

Min Xu

List of Publications by Year in descending order

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62
papers

806
citations

567281

15
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610901

24
g-index

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all docs

64
docs citations

64
times ranked

757
citing authors

#	ARTICLE	IF	CITATIONS
1	Learn to segment single cells with deep distance estimator and deep cell detector. <i>Computers in Biology and Medicine</i> , 2019, 108, 133-141.	7.0	59
2	High-throughput subtomogram alignment and classification by Fourier space constrained fast volumetric matching. <i>Journal of Structural Biology</i> , 2012, 178, 152-164.	2.8	52
3	Improved deep learning-based macromolecules structure classification from electron cryo-tomograms. <i>Machine Vision and Applications</i> , 2018, 29, 1227-1236.	2.7	44
4	An integrative approach to characterize disease-specific pathways and their coordination: a case study in cancer. <i>BMC Genomics</i> , 2008, 9, S12.	2.8	43
5	Machine Learning (ML)-Assisted Design and Fabrication for Solar Cells. <i>Energy and Environmental Materials</i> , 2019, 2, 280-291.	12.8	43
6	A convolutional autoencoder approach for mining features in cellular electron cryo-tomograms and weakly supervised coarse segmentation. <i>Journal of Structural Biology</i> , 2018, 202, 150-160.	2.8	41
7	De Novo Structural Pattern Mining in Cellular Electron Cryotomograms. <i>Structure</i> , 2019, 27, 679-691.e14.	3.3	40
8	Template-free detection of macromolecular complexes in cryo electron tomograms. <i>Bioinformatics</i> , 2011, 27, i69-i76.	4.1	37
9	Simulating cryo electron tomograms of crowded cell cytoplasm for assessment of automated particle picking. <i>BMC Bioinformatics</i> , 2016, 17, 405.	2.6	33
10	SHREC 2020: Classification in cryo-electron tomograms. <i>Computers and Graphics</i> , 2020, 91, 279-289.	2.5	33
11	Deep learning-based subdivision approach for large scale macromolecules structure recovery from electron cryo tomograms. <i>Bioinformatics</i> , 2017, 33, i13-i22.	4.1	32
12	Automatic localization and identification of mitochondria in cellular electron cryo-tomography using faster-RCNN. <i>BMC Bioinformatics</i> , 2019, 20, 132.	2.6	25
13	Automated multidimensional phenotypic profiling using large public microarray repositories. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12323-12328.	7.1	23
14	Respond-CAM: Analyzing Deep Models for 3D Imaging Data by Visualizations. <i>Lecture Notes in Computer Science</i> , 2018, , 485-492.	1.3	23
15	High precision alignment of cryo-electron subtomograms through gradient-based parallel optimization. <i>BMC Systems Biology</i> , 2012, 6, S18.	3.0	17
16	Automated target segmentation and real space fast alignment methods for high-throughput classification and averaging of crowded cryo-electron subtomograms. <i>Bioinformatics</i> , 2013, 29, i274-i282.	4.1	13
17	Improving Lesion Segmentation for Diabetic Retinopathy Using Adversarial Learning. <i>Lecture Notes in Computer Science</i> , 2019, , 333-344.	1.3	13
18	Prolificacy Assessment of Spermatozoan via State-of-the-Art Deep Learning Frameworks. <i>IEEE Access</i> , 2022, 10, 13715-13727.	4.2	13

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19	TomoMiner and TomoMinerCloud: A Software Platform for Large-Scale Subtomogram Structural Analysis. <i>Structure</i> , 2017, 25, 951-961.e2.	3.3	12
20	Adversarial domain adaptation for cross data source macromolecule <i>in situ</i> structural classification in cellular electron cryo-tomograms. <i>Bioinformatics</i> , 2019, 35, i260-i268.	4.1	12
21	Gum-Net: Unsupervised Geometric Matching for Fast and Accurate 3D Subtomogram Image Alignment and Averaging. , 2020, 2020, 4072-4082.		10
22	SCAN-ATAC-Sim: a scalable and efficient method for simulating single-cell ATAC-seq data from bulk-tissue experiments. <i>Bioinformatics</i> , 2021, 37, 1756-1758.	4.1	9
23	Poly(A)-DG: A deep-learning-based domain generalization method to identify cross-species Poly(A) signal without prior knowledge from target species. <i>PLoS Computational Biology</i> , 2020, 16, e1008297.	3.2	9
24	AttPNet: Attention-Based Deep Neural Network for 3D Point Set Analysis. <i>Sensors</i> , 2020, 20, 5455.	3.8	8
25	Active learning to classify macromolecular structures <i>in situ</i> for less supervision in cryo-electron tomography. <i>Bioinformatics</i> , 2021, 37, 2340-2346.	4.1	8
26	DECODE: a deep-learning framework for <i>Conc</i> nsing enhancers and refining boundaries with large-scale functional assays. <i>Bioinformatics</i> , 2021, 37, i280-i288.	4.1	8
27	One-Shot Learning With Attention-Guided Segmentation in Cryo-Electron Tomography. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 613347.	3.5	8
28	Deep Learning Based Supervised Semantic Segmentation of Electron Cryo-Subtomograms. , 2018, , .		7
29	An integration of fast alignment and maximum-likelihood methods for electron subtomogram averaging and classification. <i>Bioinformatics</i> , 2018, 34, i227-i236.	4.1	7
30	A joint method for marker-free alignment of tilt series in electron tomography. <i>Bioinformatics</i> , 2019, 35, i249-i259.	4.1	7
31	Model Compression for Faster Structural Separation of Macromolecules Captured by Cellular Electron Cryo-Tomography. <i>Lecture Notes in Computer Science</i> , 2018, 10882, 144-152.	1.3	6
32	Deep Learning-Based Strategy For Macromolecules Classification with Imbalanced Data from Cellular Electron Cryotomography. , 2019, , .		6
33	Few-shot learning for classification of novel macromolecular structures in cryo-electron tomograms. <i>PLoS Computational Biology</i> , 2020, 16, e1008227.	3.2	6
34	Deep Learning Predicts EBV Status in Gastric Cancer Based on Spatial Patterns of Lymphocyte Infiltration. <i>Cancers</i> , 2021, 13, 6002.	3.7	6
35	Weakly Supervised 3D Semantic Segmentation Using Cross-Image Consensus and Inter-Voxel Affinity Relations. , 2021, 2021, 2814-2824.		6
36	Feature Decomposition Based Saliency Detection in Electron Cryo-Tomograms. , 2018, 2018, 2467-2473.		5

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37	Fine-grained alignment of cryo-electron subtomograms based on MPI parallel optimization. BMC Bioinformatics, 2019, 20, 443.	2.6	5
38	A unified framework for packing deformable and non-deformable subcellular structures in crowded cryo-electron tomogram simulation. BMC Bioinformatics, 2020, 21, 399.	2.6	5
39	Macromolecules Structural Classification With a 3D Dilated Dense Network in Cryo-Electron Tomography. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 209-219.	3.0	5
40	A survey of deep learning-based methods for cryo-electron tomography data analysis. , 2021, , 63-72.		5
41	Deep-Precognitive Diagnosis: Preventing Future Pandemics by Novel Disease Detection With Biologically-Inspired Conv-Fuzzy Network. IEEE Access, 2022, 10, 23167-23185.	4.2	5
42	3D Rotation Invariant Features for the Characterization of Molecular Density Maps. , 2009, , .		4
43	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. Statistics in Biosciences, 2012, 4, 157-176.	1.2	4
44	Dilated-DenseNet for Macromolecule Classification in Cryo-electron Tomography. Lecture Notes in Computer Science, 2020, 12304, 82-94.	1.3	4
45	Template-Based and Template-Free Approaches in Cellular Cryo-Electron Tomography Structural Pattern Mining. , 0, , 175-186.		4
46	A stable iterative method for refining discriminative gene clusters. BMC Genomics, 2008, 9, S18.	2.8	3
47	Domain Randomization for Macromolecule Structure Classification and Segmentation in Electron Cyro-tomograms. , 2019, , .		3
48	PUB-SalNet: A Pre-Trained Unsupervised Self-Aware Backpropagation Network for Biomedical Salient Segmentation. Algorithms, 2020, 13, 126.	2.1	3
49	Few shot domain adaptation for <i>in situ</i> macromolecule structural classification in cryoelectron tomograms. Bioinformatics, 2021, 37, 185-191.	4.1	3
50	End-to-end robust joint unsupervised image alignment and clustering. , 2021, 2021, 3834-3846.		3
51	Deep Inductive Matrix Completion for Biomedical Interaction Prediction. , 2019, , .		2
52	Unsupervised Domain Alignment Based Open Set Structural Recognition of Macromolecules Captured By Cryo-Electron Tomography. , 2021, 2021, 106-110.		2
53	CryoETGAN: Cryo-Electron Tomography Image Synthesis via Unpaired Image Translation. Frontiers in Physiology, 2022, 13, 760404.	2.8	2
54	Cryo-shift: reducing domain shift in cryo-electron subtomograms with unsupervised domain adaptation and randomization. Bioinformatics, 2022, 38, 977-984.	4.1	2

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55	FSCC: Few-Shot Learning for Macromolecule Classification Based on Contrastive Learning and Distribution Calibration in Cryo-Electron Tomography. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	2
56	Spark-based parallel calculation of 3D fourier shell correlation for macromolecule structure local resolution estimation. <i>BMC Bioinformatics</i> , 2020, 21, 391.	2.6	1
57	A simulated annealing approach for resolution guided homogeneous cryo-electron microscopy image selection. <i>Quantitative Biology</i> , 2020, 8, 51-63.	0.5	1
58	InsuLock: A Weakly Supervised Learning Approach for Accurate Insulator Prediction, and Variant Impact Quantification. <i>Genes</i> , 2022, 13, 621.	2.4	1
59	Practical Analysis of Macromolecule Identity from Cryo-electron Tomography Images using Deep Learning. , 2021, , .		1
60	A Robust Method for Generating Discriminative Gene Clusters. , 2007, , .		0
61	Regularized Adversarial Training (RAT) for Robust Cellular Electron Cryo Tomograms Classification. , 2019, , .		0
62	Automatic analysis of cryo-electron tomography using computer vision and machine learning. <i>Microscopy and Microanalysis</i> , 2021, 27, 80-81.	0.4	0