Wei Du

List of Publications by Year
in descending order

43 papers	1,798 citations	567144 15 h-index	377752 34 g-index
44 all docs	44 docs citations	44 times ranked	4153 citing authors

#	Article	IF	Citations
1	LPInsider: a webserver for lncRNA–protein interaction extraction from the literature. BMC Bioinformatics, 2022, 23, 135.	1.2	2
2	CyanoPATH: a knowledgebase of genome-scale functional repertoire for toxic cyanobacterial blooms. Briefings in Bioinformatics, 2021, 22, .	3.2	4
3	HBFP: a new repository for human body fluid proteome. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	17
4	De novo Prediction of Moonlighting Proteins Using Multimodal Deep Ensemble Learning. Frontiers in Genetics, 2021, 12, 630379.	1.1	4
5	DeepHBSP: A Deep Learning Framework for Predicting Human Blood-Secretory Proteins Using Transfer Learning. Journal of Computer Science and Technology, 2021, 36, 234-247.	0.9	1
6	Capsule-LPI: a LncRNA–protein interaction predicting tool based on a capsule network. BMC Bioinformatics, 2021, 22, 246.	1.2	26
7	SecProCT: In Silico Prediction of Human Secretory Proteins Based on Capsule Network and Transformer. International Journal of Molecular Sciences, 2021, 22, 9054.	1.8	7
8	Deep forest ensemble learning for classification of alignments of non-coding RNA sequences based on multi-view structure representations. Briefings in Bioinformatics, 2021, 22, .	3.2	7
9	DeepUEP: Prediction of Urine Excretory Proteins Using Deep Learning. IEEE Access, 2020, 8, 100251-100261.	2.6	3
10	Classifying Breast Cancer Subtypes Using Deep Neural Networks Based on Multi-Omics Data. Genes, 2020, 11, 888.	1.0	52
11	LncLocation: Efficient Subcellular Location Prediction of Long Non-Coding RNA-Based Multi-Source Heterogeneous Feature Fusion. International Journal of Molecular Sciences, 2020, 21, 7271.	1.8	10
12	BAENET: A Brain Age Estimation Network with 3D Skipping and Outlier Constraint Loss. , 2020, , .		4
13	CapsNet-SSP: multilane capsule network for predicting human saliva-secretory proteins. BMC Bioinformatics, 2020, 21, 237.	1.2	9
14	DEEPSMP: A deep learning model for predicting the ectodomain shedding events of membrane proteins. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050017.	0.3	3
15	Computational methods for recognition of cancer protein markers in saliva. Mathematical Biosciences and Engineering, 2020, 17, 2453-2469.	1.0	3
16	LncFinder: an integrated platform for long non-coding RNA identification utilizing sequence intrinsic composition, structural information and physicochemical property. Briefings in Bioinformatics, 2019, 20, 2009-2027.	3.2	98
17	Pancreatic cancer biomarker detection by two support vector strategies for recursive feature elimination. Biomarkers in Medicine, 2019, 13, 105-121.	0.6	16
18	Predicting lncRNA-disease associations using network topological similarity based on deep mining heterogeneous networks. Mathematical Biosciences, 2019, 315, 108229.	0.9	17

#	Article	IF	Citations
19	Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model. Scientific Reports, 2019, 9, 4192.	1.6	27
20	Classifying Breast Cancer Subtypes Using Multiple Kernel Learning Based on Omics Data. Genes, 2019, 10, 200.	1.0	34
21	Integrative analysis with expanded DNA methylation data reveals common key regulators and pathways in cancers. Npj Genomic Medicine, 2019, 4, 2.	1.7	27
22	Biodiversity and dynamics of cyanobacterial communities during blooms in temperate lake (Harsha) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.2	15
23	Urine-Based Biomarkers for Alzheimer's Disease Identified Through Coupling Computational and Experimental Methods. Journal of Alzheimer's Disease, 2018, 65, 421-431.	1.2	37
24	The method for breast cancer grade prediction and pathway analysis based on improved multiple kernel learning. Journal of Bioinformatics and Computational Biology, 2017, 15, 1650037.	0.3	4
25	A Novel Unsupervised Algorithm for Biological Process-based Analysis on Cancer. Scientific Reports, 2017, 7, 4671.	1.6	4
26	A feature selection method based on multiple kernel learning with expression profiles of different types. BioData Mining, 2017, 10, 4.	2.2	26
27	Pancreatic cancer biomarker detection using recursive feature elimination based on Support Vector Machine and large margin distribution machine. , 2017, , .		5
28	Computational Analysis of Specific MicroRNA Biomarkers for Noninvasive Early Cancer Detection. BioMed Research International, 2017, 2017, 1-9.	0.9	7
29	Systematic analyses of glutamine and glutamate metabolisms across different cancer types. Chinese Journal of Cancer, 2017, 36, 88.	4.9	24
30	Lncident: A Tool for Rapid Identification of Long Noncoding RNAs Utilizing Sequence Intrinsic Composition and Open Reading Frame Information. International Journal of Genomics, 2016, 2016, 1-11.	0.8	43
31	Long Noncoding RNA Identification: Comparing Machine Learning Based Tools for Long Noncoding Transcripts Discrimination. BioMed Research International, 2016, 2016, 1-14.	0.9	1,176
32	Specific Biomarkers: Detection of Cancer Biomarkers Through High-Throughput Transcriptomics Data. Cognitive Computation, 2015, 7, 652-666.	3.6	3
33	Identification of Gene-Expression Signatures and Protein Markers for Breast Cancer Grading and Staging. PLoS ONE, 2015, 10, e0138213.	1.1	30
34	Identification of Essential Proteins Based on Ranking Edge-Weights in Protein-Protein Interaction Networks. PLoS ONE, 2014, 9, e108716.	1.1	15
35	Prokaryotic Phylogenies Inferred from Whole-Genome Sequence and Annotation Data. BioMed Research International, 2013, 2013, 1-15.	0.9	6
36	A novel multi-stage feature selection method for microarray expression data analysis. International Journal of Data Mining and Bioinformatics, 2013, 7, 58.	0.1	19

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37	Two modeling methods for near infrared spectroscopy nondestructive quantitative analysis of the protein contents in Coredyceps militaris mycelia powder. , 2010, , .		0
38	An improved normalized signal to noise ratio method for irrelevant genes removing. , 2010, , .		2
39	Clustering methods based on rough estimate of cluster core. , 2010, , .		0
40	Parameter Selection of Support Vector Regression Based on a Novel Chaotic Immune Algorithm. , 2009, , .		4
41	Operon Prediction by Decision Tree Classifier Based on VPRSM. , 2009, , .		1
42	The Application of Support Vector Machine to Operon Prediction. , 2008, , .		1
43	A Novel SVC Method Based on K-means. , 2008, , .		5