Ran Su

List of Publications by Year
in descending order

60 papers	4,136 citations	172207 29 h-index	155451 55 g-index
61 all docs	61 docs citations	61 times ranked	2672 citing authors

#	Article	IF	Citations
1	Accelerating bioactive peptide discovery via mutual information-based meta-learning. Briefings in Bioinformatics, 2022, 23, .	3.2	29
2	Distant metastasis identification based on optimized graph representation of gene interaction patterns. Briefings in Bioinformatics, 2022, 23, .	3.2	6
3	SRDFM: Siamese Response Deep Factorization Machine to improve anti-cancer drug recommendation. Briefings in Bioinformatics, 2022, 23, .	3.2	18
4	GC6mA-Pred: A deep learning approach to identify DNA N6-methyladenine sites in the rice genome. Methods, 2022, 204, 14-21.	1.9	6
5	Deep reinforcement learning with emergent communication for coalitional negotiation games. Mathematical Biosciences and Engineering, 2022, 19, 4592-4609.	1.0	8
6	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. Nucleic Acids Research, 2022, 50, 4877-4899.	6.5	12
7	An autonomous agent for negotiation with multiple communication channels using parametrized deep Q-network. Mathematical Biosciences and Engineering, 2022, 19, 7933-7951.	1.0	7
8	EOCSA: Predicting prognosis of Epithelial ovarian cancer with whole slide histopathological images. Expert Systems With Applications, 2022, 206, 117643.	4.4	8
9	Protein subcellular localization based on deep image features and criterion learning strategy. Briefings in Bioinformatics, 2021, 22, .	3.2	20
10	Computational prediction and interpretation of cell-specific replication origin sites from multiple eukaryotes by exploiting stacking framework. Briefings in Bioinformatics, 2021, 22, .	3.2	73
11	Cascade knowledge diffusion network for skin lesion diagnosis and segmentation. Applied Soft Computing Journal, 2021, 99, 106881.	4.1	57
12	Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. Briefings in Bioinformatics, 2021, 22, 428-437.	3.2	18
13	Classification and gene selection of triple-negative breast cancer subtype embedding gene connectivity matrix in deep neural network. Briefings in Bioinformatics, 2021, 22, .	3.2	26
14	Free-form tumor synthesis in computed tomography images via richer generative adversarial network. Knowledge-Based Systems, 2021, 218, 106753.	4.0	27
15	PSSP-MVIRT: peptide secondary structure prediction based on a multi-view deep learning architecture. Briefings in Bioinformatics, 2021, 22, .	3.2	8
16	Learning embedding features based on multisense-scaled attention architecture to improve the predictive performance of anticancer peptides. Bioinformatics, 2021, 37, 4684-4693.	1.8	26
17	Integrated Bioinformatic Analysis of the Expression and Prognosis of Caveolae-Related Genes in Human Breast Cancer. Frontiers in Oncology, 2021, 11, 703501.	1.3	3
18	Domain adaptation based self-correction model for COVID-19 infection segmentation in CT images. Expert Systems With Applications, 2021, 176, 114848.	4.4	34

#	Article	IF	Citations
19	Identification of glioblastoma molecular subtype and prognosis based on deep MRI features. Knowledge-Based Systems, 2021, 232, 107490.	4.0	13
20	Identification of expression signatures for non-small-cell lung carcinoma subtype classification. Bioinformatics, 2020, 36, 339-346.	1.8	26
21	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. Briefings in Bioinformatics, 2020, 21, 408-420.	3.2	122
22	Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. Briefings in Bioinformatics, 2020, 21, 996-1005.	3.2	63
23	MinE-RFE: determine the optimal subset from RFE by minimizing the subset-accuracy–defined energy. Briefings in Bioinformatics, 2020, 21, 687-698.	3.2	28
24	Construction of Retinal Vessel Segmentation Models Based on Convolutional Neural Network. Neural Processing Letters, 2020, 52, 1005-1022.	2.0	19
25	ACPred-Fuse: fusing multi-view information improves the prediction of anticancer peptides. Briefings in Bioinformatics, 2020, 21, 1846-1855.	3.2	100
26	Fusing convolutional neural network features with hand-crafted features for osteoporosis diagnoses. Neurocomputing, 2020, 385, 300-309.	3.5	26
27	RA-UNet: A Hybrid Deep Attention-Aware Network to Extract Liver and Tumor in CT Scans. Frontiers in Bioengineering and Biotechnology, 2020, 8, 605132.	2.0	187
28	WERFE: A Gene Selection Algorithm Based on Recursive Feature Elimination and Ensemble Strategy. Frontiers in Bioengineering and Biotechnology, 2020, 8, 496.	2.0	21
29	A Bioinformatics Tool for the Prediction of DNA N6-Methyladenine Modifications Based on Feature Fusion and Optimization Protocol. Frontiers in Bioengineering and Biotechnology, 2020, 8, 502.	2.0	12
30	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. Frontiers in Bioengineering and Biotechnology, 2020, 8, 227.	2.0	26
31	Developing a Multi-Dose Computational Model for Drug-Induced Hepatotoxicity Prediction Based on Toxicogenomics Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1231-1239.	1.9	120
32	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. Neurocomputing, 2019, 324, 3-9.	3.5	130
33	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. Frontiers in Neuroscience, 2019, 13, 144.	1.4	29
34	DUNet: A deformable network for retinal vessel segmentation. Knowledge-Based Systems, 2019, 178, 149-162.	4.0	535
35	Iterative feature representations improve N4-methylcytosine site prediction. Bioinformatics, 2019, 35, 4930-4937.	1.8	113
36	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. Bioinformatics, 2019, 35, 4272-4280.	1.8	116

#	Article	IF	Citations
37	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. Methods, 2019, 166, 91-102.	1.9	182
38	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. Bioinformatics, 2019, 35, 1326-1333.	1.8	156
39	Prediction of human protein subcellular localization using deep learning. Journal of Parallel and Distributed Computing, 2018, 117, 212-217.	2.7	184
40	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	3.2	60
41	M6AMRFS: Robust Prediction of N6-Methyladenosine Sites With Sequence-Based Features in Multiple Species. Frontiers in Genetics, 2018, 9, 495.	1.1	90
42	CPPred-FL: a sequence-based predictor for large-scale identification of cell-penetrating peptides by feature representation learning. Briefings in Bioinformatics, 2018, , .	3.2	62
43	ACPred-FL: a sequence-based predictor using effective feature representation to improve the prediction of anti-cancer peptides. Bioinformatics, 2018, 34, 4007-4016.	1.8	326
44	M6APred-EL: A Sequence-Based Predictor for Identifying N6-methyladenosine Sites Using Ensemble Learning. Molecular Therapy - Nucleic Acids, 2018, 12, 635-644.	2.3	167
45	Decision Variants for the Automatic Determination of Optimal Feature Subset in RF-RFE. Genes, 2018, 9, 301.	1.0	91
46	Improved prediction of protein–protein interactions using novel negative samples, features, and an ensemble classifier. Artificial Intelligence in Medicine, 2017, 83, 67-74.	3.8	220
47	Identifying N6-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. Scientific Reports, 2017, 7, 46757.	1.6	77
48	CPPred-RF: A Sequence-based Predictor for Identifying Cell-Penetrating Peptides and Their Uptake Efficiency. Journal of Proteome Research, 2017, 16, 2044-2053.	1.8	168
49	High-throughput imaging-based nephrotoxicity prediction for xenobiotics with diverse chemical structures. Archives of Toxicology, 2016, 90, 2793-2808.	1.9	51
50	Clustered nuclei splitting via curvature information and gray–scale distance transform. Journal of Microscopy, 2015, 259, 36-52.	0.8	6
51	Prediction of drug-induced nephrotoxicity and injury mechanisms with human induced pluripotent stem cell-derived cells and machine learning methods. Scientific Reports, 2015, 5, 12337.	1.6	84
52	A novel method for dendritic spines detection based on directional morphological filter and shortest path. Computerized Medical Imaging and Graphics, 2014, 38, 793-802.	3.5	9
53	A new method for linear feature and junction enhancement in 2D images based on morphological operation, oriented anisotropic Gaussian function and Hessian information. Pattern Recognition, 2014, 47, 3193-3208.	5.1	35
54	Supervised prediction of drug-induced nephrotoxicity based on interleukin-6 and -8 expression levels. BMC Bioinformatics, 2014, 15, S16.	1.2	34

#	Article	IF	Citations
55	Tubule detection in testis images using boundary weighting and circular shortest path. , 2013, 2013, 3319-22.		1
56	Dendritic spines detection based on directional morphological filter and shortest path. , 2012, 2012, 5343-6.		0
57	Segmentation of clustered nuclei based on curvature weighting. , 2012, , .		12
58	Linear feature enhancement based on morphological operation and Gabor function. , 2012, , .		2
59	Junction detection for linear structures based on Hessian, correlation and shape information. Pattern Recognition, 2012, 45, 3695-3706.	5.1	43
60	Junction Detection for Linear Structures. , 2011, , .		1