

# 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	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
2	DeepQA: improving the estimation of single protein model quality with deep belief networks. <i>BMC Bioinformatics</i> , 2016, 17, 495.	2.6	156
3	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
4	DNCON2: improved protein contact prediction using two-level deep convolutional neural networks. <i>Bioinformatics</i> , 2018, 34, 1466-1472.	4.1	148
5	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2873.	4.1	134
6	DeepSF: deep convolutional neural network for mapping protein sequences to folds. <i>Bioinformatics</i> , 2018, 34, 1295-1303.	4.1	127
7	Improving Protein Fold Recognition by Deep Learning Networks. <i>Scientific Reports</i> , 2015, 5, 17573.	3.3	107
8	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
9	QAcon: single model quality assessment using protein structural and contact information with machine learning techniques. <i>Bioinformatics</i> , 2017, 33, 586-588.	4.1	91
10	Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1361-1377.	2.6	78
11	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
12	Accelerating extended least-squares migration with weighted conjugate gradient iteration. <i>Geophysics</i> , 2016, 81, S165-S179.	2.6	70
13	Deep Learning to Predict Protein Backbone Structure from High-Resolution Cryo-EM Density Maps. <i>Scientific Reports</i> , 2020, 10, 4282.	3.3	56
14	Global impacts of chromosomal imbalance on gene expression in <i>Arabidopsis</i> and other taxa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11321-E11330.	7.1	51
15	Deep learning methods for protein torsion angle prediction. <i>BMC Bioinformatics</i> , 2017, 18, 417.	2.6	46
16	DeepDist: real-value inter-residue distance prediction with deep residual convolutional network. <i>BMC Bioinformatics</i> , 2021, 22, 30.	2.6	37
17	DeepGRN: prediction of transcription factor binding site across cell-types using attention-based deep neural networks. <i>BMC Bioinformatics</i> , 2021, 22, 38.	2.6	35
18	Analysis of several key factors influencing deep learning-based inter-residue contact prediction. <i>Bioinformatics</i> , 2020, 36, 1091-1098.	4.1	29

#	ARTICLE	IF	CITATIONS
19	Sequence of the supernumerary B chromosome of maize provides insight into its drive mechanism and evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	25
20	<scp>DNSS2</scp>: Improved ab initio protein secondary structure prediction using advanced deep learning architectures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 207-217.	2.6	24
21	ConEVA: a toolbox for comprehensive assessment of protein contacts. <i>BMC Bioinformatics</i> , 2016, 17, 517.	2.6	23
22	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
23	Genomic imbalance determines positive and negative modulation of gene expression in diploid maize. <i>Plant Cell</i> , 2021, 33, 917-939.	6.6	22
24	Predominantly inverse modulation of gene expression in genomically unbalanced disomic haploid maize. <i>Plant Cell</i> , 2021, 33, 901-916.	6.6	22
25	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	3.3	19
26	An overview of bioinformatics methods for modeling biological pathways in yeast. <i>Briefings in Functional Genomics</i> , 2016, 15, 95-108.	2.7	18
27	Improving protein tertiary structure prediction by deep learning and distance prediction in <scp>CASP14</scp>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 58-72.	2.6	18
28	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
29	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
30	Artificial intelligence advances for de novo molecular structure modeling in cryoâ€electron microscopy. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, e1542.	14.6	15
31	Recent Progress of Machine Learning in Gene Therapy. <i>Current Gene Therapy</i> , 2022, 22, 132-143.	2.0	15
32	The Gene Balance Hypothesis: Epigenetics and Dosage Effects in Plants. <i>Methods in Molecular Biology</i> , 2020, 2093, 161-171.	0.9	14
33	Improving deep learning-based protein distance prediction in CASP14. <i>Bioinformatics</i> , 2021, 37, 3190-3196.	4.1	11
34	Protein model accuracy estimation empowered by deep learning and inter-residue distance prediction in CASP14. <i>Scientific Reports</i> , 2021, 11, 10943.	3.3	10
35	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
36	DISTEVAL: a web server for evaluating predicted protein distances. <i>BMC Bioinformatics</i> , 2021, 22, 8.	2.6	9

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37	Genetic dissection of Arabidopsis MAP kinase phosphatase 1-dependent PAMP-induced transcriptional responses. <i>Journal of Experimental Botany</i> , 2017, 68, 5207-5220.	4.8	8
38	Heme oxygenase promotes Bâ€Rafâ€dependent melanosphere formation. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 850-868.	3.3	8
39	Effect of aneuploidy of a nonâ€essential chromosome on gene expression in maize. <i>Plant Journal</i> , 2022, 110, 193-211.	5.7	8
40	From Gigabyte to Kilobyte: A Bioinformatics Protocol for Mining Large RNA-Seq Transcriptomics Data. <i>PLoS ONE</i> , 2015, 10, e0125000.	2.5	7
41	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
42	Deep Ranking in Template-free Protein Structure Prediction. , 2020, , .		5
43	The renoprotective effects of soy protein in the aging kidney. <i>Medical Research Archives</i> , 2020, 8, .	0.2	4
44	Exploring soybean metabolic pathways based on probabilistic graphical model and knowledge-based methods. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2015, 2015, 5.	1.4	3
45	GNET2: an R package for constructing gene regulatory networks from transcriptomic data. <i>Bioinformatics</i> , 2020, 37, 2068-2069.	4.1	1
46	Performance Evaluation of Viral Infection Diagnosis using T-Cell Receptor Sequence and Artificial Intelligence. , 2020, , .		1
47	Dosage-sensitive miRNAs trigger modulation of gene expression during genomic imbalance in maize. <i>Nature Communications</i> , 2022, 13, .	12.8	1
48	MULTICOM2 open-source protein structure prediction system powered by deep learning and distance prediction. <i>Scientific Reports</i> , 2021, 11, 13155.	3.3	0