

# Guoqiang Yu

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

2,341  
citations

516710

16  
h-index

361022

35  
g-index

50  
all docs

50  
docs citations

50  
times ranked

4314  
citing authors

#	ARTICLE	IF	CITATIONS
1	Developmental Heterogeneity of Microglia and Brain Myeloid Cells Revealed by Deep Single-Cell RNA Sequencing. <i>Neuron</i> , 2019, 101, 207-223.e10.	8.1	695
2	DBS: a fast and informative segmentation algorithm for DNA copy number analysis. <i>BMC Bioinformatics</i> , 2019, 20, 1.	2.6	588
3	Single-Cell Transcriptomics Uncovers Glial Progenitor Diversity and Cell Fate Determinants during Development and Gliomagenesis. <i>Cell Stem Cell</i> , 2019, 24, 707-723.e8.	11.1	145
4	Accurate quantification of astrocyte and neurotransmitter fluorescence dynamics for single-cell and population-level physiology. <i>Nature Neuroscience</i> , 2019, 22, 1936-1944.	14.8	122
5	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. <i>Circulation</i> , 2018, 137, 2741-2756.	1.6	100
6	Microglial microRNAs mediate sex-specific responses to tau pathology. <i>Nature Neuroscience</i> , 2020, 23, 167-171.	14.8	79
7	Mathematical modelling of transcriptional heterogeneity identifies novel markers and subpopulations in complex tissues. <i>Scientific Reports</i> , 2016, 6, 18909.	3.3	57
8	AD-linked R47H- <i>TREM2</i> mutation induces disease-enhancing microglial states via AKT hyperactivation. <i>Science Translational Medicine</i> , 2021, 13, eabe3947.	12.4	55
9	An algorithm for learning maximum entropy probability models of disease risk that efficiently searches and sparingly encodes multilocus genomic interactions. <i>Bioinformatics</i> , 2009, 25, 2478-2485.	4.1	49
10	Astroglial dysfunctions drive aberrant synaptogenesis and social behavioral deficits in mice with neonatal exposure to lengthy general anesthesia. <i>PLoS Biology</i> , 2019, 17, e3000086.	5.6	49
11	Incorporating prior biological knowledge for network-based differential gene expression analysis using differentially weighted graphical LASSO. <i>BMC Bioinformatics</i> , 2017, 18, 99.	2.6	40
12	Aberrant Calcium Signaling in Astrocytes Inhibits Neuronal Excitability in a Human Down Syndrome Stem Cell Model. <i>Cell Reports</i> , 2018, 24, 355-365.	6.4	39
13	Biological network inference using low order partial correlation. <i>Methods</i> , 2014, 69, 266-273.	3.8	35
14	Comparative analysis of methods for detecting interacting loci. <i>BMC Genomics</i> , 2011, 12, 344.	2.8	31
15	BACOM: <i>in silico</i> detection of genomic deletion types and correction of normal cell contamination in copy number data. <i>Bioinformatics</i> , 2011, 27, 1473-1480.	4.1	30
16	INDEED: Integrated differential expression and differential network analysis of omic data for biomarker discovery. <i>Methods</i> , 2016, 111, 12-20.	3.8	28
17	SynQuant: an automatic tool to quantify synapses from microscopy images. <i>Bioinformatics</i> , 2020, 36, 1599-1606.	4.1	24
18	PUGSVM: a caBIGTM analytical tool for multiclass gene selection and predictive classification. <i>Bioinformatics</i> , 2011, 27, 736-738.	4.1	19

#	ARTICLE	IF	CITATIONS
19	A Neural Basis for Categorizing Sensory Stimuli to Enhance Decision Accuracy. <i>Current Biology</i> , 2020, 30, 4896-4909.e6.	3.9	18
20	Automated Functional Analysis of Astrocytes from Chronic Time-Lapse Calcium Imaging Data. <i>Frontiers in Neuroinformatics</i> , 2017, 11, 48.	2.5	16
21	Identification of Putative Early Atherosclerosis Biomarkers by Unsupervised Deconvolution of Heterogeneous Vascular Proteomes. <i>Journal of Proteome Research</i> , 2020, 19, 2794-2806.	3.7	16
22	Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. <i>Scientific Reports</i> , 2017, 7, 4091.	3.3	15
23	Targeted realignment of LC-MS profiles by neighbor-wise compound-specific graphical time warping with misalignment detection. <i>Bioinformatics</i> , 2020, 36, 2862-2871.	4.1	14
24	Bioinformatic Analysis Of Coronary Disease Associated SNPs And Genes To Identify Proteins Potentially Involved In The Pathogenesis Of Atherosclerosis. <i>Journal of Proteomics and Genomics Research</i> , 2017, 2, 1-12.	0.7	10
25	Data-driven detection of subtype-specific differentially expressed genes. <i>Scientific Reports</i> , 2021, 11, 332.	3.3	9
26	Comparative assessment and novel strategy on methods for imputing proteomics data. <i>Scientific Reports</i> , 2022, 12, 1067.	3.3	8
27	BACOM2.0 facilitates absolute normalization and quantification of somatic copy number alterations in heterogeneous tumor. <i>Scientific Reports</i> , 2015, 5, 13955.	3.3	6
28	Integrating prior biological knowledge and graphical LASSO for network inference. , 2015, , .		5
29	Efficient Global MOT Under Minimum-Cost Circulation Framework. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2022, 44, 1888-1904.	13.9	5
30	swCAM: estimation of subtype-specific expressions in individual samples with unsupervised sample-wise deconvolution. <i>Bioinformatics</i> , 2022, 38, 1403-1410.	4.1	5
31	COT: an efficient and accurate method for detecting marker genes among many subtypes. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	5
32	GPA: An algorithm for LC/MS based glycan profile annotation. , 2013, , .		4
33	A new approach for multi-omic data integration. , 2014, , .		4
34	FASP: A machine learning approach to functional astrocyte phenotyping from time-lapse calcium imaging data. , 2016, , .		4
35	Met is required for oligodendrocyte progenitor cell migration in <i>Danio rerio</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
36	Detection and tracking of migrating oligodendrocyte progenitor cells from in vivo fluorescence time-lapse imaging data. , 2018, 2018, 961-964.		3

#	ARTICLE	IF	CITATIONS
37	Genomic and network analysis to study the origin of ovarian cancer. Systems Biomedicine (Austin, Tex) Tj ETQq1 1 0,784314,rgBT /Ove	0.7	1
38	Biologically inspired survival analysis based on integrating gene expression as mediator with genomic variants. Computers in Biology and Medicine, 2016, 77, 231-239.	7.0	1
39	Topic model-based mass spectrometric data analysis in cancer biomarker discovery studies. BMC Genomics, 2016, 17, 545.	2.8	1
40	A Graph Based Methodology for Temporal Signature Identification from HER. AMIA ... Annual Symposium proceedings, 2015, 2015, 1269-78.	0.2	1
41	Detection of complex interactions of multi-locus SNPS. , 2008, , .		0
42	Analyzing DNA Copy Number Changes Using Fused Margin Regression. , 2009, , .		0
43	Accurate Estimation of Genomic Deletions and Normal Cell Contamination by Bayesian Analysis of Mixtures. , 2009, , .		0
44	A non-parametric approach for estimating stromal contamination in cancer samples. , 2012, , .		0
45	Accurate identification of significant aberrations in contaminated cancer genome. , 2012, , .		0
46	NMF based approach for finding recurrent aberrations in DNA copy number data. , 2012, , .		0
47	Predicting age at loss of ambulation in Duchenne muscular dystrophy with deep phenotypic measures. , 2014, , .		0
48	Asymmetric independence modeling identifies novel gene-environment interactions. Scientific Reports, 2019, 9, 2455.	3.3	0
49	An Unsupervised Approach to Detect Microglia Tip in Volumetric Fluorescence Imaging Data. , 2022, , .		0