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	Next Decade's AI-Based Drug Development Features Tight Integration of Data and Computation. Health Data Science, 2022, 2022, .	2.3	7
2	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
3	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
4	Comprehensive interactome profiling of the human Hsp70 network highlights functional differentiation of J domains. Molecular Cell, 2021, 81, 2549-2565.e8.	9.7	47
5	Bayesian information sharing enhances detection of regulatory associations in rare cell types. Bioinformatics, 2021, 37, i349-i357.	4.1	1
6	Deep geometric representations for modeling effects of mutations on protein-protein binding affinity. PLoS Computational Biology, 2021, 17, e1009284.	3.2	45
7	ECNet is an evolutionary context-integrated deep learning framework for protein engineering. Nature Communications, 2021, 12, 5743.	12.8	66
8	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
9	Jumper enables discontinuous transcript assembly in coronaviruses. Nature Communications, 2021, 12, 6728.	12.8	4
10	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
11	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
12	A marine microbiome antifungal targets urgent-threat drug-resistant fungi. Science, 2020, 370, 974-978.	12.6	102
13	When causal inference meets deep learning. Nature Machine Intelligence, 2020, 2, 426-427.	16.0	51
14	Batch equalization with a generative adversarial network. Bioinformatics, 2020, 36, i875-i883.	4.1	10
15	Metagenomic binning through low-density hashing. Bioinformatics, 2019, 35, 219-226.	4.1	21
16	Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach. Scientific Reports, 2019, 9, 690.	3.3	46
17	Robust single-cell Hi-C clustering by convolution- and random-walk–based imputation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14011-14018.	7.1	101
18	Identification of pathways associated with chemosensitivity through network embedding. PLoS Computational Biology, 2019, 15, e1006864.	3.2	12

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19	Integrating thermodynamic and sequence contexts improves protein-RNA binding prediction. PLoS Computational Biology, 2019, 15, e1007283.	3.2	27
20	Large-Margin Classification in Hyperbolic Space. Proceedings of Machine Learning Research, 2019, 89, 1832-1840.	0.3	1
21	Large-scale integration of heterogeneous pharmacogenomic data for identifying drug mechanism of action. , 2018, , .		2
22	Reconstructing spatial organizations of chromosomes through manifold learning. Nucleic Acids Research, 2018, 46, e50-e50.	14.5	50
23	Enhancing Evolutionary Couplings with Deep Convolutional Neural Networks. Cell Systems, 2018, 6, 65-74.e3.	6.2	97
24	Annotating gene sets by mining large literature collections with protein networks. , 2018, , .		6
25	Learning structural motif representations for efficient protein structure search. Bioinformatics, 2018, 34, i773-i780.	4.1	24
26	Typing tumors using pathways selected by somatic evolution. Nature Communications, 2018, 9, 4159.	12.8	19
27	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
28	DPPred: An Effective Prediction Framework with Concise Discriminative Patterns. IEEE Transactions on Knowledge and Data Engineering, 2018, 30, 1226-1239.	5.7	1
29	Generalizable and Scalable Visualization of Single-Cell Data Using Neural Networks. Cell Systems, 2018, 7, 185-191.e4.	6.2	49
30	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
31	Generalizable visualization of mega-scale single-cell data. , 2018, 10812, 251-253.		0
32	Genome-Scale Networks Link Neurodegenerative Disease Genes to Î±-Synuclein through Specific Molecular Pathways. Cell Systems, 2017, 4, 157-170.e14.	6.2	102
33	Detection of Complexes in Biological Networks Through Diversified Dense Subgraph Mining. Journal of Computational Biology, 2017, 24, 923-941.	1.6	9
34	A network integration approach for drug-target interaction prediction and computational drug repositioning from heterogeneous information. Nature Communications, 2017, 8, 573.	12.8	543
35	On the interpretability of conditional probability estimates in the agnostic setting. Electronic Journal of Statistics, 2017, 11, .	0.7	2
36	Network-assisted target identification for haploinsufficiency and homozygous profiling screens. PLoS Computational Biology, 2017, 13, e1005553.	3.2	11

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37	MACFP: Maximal Approximate Consecutive Frequent Pattern Mining under Edit Distance. , 2016, 2016, 558-566.		6
38	Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields. Scientific Reports, 2016, 6, 18962.	3.3	396
39	DPClass: An Effective but Concise Discriminative Patterns-Based Classification Framework. , 2016, 2016, 567-575.		5
40	Compressive mapping for next-generation sequencing. Nature Biotechnology, 2016, 34, 374-376.	17.5	33
41	Compact Integration of Multi-Network Topology for Functional Analysis of Genes. Cell Systems, 2016, 3, 540-548.e5.	6.2	207
42	DWCox: A density-weighted Cox model for outlier-robust prediction of prostate cancer survival. F1000Research, 2016, 5, 2806.	1.6	2
43	Reconstructing Causal Biological Networks through Active Learning. PLoS ONE, 2016, 11, e0150611.	2.5	13
44	Low-Density Locality-Sensitive Hashing Boosts Metagenomic Binning. , 2016, 9649, 255-257.		1
45	Exploiting ontology graph for predicting sparsely annotated gene function. Bioinformatics, 2015, 31, i357-i364.	4.1	97
46	Discovering What Dimensionality Reduction Really Tells Us About RNA-Seq Data. Journal of Computational Biology, 2015, 22, 715-728.	1.6	9
47	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. Cell, 2015, 161, 647-660.	28.9	482
48	Quality score compression improves genotyping accuracy. Nature Biotechnology, 2015, 33, 240-243.	17.5	57
49	Diffusion Component Analysis: Unraveling Functional Topology in Biological Networks. Lecture Notes in Computer Science, 2015, 9029, 62-64.	1.3	63
50	HapTree: A Novel Bayesian Framework for Single Individual Polyplotyping Using NGS Data. PLoS Computational Biology, 2014, 10, e1003502.	3.2	75
51	A Quantitative Chaperone Interaction Network Reveals the Architecture of Cellular Protein Homeostasis Pathways. Cell, 2014, 158, 434-448.	28.9	335
52	Computational solutions for omics data. Nature Reviews Genetics, 2013, 14, 333-346.	16.3	288
53	Protein structure alignment beyond spatial proximity. Scientific Reports, 2013, 3, 1448.	3.3	133
54	Template-based protein structure modeling using the RaptorX web server. Nature Protocols, 2012, 7, 1511-1522.	12.0	1,474