

Jin Gu

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,785
citations

394421

19
h-index

434195

31
g-index

35
all docs

35
docs citations

35
times ranked

2619
citing authors

#	ARTICLE	IF	CITATIONS
1	Multifaceted Spatial and Functional Zonation of Cardiac Cells in Adult Human Heart. <i>Circulation</i> , 2022, 145, 315-318.	1.6	8
2	JEBIN: analyzing gene co-expressions across multiple datasets by joint network embedding. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	1
3	Highly Regional Genes: graph-based gene selection for single-cell RNA-seq data. <i>Journal of Genetics and Genomics</i> , 2022, 49, 891-899.	3.9	11
4	Elucidating minimal residual disease of paediatric B-cell acute lymphoblastic leukaemia by single-cell analysis. <i>Nature Cell Biology</i> , 2022, 24, 242-252.	10.3	14
5	scCancer: a package for automated processing of single-cell RNA-seq data in cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	35
6	Integrative Genomic Analysis of Gemcitabine Resistance in Pancreatic Cancer by Patient-derived Xenograft Models. <i>Clinical Cancer Research</i> , 2021, 27, 3383-3396.	7.0	36
7	Discovery of a Carbamoyl Phosphate Synthetase 1â€‘Deficient HCC Subtype With Therapeutic Potential Through Integrative Genomic and Experimental Analysis. <i>Hepatology</i> , 2021, 74, 3249-3268.	7.3	26
8	Comprehensive analysis of spatial architecture in primary liver cancer. <i>Science Advances</i> , 2021, 7, eabg3750.	10.3	113
9	Trajectory and Functional Analysis of PDâ€‘1 ^{high} CD4 ⁺ CD8 ⁺ T Cells in Hepatocellular Carcinoma by Singleâ€‘Cell Cytometry and Transcriptome Sequencing. <i>Advanced Science</i> , 2020, 7, 2000224.	11.2	62
10	Hexosamine pathway inhibition overcomes pancreatic cancer resistance to gemcitabine through unfolded protein response and EGFR-Akt pathway modulation. <i>Oncogene</i> , 2020, 39, 4103-4117.	5.9	33
11	Effects of somatic alterations at pathway level are more mechanismâ€‘explanatory and clinically applicable to quantity of liver metastases of colorectal cancer. <i>Cancer Medicine</i> , 2019, 8, 4732-4742.	2.8	1
12	Integrative molecular analysis of metastatic hepatocellular carcinoma. <i>BMC Medical Genomics</i> , 2019, 12, 164.	1.5	11
13	Genome-wide DNA methylation analysis identifies candidate epigenetic markers and drivers of hepatocellular carcinoma. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw094.	6.5	53
14	VASC: Dimension Reduction and Visualization of Single-cell RNA-seq Data by Deep Variational Autoencoder. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 320-331.	6.9	176
15	HCCDB: A Database of Hepatocellular Carcinoma Expression Atlas. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 269-275.	6.9	218
16	Choline Kinase Î± Mediates Interactions Between the Epidermal Growth Factor Receptor and Mechanistic Target of Rapamycin Complex 2 in Hepatocellular Carcinoma Cells to Promote Drug Resistance and Xenograft Tumor Progression. <i>Gastroenterology</i> , 2017, 152, 1187-1202.	1.3	48
17	Recurrently deregulated lncRNAs in hepatocellular carcinoma. <i>Nature Communications</i> , 2017, 8, 14421.	12.8	279
18	Network embedding-based representation learning for single cell RNA-seq data. <i>Nucleic Acids Research</i> , 2017, 45, e166-e166.	14.5	54

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19	Evaluating the molecule-based prediction of clinical drug responses in cancer. <i>Bioinformatics</i> , 2016, 32, 2891-2895.	4.1	113
20	Integrative clustering methods of multi-omics data for molecule-based cancer classifications. <i>Quantitative Biology</i> , 2016, 4, 58-67.	0.5	51
21	Fast dimension reduction and integrative clustering of multi-omics data using low-rank approximation: application to cancer molecular classification. <i>BMC Genomics</i> , 2015, 16, 1022.	2.8	124
22	SCT Promoter Methylation Is a Highly Discriminative Biomarker for Lung and Many Other Cancers. <i>IEEE Life Sciences Letters</i> , 2015, 1, 30-33.	1.2	2
23	Gene module based regulator inference identifying miR-139 as a tumor suppressor in colorectal cancer. <i>Molecular BioSystems</i> , 2014, 10, 3249-3254.	2.9	13
24	Inferring the perturbed microRNA regulatory networks from gene expression data using a network propagation based method. <i>BMC Bioinformatics</i> , 2014, 15, 255.	2.6	10
25	OncomiRDB: a database for the experimentally verified oncogenic and tumor-suppressive microRNAs. <i>Bioinformatics</i> , 2014, 30, 2237-2238.	4.1	141
26	FastDMA: An Infinium HumanMethylation450 Beadchip Analyzer. <i>PLoS ONE</i> , 2013, 8, e74275.	2.5	25
27	Inferring the Perturbed microRNA Regulatory Networks in Cancer Using Hierarchical Gene Co-Expression Signatures. <i>PLoS ONE</i> , 2013, 8, e81032.	2.5	9
28	Towards integrative annotation of the cell-type specific gene functional and signaling map in vascular endothelial cells. <i>Molecular BioSystems</i> , 2012, 8, 2041.	2.9	5
29	Identification of responsive gene modules by network-based gene clustering and extending: application to inflammation and angiogenesis. <i>BMC Systems Biology</i> , 2010, 4, 47.	3.0	56
30	Computational identification of 99 insect MicroRNAs using comparative genomics. <i>Tsinghua Science and Technology</i> , 2008, 13, 425-432.	6.1	2
31	Identifications of conserved 7-mers in 3'-UTRs and microRNAs in <i>Drosophila</i> . <i>BMC Bioinformatics</i> , 2007, 8, 432.	2.6	12
32	Primary transcripts and expressions of mammal intergenic microRNAs detected by mapping ESTs to their flanking sequences. <i>Mammalian Genome</i> , 2006, 17, 1033-1041.	2.2	33