

John A G Briggs

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/9091675/john-a-g-briggs-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

129
papers

9,986
citations

56
h-index

99
g-index

137
ext. papers

12,943
ext. citations

13.9
avg, IF

6.4
L-index

#	Paper	IF	Citations
129	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts tropism and fusogenicity.. <i>Nature</i> , 2022 ,	50.4	95
128	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core.. <i>Nature Communications</i> , 2022 , 13, 1002	17.4	3
127	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	11.5	2
126	FCHO controls AP2 μ initiating role in endocytosis through a PtdIns(4,5)P-dependent switch.. <i>Science Advances</i> , 2022 , 8, eabn2018	14.3	1
125	Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. <i>Nature Communications</i> , 2021 , 12, 1564	17.4	8
124	A stable immature lattice packages IP for HIV capsid maturation. <i>Science Advances</i> , 2021 , 7,	14.3	9
123	Architecture and mechanism of metazoan retromer:SNX3 tubular coat assembly. <i>Science Advances</i> , 2021 , 7,	14.3	20
122	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core 2021 ,		1
121	SARS-CoV-2 Spike Protein Stabilized in the Closed State Induces Potent Neutralizing Responses. <i>Journal of Virology</i> , 2021 , 95, e0020321	6.6	7
120	Critical Care Workers Have Lower Seroprevalence of SARS-CoV-2 IgG Compared with Non-patient Facing Staff in First Wave of COVID19. <i>The Journal of Critical Care Medicine</i> , 2021 , 7, 199-210	1.2	2
119	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,	11.5	9
118	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021 , 592, 277-282	50.4	390
117	Determining the Patchwork Lattice of Ebola and Marburg Virus Matrix Layers Using Cryo-Electron Tomography. <i>Microscopy and Microanalysis</i> , 2021 , 27, 1884-1884	0.5	
116	Bridging length-scales from molecules to tissues using mouse genetics, cryoCLEM, and cryoET. <i>Microscopy and Microanalysis</i> , 2021 , 27, 2574-2576	0.5	
115	Maturation of the matrix and viral membrane of HIV-1. <i>Science</i> , 2021 , 373, 700-704	33.3	10
114	New structural insights into the multifunctional influenza A matrix protein 1. <i>FEBS Letters</i> , 2021 , 595, 2535-2543	3.8	0
113	Structures and distributions of SARS-CoV-2 spike proteins on intact virions. <i>Nature</i> , 2020 , 588, 498-502	50.4	461

112	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly. <i>PLoS Pathogens</i> , 2020 , 16, e1008277	7.6	19
111	Ebola and Marburg virus matrix layers are locally ordered assemblies of VP40 dimers. <i>ELife</i> , 2020 , 9,	8.9	9
110	Structures of virus-like capsids formed by the Drosophila neuronal Arc proteins. <i>Nature Neuroscience</i> , 2020 , 23, 172-175	25.5	22
109	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	18	40
108	Architecture of the AP2/clathrin coat on the membranes of clathrin-coated vesicles. <i>Science Advances</i> , 2020 , 6, eaba8381	14.3	25
107	A thermostable, closed SARS-CoV-2 spike protein trimer. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 934-941	17.6	128
106	Complexin Suppresses Spontaneous Exocytosis by Capturing the Membrane-Proximal Regions of VAMP2 and SNAP25. <i>Cell Reports</i> , 2020 , 32, 107926	10.6	9
105	Arrangements of proteins at reconstituted synaptic vesicle fusion sites depend on membrane separation. <i>FEBS Letters</i> , 2020 , 594, 3450-3463	3.8	1
104	The native structure of the assembled matrix protein 1 of influenza A virus. <i>Nature</i> , 2020 , 587, 495-498	50.4	14
103	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly 2020 , 16, e1008277		
102	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly 2020 , 16, e1008277		
101	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly 2020 , 16, e1008277		
100	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly 2020 , 16, e1008277		
99	Structures of immature EIAV Gag lattices reveal a conserved role for IP6 in lentivirus assembly 2020 , 16, e1008277		
98	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	0.5	6
97	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	11.5	20
96	High-throughput ultrastructure screening using electron microscopy and fluorescent barcoding. <i>Journal of Cell Biology</i> , 2019 , 218, 2797-2811	7.3	13
95	The Neuronal Gene Arc Encodes a Repurposed Retrotransposon Gag Protein that Mediates Intercellular RNA Transfer. <i>Cell</i> , 2018 , 172, 275-288.e18	56.2	203

94	The contributions of the actin machinery to endocytic membrane bending and vesicle formation. <i>Molecular Biology of the Cell</i> , 2018 , 29, 1346-1358	3.5	36
93	Structure and architecture of immature and mature murine leukemia virus capsids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11751-E11760	11.5	44
92	Structure of the membrane-assembled retromer coat determined by cryo-electron tomography. <i>Nature</i> , 2018 , 561, 561-564	50.4	104
91	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	11.5	37
90	New hardware and workflows for semi-automated correlative cryo-fluorescence and cryo-electron microscopy/tomography. <i>Journal of Structural Biology</i> , 2017 , 197, 83-93	3.4	79
89	Structure of the hexagonal surface layer on <i>Caulobacter crescentus</i> cells. <i>Nature Microbiology</i> , 2017 , 2, 17059	26.6	60
88	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	23.4	90
87	Efficient 3D-CTF correction for cryo-electron tomography using NovaCTF improves subtomogram averaging resolution to 3.4Å. <i>Journal of Structural Biology</i> , 2017 , 199, 187-195	3.4	139
86	Immature HIV-1 lattice assembly dynamics are regulated by scaffolding from nucleic acid and the plasma membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E10056-E10065	11.5	40
85	Structure and assembly of the Ebola virus nucleocapsid. <i>Nature</i> , 2017 , 551, 394-397	50.4	114
84	Implementation of a cryo-electron tomography tilt-scheme optimized for high resolution subtomogram averaging. <i>Journal of Structural Biology</i> , 2017 , 197, 191-198	3.4	272
83	The structure of the COPI coat determined within the cell. <i>ELife</i> , 2017 , 6,	8.9	94
82	Structure of the COPI coat reveals that the Arf1 GTPase occupies two contrasting molecular environments. <i>ELife</i> , 2017 , 6,	8.9	61
81	An atomic model of HIV-1 capsid-SP1 reveals structures regulating assembly and maturation. <i>Science</i> , 2016 , 353, 506-8	33.3	250
80	Correlative light and electron microscopy methods for the study of virus-cell interactions. <i>FEBS Letters</i> , 2016 , 590, 1877-95	3.8	51
79	Retrovirus maturation-an extraordinary structural transformation. <i>Current Opinion in Virology</i> , 2016 , 18, 27-35	7.5	44
78	A saposin-lipoprotein nanoparticle system for membrane proteins. <i>Nature Methods</i> , 2016 , 13, 345-51	21.6	152
77	The structure and flexibility of conical HIV-1 capsids determined within intact virions. <i>Science</i> , 2016 , 354, 1434-1437	33.3	149

76	Higher-order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , 2016 , 17, 1044-60	6.5	20
75	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , 2016 , 352, 363-5	33.3	216
74	Nucleic Acid Binding by Mason-Pfizer Monkey Virus CA Promotes Virus Assembly and Genome Packaging. <i>Journal of Virology</i> , 2016 , 90, 4593-4603	6.6	8
73	VESICULAR TRANSPORT. A structure of the COPI coat and the role of coat proteins in membrane vesicle assembly. <i>Science</i> , 2015 , 349, 195-8	33.3	116
72	Structural Analysis of the Roles of Influenza A Virus Membrane-Associated Proteins in Assembly and Morphology. <i>Journal of Virology</i> , 2015 , 89, 8957-66	6.6	55
71	RNA and Nucleocapsid Are Dispensable for Mature HIV-1 Capsid Assembly. <i>Journal of Virology</i> , 2015 , 89, 9739-47	6.6	13
70	ENDOCYTOSIS. Endocytic sites mature by continuous bending and remodeling of the clathrin coat. <i>Science</i> , 2015 , 348, 1369-72	33.3	164
69	An organized co-assembly of clathrin adaptors is essential for endocytosis. <i>Developmental Cell</i> , 2015 , 33, 150-62	10.2	51
68	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, 10294-302	6.6	46
67	Structure of the immature HIV-1 capsid in intact virus particles at 8.8 Å resolution. <i>Nature</i> , 2015 , 517, 505-8	50.4	212
66	Automated cryo electron tomography and sub-tomogram averaging with the FEI Volta phase plate. <i>Microscopy and Microanalysis</i> , 2015 , 21, 1833-1834	0.5	
65	Minimal tags for rapid dual-color live-cell labeling and super-resolution microscopy. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 2245-9	16.4	210
64	Correlated cryo-fluorescence and cryo-electron microscopy with high spatial precision and improved sensitivity. <i>Ultramicroscopy</i> , 2014 , 143, 24-32	3.1	90
63	Induced maturation of human immunodeficiency virus. <i>Journal of Virology</i> , 2014 , 88, 13722-31	6.6	23
62	SNARE and regulatory proteins induce local membrane protrusions to prime docked vesicles for fast calcium-triggered fusion. <i>EMBO Reports</i> , 2014 , 15, 308-14	6.5	39
61	Schnelle, zweifarbige Proteinmarkierung an lebenden Zellen für die hochauflösende Mikroskopie. <i>Angewandte Chemie</i> , 2014 , 126, 2278-2282	3.6	45
60	Insights from reconstitution reactions of COPII vesicle formation using pure components and low mechanical perturbation. <i>Biological Chemistry</i> , 2014 , 395, 801-12	4.5	9
59	The HIV mutation browser: a resource for human immunodeficiency virus mutagenesis and polymorphism data. <i>PLoS Computational Biology</i> , 2014 , 10, e1003951	5	14

58	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, 7893-903	6.6	16
57	Cryo-electron microscopy of tubular arrays of HIV-1 Gag resolves structures essential for immature virus assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 8233-8	11.5	69
56	Determination of protein structure at 8.5 Å resolution using cryo-electron tomography and sub-tomogram averaging. <i>Journal of Structural Biology</i> , 2013 , 184, 394-400	3.4	77
55	Structural biology in situ--the potential of subtomogram averaging. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 261-7	8.1	181
54	Variable internal flexibility characterizes the helical capsid formed by agrobacterium VirE2 protein on single-stranded DNA. <i>Structure</i> , 2013 , 21, 1158-67	5.2	8
53	Directing traffic into the future. <i>Developmental Cell</i> , 2013 , 27, 480-4	10.2	2
52	Vesicle coats: structure, function, and general principles of assembly. <i>Trends in Cell Biology</i> , 2013 , 23, 279-88	18.3	125
51	Tubular endocytosis drives remodelling of the apical surface during epithelial morphogenesis in <i>Drosophila</i> . <i>Nature Communications</i> , 2013 , 4, 2244	17.4	68
50	Nuclear pore scaffold structure analyzed by super-resolution microscopy and particle averaging. <i>Science</i> , 2013 , 341, 655-8	33.3	307
49	The structure of the COPII transport-vesicle coat assembled on membranes. <i>ELife</i> , 2013 , 2, e00951	8.9	84
48	Structural Biology of HIV Assembly 2013 , 1-22		1
47	Plasma membrane reshaping during endocytosis is revealed by time-resolved electron tomography. <i>Cell</i> , 2012 , 150, 508-20	56.2	257
46	Role of the SP2 domain and its proteolytic cleavage in HIV-1 structural maturation and infectivity. <i>Journal of Virology</i> , 2012 , 86, 13708-16	6.6	35
45	The structures of COPI-coated vesicles reveal alternate coatomer conformations and interactions. <i>Science</i> , 2012 , 336, 1451-4	33.3	62
44	Precise, correlated fluorescence microscopy and electron tomography of lowicryl sections using fluorescent fiducial markers. <i>Methods in Cell Biology</i> , 2012 , 111, 235-57	1.8	101
43	Structure of the immature retroviral capsid at 8 Å resolution by cryo-electron microscopy. <i>Nature</i> , 2012 , 487, 385-9	50.4	134
42	Computational identification of novel amino-acid interactions in HIV Gag via correlated evolution. <i>PLoS ONE</i> , 2012 , 7, e42468	3.7	7
41	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, 4275-80	11.5	157

40	Imaging cellular structure across scales with correlated light, superresolution, and electron microscopy. <i>Molecular Biology of the Cell</i> , 2012 , 23, 979-980	3.5	5
39	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. <i>Journal of Biological Chemistry</i> , 2012 , 287, 27659-69	5.4	80
38	In vitro assembly of virus-like particles of a gammaretrovirus, the murine leukemia virus XMRV. <i>Journal of Virology</i> , 2012 , 86, 1297-306	6.6	21
37	Complexin arrests a pool of docked vesicles for fast Ca ²⁺ -dependent release. <i>EMBO Journal</i> , 2012 , 31, 3270-81	13	72
36	The molecular architecture of HIV. <i>Journal of Molecular Biology</i> , 2011 , 410, 491-500	6.5	130
35	Multibudded tubules formed by COPII on artificial liposomes. <i>Scientific Reports</i> , 2011 , 1, 17	4.9	65
34	Correlated fluorescence and 3D electron microscopy with high sensitivity and spatial precision. <i>Journal of Cell Biology</i> , 2011 , 192, 111-9	7.3	342
33	Coatomer and dimeric ADP ribosylation factor 1 promote distinct steps in membrane scission. <i>Journal of Cell Biology</i> , 2011 , 194, 765-77	7.3	52
32	Cryo-electron tomography of Marburg virus particles and their morphogenesis within infected cells. <i>PLoS Biology</i> , 2011 , 9, e1001196	9.7	95
31	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, 3516-27	6.6	165
30	Conserved and variable features of Gag structure and arrangement in immature retrovirus particles. <i>Journal of Virology</i> , 2010 , 84, 11729-36	6.6	51
29	Electron tomography reveals the steps in filovirus budding. <i>PLoS Pathogens</i> , 2010 , 6, e1000875	7.6	47
28	Cryo electron tomography of native HIV-1 budding sites. <i>PLoS Pathogens</i> , 2010 , 6, e1001173	7.6	90
27	Structural analysis of HIV-1 maturation using cryo-electron tomography. <i>PLoS Pathogens</i> , 2010 , 6, e1001175	7.6	86
26	Computational model of membrane fission catalyzed by ESCRT-III. <i>PLoS Computational Biology</i> , 2009 , 5, e1000575	5	121
25	Contrast transfer function correction applied to cryo-electron tomography and sub-tomogram averaging. <i>Journal of Structural Biology</i> , 2009 , 168, 305-12	3.4	70
24	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, 592-9	23.4	172
23	HIV-1-cellular interactions analyzed by single virus tracing. <i>European Biophysics Journal</i> , 2008 , 37, 1291-303	30.3	24

22	Double-labelled HIV-1 particles for study of virus-cell interaction. <i>Virology</i> , 2007 , 360, 92-104	3.6	106
21	The mechanism of HIV-1 core assembly: insights from three-dimensional reconstructions of authentic virions. <i>Structure</i> , 2006 , 14, 15-20	5.2	171
20	Cryo-electron tomographic structure of an immunodeficiency virus envelope complex in situ. <i>PLoS Pathogens</i> , 2006 , 2, e83	7.6	184
19	Cryo-electron microscopy reveals conserved and divergent features of gag packing in immature particles of Rous sarcoma virus and human immunodeficiency virus. <i>Journal of Molecular Biology</i> , 2006 , 355, 157-68	6.5	79
18	Classification and three-dimensional reconstruction of unevenly distributed or symmetry mismatched features of icosahedral particles. <i>Journal of Structural Biology</i> , 2005 , 150, 332-9	3.4	31
17	Cryoelectron microscopy of mouse mammary tumor virus. <i>Journal of Virology</i> , 2004 , 78, 2606-8	6.6	18
16	The stoichiometry of Gag protein in HIV-1. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 672-5	17.6	406
15	Structural organization of authentic, mature HIV-1 virions and cores. <i>EMBO Journal</i> , 2003 , 22, 1707-15	13	344
14	Pathogenic bacteria attach to human fibronectin through a tandem beta-zipper. <i>Nature</i> , 2003 , 423, 177-81	10.4	301
13	Do lipid rafts mediate virus assembly and pseudotyping?. <i>Journal of General Virology</i> , 2003 , 84, 757-768	4.9	105
12	Multiple site-specific infrared dichroism of CD3-zeta, a transmembrane helix bundle. <i>Journal of Molecular Biology</i> , 2002 , 316, 365-74	6.5	40
11	Convergence of experimental, computational and evolutionary approaches predicts the presence of a tetrameric form for CD3-zeta. <i>Journal of Molecular Biology</i> , 2002 , 316, 375-84	6.5	33
10	Contribution of energy values to the analysis of global searching molecular dynamics simulations of transmembrane helical bundles. <i>Biophysical Journal</i> , 2002 , 82, 3063-71	2.9	23
9	The native structure of the full-length, assembled influenza A virus matrix protein, M1		2
8	The contributions of the actin machinery to endocytic membrane bending and vesicle formation		2
7	Architecture of the AP2:clathrin coat on the membranes of clathrin-coated vesicles		3
6	Maturation of the matrix and viral membrane of HIV-1		1
5	Architecture and mechanism of metazoan retromer:SNX3 tubular coat assembly		3

4	Structures and function of locked conformations of SARS-CoV-2 spike	3
3	Towards Internationally standardised humoral Immune Correlates of Protection from SARS-CoV-2 infection and COVID-19 disease	10
2	SARS-CoV-2 spike protein arrested in the closed state induces potent neutralizing responses	1
1	A Bayesian approach to single-particle electron cryo-tomography in RELION-4.0	2