Guoqiang Yu

List of Publications by Year in descending order

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	Efficient Global MOT Under Minimum-Cost Circulation Framework. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2022, 44, 1888-1904.	13.9	5
2	Comparative assessment and novel strategy on methods for imputing proteomics data. Scientific Reports, 2022, 12, 1067.	3.3	8
3	swCAM: estimation of subtype-specific expressions in individual samples with unsupervised sample-wise deconvolution. Bioinformatics, 2022, 38, 1403-1410.	4.1	5
4	An Unsupervised Approach to Detect Microglia Tip in Volumetric Fluorescence Imaging Data. , 2022, , .		0
5	COT: an efficient and accurate method for detecting marker genes among many subtypes. Bioinformatics Advances, 2022, 2, .	2.4	5
6	Met is required for oligodendrocyte progenitor cell migration in <i>Danio rerio</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	4
7	Data-driven detection of subtype-specific differentially expressed genes. Scientific Reports, 2021, 11, 332.	3.3	9
8	AD-linked R47H- <i>TREM2</i> mutation induces disease-enhancing microglial states via AKT hyperactivation. Science Translational Medicine, 2021, 13, eabe3947.	12.4	55
9	SynQuant: an automatic tool to quantify synapses from microscopy images. Bioinformatics, 2020, 36, 1599-1606.	4.1	24
10	Microglial microRNAs mediate sex-specific responses to tau pathology. Nature Neuroscience, 2020, 23, 167-171.	14.8	79
11	A Neural Basis for Categorizing Sensory Stimuli to Enhance Decision Accuracy. Current Biology, 2020, 30, 4896-4909.e6.	3.9	18
12	Identification of Putative Early Atherosclerosis Biomarkers by Unsupervised Deconvolution of Heterogeneous Vascular Proteomes. Journal of Proteome Research, 2020, 19, 2794-2806.	3.7	16
13	Targeted realignment of LC-MS profiles by neighbor-wise compound-specific graphical time warping with misalignment detection. Bioinformatics, 2020, 36, 2862-2871.	4.1	14
14	Astroglial dysfunctions drive aberrant synaptogenesis and social behavioral deficits in mice with neonatal exposure to lengthy general anesthesia. PLoS Biology, 2019, 17, e3000086.	5.6	49
15	DBS: a fast and informative segmentation algorithm for DNA copy number analysis. BMC Bioinformatics, 2019, 20, 1.	2.6	588
16	Asymmetric independence modeling identifies novel gene-environment interactions. Scientific Reports, 2019, 9, 2455.	3.3	0
17	Single-Cell Transcriptomics Uncovers Glial Progenitor Diversity and Cell Fate Determinants during Development and Gliomagenesis. Cell Stem Cell, 2019, 24, 707-723.e8.	11.1	145
18	Accurate quantification of astrocyte and neurotransmitter fluorescence dynamics for single-cell and population-level physiology. Nature Neuroscience, 2019, 22, 1936-1944.	14.8	122

#	Article	IF	Citations
19	Developmental Heterogeneity of Microglia and Brain Myeloid Cells Revealed by Deep Single-Cell RNA Sequencing. Neuron, 2019, 101, 207-223.e10.	8.1	695
20	Aberrant Calcium Signaling in Astrocytes Inhibits Neuronal Excitability in a Human Down Syndrome Stem Cell Model. Cell Reports, 2018, 24, 355-365.	6.4	39
21	Detection and tracking of migrating oligodendrocyte progenitor cells from in vivo fluorescence time-lapse imaging data. , 2018, 2018, 961-964.		3
22	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation, 2018, 137, 2741-2756.	1.6	100
23	Incorporating prior biological knowledge for network-based differential gene expression analysis using differentially weighted graphical LASSO. BMC Bioinformatics, 2017, 18, 99.	2.6	40
24	Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. Scientific Reports, 2017, 7, 4091.	3.3	15
25	Bioinformatic Analysis Of Coronary Disease Associated SNPs And Genes To Identify Proteins Potentially Involved In The Pathogenesis Of Atherosclerosis. Journal of Proteomics and Genomics Research, 2017, 2, 1-12.	0.7	10
26	Automated Functional Analysis of Astrocytes from Chronic Time-Lapse Calcium Imaging Data. Frontiers in Neuroinformatics, 2017, 11, 48.	2.5	16
27	Mathematical modelling of transcriptional heterogeneity identifies novel markers and subpopulations in complex tissues. Scientific Reports, 2016, 6, 18909.	3.3	57
28	FASP: A machine learning approach to functional astrocyte phenotyping from time-lapse calcium imaging data. , 2016, , .		4
29	INDEED: Integrated differential expression and differential network analysis of omic data for biomarker discovery. Methods, 2016, 111, 12-20.	3.8	28
30	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
31	Topic model-based mass spectrometric data analysis in cancer biomarker discovery studies. BMC Genomics, 2016, 17, 545.	2.8	1
32	BACOM2.0 facilitates absolute normalization and quantification of somatic copy number alterations in heterogeneous tumor. Scientific Reports, 2015, 5, 13955.	3.3	6
33	Integrating prior biological knowledge and graphical LASSO for network inference. , 2015, , .		5
34	A Graph Based Methodology for Temporal Signature Identification from HER. AMIA ... Annual Symposium proceedings, 2015, 2015, 1269-78.	0.2	1
35	A new approach for multi-omic data integration. , 2014, , .		4
36	Biological network inference using low order partial correlation. Methods, 2014, 69, 266-273.	3.8	35

#	Article	IF	Citations
37	Predicting age at loss of ambulation in Duchenne muscular dystrophy with deep phenotypic measures. , 2014, , .		0
38	GPA: An algorithm for LC/MS based glycan profile annotation. , 2013, , .		4
39	Genomic and network analysis to study the origin of ovarian cancer. Systems Biomedicine (Austin, Tex) Tj ETQq1 1 0.784314 rgBT /Ov	0.7	1
40	A non-parametric approach for estimating stromal contamination in cancer samples. , 2012, , .		0
41	Accurate identification of significant aberrations in contaminated cancer genome. , 2012, , .		0
42	NMF based approach for finding recurrent aberrations in DNA copy number data. , 2012, , .		0
43	Comparative analysis of methods for detecting interacting loci. BMC Genomics, 2011, 12, 344.	2.8	31
44	BACOM: <i>in silico</i> detection of genomic deletion types and correction of normal cell contamination in copy number data. Bioinformatics, 2011, 27, 1473-1480.	4.1	30
45	PUGSVM: a caBIGTM analytical tool for multiclass gene selection and predictive classification. Bioinformatics, 2011, 27, 736-738.	4.1	19
46	Analyzing DNA Copy Number Changes Using Fused Margin Regression. , 2009, , .		0
47	Accurate Estimation of Genomic Deletions and Normal Cell Contamination by Bayesian Analysis of Mixtures. , 2009, , .		0
48	An algorithm for learning maximum entropy probability models of disease risk that efficiently searches and sparingly encodes multilocus genomic interactions. Bioinformatics, 2009, 25, 2478-2485.	4.1	49
49	Detection of complex interactions of multi-locus SNPS. , 2008, , .		0