Ran Su

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/441260/publications.pdf

Version: 2024-02-01

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	DUNet: A deformable network for retinal vessel segmentation. Knowledge-Based Systems, 2019, 178, 149-162.	4.0	535
2	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
3	Improved prediction of proteinâ€“protein interactions using novel negative samples, features, and an ensemble classifier. Artificial Intelligence in Medicine, 2017, 83, 67-74.	3.8	220
4	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
5	Prediction of human protein subcellular localization using deep learning. Journal of Parallel and Distributed Computing, 2018, 117, 212-217.	2.7	184
6	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. Methods, 2019, 166, 91-102.	1.9	182
7	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
8	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
9	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. Bioinformatics, 2019, 35, 1326-1333.	1.8	156
10	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. Neurocomputing, 2019, 324, 3-9.	3.5	130
11	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. Briefings in Bioinformatics, 2020, 21, 408-420.	3.2	122
12	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
13	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. Bioinformatics, 2019, 35, 4272-4280.	1.8	116
14	Iterative feature representations improve N4-methylcytosine site prediction. Bioinformatics, 2019, 35, 4930-4937.	1.8	113
15	ACPred-Fuse: fusing multi-view information improves the prediction of anticancer peptides. Briefings in Bioinformatics, 2020, 21, 1846-1855.	3.2	100
16	Decision Variants for the Automatic Determination of Optimal Feature Subset in RF-RFE. Genes, 2018, 9, 301.	1.0	91
17	M6AMRFS: Robust Prediction of N6-Methyladenosine Sites With Sequence-Based Features in Multiple Species. Frontiers in Genetics, 2018, 9, 495.	1.1	90
18	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

#	ARTICLE	IF	CITATIONS
19	Identifying N6-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. Scientific Reports, 2017, 7, 46757.	1.6	77
20	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
21	Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. Briefings in Bioinformatics, 2020, 21, 996-1005.	3.2	63
22	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
23	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	3.2	60
24	Cascade knowledge diffusion network for skin lesion diagnosis and segmentation. Applied Soft Computing Journal, 2021, 99, 106881.	4.1	57
25	High-throughput imaging-based nephrotoxicity prediction for xenobiotics with diverse chemical structures. Archives of Toxicology, 2016, 90, 2793-2808.	1.9	51
26	Junction detection for linear structures based on Hessian, correlation and shape information. Pattern Recognition, 2012, 45, 3695-3706.	5.1	43
27	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
28	Supervised prediction of drug-induced nephrotoxicity based on interleukin-6 and -8 expression levels. BMC Bioinformatics, 2014, 15, S16.	1.2	34
29	Domain adaptation based self-correction model for COVID-19 infection segmentation in CT images. Expert Systems With Applications, 2021, 176, 114848.	4.4	34
30	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. Frontiers in Neuroscience, 2019, 13, 144.	1.4	29
31	Accelerating bioactive peptide discovery via mutual information-based meta-learning. Briefings in Bioinformatics, 2022, 23, .	3.2	29
32	MinE-RFE: determine the optimal subset from RFE by minimizing the subset-accuracyâ€“defined energy. Briefings in Bioinformatics, 2020, 21, 687-698.	3.2	28
33	Free-form tumor synthesis in computed tomography images via richer generative adversarial network. Knowledge-Based Systems, 2021, 218, 106753.	4.0	27
34	Identification of expression signatures for non-small-cell lung carcinoma subtype classification. Bioinformatics, 2020, 36, 339-346.	1.8	26
35	Fusing convolutional neural network features with hand-crafted features for osteoporosis diagnoses. Neurocomputing, 2020, 385, 300-309.	3.5	26
36	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. Frontiers in Bioengineering and Biotechnology, 2020, 8, 227.	2.0	26

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	WERFE: A Gene Selection Algorithm Based on Recursive Feature Elimination and Ensemble Strategy. Frontiers in Bioengineering and Biotechnology, 2020, 8, 496.	2.0	21
40	Protein subcellular localization based on deep image features and criterion learning strategy. Briefings in Bioinformatics, 2021, 22, .	3.2	20
41	Construction of Retinal Vessel Segmentation Models Based on Convolutional Neural Network. Neural Processing Letters, 2020, 52, 1005-1022.	2.0	19
42	Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. Briefings in Bioinformatics, 2021, 22, 428-437.	3.2	18
43	SRDFM: Siamese Response Deep Factorization Machine to improve anti-cancer drug recommendation. Briefings in Bioinformatics, 2022, 23, .	3.2	18
44	Identification of glioblastoma molecular subtype and prognosis based on deep MRI features. Knowledge-Based Systems, 2021, 232, 107490.	4.0	13
45	Segmentation of clustered nuclei based on curvature weighting. , 2012, , .		12
46	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
47	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
48	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
49	PSSP-MVIRT: peptide secondary structure prediction based on a multi-view deep learning architecture. Briefings in Bioinformatics, 2021, 22, .	3.2	8
50	Deep reinforcement learning with emergent communication for coalitional negotiation games. Mathematical Biosciences and Engineering, 2022, 19, 4592-4609.	1.0	8
51	EOCSA: Predicting prognosis of Epithelial ovarian cancer with whole slide histopathological images. Expert Systems With Applications, 2022, 206, 117643.	4.4	8
52	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
53	Clustered nuclei splitting via curvature information and grayâ€scale distance transform. Journal of Microscopy, 2015, 259, 36-52.	0.8	6
54	Distant metastasis identification based on optimized graph representation of gene interaction patterns. Briefings in Bioinformatics, 2022, 23, .	3.2	6

#	Article	IF	Citations
55	GC6mA-Pred: A deep learning approach to identify DNA N6-methyladenine sites in the rice genome. Methods, 2022, 204, 14-21.	1.9	6
56	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
57	Linear feature enhancement based on morphological operation and Gabor function. , 2012, , .		2
58	Junction Detection for Linear Structures. , 2011, , .		1
59	Tubule detection in testis images using boundary weighting and circular shortest path. , 2013, 2013, 3319-22.		1
60	Dendritic spines detection based on directional morphological filter and shortest path. , 2012, 2012, 5343-6.		0