

Yang Yang

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

371
citations

933447

10
h-index

794594

19
g-index

21
all docs

21
docs citations

21
times ranked

473
citing authors

#	ARTICLE	IF	CITATIONS
1	Hum-mPloc 3.0: prediction enhancement of human protein subcellular localization through modeling the hidden correlations of gene ontology and functional domain features. <i>Bioinformatics</i> , 2017, 33, 843-853.	4.1	88
2	Predicting gene regulatory interactions based on spatial gene expression data and deep learning. <i>PLoS Computational Biology</i> , 2019, 15, e1007324.	3.2	42
3	A clustering-based approach for efficient identification of microRNA combinatorial biomarkers. <i>BMC Genomics</i> , 2017, 18, 210.	2.8	36
4	ImPloc: a multi-instance deep learning model for the prediction of protein subcellular localization based on immunohistochemistry images. <i>Bioinformatics</i> , 2020, 36, 2244-2250.	4.1	35
5	PROTEIN SUBCELLULAR MULTI-LOCALIZATION PREDICTION USING A MIN-MAX MODULAR SUPPORT VECTOR MACHINE. <i>International Journal of Neural Systems</i> , 2010, 20, 13-28.	5.2	33
6	Missing value imputation for microRNA expression data by using a GO-based similarity measure. <i>BMC Bioinformatics</i> , 2016, 17, 10.	2.6	27
7	Artificial intelligence-based multi-objective optimization protocol for protein structure refinement. <i>Bioinformatics</i> , 2020, 36, 437-448.	4.1	21
8	When SMILES Smiles, Practicality Judgment and Yield Prediction of Chemical Reaction via Deep Chemical Language Processing. <i>IEEE Access</i> , 2021, 9, 85071-85083.	4.2	12
9	Accurate inference of gene regulatory interactions from spatial gene expression with deep contrastive learning. <i>Bioinformatics</i> , 2022, 38, 746-753.	4.1	11
10	SIFLoc: a self-supervised pre-training method for enhancing the recognition of protein subcellular localization in immunofluorescence microscopic images. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	11
11	CrepHAN: cross-species prediction of enhancers by using hierarchical attention networks. <i>Bioinformatics</i> , 2021, 37, 3436-3443.	4.1	9
12	Incorporating label correlations into deep neural networks to classify protein subcellular location patterns in immunohistochemistry images. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 493-503.	2.6	9
13	KenDTI: An Ensemble Model for Predicting Drug-Target Interaction by Integrating Multi-Source Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1305-1314.	3.0	8
14	EmbedDTI: Enhancing the Molecular Representations via Sequence Embedding and Graph Convolutional Network for the Prediction of Drug-Target Interaction. <i>Biomolecules</i> , 2021, 11, 1783.	4.0	8
15	WEDeepT3: predicting type III secreted effectors based on word embedding and deep learning. <i>Quantitative Biology</i> , 2019, 7, 293-301.	0.5	7
16	AnnoFly: annotating <i>Drosophila</i> embryonic images based on an attention-enhanced RNN model. <i>Bioinformatics</i> , 2019, 35, 2834-2842.	4.1	6
17	Line Junction Detection Without Prior-Delineation of Curvilinear Structure in Biomedical Images. <i>IEEE Access</i> , 2018, 6, 2016-2027.	4.2	3
18	Detection of Curvilinear Structure in Images by a Multi-Centered Hough Forest Method. <i>IEEE Access</i> , 2018, 6, 22684-22694.	4.2	2

#	ARTICLE	IF	CITATIONS
19	ProtPlat: an efficient pre-training platform for protein classification based on FastText. BMC Bioinformatics, 2022, 23, 66.	2.6	2
20	FlyIT: Drosophila Embryogenesis Image Annotation based on Image Tiling and Convolutional Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	3.0	0