Min Xu

List of Publications by Year
in descending order

62 papers	806 citations	567281 15 h-index	610901 24 g-index
64 all docs	64 docs citations	64 times ranked	757 citing authors

#	Article	IF	Citations
1	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
2	Prolificacy Assessment of Spermatozoan via State-of-the-Art Deep Learning Frameworks. IEEE Access, 2022, 10, 13715-13727.	4.2	13
3	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
4	CryoETGAN: Cryo-Electron Tomography Image Synthesis via Unpaired Image Translation. Frontiers in Physiology, 2022, 13, 760404.	2.8	2
5	InsuLock: A Weakly Supervised Learning Approach for Accurate Insulator Prediction, and Variant Impact Quantification. Genes, 2022, 13, 621.	2.4	1
6	Cryo-shift: reducing domain shift in cryo-electron subtomograms with unsupervised domain adaptation and randomization. Bioinformatics, 2022, 38, 977-984.	4.1	2
7	Few shot domain adaptation for *in situ* macromolecule structural classification in cryoelectron tomograms. Bioinformatics, 2021, 37, 185-191.	4.1	3
8	SCAN-ATAC-Sim: a scalable and efficient method for simulating single-cell ATAC-seq data from bulk-tissue experiments. Bioinformatics, 2021, 37, 1756-1758.	4.1	9
9	Active learning to classify macromolecular structures *in situ* for less supervision in cryo-electron tomography. Bioinformatics, 2021, 37, 2340-2346.	4.1	8
10	Automatic analysis of cryo-electron tomography using computer vision and machine learning. Microscopy and Microanalysis, 2021, 27, 80-81.	0.4	0
11	DECODE: a *De*ep-learning framework for *Co*n*de*nsing enhancers and refining boundaries with large-scale functional assays. Bioinformatics, 2021, 37, i280-i288.	4.1	8
12	Unsupervised Domain Alignment Based Open Set Structural Recognition of Macromolecules Captured By Cryo-Electron Tomography. , 2021, 2021, 106-110.		2
13	A survey of deep learning-based methods for cryo-electron tomography data analysis. , 2021, , 63-72.		5
14	Deep Learning Predicts EBV Status in Gastric Cancer Based on Spatial Patterns of Lymphocyte Infiltration. Cancers, 2021, 13, 6002.	3.7	6
15	Weakly Supervised 3D Semantic Segmentation Using Cross-Image Consensus and Inter-Voxel Affinity Relations. , 2021, 2021, 2814-2824.		6
16	End-to-end robust joint unsupervised image alignment and clustering. , 2021, 2021, 3834-3846.		3
17	Practical Analysis of Macromolecule Identity from Cryo-electron Tomography Images using Deep Learning. , 2021, , .		1
18	AttPNet: Attention-Based Deep Neural Network for 3D Point Set Analysis. Sensors, 2020, 20, 5455.	3.8	8

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19	PUB-SalNet: A Pre-Trained Unsupervised Self-Aware Backpropagation Network for Biomedical Salient Segmentation. Algorithms, 2020, 13, 126.	2.1	3
20	SHREC 2020: Classification in cryo-electron tomograms. Computers and Graphics, 2020, 91, 279-289.	2.5	33
21	Gum-Net: Unsupervised Geometric Matching for Fast and Accurate 3D Subtomogram Image Alignment and Averaging. , 2020, 2020, 4072-4082.		10
22	Spark-based parallel calculation of 3D fourier shell correlation for macromolecule structure local resolution estimation. BMC Bioinformatics, 2020, 21, 391.	2.6	1
23	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
24	A simulated annealing approach for resolution guided homogeneous cryo–electron microscopy image selection. Quantitative Biology, 2020, 8, 51-63.	0.5	1
25	One-Shot Learning With Attention-Guided Segmentation in Cryo-Electron Tomography. Frontiers in Molecular Biosciences, 2020, 7, 613347.	3.5	8
26	Dilated-DenseNet for Macromolecule Classification in Cryo-electron Tomography. Lecture Notes in Computer Science, 2020, 12304, 82-94.	1.3	4
27	Few-shot learning for classification of novel macromolecular structures in cryo-electron tomograms. PLoS Computational Biology, 2020, 16, e1008227.	3.2	6
28	Poly(A)-DG: A deep-learning-based domain generalization method to identify cross-species Poly(A) signal without prior knowledge from target species. PLoS Computational Biology, 2020, 16, e1008297.	3.2	9
29	Improving Lesion Segmentation for Diabetic Retinopathy Using Adversarial Learning. Lecture Notes in Computer Science, 2019, , 333-344.	1.3	13
30	A joint method for marker-free alignment of tilt series in electron tomography. Bioinformatics, 2019, 35, i249-i259.	4.1	7
31	Adversarial domain adaptation for cross data source macromolecule <i>in situ</i> structural classification in cellular electron cryo-tomograms. Bioinformatics, 2019, 35, i260-i268.	4.1	12
32	Machine Learning (ML)–Assisted Design and Fabrication for Solar Cells. Energy and Environmental Materials, 2019, 2, 280-291.	12.8	43
33	Fine-grained alignment of cryo-electron subtomograms based on MPI parallel optimization. BMC Bioinformatics, 2019, 20, 443.	2.6	5
34	Learn to segment single cells with deep distance estimator and deep cell detector. Computers in Biology and Medicine, 2019, 108, 133-141.	7.0	59
35	Automatic localization and identification of mitochondria in cellular electron cryo-tomography using faster-RCNN. BMC Bioinformatics, 2019, 20, 132.	2.6	25
36	De Novo Structural Pattern Mining in Cellular Electron Cryotomograms. Structure, 2019, 27, 679-691.e14.	3.3	40

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37	Deep Inductive Matrix Completion for Biomedical Interaction Prediction. , 2019, , .		2
38	Domain Randomization for Macromolecule Structure Classification and Segmentation in Electron Cyro-tomograms. , 2019, , .		3
39	Regularized Adversarial Training (RAT) for Robust Cellular Electron Cryo Tomograms Classification. , 2019, , .		0
40	Deep Learning-Based Strategy For Macromolecules Classification with Imbalanced Data from Cellular Electron Cryotomography. , 2019, , .		6
41	A convolutional autoencoder approach for mining features in cellular electron cryo-tomograms and weakly supervised coarse segmentation. Journal of Structural Biology, 2018, 202, 150-160.	2.8	41
42	Deep Learning Based Supervised Semantic Segmentation of Electron Cryo-Subtomograms. , 2018, , .		7
43	Feature Decomposition Based Saliency Detection in Electron Cryo-Tomograms. , 2018, 2018, 2467-2473.		5
44	An integration of fast alignment and maximum-likelihood methods for electron subtomogram averaging and classification. Bioinformatics, 2018, 34, i227-i236.	4.1	7
45	Improved deep learning-based macromolecules structure classification from electron cryo-tomograms. Machine Vision and Applications, 2018, 29, 1227-1236.	2.7	44
46	Model Compression for Faster Structural Separation of Macromolecules Captured by Cellular Electron Cryo-Tomography. Lecture Notes in Computer Science, 2018, 10882, 144-152.	1.3	6
47	Respond-CAM: Analyzing Deep Models for 3D Imaging Data by Visualizations. Lecture Notes in Computer Science, 2018, , 485-492.	1.3	23
48	TomoMiner and TomoMinerCloud: A Software Platform for Large-Scale Subtomogram Structural Analysis. Structure, 2017, 25, 951-961.e2.	3.3	12
49	Deep learning-based subdivision approach for large scale macromolecules structure recovery from electron cryo tomograms. Bioinformatics, 2017, 33, i13-i22.	4.1	32
50	Simulating cryo electron tomograms of crowded cell cytoplasm for assessment of automated particle picking. BMC Bioinformatics, 2016, 17, 405.	2.6	33
51	Automated target segmentation and real space fast alignment methods for high-throughput classification and averaging of crowded cryo-electron subtomograms. Bioinformatics, 2013, 29, i274-i282.	4.1	13
52	High-throughput subtomogram alignment and classification by Fourier space constrained fast volumetric matching. Journal of Structural Biology, 2012, 178, 152-164.	2.8	52
53	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. Statistics in Biosciences, 2012, 4, 157-176.	1.2	4
54	High precision alignment of cryo-electron subtomograms through gradient-based parallel optimization. BMC Systems Biology, 2012, 6, S18.	3.0	17

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55	Template-free detection of macromolecular complexes in cryo electron tomograms. Bioinformatics, 2011, 27, i69-i76.	4.1	37
56	Automated multidimensional phenotypic profiling using large public microarray repositories. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12323-12328.	7.1	23
57	3D Rotation Invariant Features for the Characterization of Molecular Density Maps. , 2009, , .		4
58	An integrative approach to characterize disease-specific pathways and their coordination: a case study in cancer. BMC Genomics, 2008, 9, S12.	2.8	43
59	A stable iterative method for refining discriminative gene clusters. BMC Genomics, 2008, 9, S18.	2.8	3
60	A Robust Method for Generating Discriminative Gene Clusters. , 2007, , .		0
61	Template-Based and Template-Free Approaches in Cellular Cryo-Electron Tomography Structural Pattern Mining. , 0, , 175-186.		4
62	FSCC: Few-Shot Learning for Macromolecule Classification Based on Contrastive Learning and Distribution Calibration in Cryo-Electron Tomography. Frontiers in Molecular Biosciences, 0, 9, .	3.5	2