

Jie Hou

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,108
citations

361413

20
h-index

265206

42
g-index

50
all docs

50
docs citations

50
times ranked

2238
citing authors

#	ARTICLE	IF	CITATIONS
1	Artificial intelligence advances for de novo molecular structure modeling in cryo-electron microscopy. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1542.	14.6	15
2	Recent Progress of Machine Learning in Gene Therapy. Current Gene Therapy, 2022, 22, 132-143.	2.0	15
3	Improving protein tertiary structure prediction by deep learning and distance prediction in CASP14. Proteins: Structure, Function and Bioinformatics, 2022, 90, 58-72.	2.6	18
4	Effect of aneuploidy of a non-essential chromosome on gene expression in maize. Plant Journal, 2022, 110, 193-211.	5.7	8
5	Dosage-sensitive miRNAs trigger modulation of gene expression during genomic imbalance in maize. Nature Communications, 2022, 13, .	12.8	1
6	DNSS2: Improved ab initio protein secondary structure prediction using advanced deep learning architectures. Proteins: Structure, Function and Bioinformatics, 2021, 89, 207-217.	2.6	24
7	DeepDist: real-value inter-residue distance prediction with deep residual convolutional network. BMC Bioinformatics, 2021, 22, 30.	2.6	37
8	DISTEVAL: a web server for evaluating predicted protein distances. BMC Bioinformatics, 2021, 22, 8.	2.6	9
9	Genomic imbalance determines positive and negative modulation of gene expression in diploid maize. Plant Cell, 2021, 33, 917-939.	6.6	22
10	DeepGRN: prediction of transcription factor binding site across cell-types using attention-based deep neural networks. BMC Bioinformatics, 2021, 22, 38.	2.6	35
11	Predominantly inverse modulation of gene expression in genomically unbalanced disomic haploid maize. Plant Cell, 2021, 33, 901-916.	6.6	22
12	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.0	73
13	Improving deep learning-based protein distance prediction in CASP14. Bioinformatics, 2021, 37, 3190-3196.	4.1	11
14	Protein model accuracy estimation empowered by deep learning and inter-residue distance prediction in CASP14. Scientific Reports, 2021, 11, 10943.	3.3	10
15	Sequence of the supernumerary B chromosome of maize provides insight into its drive mechanism and evolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	25
16	MULTICOM2 open-source protein structure prediction system powered by deep learning and distance prediction. Scientific Reports, 2021, 11, 13155.	3.3	0
17	Analysis of several key factors influencing deep learning-based inter-residue contact prediction. Bioinformatics, 2020, 36, 1091-1098.	4.1	29
18	GNET2: an R package for constructing gene regulatory networks from transcriptomic data. Bioinformatics, 2020, 37, 2068-2069.	4.1	1

#	ARTICLE	IF	CITATIONS
19	Heme oxygenase promotes Bâ€Rafâ€dependent melanosphere formation. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 850-868.	3.3	8
20	Deep Learning to Predict Protein Backbone Structure from High-Resolution Cryo-EM Density Maps. <i>Scientific Reports</i> , 2020, 10, 4282.	3.3	56
21	Magnitude of modulation of gene expression in aneuploid maize depends on the extent of genomic imbalance. <i>Journal of Genetics and Genomics</i> , 2020, 47, 93-103.	3.9	15
22	SAXSDom: Modeling multidomain protein structures using smallâ€angle Xâ€ray scattering data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 775-787.	2.6	9
23	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2873.	4.1	134
24	The Gene Balance Hypothesis: Epigenetics and Dosage Effects in Plants. <i>Methods in Molecular Biology</i> , 2020, 2093, 161-171.	0.9	14
25	The MULTICOM Protein Structure Prediction Server Empowered by Deep Learning and Contact Distance Prediction. <i>Methods in Molecular Biology</i> , 2020, 2165, 13-26.	0.9	23
26	Deep Ranking in Template-free Protein Structure Prediction. , 2020, , .		5
27	The renoprotective effects of soy protein in the aging kidney. <i>Medical Research Archives</i> , 2020, 8, .	0.2	4
28	Performance Evaluation of Viral Infection Diagnosis using T-Cell Receptor Sequence and Artificial Intelligence. , 2020, , .		1
29	PairedFB: a full hierarchical Bayesian model for paired RNA-seq data with heterogeneous treatment effects. <i>Bioinformatics</i> , 2019, 35, 787-797.	4.1	5
30	Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1361-1377.	2.6	78
31	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
32	Protein tertiary structure modeling driven by deep learning and contact distance prediction in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1165-1178.	2.6	149
33	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
34	DeepSF: deep convolutional neural network for mapping protein sequences to folds. <i>Bioinformatics</i> , 2018, 34, 1295-1303.	4.1	127
35	DNCON2: improved protein contact prediction using two-level deep convolutional neural networks. <i>Bioinformatics</i> , 2018, 34, 1466-1472.	4.1	148
36	Protein contact prediction by integrating deep multiple sequence alignments, coevolution and machine learning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 84-96.	2.6	15

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37	Global impacts of chromosomal imbalance on gene expression in <i>Arabidopsis</i> and other taxa. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11321-E11330.	7.1	51
38	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	3.3	19
39	QAcon: single model quality assessment using protein structural and contact information with machine learning techniques. Bioinformatics, 2017, 33, 586-588.	4.1	91
40	Deep learning methods for protein torsion angle prediction. BMC Bioinformatics, 2017, 18, 417.	2.6	46
41	Genetic dissection of Arabidopsis MAP kinase phosphatase 1-dependent PAMP-induced transcriptional responses. Journal of Experimental Botany, 2017, 68, 5207-5220.	4.8	8
42	DeepQA: improving the estimation of single protein model quality with deep belief networks. BMC Bioinformatics, 2016, 17, 495.	2.6	156
43	Accelerating extended least-squares migration with weighted conjugate gradient iteration. Geophysics, 2016, 81, S165-S179.	2.6	70
44	ConEVA: a toolbox for comprehensive assessment of protein contacts. BMC Bioinformatics, 2016, 17, 517.	2.6	23
45	An overview of bioinformatics methods for modeling biological pathways in yeast. Briefings in Functional Genomics, 2016, 15, 95-108.	2.7	18
46	Improving Protein Fold Recognition by Deep Learning Networks. Scientific Reports, 2015, 5, 17573.	3.3	107
47	Exploring soybean metabolic pathways based on probabilistic graphical model and knowledge-based methods. Eurasip Journal on Bioinformatics and Systems Biology, 2015, 2015, 5.	1.4	3
48	From Gigabyte to Kilobyte: A Bioinformatics Protocol for Mining Large RNA-Seq Transcriptomics Data. PLoS ONE, 2015, 10, e0125000.	2.5	7