

Yuanfang Guan

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

103
papers

2,544
citations

28
h-index

48
g-index

109
ext. papers

3,492
ext. citations

9
avg, IF

5.51
L-index

#	Paper	IF	Citations
103	Clinical applications of machine learning in cardiovascular disease and its relevance to cardiac imaging. <i>European Heart Journal</i> , 2019 , 40, 1975-1986	9.5	180
102	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016 , 13, 310-8	21.6	158
101	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019 , 10, 2674	17.4	119
100	Predicting human olfactory perception from chemical features of odor molecules. <i>Science</i> , 2017 , 355, 820-826	33.3	117
99	Tissue-specific functional networks for prioritizing phenotype and disease genes. <i>PLoS Computational Biology</i> , 2012 , 8, e1002694	5	114
98	Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. <i>JAMA Network Open</i> , 2020 , 3, e200265	10.4	105
97	Predicting gene function in a hierarchical context with an ensemble of classifiers. <i>Genome Biology</i> , 2008 , 9 Suppl 1, S3	18.3	98
96	A genomewide functional network for the laboratory mouse. <i>PLoS Computational Biology</i> , 2008 , 4, e1000165	9.165	94
95	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. <i>Lancet Oncology</i> , 2017 , 18, 132-142	21.7	90
94	miRmine: a database of human miRNA expression profiles. <i>Bioinformatics</i> , 2017 , 33, 1554-1560	7.2	87
93	The emerging era of genomic data integration for analyzing splice isoform function. <i>Trends in Genetics</i> , 2014 , 30, 340-7	8.5	61
92	Systematically differentiating functions for alternatively spliced isoforms through integrating RNA-seq data. <i>PLoS Computational Biology</i> , 2013 , 9, e1003314	5	58
91	Effects of Antioxidants in Human Cancers: Differential Effects on Non-Coding Intronic RNA Expression. <i>Antioxidants</i> , 2016 , 5,	7.1	58
90	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2016 , 12, 645-53	1.2	58
89	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016 , 7, 12460	17.4	54
88	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015 , 14, 3415-31	5.6	50
87	Machine Learning to Predict Anti-Tumor Necrosis Factor Drug Responses of Rheumatoid Arthritis Patients by Integrating Clinical and Genetic Markers. <i>Arthritis and Rheumatology</i> , 2019 , 71, 1987-1996	9.5	49

86	Functional genomics complements quantitative genetics in identifying disease-gene associations. <i>PLoS Computational Biology</i> , 2010 , 6, e1000991	5	46
85	Single-cell ATAC-Seq in human pancreatic islets and deep learning upscaling of rare cells reveals cell-specific type 2 diabetes regulatory signatures. <i>Molecular Metabolism</i> , 2020 , 32, 109-121	8.8	46
84	COVID-19 drug repurposing: A review of computational screening methods, clinical trials, and protein interaction assays. <i>Medicinal Research Reviews</i> , 2021 , 41, 5-28	14.4	43
83	Network Propagation Predicts Drug Synergy in Cancers. <i>Cancer Research</i> , 2018 , 78, 5446-5457	10.1	42
82	Transcriptional regulation of microalgae for concurrent lipid overproduction and secretion. <i>Science Advances</i> , 2019 , 5, eaau3795	14.3	41
81	Identification of stage-specific genes associated with lupus nephritis and response to remission induction in (NZB [NZW]F1 and NZM2410 mice. <i>Arthritis and Rheumatology</i> , 2014 , 66, 2246-2258	9.5	37
80	Developmental transcriptome analysis of human erythropoiesis. <i>Human Molecular Genetics</i> , 2014 , 23, 4528-42	5.6	36
79	A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020 , 38, 97-107	44.5	35
78	Brain-specific functional relationship networks inform autism spectrum disorder gene prediction. <i>Translational Psychiatry</i> , 2018 , 8, 56	8.6	30
77	A new class of protein cancer biomarker candidates: differentially expressed splice variants of ERBB2 (HER2/neu) and ERBB1 (EGFR) in breast cancer cell lines. <i>Journal of Proteomics</i> , 2014 , 107, 103-123	3.9	30
76	Anchor: trans-cell type prediction of transcription factor binding sites. <i>Genome Research</i> , 2019 , 29, 281-292	2.7	30
75	Revisiting the identification of canonical splice isoforms through integration of functional genomics and proteomics evidence. <i>Proteomics</i> , 2014 , 14, 2709-18	4.8	28
74	Comparison of spinocerebellar ataxia type 3 mouse models identifies early gain-of-function, cell-autonomous transcriptional changes in oligodendrocytes. <i>Human Molecular Genetics</i> , 2017 , 26, 3362-3374	5.6	27
73	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. <i>Leukemia</i> , 2020 , 34, 1866-1874	10.7	27
72	Functional Networks of Highest-Connected Splice Isoforms: From The Chromosome 17 Human Proteome Project. <i>Journal of Proteome Research</i> , 2015 , 14, 3484-91	5.6	26
71	Rescue of Metabolic Alterations in AR113Q Skeletal Muscle by Peripheral Androgen Receptor Gene Silencing. <i>Cell Reports</i> , 2016 , 17, 125-136	10.6	26
70	Genome-Wide Functional Annotation of Human Protein-Coding Splice Variants Using Multiple Instance Learning. <i>Journal of Proteome Research</i> , 2016 , 15, 1747-53	5.6	23
69	Complete hazard ranking to analyze right-censored data: An ALS survival study. <i>PLoS Computational Biology</i> , 2017 , 13, e1005887	5	22

68	Accurate prediction of personalized olfactory perception from large-scale chemoinformatic features. <i>GigaScience</i> , 2018 , 7,	7.6	20
67	Cellular, transcriptomic and isoform heterogeneity of breast cancer cell line revealed by full-length single-cell RNA sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 676-685	6.8	16
66	Genetic variants in PLG, LPA, and SIGLEC 14 as well as smoking contribute to plasma plasminogen levels. <i>Blood</i> , 2014 , 124, 3155-64	2.2	16
65	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017 , 5, 485-497.e3	10.6	14
64	Deep Learning Identifies Digital Biomarkers for Self-Reported Parkinson's Disease. <i>Patterns</i> , 2020 , 1,	5.1	14
63	MIsoMine: a genome-scale high-resolution data portal of expression, function and networks at the splice isoform level in the mouse. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav045	5	14
62	A Network of Splice Isoforms for the Mouse. <i>Scientific Reports</i> , 2016 , 6, 24507	4.9	14
61	Three-Plane-assembled Deep Learning Segmentation of Gliomas. <i>Radiology: Artificial Intelligence</i> , 2020 , 2, e190011	8.7	12
60	COMPASS: A computational model to predict changes in MMSE scores 24-months after initial assessment of Alzheimer's disease. <i>Scientific Reports</i> , 2016 , 6, 34567	4.9	12
59	FastClone is a probabilistic tool for deconvoluting tumor heterogeneity in bulk-sequencing samples. <i>Nature Communications</i> , 2020 , 11, 4469	17.4	12
58	Model-Based and Model-Free Techniques for Amyotrophic Lateral Sclerosis Diagnostic Prediction and Patient Clustering. <i>Neuroinformatics</i> , 2019 , 17, 407-421	3.2	12
57	DNAP: A Pipeline for DNA-seq Data Analysis. <i>Scientific Reports</i> , 2018 , 8, 6793	4.9	11
56	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020 , 11, 186-195.e9	10.6	11
55	Predicting dynamic signaling network response under unseen perturbations. <i>Bioinformatics</i> , 2014 , 30, 2772-8	7.2	10
54	DeepSleep convolutional neural network allows accurate and fast detection of sleep arousal. <i>Communications Biology</i> , 2021 , 4, 18	6.7	10
53	Modeling dynamic functional relationship networks and application to ex vivo human erythroid differentiation. <i>Bioinformatics</i> , 2014 , 30, 3325-33	7.2	9
52	Deep Residual Neural Networks Resolve Quartet Molecular Phylogenies. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1495-1507	8.3	9
51	Graph2GO: a multi-modal attributed network embedding method for inferring protein functions. <i>GigaScience</i> , 2020 , 9,	7.6	9

50	Prognostic model for multiple myeloma progression integrating gene expression and clinical features. <i>GigaScience</i> , 2019 , 8,	7.6	9
49	Crowdsourcing digital health measures to predict Parkinson's disease severity: the Parkinson's Disease Digital Biomarker DREAM Challenge. <i>Npj Digital Medicine</i> , 2021 , 4, 53	15.7	8
48	Machine learning empowers phosphoproteome prediction in cancers. <i>Bioinformatics</i> , 2020 , 36, 859-864	7.2	8
47	Regulatory network inferred using expression data of small sample size: application and validation in erythroid system. <i>Bioinformatics</i> , 2015 , 31, 2537-44	7.2	7
46	TAJI: approaching experimental replicates-level accuracy for drug synergy prediction. <i>Bioinformatics</i> , 2019 , 35, 2338-2339	7.2	7
45	BaiHui: cross-species brain-specific network built with hundreds of hand-curated datasets. <i>Bioinformatics</i> , 2019 , 35, 2486-2488	7.2	7
44	Antisense Oligonucleotide Therapy Targeted Against ATXN3 Improves Potassium Channel-Mediated Purkinje Neuron Dysfunction in Spinocerebellar Ataxia Type 3. <i>Cerebellum</i> , 2021 , 20, 41-53	4.3	7
43	A proteogenomic approach to understand splice isoform functions through sequence and expression-based computational modeling. <i>Briefings in Bioinformatics</i> , 2016 , 17, 1024-1031	13.4	6
42	Biased, non-equivalent gene-proximal and -distal binding motifs of orphan nuclear receptor TR4 in primary human erythroid cells. <i>PLoS Genetics</i> , 2014 , 10, e1004339	6	6
41	Chromosome 17 Missing Proteins: Recent Progress and Future Directions as Part of the neXt-MP50 Challenge. <i>Journal of Proteome Research</i> , 2018 , 17, 4061-4071	5.6	6
40	Treatment Stratification of Patients with Metastatic Castration-Resistant Prostate Cancer by Machine Learning. <i>IScience</i> , 2020 , 23, 100804	6.1	5
39	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. <i>Cell Reports Medicine</i> , 2021 , 2, 100323	18	5
38	Deep learning prediction of patient response time course from early data via neural-pharmacokinetic/pharmacodynamic modelling. <i>Nature Machine Intelligence</i> , 2021 , 3, 696-704	22.5	5
37	Neural-ODE for pharmacokinetics modeling and its advantage to alternative machine learning models in predicting new dosing regimens. <i>IScience</i> , 2021 , 24, 102804	6.1	5
36	Waking up to data challenges. <i>Nature Machine Intelligence</i> , 2019 , 1,	22.5	5
35	GATA3 Abundance Is a Critical Determinant of T Cell Receptor Allelic Exclusion. <i>Molecular and Cellular Biology</i> , 2017 , 37,	4.8	4
34	TissueNexus: a database of human tissue functional gene networks built with a large compendium of curated RNA-seq data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	4
33	Detecting Asymmetric Patterns and Localizing Cancers on Mammograms. <i>Patterns</i> , 2020 , 1,	5.1	4

32	Gene expression profiles of diabetic kidney disease and neuropathy in eNOS knockout mice: Predictors of pathology and RAS blockade effects. <i>FASEB Journal</i> , 2021 , 35, e21467	0.9	4
31	Joint learning improves protein abundance prediction in cancers. <i>BMC Biology</i> , 2019 , 17, 107	7.3	4
30	High-Throughput Single-Cell Sequencing of both Alleles. <i>Journal of Immunology</i> , 2018 , 201, 3465-3470	5.3	4
29	YAMDA: thousandfold speedup of EM-based motif discovery using deep learning libraries and GPU. <i>Bioinformatics</i> , 2018 , 34, 3578-3580	7.2	4
28	Benchmarked approaches for reconstruction of in vitro cell lineages and in silico models of <i>C. elegans</i> and <i>M. musculus</i> developmental trees. <i>Cell Systems</i> , 2021 , 12, 810-826.e4	10.6	4
27	MI-PVT: A Tool for Visualizing the Chromosome-Centric Human Proteome. <i>Journal of Proteome Research</i> , 2015 , 14, 3762-7	5.6	3
26	Machine Learning for Cancer Drug Combination. <i>Clinical Pharmacology and Therapeutics</i> , 2020 , 107, 749-752		3
25	A similarity-based approach to leverage multi-cohort medical data on the diagnosis and prognosis of Alzheimer's disease. <i>GigaScience</i> , 2018 , 7,	7.6	3
24	Fast decoding cell type-specific transcription factor binding landscape at single-nucleotide resolution. <i>Genome Research</i> , 2021 , 31, 721-731	9.7	3
23	A survival model generalized to regression learning algorithms. <i>Nature Computational Science</i> , 2021 , 1, 433-440		3
22	Comparative analysis of molecular fingerprints in prediction of drug combination effects. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
21	An integrated brain-specific network identifies genes associated with neuropathologic and clinical traits of Alzheimer's disease.. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	2
20	Multiple Myeloma DREAM Challenge Reveals Epigenetic Regulator PHF19As Marker of Aggressive Disease		2
19	Annotation of Alternatively Spliced Proteins and Transcripts with Protein-Folding Algorithms and Isoform-Level Functional Networks. <i>Methods in Molecular Biology</i> , 2017 , 1558, 415-436	1.4	2
18	Challenge-Enabled Machine Learning to Drug-Response Prediction. <i>AAPS Journal</i> , 2020 , 22, 106	3.7	2
17	Assessment of the timeliness and robustness for predicting adult sepsis. <i>iScience</i> , 2021 , 24, 102106	6.1	2
16	Genes Caught In Flagranti: Integrating Renal Transcriptional Profiles With Genotypes and Phenotypes. <i>Seminars in Nephrology</i> , 2015 , 35, 237-44	4.8	1
15	Prioritizing predictive biomarkers for gene essentiality in cancer cells with mRNA expression data and DNA copy number profile. <i>Bioinformatics</i> , 2018 , 34, 3975-3982	7.2	1

14	Leopard: fast decoding cell type-specific transcription factor binding landscape at single-nucleotide resolution	1
13	DeepSleep: Fast and Accurate Delineation of Sleep Arousals at Millisecond Resolution by Deep Learning	1
12	Auto-annotating sleep stages based on polysomnographic data.. <i>Patterns</i> , 2022 , 3, 100371	5.1 1
11	Evidence of widespread, independent sequence signature for transcription factor cobinding. <i>Genome Research</i> , 2020 ,	9.7 1
10	Crowdsourcing digital health measures to predict Parkinson's disease severity: the Parkinson's Disease Digital Biomarker DREAM Challenge	1
9	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth	1
8	High throughput single cell sequencing of both T-cell-receptor-beta alleles	1
7	Comparative analysis of molecular representations in prediction of drug combination effects	1
6	Asymmetric Predictive Relationships Across Histone Modifications.. <i>Nature Machine Intelligence</i> , 2022 , 4, 288-299	22.5 1
5	Heterogeneous digital biomarker integration out-performs patient self-reports in predicting Parkinson's disease.. <i>Communications Biology</i> , 2022 , 5, 58	6.7 0
4	Enabling Eating Detection in a Free-living Environment: Integrative Engineering and Machine Learning Study.. <i>Journal of Medical Internet Research</i> , 2022 , 24, e27934	7.6 0
3	Deep learning identifies erroneous microarray-based, gene-level conclusions in literature. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab089	3.7
2	Timesias: A machine learning pipeline for predicting outcomes from time-series clinical records. <i>STAR Protocols</i> , 2021 , 2, 100639	1.4
1	Micro-dissection and integration of long and short reads to create a robust catalog of kidney compartment-specific isoforms.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010040	5