Jian Peng

List of Publications by Year
in descending order

54 papers	5,557 citations	186265 28 h-index	206112 48 g-index
61 all docs	61 docs citations	61 times ranked	10010 citing authors

#	Article	IF	Citations
1	Template-based protein structure modeling using the RaptorX web server. Nature Protocols, 2012, 7, 1511-1522.	12.0	1,474
2	A network integration approach for drug-target interaction prediction and computational drug repositioning from heterogeneous information. Nature Communications, 2017, 8, 573.	12.8	543
3	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. Cell, 2015, 161, 647-660.	28.9	482
4	Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields. Scientific Reports, 2016, 6, 18962.	3.3	396
5	A Quantitative Chaperone Interaction Network Reveals the Architecture of Cellular Protein Homeostasis Pathways. Cell, 2014, 158, 434-448.	28.9	335
6	Computational solutions for omics data. Nature Reviews Genetics, 2013, 14, 333-346.	16.3	288
7	Compact Integration of Multi-Network Topology for Functional Analysis of Genes. Cell Systems, 2016, 3, 540-548.e5.	6.2	207
8	Protein structure alignment beyond spatial proximity. Scientific Reports, 2013, 3, 1448.	3.3	133
9	Genome-Scale Networks Link Neurodegenerative Disease Genes to Î±-Synuclein through Specific Molecular Pathways. Cell Systems, 2017, 4, 157-170.e14.	6.2	102
10	A marine microbiome antifungal targets urgent-threat drug-resistant fungi. Science, 2020, 370, 974-978.	12.6	102
11	Robust single-cell Hi-C clustering by convolution- and random-walkâ€"based imputation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14011-14018.	7.1	101
12	Exploiting ontology graph for predicting sparsely annotated gene function. Bioinformatics, 2015, 31, i357-i364.	4.1	97
13	Enhancing Evolutionary Couplings with Deep Convolutional Neural Networks. Cell Systems, 2018, 6, 65-74.e3.	6.2	97
14	Few-shot learning creates predictive models of drug response that translate from high-throughput screens to individual patients. Nature Cancer, 2021, 2, 233-244.	13.2	92
15	STAIR: A generic and fully-automated method to fuse multiple sources of optical satellite data to generate a high-resolution, daily and cloud-/gap-free surface reflectance product. Remote Sensing of Environment, 2018, 214, 87-99.	11.0	84
16	Deriving high-spatiotemporal-resolution leaf area index for agroecosystems in the U.S. Corn Belt using Planet Labs CubeSat and STAIR fusion data. Remote Sensing of Environment, 2020, 239, 111615.	11.0	84
17	HapTree: A Novel Bayesian Framework for Single Individual Polyplotyping Using NGS Data. PLoS Computational Biology, 2014, 10, e1003502.	3.2	75
18	ECNet is an evolutionary context-integrated deep learning framework for protein engineering. Nature Communications, 2021, 12, 5743.	12.8	66

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19	Diffusion Component Analysis: Unraveling Functional Topology in Biological Networks. Lecture Notes in Computer Science, 2015, 9029, 62-64.	1.3	63
20	Quality score compression improves genotyping accuracy. Nature Biotechnology, 2015, 33, 240-243.	17.5	57
21	Deep learning guided optimization of human antibody against SARS-CoV-2 variants with broad neutralization. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2122954119.	7.1	57
22	When causal inference meets deep learning. Nature Machine Intelligence, 2020, 2, 426-427.	16.0	51
23	Reconstructing spatial organizations of chromosomes through manifold learning. Nucleic Acids Research, 2018, 46, e50-e50.	14.5	50
24	Generalizable and Scalable Visualization of Single-Cell Data Using Neural Networks. Cell Systems, 2018, 7, 185-191.e4.	6.2	49
25	Comprehensive interactome profiling of the human Hsp70 network highlights functional differentiation of J domains. Molecular Cell, 2021, 81, 2549-2565.e8.	9.7	47
26	Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach. Scientific Reports, 2019, 9, 690.	3.3	46
27	Deep geometric representations for modeling effects of mutations on protein-protein binding affinity. PLoS Computational Biology, 2021, 17, e1009284.	3.2	45
28	A large-scale systematic survey reveals recurring molecular features of public antibody responses to SARS-CoV-2. Immunity, 2022, 55, 1105-1117.e4.	14.3	44
29	Compressive mapping for next-generation sequencing. Nature Biotechnology, 2016, 34, 374-376.	17.5	33
30	Integrating thermodynamic and sequence contexts improves protein-RNA binding prediction. PLoS Computational Biology, 2019, 15, e1007283.	3.2	27
31	Learning structural motif representations for efficient protein structure search. Bioinformatics, 2018, 34, i773-i780.	4.1	24
32	Metagenomic binning through low-density hashing. Bioinformatics, 2019, 35, 219-226.	4.1	21
33	Typing tumors using pathways selected by somatic evolution. Nature Communications, 2018, 9, 4159.	12.8	19
34	STAIR 2.0: A Generic and Automatic Algorithm to Fuse Modis, Landsat, and Sentinel-2 to Generate 10 m, Daily, and Cloud-/Gap-Free Surface Reflectance Product. Remote Sensing, 2020, 12, 3209.	4.0	15
35	Reconstructing Causal Biological Networks through Active Learning. PLoS ONE, 2016, 11, e0150611.	2.5	13
36	Identification of pathways associated with chemosensitivity through network embedding. PLoS Computational Biology, 2019, 15, e1006864.	3.2	12

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37	Network-assisted target identification for haploinsufficiency and homozygous profiling screens. PLoS Computational Biology, 2017, 13, e1005553.	3.2	11
38	Batch equalization with a generative adversarial network. Bioinformatics, 2020, 36, i875-i883.	4.1	10
39	Discovering What Dimensionality Reduction Really Tells Us About RNA-Seq Data. Journal of Computational Biology, 2015, 22, 715-728.	1.6	9
40	Detection of Complexes in Biological Networks Through Diversified Dense Subgraph Mining. Journal of Computational Biology, 2017, 24, 923-941.	1.6	9
41	Next Decade's AI-Based Drug Development Features Tight Integration of Data and Computation. Health Data Science, 2022, 2022, .	2.3	7
42	MACFP: Maximal Approximate Consecutive Frequent Pattern Mining under Edit Distance. , 2016, 2016, 558-566.		6
43	Annotating gene sets by mining large literature collections with protein networks. , 2018, , .		6
44	Annotating gene sets by mining large literature collections with protein networks. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 602-613.	0.7	6
45	DPClass: An Effective but Concise Discriminative Patterns-Based Classification Framework. , 2016, 2016, 567-575.		5
46	Jumper enables discontinuous transcript assembly in coronaviruses. Nature Communications, 2021, 12, 6728.	12.8	4
47	On the interpretability of conditional probability estimates in the agnostic setting. Electronic Journal of Statistics, 2017, 11, .	0.7	2
48	Large-scale integration of heterogeneous pharmacogenomic data for identifying drug mechanism of action. , 2018, , .		2
49	DWCox: A density-weighted Cox model for outlier-robust prediction of prostate cancer survival. F1000Research, 2016, 5, 2806.	1.6	2
50	DPPred: An Effective Prediction Framework with Concise Discriminative Patterns. IEEE Transactions on Knowledge and Data Engineering, 2018, 30, 1226-1239.	5.7	1
51	Bayesian information sharing enhances detection of regulatory associations in rare cell types. Bioinformatics, 2021, 37, i349-i357.	4.1	1
52	Low-Density Locality-Sensitive Hashing Boosts Metagenomic Binning. , 2016, 9649, 255-257.		1
53	Large-Margin Classification in Hyperbolic Space. Proceedings of Machine Learning Research, 2019, 89, 1832-1840.	0.3	1
54	Generalizable visualization of mega-scale single-cell data. , 2018, 10812, 251-253.		0