

Slavica Jonic

List of Publications by Year in descending order

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57
papers

1,322
citations

361413

20
h-index

395702

33
g-index

62
all docs

62
docs citations

62
times ranked

1126
citing authors

#	ARTICLE	IF	CITATIONS
1	TomoFlow: Analysis of Continuous Conformational Variability of Macromolecules in Cryogenic Subtomograms based on 3D Dense Optical Flow. <i>Journal of Molecular Biology</i> , 2022, 434, 167381.	4.2	14
2	NMMD: Efficient Cryo-EM Flexible Fitting Based on Simultaneous Normal Mode and Molecular Dynamics atomic displacements. <i>Journal of Molecular Biology</i> , 2022, 434, 167483.	4.2	26
3	HEMNMA-3D: Cryo Electron Tomography Method Based on Normal Mode Analysis to Study Continuous Conformational Variability of Macromolecular Complexes. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 663121.	3.5	30
4	Advances in Xmipp for Cryo-EM Electron Microscopy: From Xmipp to Scipion. <i>Molecules</i> , 2021, 26, 6224.	3.8	22
5	Deep learning of elastic 3D shapes for cryo electron microscopy analysis of continuous conformational changes of biomolecules. , 2021, , .		3
6	Combined Bayesian and Normal Mode Flexible Fitting with Hamiltonian Monte Carlo Sampling for Cryo Electron Microscopy. , 2021, , .		1
7	Comparison between HEMNMA-3D and Traditional Classification Techniques for Analyzing Biomolecular Continuous Shape Variability in Cryo Electron Subtomograms. , 2021, , .		0
8	Hybrid Electron Microscopy Normal Mode Analysis with Scipion. <i>Protein Science</i> , 2020, 29, 223-236.	7.6	24
9	Insulin Modulates the Bioenergetic and Thermogenic Capacity of Rat Brown Adipocytes In Vivo by Modulating Mitochondrial Mosaicism. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9204.	4.1	5
10	PEBP1/RKIP behavior: a mirror of actin-membrane organization. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 859-874.	5.4	17
11	Survey of the analysis of continuous conformational variability of biological macromolecules by electron microscopy. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 19-32.	0.8	49
12	Validation of electron microscopy initial models via small angle X-ray scattering curves. <i>Bioinformatics</i> , 2019, 35, 2427-2433.	4.1	7
13	Editorial: Hybrid Biomolecular Modeling. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 98.	3.5	0
14	Poisson image denoising by piecewise principal component analysis and its application in single-particle X-ray diffraction imaging. <i>IET Image Processing</i> , 2018, 12, 2264-2274.	2.5	5
15	Single-particle XFEL 3D reconstruction of ribosome-size particles based on Fourier slice matching: requirements to reach subnanometer resolution. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1010-1021.	2.4	16
16	A methodology using Gaussian-based density map approximation to assess sets of cryo-electron microscopy density maps. <i>Journal of Structural Biology</i> , 2018, 204, 344-350.	2.8	3
17	The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018, 204, 291-300.	2.8	17
18	Computational methods for analyzing conformational variability of macromolecular complexes from cryo-electron microscopy images. <i>Current Opinion in Structural Biology</i> , 2017, 43, 114-121.	5.7	37

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19	Three-dimensional reconstruction for coherent diffraction patterns obtained by XFEL. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 727-737.	2.4	13
20	Versatility of Approximating Single-Particle Electron Microscopy Density Maps Using Pseudoatoms and Approximation-Accuracy Control. <i>BioMed Research International</i> , 2016, 2016, 1-11.	1.9	11
21	Cryo-electron Microscopy Analysis of Structurally Heterogeneous Macromolecular Complexes. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 385-390.	4.1	27
22	Denoising of high-resolution single-particle electron-microscopy density maps by their approximation using three-dimensional Gaussian functions. <i>Journal of Structural Biology</i> , 2016, 194, 423-433.	2.8	16
23	Local analysis of strains and rotations for macromolecular electron microscopy maps. <i>Journal of Structural Biology</i> , 2016, 195, 123-128.	2.8	9
24	StructMap: Elastic Distance Analysis of Electron Microscopy Maps for Studying Conformational Changes. <i>Biophysical Journal</i> , 2016, 110, 1753-1765.	0.5	25
25	Hybrid approach for structural modeling of biological systems from X-ray free electron laser diffraction patterns. <i>Journal of Structural Biology</i> , 2016, 194, 325-336.	2.8	18
26	Coarse-Graining of Volumes for Modeling of Structure and Dynamics in Electron Microscopy: Algorithm to Automatically Control Accuracy of Approximation. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2016, 10, 161-173.	10.8	30
27	Methods for studying the localization of mitochondrial complexes III and IV by immunofluorescent and immunogold microscopy. <i>Archives of Biological Sciences</i> , 2016, 68, 767-772.	0.5	7
28	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359.	2.8	34
29	Full-open and closed CFTR channels, with lateral tunnels from the cytoplasm and an alternative position of the F508 region, as revealed by molecular dynamics. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 1377-1403.	5.4	79
30	Elastic image registration to fully explore macromolecular dynamics by electron microscopy. , 2014, , .		0
31	Hybrid Electron Microscopy Normal Mode Analysis graphical interface and protocol. <i>Journal of Structural Biology</i> , 2014, 188, 134-141.	2.8	18
32	Insulin induces cristae remodeling by decreasing complex I and increasing UCP1 expression in rat brown adipose tissue. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, e26-e27.	1.0	0
33	Iterative Elastic 3D-to-2D Alignment Method Using Normal Modes for Studying Structural Dynamics of Large Macromolecular Complexes. <i>Structure</i> , 2014, 22, 496-506.	3.3	90
34	Macromolecular Dynamics by Hybrid Electron Microscopy Normal Mode Analysis. <i>Microscopy and Microanalysis</i> , 2014, 20, 1218-1219.	0.4	7
35	Conformational heterogeneity of the AAA ATPase p97 characterized by single particle cryo-EM. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C853-C853.	0.1	0
36	FASTDEF: Fast defocus and astigmatism estimation for high-throughput transmission electron microscopy. <i>Journal of Structural Biology</i> , 2013, 181, 136-148.	2.8	31

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37	3DEM Loupe: analysis of macromolecular dynamics using structures from electron microscopy. <i>Nucleic Acids Research</i> , 2013, 41, W363-W367.	14.5	14
38	Processing of Transmission Electron Microscopy Images for Single-Particle Analysis of Macromolecular Complexes. <i>Methods in Cell Biology</i> , 2012, 112, 295-310.	1.1	2
39	The Structure of Phosphorylase Kinase Holoenzyme at 9.9 Å... Resolution and Location of the Catalytic Subunit and the Substrate Glycogen Phosphorylase. <i>Structure</i> , 2009, 17, 117-127.	3.3	28
40	Protein structure determination by electron cryo-microscopy. <i>Current Opinion in Pharmacology</i> , 2009, 9, 636-642.	3.5	34
41	The Structure Of Phosphorylase Kinase Holoenzyme At Subnanometer Resolution, Location Of The Catalytic Subunit And The Substrate Glycogen Phosphorylase. <i>Biophysical Journal</i> , 2009, 96, 413a.	0.5	0
42	Comparison of single-particle analysis and electron tomography approaches: an overview. <i>Journal of Microscopy</i> , 2008, 232, 562-579.	1.8	25
43	3D mapping of glycogenosis-causing mutations in the large regulatory alpha subunit of phosphorylase kinase. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2008, 1782, 664-670.	3.8	19
44	The Subnanometer Resolution Structure of the Glutamate Synthase 1.2-MDa Hexamer by Cryoelectron Microscopy and Its Oligomerization Behavior in Solution. <i>Journal of Biological Chemistry</i> , 2008, 283, 8237-8249.	3.4	30
45	A novel method for improvement of visualization of power spectra for sorting cryo-electron micrographs and their local areas. <i>Journal of Structural Biology</i> , 2007, 157, 156-167.	2.8	20
46	Fast, robust, and accurate determination of transmission electron microscopy contrast transfer function. <i>Journal of Structural Biology</i> , 2007, 160, 249-262.	2.8	47
47	Radiation-Induced Synthesis and Cryo-TEM Characterization of Silver Nanoshells on Linoleate Spherical Micelles. <i>Langmuir</i> , 2007, 23, 9523-9526.	3.5	16
48	3D electron microscopy of biological nanomachines: principles and applications. <i>European Biophysics Journal</i> , 2007, 36, 995-1013.	2.2	13
49	An Optimized Spline-Based Registration of a 3D CT to a Set of C-Arm Images. <i>International Journal of Biomedical Imaging</i> , 2006, 2006, 1-12.	3.9	12
50	Spline-based image-to-volume registration for three-dimensional electron microscopy. <i>Ultramicroscopy</i> , 2005, 103, 303-317.	1.9	26
51	Spectral signal-to-noise ratio and resolution assessment of 3D reconstructions. <i>Journal of Structural Biology</i> , 2005, 149, 243-255.	2.8	51
52	A multiresolution approach to orientation assignment in 3D electron microscopy of single particles. <i>Journal of Structural Biology</i> , 2004, 146, 381-392.	2.8	40
53	Multiresolution-based registration of a volume to a set of its projections. , 2003, , .		9
54	<title>Multiresolution spline-based 3D/2D registration of CT volume and C-arm images for computer-assisted surgery</title>. , 2001, , .		5

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55	Automatic synthesis of synergies for control of reaching â€” hierarchical clustering. Medical Engineering and Physics, 1999, 21, 329-341.	1.7	6
56	Three machine learning techniques for automatic determination of rules to control locomotion. IEEE Transactions on Biomedical Engineering, 1999, 46, 300-310.	4.2	97
57	Optimal control of walking with functional electrical stimulation: a computer simulation study. IEEE Transactions on Rehabilitation Engineering: A Publication of the IEEE Engineering in Medicine and Biology Society, 1999, 7, 69-79.	1.4	124