genetics, cryoCLEM, and cryoET. Microscopy and Microanalysis, 2021, 27, 2574-2576.	0.2	0
115	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly. , 2020, 16, e1008277.		0
116	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly. , 2020, 16, e1008277.		0
117	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly. , 2020, 16, e1008277.		0
118	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly. , 2020, 16, e1008277.		0
119	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly. , 2020, 16, e1008277.		0