Ao Li

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	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
2	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
3	HFBSurv: hierarchical multimodal fusion with factorized bilinear models for cancer survival prediction. Bioinformatics, 2022, 38, 2587-2594.	4.1	18
4	PhosVarDeep: deep-learning based prediction of phospho-variants using sequence information. PeerJ, 2022, 10, e12847.	2.0	2
5	Semi-Supervised Nuclei Detection in Histopathology Images via Location-Aware Adversarial Image Reconstruction. IEEE Access, 2022, 10, 42739-42749.	4.2	0
6	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
7	DeepTL-Ubi: A novel deep transfer learning method for effectively predicting ubiquitination sites of multiple species. Methods, 2021, 192, 103-111.	3.8	18
8	Multimodal Deep Reinforcement Learning with Auxiliary Task for Obstacle Avoidance of Indoor Mobile Robot. Sensors, 2021, 21, 1363.	3.8	14
9	GPDBN: deep bilinear network integrating both genomic data and pathological images for breast cancer prognosis prediction. Bioinformatics, 2021, 37, 2963-2970.	4.1	39
10	PhosIDN: an integrated deep neural network for improving protein phosphorylation site prediction by combining sequence and protein–protein interaction information. Bioinformatics, 2021, 37, 4668-4676.	4.1	37
11	Learning rich features with hybrid loss for brain tumor segmentation. BMC Medical Informatics and Decision Making, 2021, 21, 63.	3.0	4
12	Semi-HIC: A novel semi-supervised deep learning method for histopathological image classification. Computers in Biology and Medicine, 2021, 137, 104788.	7.0	15
13	Coarse-to-Fine Hand–Object Pose Estimation with Interaction-Aware Graph Convolutional Network. Sensors, 2021, 21, 8092.	3.8	2
14	Inferring subgroup-specific driver genes from heterogeneous cancer samples via subspace learning with subgroup indication. Bioinformatics, 2020, 36, 1855-1863.	4.1	53
15	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
16	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
17	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
18	Globally learning gene regulatory networks based on hidden atomic regulators from transcriptomic big data. BMC Genomics, 2020, 21, 711.	2.8	1

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19	GANcon: Protein Contact Map Prediction With Deep Generative Adversarial Network. IEEE Access, 2020, 8, 80899-80907.	4.2	25
20	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
21	Adversarially Regularized U-Net-based GANs for Facial Attribute Modification and Generation. IEEE Access, 2019, 7, 86453-86462.	4.2	6
22	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
23	Gene Expression Profiling Reveals Distinct Molecular Subtypes of Esophageal Squamous Cell Carcinoma in Asian Populations. Neoplasia, 2019, 21, 571-581.	5.3	21
24	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
25	CapSurv: Capsule Network for Survival Analysis With Whole Slide Pathological Images. IEEE Access, 2019, 7, 26022-26030.	4.2	40
26	DeepPhos: prediction of protein phosphorylation sites with deep learning. Bioinformatics, 2019, 35, 2766-2773.	4.1	132
27	A novel approach for drug response prediction in cancer cell lines via network representation learning. Bioinformatics, 2019, 35, 1527-1535.	4.1	58
28	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
29	A novel heterogeneous network-based method for drug response prediction in cancer cell lines. Scientific Reports, 2018, 8, 3355.	3.3	72
30	TPGLDA: Novel prediction of associations between lncRNAs and diseases via lncRNA-disease-gene tripartite graph. Scientific Reports, 2018, 8, 1065.	3.3	97
31	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
32	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
33	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
34	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
35	An efficient nonnegative matrix factorization model for finding cancer associated genes by integrating data from genome, transcriptome and interactome. , 2018, , .		1
36	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

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37	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
38	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
39	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
40	MPTM: A tool for mining protein post-translational modifications from literature. Journal of Bioinformatics and Computational Biology, 2017, 15, 1740005.	0.8	7
41	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
42	A novel method for identifying potential disease-related miRNAs via a disease–miRNA–target heterogeneous network. Molecular BioSystems, 2017, 13, 2328-2337.	2.9	11
43	Discovery of Bladder Cancer-related Genes Using Integrative Heterogeneous Network Modeling of Multi-omics Data. Scientific Reports, 2017, 7, 15639.	3.3	13
44	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
45	Identification of driver network modules in protein-protein interaction network using patient mutation profiles. , 2017, , .		1
46	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
47	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
48	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
49	Prediction of post-translational modification sites using multiple kernel support vector machine. PeerJ, 2017, 5, e3261.	2.0	12
50	ksrMKL: a novel method for identification of kinase–substrate relationships using multiple kernel learning. PeerJ, 2017, 5, e4182.	2.0	5
51	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
52	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
53	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
54	NTSMDA: prediction of miRNA–disease associations by integrating network topological similarity. Molecular BioSystems, 2016, 12, 2224-2232.	2.9	66

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55	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
56	CloneCNA: detecting subclonal somatic copy number alterations in heterogeneous tumor samples from whole-exome sequencing data. BMC Bioinformatics, 2016, 17, 310.	2.6	27
57	Heterogeneous network-based propagation algorithm for discovering bladder cancer-related genes. , 2016, , .		0
58	A text feature-based approach for literature mining of lncRNAâ€"protein interactions. Neurocomputing, 2016, 206, 73-80.	5.9	16
59	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
60	IsomiR Bank: a research resource for tracking IsomiRs. Bioinformatics, 2016, 32, 2069-2071.	4.1	52
61	A novel method for predicting protein phosphorylation via site-modification network profiles. , 2015, , .		0
62	Extracting LncRNA-protein Interactions from Literature Using a Text Feature-based Approach. IFAC-PapersOnLine, 2015, 48, 22-26.	0.9	1
63	LncReg: a reference resource for lncRNA-associated regulatory networks. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav083.	3.0	55
64	TAFFYS: An Integrated Tool for Comprehensive Analysis of Genomic Aberrations in Tumor Samples. PLoS ONE, 2015, 10, e0129835.	2.5	2
65	Systematic Analysis and Prediction of *In Situ* Cross Talk of O-GlcNAcylation and Phosphorylation. BioMed Research International, 2015, 2015, 1-12.	1.9	9
66	Predicting Long Noncoding RNA and Protein Interactions Using Heterogeneous Network Model. BioMed Research International, 2015, 2015, 1-11.	1.9	73
67	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
68	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
69	RPdb: a database of experimentally verified cellular reprogramming records. Bioinformatics, 2015, 31, 3237-3239.	4.1	4
70	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
71	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
72	Prediction of interactions between lncRNA and protein by using relevance search in a heterogeneous lncRNA-protein network. , 2015, , .		4

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73	Prediction of human disease–associated phosphorylation sites with combined feature selection approach and support vector machine. IET Systems Biology, 2015, 9, 155-163.	1.5	11
74	Kinase Identification with Supervised Laplacian Regularized Least Squares. PLoS ONE, 2015, 10, e0139676.	2.5	5
75	Prediction of human disease-specific phosphorylation sites with combined feature selection approach and support vector machine. , 2014, , .		1
76	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
77	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
78	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
79	Literature mining of protein phosphorylation using dependency parse trees. Methods, 2014, 67, 386-393.	3.8	4
80	Genome-Wide Identification of Somatic Aberrations from Paired Normal-Tumor Samples. PLoS ONE, 2014, 9, e87212.	2.5	8
81	A Kinect based gesture recognition algorithm using GMM and HMM. , 2013, , .		19
82	A novel HMM for analyzing chromosomal aberrations in heterogeneous tumor samples. , 2013, , .		1
83	Human Action Recognition Based on Depth Images from Microsoft Kinect. , 2013, , .		19
84	miRNA Target Prediction Based on Gene Ontology. , 2013, , .		3
85	Reconstruction and Analysis of Transcription Factor–miRNA Co-Regulatory Feed-Forward Loops in Human Cancers Using Filter-Wrapper Feature Selection. PLoS ONE, 2013, 8, e78197.	2.5	20
86	Prediction of protein kinase-specific phosphorylation sites using Random forest algorithm. , 2012, , .		0
87	Construction and analysis of human phosphorylation network. , 2012, , .		0
88	PISV: A novel algorithm for peptide identification using spectrum vector. , 2012, , .		0
89	A gene signature for breast cancer prognosis using support vector machine. , 2012, , .		49
90	A genome-wide association study of Alzheimer's disease using random forests and enrichment analysis. Science China Life Sciences, 2012, 55, 618-625.	4.9	12

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91	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
92	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
93	PPSP: prediction of PK-specific phosphorylation site with Bayesian decision theory. BMC Bioinformatics, 2006, 7, 163.	2.6	183
94	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