

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	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
2	Three machine learning techniques for automatic determination of rules to control locomotion. IEEE Transactions on Biomedical Engineering, 1999, 46, 300-310.	4.2	97
3	Iterative Elastic 3D-to-2D Alignment Method Using Normal Modes for Studying Structural Dynamics of Large Macromolecular Complexes. Structure, 2014, 22, 496-506.	3.3	90
4	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. Cellular and Molecular Life Sciences, 2015, 72, 1377-1403.	5.4	79
5	Spectral signal-to-noise ratio and resolution assessment of 3D reconstructions. Journal of Structural Biology, 2005, 149, 243-255.	2.8	51
6	Survey of the analysis of continuous conformational variability of biological macromolecules by electron microscopy. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 19-32.	0.8	49
7	Fast, robust, and accurate determination of transmission electron microscopy contrast transfer function. Journal of Structural Biology, 2007, 160, 249-262.	2.8	47
8	A multiresolution approach to orientation assignment in 3D electron microscopy of single particles. Journal of Structural Biology, 2004, 146, 381-392.	2.8	40
9	Computational methods for analyzing conformational variability of macromolecular complexes from cryo-electron microscopy images. Current Opinion in Structural Biology, 2017, 43, 114-121.	5.7	37
10	Protein structure determination by electron cryo-microscopy. Current Opinion in Pharmacology, 2009, 9, 636-642.	3.5	34
11	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	2.8	34
12	FASTDEF: Fast defocus and astigmatism estimation for high-throughput transmission electron microscopy. Journal of Structural Biology, 2013, 181, 136-148.	2.8	31
13	The Subnanometer Resolution Structure of the Glutamate Synthase 1.2-MDa Hexamer by Cryoelectron Microscopy and Its Oligomerization Behavior in Solution. Journal of Biological Chemistry, 2008, 283, 8237-8249.	3.4	30
14	Coarse-Graining of Volumes for Modeling of Structure and Dynamics in Electron Microscopy: Algorithm to Automatically Control Accuracy of Approximation. IEEE Journal on Selected Topics in Signal Processing, 2016, 10, 161-173.	10.8	30
15	HEMNMA-3D: Cryo Electron Tomography Method Based on Normal Mode Analysis to Study Continuous Conformational Variability of Macromolecular Complexes. Frontiers in Molecular Biosciences, 2021, 8, 663121.	3.5	30
16	The Structure of Phosphorylase Kinase Holoenzyme at 9.9 Å... Resolution and Location of the Catalytic Subunit and the Substrate Glycogen Phosphorylase. Structure, 2009, 17, 117-127.	3.3	28
17	Cryo-electron Microscopy Analysis of Structurally Heterogeneous Macromolecular Complexes. Computational and Structural Biotechnology Journal, 2016, 14, 385-390.	4.1	27
18	Spline-based image-to-volume registration for three-dimensional electron microscopy. Ultramicroscopy, 2005, 103, 303-317.	1.9	26

#	ARTICLE	IF	CITATIONS
19	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
20	Comparison of single-particle analysis and electron tomography approaches: an overview. <i>Journal of Microscopy</i> , 2008, 232, 562-579.	1.8	25
21	StructMap: Elastic Distance Analysis of Electron Microscopy Maps for Studying Conformational Changes. <i>Biophysical Journal</i> , 2016, 110, 1753-1765.	0.5	25
22	Hybrid Electron Microscopy Normal Mode Analysis with Scipion. <i>Protein Science</i> , 2020, 29, 223-236.	7.6	24
23	Advances in Xmipp for Cryo-EM Electron Microscopy: From Xmipp to Scipion. <i>Molecules</i> , 2021, 26, 6224.	3.8	22
24	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
25	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
26	Hybrid Electron Microscopy Normal Mode Analysis graphical interface and protocol. <i>Journal of Structural Biology</i> , 2014, 188, 134-141.	2.8	18
27	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
28	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
29	PEBP1/RKIP behavior: a mirror of actin-membrane organization. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 859-874.	5.4	17
30	Radiation-Induced Synthesis and Cryo-TEM Characterization of Silver Nanoshells on Linoleate Spherical Micelles. <i>Langmuir</i> , 2007, 23, 9523-9526.	3.5	16
31	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
32	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
33	3DEM Loupe: analysis of macromolecular dynamics using structures from electron microscopy. <i>Nucleic Acids Research</i> , 2013, 41, W363-W367.	14.5	14
34	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
35	3D electron microscopy of biological nanomachines: principles and applications. <i>European Biophysics Journal</i> , 2007, 36, 995-1013.	2.2	13
36	Three-dimensional reconstruction for coherent diffraction patterns obtained by XFEL. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 727-737.	2.4	13

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37	An Optimized Spline-Based Registration of a 3D CT to a Set of C-Arm Images. International Journal of Biomedical Imaging, 2006, 2006, 1-12.	3.9	12
38	Versatility of Approximating Single-Particle Electron Microscopy Density Maps Using Pseudoatoms and Approximation-Accuracy Control. BioMed Research International, 2016, 2016, 1-11.	1.9	11
39	Multiresolution-based registration of a volume to a set of its projections. , 2003, , .		9
40	Local analysis of strains and rotations for macromolecular electron microscopy maps. Journal of Structural Biology, 2016, 195, 123-128.	2.8	9
41	Macromolecular Dynamics by Hybrid Electron Microscopy Normal Mode Analysis. Microscopy and Microanalysis, 2014, 20, 1218-1219.	0.4	7
42	Validation of electron microscopy initial models via small angle X-ray scattering curves. Bioinformatics, 2019, 35, 2427-2433.	4.1	7
43	Methods for studying the localization of mitochondrial complexes III and IV by immunofluorescent and immunogold microscopy. Archives of Biological Sciences, 2016, 68, 767-772.	0.5	7
44	Automatic synthesis of synergies for control of reaching " hierarchical clustering. Medical Engineering and Physics, 1999, 21, 329-341.	1.7	6
45	Poisson image denoising by piecewise principal component analysis and its application in single-particle X-ray diffraction imaging. IET Image Processing, 2018, 12, 2264-2274.	2.5	5
46	Insulin Modulates the Bioenergetic and Thermogenic Capacity of Rat Brown Adipocytes In Vivo by Modulating Mitochondrial Mosaicism. International Journal of Molecular Sciences, 2020, 21, 9204.	4.1	5
47	<title>Multiresolution spline-based 3D/2D registration of CT volume and C-arm images for computer-assisted surgery</title>. , 2001, , .		5
48	A methodology using Gaussian-based density map approximation to assess sets of cryo-electron microscopy density maps. Journal of Structural Biology, 2018, 204, 344-350.	2.8	3
49	Deep learning of elastic 3D shapes for cryo electron microscopy analysis of continuous conformational changes of biomolecules. , 2021, , .		3
50	Processing of Transmission Electron Microscopy Images for Single-Particle Analysis of Macromolecular Complexes. Methods in Cell Biology, 2012, 112, 295-310.	1.1	2
51	Combined Bayesian and Normal Mode Flexible Fitting with Hamiltonian Monte Carlo Sampling for Cryo Electron Microscopy. , 2021, , .		1
52	The Structure Of Phosphorylase Kinase Holoenzyme At Subnanometer Resolution, Location Of The Catalytic Subunit And The Substrate Glycogen Phosphorylase. Biophysical Journal, 2009, 96, 413a.	0.5	0
53	Elastic image registration to fully explore macromolecular dynamics by electron microscopy. , 2014, , .		0
54	Insulin induces cristae remodeling by decreasing complex I and increasing UCP1 expression in rat brown adipose tissue. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, e26-e27.	1.0	0

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55	Editorial: Hybrid Biomolecular Modeling. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 98.	3.5	0
56	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
57	Comparison between HEMNMA-3D and Traditional Classification Techniques for Analyzing Biomolecular Continuous Shape Variability in Cryo Electron Subtomograms. , 2021, , .		0