

Hui Jiang

List of Publications by Year in descending order

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99
papers

20,131
citations

94269

37
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37111

96
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101
all docs

101
docs citations

101
times ranked

42923
citing authors

#	ARTICLE	IF	CITATIONS
1	Collaborative Multilabel Classification. <i>Journal of the American Statistical Association</i> , 2023, 118, 913-924.	1.8	1
2	A Cross-Validation Statistical Framework for Asymmetric Data Integration. <i>Biometrics</i> , 2023, 79, 1280-1292.	0.8	0
3	A Two-Part Mixed Model for Differential Expression Analysis in Single-Cell High-Throughput Gene Expression Data. <i>Genes</i> , 2022, 13, 377.	1.0	3
4	Therapeutic Effects of Xianlu Oral Solution on Rats with Oligoasthenozoospermia through Alleviating Apoptosis and Oxidative Stress. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	2
5	Microbe-Mediated Activation of Toll-like Receptor 2 Drives PDL1 Expression in HNSCC. <i>Cancers</i> , 2021, 13, 4782.	1.7	4
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	Statistics in the Genomic Era. <i>Genes</i> , 2020, 11, 443.	1.0	1
10	The in vivo endothelial cell translome 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	Silencing of hsa_circ_0004771 inhibits proliferation and induces apoptosis in breast cancer through activation of miR-653 by targeting ZEB2 signaling pathway. <i>Bioscience Reports</i> , 2019, 39, .	1.1	62
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	Balanced Chromosomal Rearrangement Detection by Low-Pass Whole-Genome Sequencing. <i>Current Protocols in Human Genetics</i> , 2018, 96, 8.18.1-8.18.16.	3.5	10
22	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
23	Identification of balanced chromosomal rearrangements previously unknown among participants in the 1000 Genomes Project: implications for interpretation of structural variation in genomes and the future of clinical cytogenetics. <i>Genetics in Medicine</i> , 2018, 20, 697-707.	1.1	52
24	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
25	Fast Approximation of Small P-values in Permutation Tests by Partitioning the Permutations. <i>Biometrics</i> , 2018, 74, 196-206.	0.8	15
26	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
27	The genomic landscape of UM-SCC oral cavity squamous cell carcinoma cell lines. <i>Oral Oncology</i> , 2018, 87, 144-151.	0.8	27
28	Targeting LRP8 inhibits breast cancer stem cells in triple-negative breast cancer. <i>Cancer Letters</i> , 2018, 438, 165-173.	3.2	28
29	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
30	Comprehensive multi-center assessment of small RNA-seq methods for quantitative miRNA profiling. <i>Nature Biotechnology</i> , 2018, 36, 746-757.	9.4	134
31	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
32	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. <i>Bayesian Analysis</i> , 2018, 13, 411-436.	1.6	5
33	P-splines with an ℓ_1 penalty for repeated measures. <i>Electronic Journal of Statistics</i> , 2018, 12, .	0.4	3
34	Programmed Death-ligand 1 Expression in Upper Tract Urothelial Carcinoma. <i>European Urology Focus</i> , 2017, 3, 502-509.	1.6	25
35	Targeted Degradation of BET Proteins in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2476-2487.	0.4	173
36	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

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37	Unit-Free and Robust Detection of Differential Expression from RNA-Seq Data. <i>Statistics in Biosciences</i> , 2017, 9, 178-199.	0.6	4
38	Copy Number Variants Detection by Low-Pass Whole-Genome Sequencing. <i>Current Protocols in Human Genetics</i> , 2017, 94, 8.17.1-8.17.16.	3.5	19
39	Isolation and whole genome sequencing of fetal cells from maternal blood towards the ultimate non-invasive prenatal testing. <i>Prenatal Diagnosis</i> , 2017, 37, 1311-1321.	1.1	36
40	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	137
41	Identification of gene pairs through penalized regression subject to constraints. <i>BMC Bioinformatics</i> , 2017, 18, 466.	1.2	6
42	Differential regulation of the c-Myc/Lin28 axis discriminates subclasses of rearranged MLL leukemia. <i>Oncotarget</i> , 2016, 7, 25208-25223.	0.8	19
43	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
44	Clinical experience from Thailand: noninvasive prenatal testing as screening tests for trisomies 21, 18 and 13 in 4736 pregnancies. <i>Prenatal Diagnosis</i> , 2016, 36, 224-231.	1.1	18
45	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <i>Nature Communications</i> , 2016, 7, 11764.	5.8	114
46	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
47	First report of human salivirus/klassivirus in respiratory specimens of a child with fatal adenovirus infection. <i>Virus Genes</i> , 2016, 52, 620-624.	0.7	2
48	Dissecting the biological relationship between TCGA miRNA and mRNA sequencing data using MMiRNA-Viewer. <i>BMC Bioinformatics</i> , 2016, 17, 336.	1.2	10
49	Complete mitochondrial genome of the Saker falcon, <i>Falco cherrug</i> (Falco, Falconidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3226-3227.	0.7	3
50	Low-pass whole-genome sequencing in clinical cytogenetics: a validated approach. <i>Genetics in Medicine</i> , 2016, 18, 940-948.	1.1	138
51	Promoter targeted bisulfite sequencing reveals DNA methylation profiles associated with low sperm motility in asthenozoospermia. <i>Human Reproduction</i> , 2016, 31, 24-33.	0.4	47
52	Computational Aspects of Optional \mathbb{P}^3 Tree. <i>Journal of Computational and Graphical Statistics</i> , 2016, 25, 301-320.	0.9	4
53	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
54	Performance Evaluation of NIPT in Detection of Chromosomal Copy Number Variants Using Low-Coverage Whole-Genome Sequencing of Plasma DNA. <i>PLoS ONE</i> , 2016, 11, e0159233.	1.1	42

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55	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
56	Rapid diagnosis of <i>Propionibacterium acnes</i> infection in patient with hyperpyrexia after hematopoietic stem cell transplantation by next-generation sequencing: a case report. <i>BMC Infectious Diseases</i> , 2015, 16, 5.	1.3	18
57	Trastuzumab resistance induces EMT to transform HER2+ PTEN ^Δ to a triple negative breast cancer that requires unique treatment options. <i>Scientific Reports</i> , 2015, 5, 15821.	1.6	50
58	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
59	Clustering of Cancer Cell Lines Using A Promoter- Targeted Liquid Hybridization Capture-Based Bisulfite Sequencing Approach. <i>Technology in Cancer Research and Treatment</i> , 2015, 14, 383-394.	0.8	9
60	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
61	Correlating Bladder Cancer Risk Genes with Their Targeting MicroRNAs Using M ² IRNA-Tar. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 177-182.	3.0	8
62	An atypical form of AOA2 with myoclonus associated with mutations in SETX and AFG3L2. <i>BMC Medical Genetics</i> , 2015, 16, 16.	2.1	12
63	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
64	Clinicopathologic characteristics of anterior prostate cancer (APC), including correlation with previous biopsy pathology. <i>Medical Oncology</i> , 2015, 32, 249.	1.2	10
65	A penalized likelihood approach for robust estimation of isoform expression. <i>Statistics and Its Interface</i> , 2015, 8, 437-445.	0.2	11
66	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
67	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
68	Frequent discordance between <i>ERG</i> 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
69	RNA-Seq Accurately Identifies Cancer Biomarker Signatures to Distinguish Tissue of Origin. <i>Neoplasia</i> , 2014, 16, 918-927.	2.3	37
70	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. <i>Reproductive Sciences</i> , 2014, 21, 32-40.	1.1	259
71	A Robust Approach for Blind Detection of Balanced Chromosomal Rearrangements with Whole-Genome Low-Coverage Sequencing. <i>Human Mutation</i> , 2014, 35, 625-636.	1.1	65
72	PSCC: Sensitive and Reliable Population-Scale Copy Number Variation Detection Method Based on Low Coverage Sequencing. <i>PLoS ONE</i> , 2014, 9, e85096.	1.1	30

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73	Performance Comparison between Rapid Sequencing Platforms for Ultra-Low Coverage Sequencing Strategy. PLoS ONE, 2014, 9, e92192.	1.1	23
74	Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq. Nature Cell Biology, 2013, 15, 1244-1252.	4.6	88
75	Multivariate Density Estimation by Bayesian Sequential Partitioning. Journal of the American Statistical Association, 2013, 108, 1402-1410.	1.8	39
76	rSeqDiff: Detecting Differential Isoform Expression from RNA-Seq Data Using Hierarchical Likelihood Ratio Test. PLoS ONE, 2013, 8, e79448.	1.1	29
77	Statistical properties of an early stopping rule for resampling-based multiple testing. Biometrika, 2012, 99, 973-980.	1.3	17
78	Clinical application of massively parallel sequencing-based prenatal noninvasive fetal trisomy test for trisomies 21 and 18 in 11% pregnancies with mixed risk factors. Prenatal Diagnosis, 2012, 32, 1225-1232.	1.1	197
79	Fast and accurate read alignment for resequencing. Bioinformatics, 2012, 28, 2366-2373.	1.8	48
80	Noninvasive prenatal genetic testing for fetal aneuploidy detects maternal trisomy X. Prenatal Diagnosis, 2012, 32, 1114-1116.	1.1	51
81	Noninvasive prenatal diagnosis of common fetal chromosomal aneuploidies by maternal plasma DNA sequencing. Journal of Maternal-Fetal and Neonatal Medicine, 2012, 25, 1370-1374.	0.7	106
82	The dynamics of the vaginal microbiome during infertility therapy with in vitro fertilization-embryo transfer. Journal of Assisted Reproduction and Genetics, 2012, 29, 105-115.	1.2	124
83	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	1.1	7
84	Using CisGenome to Analyze ChIP-chip and ChIP-seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
85	Statistical Modeling of RNA-Seq Data. Statistical Science, 2011, 26, .	1.6	64
86	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	3.3	122
87	A direct comparison of the KB, Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. BMC Research Notes, 2010, 3, 257.	0.6	9
88	CisGenome Browser: a flexible tool for genomic data visualization. Bioinformatics, 2010, 26, 1781-1782.	1.8	37
89	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	6.5	300
90	Modeling non-uniformity in short-read rates in RNA-Seq data. Genome Biology, 2010, 11, R50.	13.9	165

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91	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 3056-3059.	1.8	54
92	Statistical inferences for isoform expression in RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1026-1032.	1.8	405
93	An integrated software system for analyzing ChIP-chip and ChIP-seq data. <i>Nature Biotechnology</i> , 2008, 26, 1293-1300.	9.4	662
94	An optimization algorithm for designing phase I cancer clinical trials. <i>Contemporary Clinical Trials</i> , 2008, 29, 102-108.	0.8	6
95	SeqMap: mapping massive amount of oligonucleotides to the genome. <i>Bioinformatics</i> , 2008, 24, 2395-2396.	1.8	459
96	Cross-hybridization modeling on Affymetrix exon arrays. <i>Bioinformatics</i> , 2008, 24, 2887-2893.	1.8	35
97	MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. <i>Rna</i> , 2008, 14, 1470-1479.	1.6	86
98	Gestalt-based feature similarity measure in trademark database. <i>Pattern Recognition</i> , 2006, 39, 988-1001.	5.1	32
99	Graph based image matching. , 2004, , .		0