

Elizabeth Villa

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

22,378
citations

94269

37
h-index

161609

54
g-index

85
all docs

85
docs citations

85
times ranked

27811
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive structure and functional adaptations of the yeast nuclear pore complex. <i>Cell</i> , 2022, 185, 361-378.e25.	13.5	87
2	Subcellular organization of viral particles during maturation of nucleus-forming jumbo phage. <i>Science Advances</i> , 2022, 8, eabj9670.	4.7	18
3	Revealing bacterial cell biology using cryo-electron tomography. <i>Current Opinion in Structural Biology</i> , 2022, 75, 102419.	2.6	12
4	HSP70 chaperones RNA-free TDP-43 into anisotropic intranuclear liquid spherical shells. <i>Science</i> , 2021, 371, .	6.0	200
5	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.	5.8	307
6	Stochastic Spatial Simulation of Genetic Information Processes in the Minimal Cell. <i>Biophysical Journal</i> , 2021, 120, 109a.	0.2	0
7	Generating Chromosome Geometries at the Single-Cell Level from Cryo-Electron Tomograms. <i>Biophysical Journal</i> , 2021, 120, 222a.	0.2	0
8	Asymmetric localization of the cell division machinery during <i>Bacillus subtilis</i> sporulation. <i>ELife</i> , 2021, 10, .	2.8	24
9	Selective transport of fluorescent proteins into the phage nucleus. <i>PLoS ONE</i> , 2021, 16, e0251429.	1.1	16
10	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.	1.6	13
11	Practical Approaches for Cryo-FIB Milling and Applications for Cellular Cryo-Electron Tomography. <i>Methods in Molecular Biology</i> , 2021, 2215, 49-82.	0.4	19
12	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, .	3.3	11
13	The In Situ Structure of Parkinson's Disease-Linked LRRK2. <i>Cell</i> , 2020, 182, 1508-1518.e16.	13.5	135
14	Structure of LRRK2 in Parkinson's disease and model for microtubule interaction. <i>Nature</i> , 2020, 588, 344-349.	13.7	147
15	Preparing samples from whole cells using focused-ion-beam milling for cryo-electron tomography. <i>Nature Protocols</i> , 2020, 15, 2041-2070.	5.5	114
16	The In situ Structure of Parkinson's Disease-Linked LRRK2. <i>Biophysical Journal</i> , 2020, 118, 486a.	0.2	11
17	A novel vibriophage exhibits inhibitory activity against host protein synthesis machinery. <i>Scientific Reports</i> , 2020, 10, 2347.	1.6	20
18	Viral Capsid Trafficking along Treadmilling Tubulin Filaments in Bacteria. <i>Cell</i> , 2019, 177, 1771-1780.e12.	13.5	62

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19	The molecular architecture of engulfment during <i>Bacillus subtilis</i> sporulation. <i>ELife</i> , 2019, 8, .	2.8	34
20	Chromosome Translocation Inflates <i>Bacillus</i> Forespores and Impacts Cellular Morphology. <i>Cell</i> , 2018, 172, 758-770.e14.	13.5	42
21	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.	0.2	0
22	Assembly of a nucleus-like structure during viral replication in bacteria. <i>Science</i> , 2017, 355, 194-197.	6.0	207
23	Biography of Klaus Schulten. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3206-3206.	1.2	0
24	Challenges of Integrating Stochastic Dynamics and Cryo-Electron Tomograms in Whole-Cell Simulations. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3871-3881.	1.2	14
25	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.	0.2	1
26	Opening windows into the cell: bringing structure to cell biology using cryo-electron microscopy. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a417-a417.	0.0	0
27	Optical probes for molecular-guided surgery: Using photomedicine to prevent recurrence in the surgical bed (Conference Presentation). , 2016, , .		0
28	Photodynamic therapy with simultaneous suppression of multiple treatment escape pathways (Conference Presentation). , 2016, , .		0
29	A photoactivable multi-inhibitor nanoliposome for tumour control and simultaneous inhibition of treatment escape pathways. <i>Nature Nanotechnology</i> , 2016, 11, 378-387.	15.6	201
30	Visualizing the molecular sociology at the HeLa cell nuclear periphery. <i>Science</i> , 2016, 351, 969-972.	6.0	493
31	Native architecture of the <i>Chlamydomonas</i> chloroplast revealed by in situ cryo-electron tomography. <i>ELife</i> , 2015, 4, .	2.8	224
32	Architecture of the RNA polymerase II "Mediator core initiation complex. <i>Nature</i> , 2015, 518, 376-380.	13.7	259
33	Structural Cell Biology: Preparing Specimens for Cryo-Electron Tomography Using Focused-Ion-Beam Milling. <i>Microscopy and Microanalysis</i> , 2014, 20, 1222-1223.	0.2	0
34	Finding the right fit: chiseling structures out of cryo-electron microscopy maps. <i>Current Opinion in Structural Biology</i> , 2014, 25, 118-125.	2.6	49
35	Opening Windows into the Cell: Focused-Ion-Beam Milling for Cryo-Electron Tomography. <i>Biophysical Journal</i> , 2014, 106, 600a.	0.2	3
36	Opening Windows into the Cell: Focused Ion Beam Micromachining of Eukaryotic Cells for Cryo-Electron Tomography. <i>Biophysical Journal</i> , 2013, 104, 353a-354a.	0.2	1

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37	Opening windows into the cell: focused-ion-beam milling for cryo-electron tomography. <i>Current Opinion in Structural Biology</i> , 2013, 23, 771-777.	2.6	179
38	Promiscuous behaviour of archaeal ribosomal proteins: Implications for eukaryotic ribosome evolution. <i>Nucleic Acids Research</i> , 2013, 41, 1284-1293.	6.5	59
39	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, 20521-20526.	3.3	81
40	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, 4449-4454.	3.3	356
41	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, 14870-14875.	3.3	242
42	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, 1380-1387.	3.3	422
43	Dynein achieves processive motion using both stochastic and coordinated stepping. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 193-200.	3.6	198
44	Integrative Approaches for Cellular Cryo-electron Tomography. <i>Methods in Cell Biology</i> , 2012, 111, 259-281.	0.5	59
45	1.14 Structure Determination of Macromolecular Complexes by Cryo-Electron Microscopy in vitro and in situ. , 2012, , 245-276.		1
46	The Structure of Human Tripeptidyl Peptidase II as Determined by a Hybrid Approach. <i>Structure</i> , 2012, 20, 593-603.	1.6	19
47	Applications of the molecular dynamics flexible fitting method. <i>Journal of Structural Biology</i> , 2011, 173, 420-427.	1.3	44
48	Hybrid Imaging-Novel Approaches and Recent Advances in Correlative Microscopy. <i>Microscopy and Microanalysis</i> , 2011, 17, 964-965.	0.2	1
49	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, 715-720.	3.6	150
50	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, 19754-19759.	3.3	122
51	Visualizing cellular processes at the molecular level by cryo-electron tomography. <i>Journal of Cell Science</i> , 2010, 123, 7-12.	1.2	59
52	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19748-19753.	3.3	196
53	Integration of Cryo-EM with Atomic and Protein-Protein Interaction Data. <i>Methods in Enzymology</i> , 2010, 483, 47-72.	0.4	12
54	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, 1063-1068.	3.3	219

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55	Regulation of the Protein-Conducting Channel by a Bound Ribosome. <i>Structure</i> , 2009, 17, 1453-1464.	1.6	107
56	Structural model and excitonic properties of the dimeric RCâ€“LH1â€“PufX complex from <i>Rhodospira rubra</i> . <i>Chemical Physics</i> , 2009, 357, 188-197.	0.9	48
57	Molecular dynamics flexible fitting: A practical guide to combine cryo-electron microscopy and X-ray crystallography. <i>Methods</i> , 2009, 49, 174-180.	1.9	305
58	Protein-Induced Membrane Curvature Investigated through Molecular Dynamics Flexible Fitting. <i>Biophysical Journal</i> , 2009, 97, 321-329.	0.2	68
59	Structural Insight into Nascent Polypeptide Chainâ€“Mediated Translational Stalling. <i>Science</i> , 2009, 326, 1412-1415.	6.0	263
60	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. <i>Structure</i> , 2008, 16, 673-683.	1.6	833
61	Merging data from cryo-EM and X-ray crystallography to reveal biomolecular function. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, C47-C47.	0.3	0
62	Molecular mechanisms of cellular mechanics. <i>Physical Chemistry Chemical Physics</i> , 2006, 8, 3692.	1.3	76
63	Scalable molecular dynamics with NAMD. <i>Journal of Computational Chemistry</i> , 2005, 26, 1781-1802.	1.5	15,208
64	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, 6783-6788.	3.3	135
65	Multiscale Method for Simulating Protein-DNA Complexes. <i>Multiscale Modeling and Simulation</i> , 2004, 2, 527-553.	0.6	68
66	Chromosome Translocation Inflates <i>Bacillus subtilis</i> Forespores and Impacts Cellular Morphology. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0