Ao Li

List of Publications by Year
in descending order

94 papers	2,496 citations	218677 26 h-index	223800 46 g-index
96 all docs	96 docs citations	96 times ranked	2754 citing authors

#	Article	IF	Citations
1	A Multimodal Deep Neural Network for Human Breast Cancer Prognosis Prediction by Integrating Multi-Dimensional Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 841-850.	3.0	195
2	PPSP: prediction of PK-specific phosphorylation site with Bayesian decision theory. BMC Bioinformatics, 2006, 7, 163.	2.6	183
3	DeepPhos: prediction of protein phosphorylation sites with deep learning. Bioinformatics, 2019, 35, 2766-2773.	4.1	132
4	A novel end-to-end brain tumor segmentation method using improved fully convolutional networks. Computers in Biology and Medicine, 2019, 108, 150-160.	7.0	124
5	TPGLDA: Novel prediction of associations between lncRNAs and diseases via lncRNA-disease-gene tripartite graph. Scientific Reports, 2018, 8, 1065.	3.3	97
6	A Bipartite Network-based Method for Prediction of Long Non-coding RNAâ€“protein Interactions. Genomics, Proteomics and Bioinformatics, 2016, 14, 62-71.	6.9	88
7	Integrating genomic data and pathological images to effectively predict breast cancer clinical outcome. Computer Methods and Programs in Biomedicine, 2018, 161, 45-53.	4.7	84
8	GPHMM: an integrated hidden Markov model for identification of copy number alteration and loss of heterozygosity in complex tumor samples using whole genome SNP arrays. Nucleic Acids Research, 2011, 39, 4928-4941.	14.5	76
9	Predicting Long Noncoding RNA and Protein Interactions Using Heterogeneous Network Model. BioMed Research International, 2015, 2015, 1-11.	1.9	73
10	A novel heterogeneous network-based method for drug response prediction in cancer cell lines. Scientific Reports, 2018, 8, 3355.	3.3	72
11	NTSMDA: prediction of miRNAâ€“disease associations by integrating network topological similarity. Molecular BioSystems, 2016, 12, 2224-2232.	2.9	66
12	Improve Glioblastoma Multiforme Prognosis Prediction by Using Feature Selection and Multiple Kernel Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 825-835.	3.0	62
13	A novel approach for drug response prediction in cancer cell lines via network representation learning. Bioinformatics, 2019, 35, 1527-1535.	4.1	58
14	Prediction of protein kinase-specific phosphorylation sites in hierarchical structure using functional information and random forest. Amino Acids, 2014, 46, 1069-1078.	2.7	55
15	LncReg: a reference resource for lncRNA-associated regulatory networks. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav083.	3.0	55
16	Inferring subgroup-specific driver genes from heterogeneous cancer samples via subspace learning with subgroup indication. Bioinformatics, 2020, 36, 1855-1863.	4.1	53
17	IsomiR Bank: a research resource for tracking IsomiRs. Bioinformatics, 2016, 32, 2069-2071.	4.1	52
18	A gene signature for breast cancer prognosis using support vector machine. , 2012, , .		49

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19	PTM-ssMP: A Web Server for Predicting Different Types of Post-translational Modification Sites Using Novel Site-specific Modification Profile. International Journal of Biological Sciences, 2018, 14, 946-956.	6.4	45
20	CLImAT: accurate detection of copy number alteration and loss of heterozygosity in impure and aneuploid tumor samples using whole-genome sequencing data. Bioinformatics, 2014, 30, 2576-2583.	4.1	43
21	DeAnnIso: a tool for online detection and annotation of isomiRs from small RNA sequencing data. Nucleic Acids Research, 2016, 44, W166-W175.	14.5	41
22	CapSurv: Capsule Network for Survival Analysis With Whole Slide Pathological Images. IEEE Access, 2019, 7, 26022-26030.	4.2	40
23	GPDBN: deep bilinear network integrating both genomic data and pathological images for breast cancer prognosis prediction. Bioinformatics, 2021, 37, 2963-2970.	4.1	39
24	PhosIDN: an integrated deep neural network for improving protein phosphorylation site prediction by combining sequence and proteinâ€“protein interaction information. Bioinformatics, 2021, 37, 4668-4676.	4.1	37
25	MixHMM: Inferring Copy Number Variation and Allelic Imbalance Using SNP Arrays and Tumor Samples Mixed with Stromal Cells. PLoS ONE, 2010, 5, e10909.	2.5	30
26	DeAnnCNV: a tool for online detection and annotation of copy number variations from whole-exome sequencing data. Nucleic Acids Research, 2015, 43, W289-W294.	14.5	29
27	LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 189-197.	3.0	29
28	CloneCNA: detecting subclonal somatic copy number alterations in heterogeneous tumor samples from whole-exome sequencing data. BMC Bioinformatics, 2016, 17, 310.	2.6	27
29	GANcon: Protein Contact Map Prediction With Deep Generative Adversarial Network. IEEE Access, 2020, 8, 80899-80907.	4.2	25
30	Discovering Recurrent Copy Number Aberrations in Complex Patterns via Non-Negative Sparse Singular Value Decomposition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 656-668.	3.0	24
31	Discovering mutated driver genes through a robust and sparse co-regularized matrix factorization framework with prior information from mRNA expression patterns and interaction network. BMC Bioinformatics, 2018, 19, 214.	2.6	24
32	A Novel MKL Method for GBM Prognosis Prediction by Integrating Histopathological Image and Multi-Omics Data. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 171-179.	6.3	23
33	CSCdb: a cancer stem cells portal for markers, related genes and functional information. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw023.	3.0	21
34	Gene Expression Profiling Reveals Distinct Molecular Subtypes of Esophageal Squamous Cell Carcinoma in Asian Populations. Neoplasia, 2019, 21, 571-581.	5.3	21
35	Discovering potential driver genes through an integrated model of somatic mutation profiles and gene functional information. Molecular BioSystems, 2017, 13, 2135-2144.	2.9	20
36	HetRCNA: A Novel Method to Identify Recurrent Copy Number Alternations from Heterogeneous Tumor Samples Based on Matrix Decomposition Framework. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 422-434.	3.0	20

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37	Reconstruction and Analysis of Transcription Factorâ€“miRNA Co-Regulatory Feed-Forward Loops in Human Cancers Using Filter-Wrapper Feature Selection. PLoS ONE, 2013, 8, e78197.	2.5	20
38	A Kinect based gesture recognition algorithm using GMM and HMM. , 2013, , .		19
39	Human Action Recognition Based on Depth Images from Microsoft Kinect. , 2013, , .		19
40	CLImAT-HET: detecting subclonal copy number alterations and loss of heterozygosity in heterogeneous tumor samples from whole-genome sequencing data. BMC Medical Genomics, 2017, 10, 15.	1.5	19
41	DeepTL-Ubi: A novel deep transfer learning method for effectively predicting ubiquitination sites of multiple species. Methods, 2021, 192, 103-111.	3.8	18
42	HFBSurv: hierarchical multimodal fusion with factorized bilinear models for cancer survival prediction. Bioinformatics, 2022, 38, 2587-2594.	4.1	18
43	A text feature-based approach for literature mining of lncRNAâ€“protein interactions. Neurocomputing, 2016, 206, 73-80.	5.9	16
44	Semi-HIC: A novel semi-supervised deep learning method for histopathological image classification. Computers in Biology and Medicine, 2021, 137, 104788.	7.0	15
45	Multimodal Deep Reinforcement Learning with Auxiliary Task for Obstacle Avoidance of Indoor Mobile Robot. Sensors, 2021, 21, 1363.	3.8	14
46	Discovery of Bladder Cancer-related Genes Using Integrative Heterogeneous Network Modeling of Multi-omics Data. Scientific Reports, 2017, 7, 15639.	3.3	13
47	A genome-wide association study of Alzheimerâ€™s disease using random forests and enrichment analysis. Science China Life Sciences, 2012, 55, 618-625.	4.9	12
48	Prognosis prediction of human breast cancer by integrating deep neural network and support vector machine: Supervised feature extraction and classification for breast cancer prognosis prediction. , 2017, , .		12
49	Prediction of post-translational modification sites using multiple kernel support vector machine. PeerJ, 2017, 5, e3261.	2.0	12
50	Prediction of human diseaseâ€associated phosphorylation sites with combined feature selection approach and support vector machine. IET Systems Biology, 2015, 9, 155-163.	1.5	11
51	A Heterogeneous Network Based Method for Identifying GBM-Related Genes by Integrating Multi-Dimensional Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 713-720.	3.0	11
52	A novel method for identifying potential disease-related miRNAs via a diseaseâ€“miRNAâ€“target heterogeneous network. Molecular BioSystems, 2017, 13, 2328-2337.	2.9	11
53	A novel network regularized matrix decomposition method to detect mutated cancer genes in tumour samples with inter-patient heterogeneity. Scientific Reports, 2017, 7, 2855.	3.3	10
54	Systematic Analysis and Prediction ofIn SituCross Talk of O-GlcNAcylation and Phosphorylation. BioMed Research International, 2015, 2015, 1-12.	1.9	9

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55	A Novel Phosphorylation Site-Kinase Network-Based Method for the Accurate Prediction of Kinase-Substrate Relationships. BioMed Research International, 2017, 2017, 1-11.	1.9	9
56	Anaconda: AN automated pipeline for somatic COpy Number variation Detection and Annotation from tumor exome sequencing data. BMC Bioinformatics, 2017, 18, 436.	2.6	9
57	Genome-Wide Identification of Somatic Aberrations from Paired Normal-Tumor Samples. PLoS ONE, 2014, 9, e87212.	2.5	8
58	Reconstruction-Assisted Feature Encoding Network for Histologic Subtype Classification of Non-Small Cell Lung Cancer. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 4563-4574.	6.3	8
59	MPTM: A tool for mining protein post-translational modifications from literature. Journal of Bioinformatics and Computational Biology, 2017, 15, 1740005.	0.8	7
60	Adversarially Regularized U-Net-based GANs for Facial Attribute Modification and Generation. IEEE Access, 2019, 7, 86453-86462.	4.2	6
61	High Sensitive and Non-invasive ctDNAs Sequencing Facilitate Clinical Diagnosis And Clinical Guidance of Non-small Cell Lung Cancer Patient: A Time Course Study. Frontiers in Oncology, 2018, 8, 491.	2.8	5
62	LSCDFS-MKL: A multiple kernel based method for lung squamous cell carcinomas disease-free survival prediction with pathological and genomic data. Journal of Biomedical Informatics, 2019, 94, 103194.	4.3	5
63	TSDLPP: A Novel Two-Stage Deep Learning Framework For Prognosis Prediction Based on Whole Slide Histopathological Images. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2523-2532.	3.0	5
64	Kinase Identification with Supervised Laplacian Regularized Least Squares. PLoS ONE, 2015, 10, e0139676.	2.5	5
65	ksrMKL: a novel method for identification of kinaseâ€“substrate relationships using multiple kernel learning. PeerJ, 2017, 5, e4182.	2.0	5
66	Literature mining of protein phosphorylation using dependency parse trees. Methods, 2014, 67, 386-393.	3.8	4
67	RPdb: a database of experimentally verified cellular reprogramming records. Bioinformatics, 2015, 31, 3237-3239.	4.1	4
68	Prediction of interactions between lncRNA and protein by using relevance search in a heterogeneous lncRNA-protein network. , 2015, , .		4
69	Learning rich features with hybrid loss for brain tumor segmentation. BMC Medical Informatics and Decision Making, 2021, 21, 63.	3.0	4
70	DGPathinter: a novel model for identifying driver genes via knowledge-driven matrix factorization with prior knowledge from interactome and pathways. PeerJ Computer Science, 0, 3, e133.	4.5	4
71	AIR-Net: A novel multi-task learning method with auxiliary image reconstruction for predicting EGFR mutation status on CT images of NSCLC patients. Computers in Biology and Medicine, 2022, 141, 105157.	7.0	4
72	miRNA Target Prediction Based on Gene Ontology. , 2013, , .		3

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73	TAFFYS: An Integrated Tool for Comprehensive Analysis of Genomic Aberrations in Tumor Samples. PLoS ONE, 2015, 10, e0129835.	2.5	2
74	A novel framework for analyzing somatic copy number aberrations and tumor subclones for paired heterogeneous tumor samples. Bio-Medical Materials and Engineering, 2015, 26, S1845-S1853.	0.6	2
75	Discovering key regulatory mechanisms from single-factor and multi-factor regulations in glioblastoma utilizing multi-dimensional data. Molecular BioSystems, 2015, 11, 2345-2353.	2.9	2
76	Detection of copy number variants and loss of heterozygosity from impure tumor samples using whole exome sequencing data. Oncology Letters, 2018, 16, 4713-4720.	1.8	2
77	Dual-layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	2
78	PhosVarDeep: deep-learning based prediction of phospho-variants using sequence information. PeerJ, 2022, 10, e12847.	2.0	2
79	Coarse-to-Fine Handâ€“Object Pose Estimation with Interaction-Aware Graph Convolutional Network. Sensors, 2021, 21, 8092.	3.8	2
80	A novel HMM for analyzing chromosomal aberrations in heterogeneous tumor samples. , 2013, , .		1
81	Prediction of human disease-specific phosphorylation sites with combined feature selection approach and support vector machine. , 2014, , .		1
82	Comprehensive study of tumour single nucleotide polymorphism array data reveals significant driver aberrations and disrupted signalling pathways in human hepatocellular cancer. IET Systems Biology, 2014, 8, 24-32.	1.5	1
83	Extracting LncRNA-protein Interactions from Literature Using a Text Feature-based Approach. IFAC-PapersOnLine, 2015, 48, 22-26.	0.9	1
84	Identification of Genomic Aberrations in Cancer Subclones from Heterogeneous Tumor Samples. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 679-685.	3.0	1
85	Identification of driver network modules in protein-protein interaction network using patient mutation profiles. , 2017, , .		1
86	An efficient nonnegative matrix factorization model for finding cancer associated genes by integrating data from genome, transcriptome and interactome. , 2018, , .		1
87	Globally learning gene regulatory networks based on hidden atomic regulators from transcriptomic big data. BMC Genomics, 2020, 21, 711.	2.8	1
88	Prediction of protein kinase-specific phosphorylation sites using Random forest algorithm. , 2012, , .		0
89	Construction and analysis of human phosphorylation network. , 2012, , .		0
90	PISV: A novel algorithm for peptide identification using spectrum vector. , 2012, , .		0

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91	A novel method for predicting protein phosphorylation via site-modification network profiles. , 2015, , .		0
92	Heterogeneous network-based propagation algorithm for discovering bladder cancer-related genes. , 2016, , .		0
93	Integrated Modeling of GC-Content, Mappability, Tumor Impurity and Aneuploidy for Accurate Detection of Genomic Aberrations. IEEE Access, 2018, 6, 64096-64106.	4.2	0
94	Semi-Supervised Nuclei Detection in Histopathology Images via Location-Aware Adversarial Image Reconstruction. IEEE Access, 2022, 10, 42739-42749.	4.2	0