Jin Gu

List of Publications by Year
in descending order

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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	Recurrently deregulated lncRNAs in hepatocellular carcinoma. Nature Communications, 2017, 8, 14421.	12.8	279
2	HCCDB: A Database of Hepatocellular Carcinoma Expression Atlas. Genomics, Proteomics and Bioinformatics, 2018, 16, 269-275.	6.9	218
3	VASC: Dimension Reduction and Visualization of Single-cell RNA-seq Data by Deep Variational Autoencoder. Genomics, Proteomics and Bioinformatics, 2018, 16, 320-331.	6.9	176
4	OncomiRDB: a database for the experimentally verified oncogenic and tumor-suppressive microRNAs. Bioinformatics, 2014, 30, 2237-2238.	4.1	141
5	Fast dimension reduction and integrative clustering of multi-omics data using low-rank approximation: application to cancer molecular classification. BMC Genomics, 2015, 16, 1022.	2.8	124
6	Evaluating the molecule-based prediction of clinical drug responses in cancer. Bioinformatics, 2016, 32, 2891-2895.	4.1	113
7	Comprehensive analysis of spatial architecture in primary liver cancer. Science Advances, 2021, 7, eabg3750.	10.3	113
8	Trajectory and Functional Analysis of PDâ€1 ^{high} CD4⁺CD8⁺ T Cells in Hepatocellular Carcinoma by Singleâ€Cell Cytometry and Transcriptome Sequencing. Advanced Science, 2020, 7, 2000224.	11.2	62
9	Identification of responsive gene modules by network-based gene clustering and extending: application to inflammation and angiogenesis. BMC Systems Biology, 2010, 4, 47.	3.0	56
10	Network embedding-based representation learning for single cell RNA-seq data. Nucleic Acids Research, 2017, 45, e166-e166.	14.5	54
11	Genome-wide DNA methylation analysis identifies candidate epigenetic markers and drivers of hepatocellular carcinoma. Briefings in Bioinformatics, 2018, 19, bbw094.	6.5	53
12	Integrative clustering methods of multiâ€omics data for moleculeâ€based cancer classifications. Quantitative Biology, 2016, 4, 58-67.	0.5	51
13	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. Gastroenterology, 2017, 152, 1187-1202.	1.3	48
14	Integrative Genomic Analysis of Gemcitabine Resistance in Pancreatic Cancer by Patient-derived Xenograft Models. Clinical Cancer Research, 2021, 27, 3383-3396.	7.0	36
15	scCancer: a package for automated processing of single-cell RNA-seq data in cancer. Briefings in Bioinformatics, 2021, 22, .	6.5	35
16	Primary transcripts and expressions of mammal intergenic microRNAs detected by mapping ESTs to their flanking sequences. Mammalian Genome, 2006, 17, 1033-1041.	2.2	33
17	Hexosamine pathway inhibition overcomes pancreatic cancer resistance to gemcitabine through unfolded protein response and EGFR-Akt pathway modulation. Oncogene, 2020, 39, 4103-4117.	5.9	33
18	Discovery of a Carbamoyl Phosphate Synthetase 1â€"Deficient HCC Subtype With Therapeutic Potential Through Integrative Genomic and Experimental Analysis. Hepatology, 2021, 74, 3249-3268.	7.3	26

#	Article	IF	Citations
19	FastDMA: An Infinium HumanMethylation450 Beadchip Analyzer. PLoS ONE, 2013, 8, e74275.	2.5	25
20	Elucidating minimal residual disease of paediatric B-cell acute lymphoblastic leukaemia by single-cell analysis. Nature Cell Biology, 2022, 24, 242-252.	10.3	14
21	Gene module based regulator inference identifying miR-139 as a tumor suppressor in colorectal cancer. Molecular BioSystems, 2014, 10, 3249-3254.	2.9	13
22	Identifications of conserved 7-mers in 3'-UTRs and microRNAs in Drosophila. BMC Bioinformatics, 2007, 8, 432.	2.6	12
23	Integrative molecular analysis of metastatic hepatocellular carcinoma. BMC Medical Genomics, 2019, 12, 164.	1.5	11
24	Highly Regional Genes: graph-based gene selection for single-cell RNA-seq data. Journal of Genetics and Genomics, 2022, 49, 891-899.	3.9	11
25	Inferring the perturbed microRNA regulatory networks from gene expression data using a network propagation based method. BMC Bioinformatics, 2014, 15, 255.	2.6	10
26	Inferring the Perturbed microRNA Regulatory Networks in Cancer Using Hierarchical Gene Co-Expression Signatures. PLoS ONE, 2013, 8, e81032.	2.5	9
27	Multifaceted Spatial and Functional Zonation of Cardiac Cells in Adult Human Heart. Circulation, 2022, 145, 315-318.	1.6	8
28	Towards integrative annotation of the cell-type specific gene functional and signaling map in vascular endothelial cells. Molecular BioSystems, 2012, 8, 2041.	2.9	5
29	Computational identification of 99 insect MicroRNAs using comparative genomics. Tsinghua Science and Technology, 2008, 13, 425-432.	6.1	2
30	SCT Promoter Methylation Is a Highly Discriminative Biomarker for Lung and Many Other Cancers. IEEE Life Sciences Letters, 2015, 1, 30-33.	1.2	2
31	Effects of somatic alterations at pathway level are more mechanismâ€explanatory and clinically applicable to quantity of liver metastases of colorectal cancer. Cancer Medicine, 2019, 8, 4732-4742.	2.8	1
32	JEBIN: analyzing gene co-expressions across multiple datasets by joint network embedding. Briefings in Bioinformatics, 2022, 23, .	6.5	1