

Elizabeth Villa

List of Publications by Year in Descending Order

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

67
papers

17,841
citations

35
h-index

85
g-index

85
ext. papers

20,677
ext. citations

12.8
avg, IF

6.11
L-index

#	Paper	IF	Citations
67	Subcellular organization of viral particles during maturation of nucleus-forming jumbo phage.. <i>Science Advances</i> , 2022 , 8, eabj9670	14.3	1
66	Comprehensive structure and functional adaptations of the yeast nuclear pore complex.. <i>Cell</i> , 2021 ,	56.2	18
65	Practical Approaches for Cryo-FIB Milling and Applications for Cellular Cryo-Electron Tomography. <i>Methods in Molecular Biology</i> , 2021 , 2215, 49-82	1.4	4
64	Asymmetric localization of the cell division machinery during sporulation. <i>ELife</i> , 2021 , 10,	8.9	7
63	Selective transport of fluorescent proteins into the phage nucleus. <i>PLoS ONE</i> , 2021 , 16, e0251429	3.7	3
62	HSP70 chaperones RNA-free TDP-43 into anisotropic intranuclear liquid spherical shells. <i>Science</i> , 2021 , 371,	33.3	73
61	The SARS-CoV-2 nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein. <i>Nature Communications</i> , 2021 , 12, 502	17.4	101
60	Generating Chromosome Geometries in a Minimal Cell From Cryo-Electron Tomograms and Chromosome Conformation Capture Maps. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 644133	5.6	3
59	Entropy-regularized deconvolution of cellular cryotransmission electron tomograms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
58	Structure of LRRK2 in Parkinson's disease and model for microtubule interaction. <i>Nature</i> , 2020 , 588, 344-349	50.4	60
57	Preparing samples from whole cells using focused-ion-beam milling for cryo-electron tomography. <i>Nature Protocols</i> , 2020 , 15, 2041-2070	18.8	38
56	The In situ Structure of Parkinson's Disease-Linked LRRK2. <i>Biophysical Journal</i> , 2020 , 118, 486a	2.9	8
55	A novel vibriophage exhibits inhibitory activity against host protein synthesis machinery. <i>Scientific Reports</i> , 2020 , 10, 2347	4.9	6
54	The SARS-CoV-2 Nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein 2020 ,		10
53	The In Situ Structure of Parkinson's Disease-Linked LRRK2. <i>Cell</i> , 2020 , 182, 1508-1518.e16	56.2	57
52	Viral Capsid Trafficking along Treadmilling Tubulin Filaments in Bacteria. <i>Cell</i> , 2019 , 177, 1771-1780.e12	56.2	30
51	The molecular architecture of engulfment during sporulation. <i>ELife</i> , 2019 , 8,	8.9	17

50	Chromosome Translocation Inflates Bacillus Forespores and Impacts Cellular Morphology. <i>Cell</i> , 2018 , 172, 758-770.e14	56.2	23
49	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. <i>Journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 433-443	0.5	
48	Assembly of a nucleus-like structure during viral replication in bacteria. <i>Science</i> , 2017 , 355, 194-197	33.3	115
47	Biography of Klaus Schulten. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 3206	3.4	
46	Challenges of Integrating Stochastic Dynamics and Cryo-Electron Tomograms in Whole-Cell Simulations. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 3871-3881	3.4	9
45	Revealing the Native Molecular Architecture of the Nuclear Periphery using Cryo-Focused-Ion-Beam Milling, Light Microscopy and Electron Tomography. <i>Microscopy and Microanalysis</i> , 2017 , 23, 1248-1249	0.5	
44	A photoactivable multi-inhibitor nanoliposome for tumour control and simultaneous inhibition of treatment escape pathways. <i>Nature Nanotechnology</i> , 2016 , 11, 378-87	28.7	169
43	Visualizing the molecular sociology at the HeLa cell nuclear periphery. <i>Science</i> , 2016 , 351, 969-72	33.3	344
42	Native architecture of the Chlamydomonas chloroplast revealed by in situ cryo-electron tomography. <i>ELife</i> , 2015 , 4,	8.9	166
41	Architecture of the RNA polymerase II-Mediator core initiation complex. <i>Nature</i> , 2015 , 518, 376-80	50.4	205
40	Finding the right fit: chiseling structures out of cryo-electron microscopy maps. <i>Current Opinion in Structural Biology</i> , 2014 , 25, 118-25	8.1	38
39	Opening Windows into the Cell: Focused-Ion-Beam Milling for Cryo-Electron Tomography. <i>Biophysical Journal</i> , 2014 , 106, 600a	2.9	3
38	Structural Cell Biology: Preparing Specimens for Cryo-Electron Tomography Using Focused-Ion-Beam Milling. <i>Microscopy and Microanalysis</i> , 2014 , 20, 1222-1223	0.5	
37	Opening windows into the cell: focused-ion-beam milling for cryo-electron tomography. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 771-7	8.1	127
36	Promiscuous behaviour of archaeal ribosomal proteins: implications for eukaryotic ribosome evolution. <i>Nucleic Acids Research</i> , 2013 , 41, 1284-93	20.1	48
35	Three-dimensional architecture of actin filaments in <i>Listeria monocytogenes</i> comet tails. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20521-6	11.5	58
34	The structure of human tripeptidyl peptidase II as determined by a hybrid approach. <i>Structure</i> , 2012 , 20, 593-603	5.2	15
33	Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1380-7	11.5	380

32	Dynein achieves processive motion using both stochastic and coordinated stepping. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 193-200	17.6	159
31	Integrative approaches for cellular cryo-electron tomography: correlative imaging and focused ion beam micromachining. <i>Methods in Cell Biology</i> , 2012 , 111, 259-81	1.8	51
30	1.14 Structure Determination of Macromolecular Complexes by Cryo-Electron Microscopy in vitro and in situ 2012 , 245-276		
29	Focused ion beam micromachining of eukaryotic cells for cryoelectron tomography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 4449-54	11.5	260
28	Near-atomic resolution structural model of the yeast 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 14870-5	11.5	212
27	Applications of the molecular dynamics flexible fitting method. <i>Journal of Structural Biology</i> , 2011 , 173, 420-7	3.4	38
26	Hybrid Imaging-Novel Approaches and Recent Advances in Correlative Microscopy. <i>Microscopy and Microanalysis</i> , 2011 , 17, 964-965	0.5	1
25	Structure of the no-go mRNA decay complex Dom34-Hbs1 bound to a stalled 80S ribosome. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 715-20	17.6	132
24	Visualizing cellular processes at the molecular level by cryo-electron tomography. <i>Journal of Cell Science</i> , 2010 , 123, 7-12	5.3	56
23	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-A resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 19748-53	11.5	158
22	Integration of cryo-EM with atomic and protein-protein interaction data. <i>Methods in Enzymology</i> , 2010 , 483, 47-72	1.7	12
21	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 19754-9	11.5	112
20	Ribosome-induced changes in elongation factor Tu conformation control GTP hydrolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1063-8	11.5	199
19	Regulation of the protein-conducting channel by a bound ribosome. <i>Structure</i> , 2009 , 17, 1453-64	5.2	95
18	Structural model and excitonic properties of the dimeric RC-LH1-PufX complex from Rhodospira rubra. <i>Chemical Physics</i> , 2009 , 357, 188-197	2.3	45
17	Molecular dynamics flexible fitting: a practical guide to combine cryo-electron microscopy and X-ray crystallography. <i>Methods</i> , 2009 , 49, 174-80	4.6	246
16	Protein-induced membrane curvature investigated through molecular dynamics flexible fitting. <i>Biophysical Journal</i> , 2009 , 97, 321-9	2.9	64
15	Structural insight into nascent polypeptide chain-mediated translational stalling. <i>Science</i> , 2009 , 326, 1412-5	33.3	233

14	Flexible fitting of atomic structures into electron microscopy maps using molecular dynamics. <i>Structure</i> , 2008 , 16, 673-83	5.2	678
13	Molecular mechanisms of cellular mechanics. <i>Physical Chemistry Chemical Physics</i> , 2006 , 8, 3692-706	3.6	59
12	Scalable molecular dynamics with NAMD. <i>Journal of Computational Chemistry</i> , 2005 , 26, 1781-802	3.5	12650
11	Structural dynamics of the lac repressor-DNA complex revealed by a multiscale simulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 6783-8	11.5	123
10	Multiscale Method for Simulating Protein-DNA Complexes. <i>Multiscale Modeling and Simulation</i> , 2004 , 2, 527-553	1.8	64
9	A Cytoskeletal Vortex Drives Phage Nucleus Rotation During Jumbo Phage Replication in E. coli		2
8	Parkinson's Disease-linked LRRK2 structure and model for microtubule interaction		9
7	TDP-43 and HSP70 phase separate into anisotropic, intranuclear liquid spherical annuli		2
6	Asymmetric localization of the cell division machinery during Bacillus subtilis sporulation		2
5	Selective transport of fluorescent proteins into the phage nucleus		2
4	The in situ structure of Parkinson's disease-linked LRRK2		8
3	Subcellular Organization of Viral Particles During Maturation of Nucleus-Forming Jumbo Phage		1
2	Entropy Regularized Deconvolution of Cellular Cryo-Transmission Electron Tomograms		2
1	A modular platform for engineering function of natural and synthetic biomolecular condensates		6