

Jingyang Gao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7789155/publications.pdf>

Version: 2024-02-01

18
papers

107
citations

1937685

4
h-index

1474206

9
g-index

19
all docs

19
docs citations

19
times ranked

105
citing authors

#	ARTICLE	IF	CITATIONS
1	Resource optimization model using novel extreme learning machine with t-distributed stochastic neighbor embedding: Application to complex industrial processes. Energy, 2021, 225, 120255.	8.8	40
2	DeepSV: accurate calling of genomic deletions from high-throughput sequencing data using deep convolutional neural network. BMC Bioinformatics, 2019, 20, 665.	2.6	27
3	Classification of G-protein coupled receptors based on a rich generation of convolutional neural network, N-gram transformation and multiple sequence alignments. Amino Acids, 2018, 50, 255-266.	2.7	8
4	Concod: an effective integration framework of consensus-based calling deletions from next-generation sequencing data. International Journal of Data Mining and Bioinformatics, 2017, 17, 153.	0.1	5
5	An efficient scRNA-seq dropout imputation method using graph attention network. BMC Bioinformatics, 2021, 22, 582.	2.6	5
6	An efficient CNN-based classification on G-protein Coupled Receptors using TF-IDF and N-gram. , 2017, , .		4
7	InvBFM: finding genomic inversions from high-throughput sequence data based on feature mining. BMC Genomics, 2020, 21, 173.	2.8	4
8	CNNdel: Calling Structural Variations on Low Coverage Data Based on Convolutional Neural Networks. BioMed Research International, 2017, 2017, 1-8.	1.9	3
9	Cnngeno: A high-precision deep learning based strategy for the calling of structural variation genotype. Computational Biology and Chemistry, 2021, 94, 107417.	2.3	3
10	Concod: Accurate consensus-based approach of calling deletions from high-throughput sequencing data. , 2016, , .		2
11	Structural variation discovery with next-generation sequencing. , 2013, , .		1
12	Strategies for Improving Accuracy of Structural Variation Prediction Using Read Pairs. , 2013, , .		1
13	MrBayes 3.2.6 on Tianhe-1A: A High Performance and Distributed Implementation of Phylogenetic Analysis. , 2016, , .		1
14	Phylogenetic Likelihood Estimation on GPUs Using Vertical Partitioning Scheme. , 2016, , .		1
15	A high-precision shallow Convolutional Neural Network based strategy for the detection of Genomic Deletions. , 2016, , .		1
16	Deletion genotype calling on the basis of sequence visualisation and image classification. International Journal of Data Mining and Bioinformatics, 2018, 20, 109.	0.1	1
17	iSchool: a Tool Software for Identifying Suspicious Copied Homework Documents with Definitive Contents. , 2020, , .		0
18	IMDSVs: An integrated method based on machine learning and deep learning of calling structural variations from long-read data. , 2021, , .		0