

Hui Jiang

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

19,446
citations

126708

33
h-index

74018

75
g-index

80
all docs

80
docs citations

80
times ranked

42106
citing authors

#	ARTICLE	IF	CITATIONS
1	Advancement of PI3 Kinase Inhibitor Combination Therapies for PI3K-Aberrant Chordoma. <i>Journal of Neurological Surgery, Part B: Skull Base</i> , 2022, 83, 087-098.	0.4	3
2	Small molecule profiling to define synergistic EGFR inhibitor combinations in head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2022, 44, 1192-1205.	0.9	5
3	Genetic analysis of sinonasal undifferentiated carcinoma discovers recurrent SWI/SNF alterations and a novel PGAP3-SRPK1 fusion gene. <i>BMC Cancer</i> , 2021, 21, 636.	1.1	9
4	Microbe-Mediated Activation of Toll-like Receptor 2 Drives PDL1 Expression in HNSCC. <i>Cancers</i> , 2021, 13, 4782.	1.7	4
5	Genome-wide pQTL analysis of protein expression regulatory networks in the human liver. <i>BMC Biology</i> , 2020, 18, 97.	1.7	49
6	Combined p53- and PTEN-deficiency activates expression of mesenchyme homeobox 1 (MEOX1) required for growth of triple-negative breast cancer. <i>Journal of Biological Chemistry</i> , 2020, 295, 12188-12202.	1.6	16
7	Single-Cell Transcriptomics Analysis Identifies Nuclear Protein 1 as a Regulator of Docetaxel Resistance in Prostate Cancer Cells. <i>Molecular Cancer Research</i> , 2020, 18, 1290-1301.	1.5	25
8	Variability in protein cargo detection in technical and biological replicates of exosome-enriched extracellular vesicles. <i>PLoS ONE</i> , 2020, 15, e0228871.	1.1	14
9	A Potent and Selective Small-Molecule Degradator of STAT3 Achieves Complete Tumor Regression In Vivo. <i>Cancer Cell</i> , 2019, 36, 498-511.e17.	7.7	364
10	The in vivo endothelial cell transcriptome is highly heterogeneous across vascular beds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23618-23624.	3.3	89
11	Identifying Interaction Clusters for miRNA and mRNA Pairs in TCGA Network. <i>Genes</i> , 2019, 10, 702.	1.0	13
12	False Discovery Rate Control in Cancer Biomarker Selection Using Knockoffs. <i>Cancers</i> , 2019, 11, 744.	1.7	12
13	The molecular landscape of the University of Michigan laryngeal squamous cell carcinoma cell line panel. <i>Head and Neck</i> , 2019, 41, 3114-3124.	0.9	23
14	Label-free absolute protein quantification with data-independent acquisition. <i>Journal of Proteomics</i> , 2019, 200, 51-59.	1.2	60
15	Rationale for Using Irreversible Epidermal Growth Factor Receptor Inhibitors in Combination with Phosphatidylinositol 3-Kinase Inhibitors for Advanced Head and Neck Squamous Cell Carcinoma. <i>Molecular Pharmacology</i> , 2019, 95, 528-536.	1.0	17
16	Joint between-sample normalization and differential expression detection through λ_0 -regularized regression. <i>BMC Bioinformatics</i> , 2019, 20, 593.	1.2	1
17	Response to the Comments on "Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Proteomics Method". <i>Journal of Proteome Research</i> , 2019, 18, 1458-1459.	1.8	0
18	Accurate and efficient estimation of small P -values with the cross-entropy method: applications in genomic data analysis. <i>Bioinformatics</i> , 2019, 35, 2441-2448.	1.8	6

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19	Minimizing Sum of Truncated Convex Functions and Its Applications. <i>Journal of Computational and Graphical Statistics</i> , 2019, 28, 1-10.	0.9	17
20	A Unified Model for Joint Normalization and Differential Gene Expression Detection in RNA-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 442-454.	1.9	13
21	Comparison of protein expression between human livers and the hepatic cell lines HepG2, Hep3B, and Huh7 using SWATH and MRM-HR proteomics: Focusing on drug-metabolizing enzymes. <i>Drug Metabolism and Pharmacokinetics</i> , 2018, 33, 133-140.	1.1	42
22	Testing the performance of a prototype lateral flow device using bronchoalveolar lavage fluid for the diagnosis of invasive pulmonary aspergillosis in high-risk patients. <i>Mycoses</i> , 2018, 61, 4-10.	1.8	15
23	Fast Approximation of Small P-values in Permutation Tests by Partitioning the Permutations. <i>Biometrics</i> , 2018, 74, 196-206.	0.8	15
24	A Unified Model for Robust Differential Expression Analysis of RNA-Seq Data. , 2018, , .		0
25	False discovery control for penalized variable selections with high-dimensional covariates. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2018, 17, .	0.2	1
26	The genomic landscape of UM-SCC oral cavity squamous cell carcinoma cell lines. <i>Oral Oncology</i> , 2018, 87, 144-151.	0.8	27
27	Targeting LRP8 inhibits breast cancer stem cells in triple-negative breast cancer. <i>Cancer Letters</i> , 2018, 438, 165-173.	3.2	28
28	Analysis of the androgen receptor-regulated lncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. <i>Nature Genetics</i> , 2018, 50, 814-824.	9.4	196
29	Comprehensive multi-center assessment of small RNA-seq methods for quantitative miRNA profiling. <i>Nature Biotechnology</i> , 2018, 36, 746-757.	9.4	134
30	Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Based Proteomics Method. <i>Journal of Proteome Research</i> , 2018, 17, 3606-3612.	1.8	20
31	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. <i>Bayesian Analysis</i> , 2018, 13, 411-436.	1.6	5
32	Programmed Death-ligand 1 Expression in Upper Tract Urothelial Carcinoma. <i>European Urology Focus</i> , 2017, 3, 502-509.	1.6	25
33	Targeted Degradation of BET Proteins in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2476-2487.	0.4	173
34	Development of Peptidomimetic Inhibitors of the ERG Gene Fusion Product in Prostate Cancer. <i>Cancer Cell</i> , 2017, 31, 532-548.e7.	7.7	85
35	Unit-Free and Robust Detection of Differential Expression from RNA-Seq Data. <i>Statistics in Biosciences</i> , 2017, 9, 178-199.	0.6	4
36	Differential regulation of the c-Myc/Lin28 axis discriminates subclasses of rearranged MLL leukemia. <i>Oncotarget</i> , 2016, 7, 25208-25223.	0.8	19

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37	Concurrent nuclear ERG and MYC protein overexpression defines a subset of locally advanced prostate cancer: Potential opportunities for synergistic targeted therapeutics. <i>Prostate</i> , 2016, 76, 845-853.	1.2	9
38	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <i>Nature Communications</i> , 2016, 7, 11764.	5.8	114
39	Comparative analysis of circulating tumor DNA stability In K3EDTA, Streck, and CellSave blood collection tubes. <i>Clinical Biochemistry</i> , 2016, 49, 1354-1360.	0.8	175
40	Dissecting the biological relationship between TCGA miRNA and mRNA sequencing data using MMiRNA-Viewer. <i>BMC Bioinformatics</i> , 2016, 17, 336.	1.2	10
41	Computational Aspects of Optional P ³ ly Tree. <i>Journal of Computational and Graphical Statistics</i> , 2016, 25, 301-320.	0.9	4
42	Expression of PDL1 (B7-H1) Before and After Neoadjuvant Chemotherapy in Urothelial Carcinoma. <i>European Urology Focus</i> , 2016, 1, 265-268.	1.6	45
43	Novel cancer stem cell targets during epithelial to mesenchymal transition in PTEN-deficient trastuzumab-resistant breast cancer. <i>Oncotarget</i> , 2016, 7, 51408-51422.	0.8	37
44	Trastuzumab resistance induces EMT to transform HER2+ PTEN ⁺ to a triple negative breast cancer that requires unique treatment options. <i>Scientific Reports</i> , 2015, 5, 15821.	1.6	50
45	Performance of lateral flow device and galactomannan for the detection of <i>Aspergillus</i> species in bronchoalveolar fluid of patients at risk for invasive pulmonary aspergillosis. <i>Mycoses</i> , 2015, 58, 368-374.	1.8	26
46	rSeqNP: a non-parametric approach for detecting differential expression and splicing from RNA-Seq data. <i>Bioinformatics</i> , 2015, 31, 2222-2224.	1.8	13
47	Correlating Bladder Cancer Risk Genes with Their Targeting MicroRNAs Using MMiRNA-Tar. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 177-182.	3.0	8
48	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
49	Clinicopathologic characteristics of anterior prostate cancer (APC), including correlation with previous biopsy pathology. <i>Medical Oncology</i> , 2015, 32, 249.	1.2	10
50	A penalized likelihood approach for robust estimation of isoform expression. <i>Statistics and Its Interface</i> , 2015, 8, 437-445.	0.2	11
51	Differential Regulation of c-Myc/Lin28 Discriminates Subclasses of Rearranged MLL Leukemia. <i>Blood</i> , 2015, 126, 163-163.	0.6	0
52	Expansion of CTCs from early stage lung cancer patients using a microfluidic co-culture model. <i>Oncotarget</i> , 2014, 5, 12383-12397.	0.8	175
53	A Novel RNA In Situ Hybridization Assay for the Long Noncoding RNA SchLAP1 Predicts Poor Clinical Outcome After Radical Prostatectomy in Clinically Localized Prostate Cancer. <i>Neoplasia</i> , 2014, 16, 1121-1127.	2.3	81
54	Frequent discordance between ERG gene rearrangement and ERG protein expression in a rapid autopsy cohort of patients with lethal, metastatic, castration-resistant prostate cancer. <i>Prostate</i> , 2014, 74, 1199-1208.	1.2	33

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55	RNA-Seq Accurately Identifies Cancer Biomarker Signatures to Distinguish Tissue of Origin. <i>Neoplasia</i> , 2014, 16, 918-927.	2.3	37
56	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. <i>Reproductive Sciences</i> , 2014, 21, 32-40.	1.1	259
57	Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq. <i>Nature Cell Biology</i> , 2013, 15, 1244-1252.	4.6	88
58	Multivariate Density Estimation by Bayesian Sequential Partitioning. <i>Journal of the American Statistical Association</i> , 2013, 108, 1402-1410.	1.8	39
59	rSeqDiff: Detecting Differential Isoform Expression from RNA-Seq Data Using Hierarchical Likelihood Ratio Test. <i>PLoS ONE</i> , 2013, 8, e79448.	1.1	29
60	Statistical properties of an early stopping rule for resampling-based multiple testing. <i>Biometrika</i> , 2012, 99, 973-980.	1.3	17
61	Fast and accurate read alignment for resequencing. <i>Bioinformatics</i> , 2012, 28, 2366-2373.	1.8	48
62	The dynamics of the vaginal microbiome during infertility therapy with in vitro fertilization-embryo transfer. <i>Journal of Assisted Reproduction and Genetics</i> , 2012, 29, 105-115.	1.2	124
63	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. <i>PLoS ONE</i> , 2012, 7, e31440.	1.1	7
64	Using CisGenome to Analyze ChIP-chip and ChIP-seq Data. <i>Current Protocols in Bioinformatics</i> , 2011, 33, Unit2.13.	25.8	34
65	Statistical Modeling of RNA-Seq Data. <i>Statistical Science</i> , 2011, 26, .	1.6	64
66	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	3.3	122
67	A direct comparison of the KB ₊ Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. <i>BMC Research Notes</i> , 2010, 3, 257.	0.6	9
68	CisGenome Browser: a flexible tool for genomic data visualization. <i>Bioinformatics</i> , 2010, 26, 1781-1782.	1.8	37
69	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. <i>Nucleic Acids Research</i> , 2010, 38, 4570-4578.	6.5	300
70	Modeling non-uniformity in short-read rates in RNA-Seq data. <i>Genome Biology</i> , 2010, 11, R50.	13.9	165
71	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 3056-3059.	1.8	54
72	Statistical inferences for isoform expression in RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1026-1032.	1.8	405

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73	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	9.4	662
74	An optimization algorithm for designing phase I cancer clinical trials. Contemporary Clinical Trials, 2008, 29, 102-108.	0.8	6
75	SeqMap: mapping massive amount of oligonucleotides to the genome. Bioinformatics, 2008, 24, 2395-2396.	1.8	459
76	Cross-hybridization modeling on Affymetrix exon arrays. Bioinformatics, 2008, 24, 2887-2893.	1.8	35
77	MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. Rna, 2008, 14, 1470-1479.	1.6	86
78	Gestalt-based feature similarity measure in trademark database. Pattern Recognition, 2006, 39, 988-1001.	5.1	32
79	Graph based image matching. , 2004, , .		0