Willy Wriggers

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Conserved Intramolecular Interactions Maintain Myosin Interacting-Heads Motifs Explaining Tarantula Muscle Super-Relaxed State Structural Basis. Journal of Molecular Biology, 2016, 428, 1142-1164.	2.0	82
2	Automated tracing of filaments in 3D electron tomography reconstructions using Sculptor and Situs. Journal of Structural Biology, 2012, 178, 121-128.	1.3	47
3	Accurate flexible refinement of atomic models against medium-resolution cryo-EM maps using damped dynamics. BMC Structural Biology, 2018, 18, 12.	2.3	29
4	Numerical geometry of map and model assessment. Journal of Structural Biology, 2015, 192, 255-261.	1.3	18
5	Tracing Actin Filament Bundles in Three-Dimensional Electron Tomography Density Maps of Hair Cell Stereocilia. Molecules, 2018, 23, 882.	1.7	15
6	A cryo-tomography-based volumetric model of the actin core of mouse vestibular hair cell stereocilia lacking plastin 1. Journal of Structural Biology, 2020, 210, 107461.	1.3	14
7	Cylindrical Similarity Measurement for Helices in Medium-Resolution Cryo-Electron Microscopy Density Maps. Journal of Chemical Information and Modeling, 2020, 60, 2644-2650.	2.5	12
8	Spatial Heat Maps from Fast Information Matching of Fast and Slow Degrees of Freedom: Application to Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2016, 120, 8473-8484.	1.2	11
9	Multi-scale Visualization of Molecular Architecture Using Real-Time Ambient Occlusion in Sculptor. PLoS Computational Biology, 2015, 11, e1004516.	1.5	10
10	Correction of Missing-Wedge Artifacts in Filamentous Tomograms by Template-Based Constrained Deconvolution. Journal of Chemical Information and Modeling, 2020, 60, 2626-2633.	2.5	9
11	Comparing an Atomic Model or Structure to a Corresponding Cryo-electron Microscopy Image at the Central Axis of a Helix. Journal of Computational Biology, 2017, 24, 52-67.	0.8	8
12	TomoSim: Simulation of Filamentous Cryo-Electron Tomograms. , 2021, , .		5
13	Tracing Filaments in Simulated 3D Cryo-Electron Tomography Maps Using a Fast Dynamic Programming Algorithm. , 2021, , .		4
14	Frontiers in CryoEM Modeling. Journal of Chemical Information and Modeling, 2019, 59, 3091-3093.	2.5	2
15	Comparison of an atomic model and its cryo-EM image at the central axis of a helix. , 2015, 2015, 1253-1259.		1
16	Detection of Protein Secondary Structure Patterns from 3D Cryo-TEM Maps at Medium Resolution - Combining the Best of SSETracer and VolTrac. Microscopy and Microanalysis, 2017, 23, 242-243.	0.2	1
17	An Experimental Approach to Mapping of Magnetic Fields of CubeSat Attitude Actuator Representations. , 2020, , .		1
18	Faces of Contemporary CryoEM Information and Modeling. Journal of Chemical Information and Modeling, 2020, 60, 2407-2409.	2.5	1

#	Article	IF	CITATIONS
19	Tracing Filaments in Simulated and Experimental 3D Cryo-Electron Tomography Maps Using a Fast Dynamic Programming Algorithm. Microscopy and Microanalysis, 2021, 27, 3236-3237.	0.2	1
20	Mechanism for the Unfolding of the TOP7 Protein in Steered Molecular Dynamics Simulations as Revealed by Mutual Information Analysis. Frontiers in Molecular Biosciences, 2021, 8, 696609.	1.6	1
21	Flexible Fitting and Refinement of Atomic Structures Using the Coarse-Grained DDFF Force Field Tailored to 5-10A Resolution Cryo-TEM Maps. Microscopy and Microanalysis, 2017, 23, 1226-1227.	0.2	0
22	An Information Theoretic Approach for Creating 3D Spatial Images from 4D Time Series Data. Microscopy and Microanalysis, 2017, 23, 100-101.	0.2	0
23	Interpreting Cytoskeletal Filaments in Cryo-Electron Tomograms with Shape-Constrained Deconvolution. Microscopy and Microanalysis, 2021, 27, 72-73.	0.2	0