Hui Jiang

List of Publications by Year
in descending order

99 papers	20,131 citations	94433 37 h-index	37204 96 g-index
101 all docs	101 docs citations	101 times ranked	42923 citing authors

#	Article	IF	Citations
1	Collaborative Multilabel Classification. Journal of the American Statistical Association, 2023, 118, 913-924.	3.1	1
2	A Cross-Validation Statistical Framework for Asymmetric Data Integration. Biometrics, 2023, 79, 1280-1292.	1.4	0
3	A Two-Part Mixed Model for Differential Expression Analysis in Single-Cell High-Throughput Gene Expression Data. Genes, 2022, 13, 377.	2.4	3
4	Therapeutic Effects of Xianlu Oral Solution on Rats with Oligoasthenozoospermia through Alleviating Apoptosis and Oxidative Stress. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-11.	1.2	2
5	Microbe-Mediated Activation of Toll-like Receptor 2 Drives PDL1 Expression in HNSCC. Cancers, 2021, 13, 4782.	3.7	4
6	Combined p53- and PTEN-deficiency activates expression of mesenchyme homeobox 1 (MEOX1) required for growth of triple-negative breast cancer. Journal of Biological Chemistry, 2020, 295, 12188-12202.	3.4	16
7	Single-Cell Transcriptomics Analysis Identifies Nuclear Protein 1 as a Regulator of Docetaxel Resistance in Prostate Cancer Cells. Molecular Cancer Research, 2020, 18, 1290-1301.	3.4	25
8	Variability in protein cargo detection in technical and biological replicates of exosome-enriched extracellular vesicles. PLoS ONE, 2020, 15, e0228871.	2.5	14
9	Statistics in the Genomic Era. Genes, 2020, 11, 443.	2.4	1
10	The in vivo endothelial cell translatome is highly heterogeneous across vascular beds. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23618-23624.	7.1	89
11	Identifying Interaction Clusters for MiRNA and MRNA Pairs in TCGA Network. Genes, 2019, 10, 702.	2.4	13
12	False Discovery Rate Control in Cancer Biomarker Selection Using Knockoffs. Cancers, 2019, 11, 744.	3.7	12
13	The molecular landscape of the University of Michigan laryngeal squamous cell carcinoma cell line panel. Head and Neck, 2019, 41, 3114-3124.	2.0	23
14	Label-free absolute protein quantification with data-independent acquisition. Journal of Proteomics, 2019, 200, 51-59.	2.4	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. Molecular Pharmacology, 2019, 95, 528-536.	2.3	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. Bioscience Reports, 2019, 39, .	2.4	62
17	Response to the Comments on â€œDetermining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Proteomics Methodâ€• Journal of Proteome Research, 2019, 18, 1458-1459.	3.7	0
18	Accurate and efficient estimation of small P-values with the cross-entropy method: applications in genomic data analysis. Bioinformatics, 2019, 35, 2441-2448.	4.1	6

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19	Minimizing Sum of Truncated Convex Functions and Its Applications. Journal of Computational and Graphical Statistics, 2019, 28, 1-10.	1.7	17
20	A Unified Model for Joint Normalization and Differential Gene Expression Detection in RNA-Seq Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 442-454.	3.0	13
21	Balanced Chromosomal Rearrangement Detection by Lowâ€Pass Wholeâ€Genome Sequencing. Current Protocols in Human Genetics, 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. Drug Metabolism and Pharmacokinetics, 2018, 33, 133-140.	2.2	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. Genetics in Medicine, 2018, 20, 697-707.	2.4	52
24	Testing the performance of a prototype lateral flow device using bronchoalveolar lavage fluid for the diagnosis of invasive pulmonary aspergillosis in highâ€risk patients. Mycoses, 2018, 61, 4-10.	4.0	15
25	Fast Approximation of Small P-values in Permutation Tests by Partitioning the Permutations. Biometrics, 2018, 74, 196-206.	1.4	15
26	False discovery control for penalized variable selections with high-dimensional covariates. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	1
27	The genomic landscape of UM-SCC oral cavity squamous cell carcinoma cell lines. Oral Oncology, 2018, 87, 144-151.	1.5	27
28	Targeting LRP8 inhibits breast cancer stem cells in triple-negative breast cancer. Cancer Letters, 2018, 438, 165-173.	7.2	28
29	Analysis of the androgen receptorâ€“regulated lncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. Nature Genetics, 2018, 50, 814-824.	21.4	196
30	Comprehensive multi-center assessment of small RNA-seq methods for quantitative miRNA profiling. Nature Biotechnology, 2018, 36, 746-757.	17.5	134
31	Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Based Proteomics Method. Journal of Proteome Research, 2018, 17, 3606-3612.	3.7	20
32	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. Bayesian Analysis, 2018, 13, 411-436.	3.0	5
33	P-splines with an ell_{1} penalty for repeated measures. Electronic Journal of Statistics, 2018, 12, .	0.7	3
34	Programmed Death-ligand 1 Expression in Upper Tract Urothelial Carcinoma. European Urology Focus, 2017, 3, 502-509.	3.1	25
35	Targeted Degradation of BET Proteins in Triple-Negative Breast Cancer. Cancer Research, 2017, 77, 2476-2487.	0.9	173
36	Development of Peptidomimetic Inhibitors of the ERG Gene Fusion Product in Prostate Cancer. Cancer Cell, 2017, 31, 532-548.e7.	16.8	85

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37	Unit-Free and Robust Detection of Differential Expression from RNA-Seq Data. Statistics in Biosciences, 2017, 9, 178-199.	1.2	4
38	Copyâ€Number Variants Detection by Lowâ€Pass Wholeâ€Genome Sequencing. Current Protocols in Human Genetics, 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 nonâ€invasive prenatal testing. Prenatal Diagnosis, 2017, 37, 1311-1321.	2.3	36
40	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 2017, 6, 1-13.	6.4	137
41	Identification of gene pairs through penalized regression subject to constraints. BMC Bioinformatics, 2017, 18, 466.	2.6	6
42	Differential regulation of the c-Myc/Lin28 axis discriminates subclasses of rearranged MLL leukemia. Oncotarget, 2016, 7, 25208-25223.	1.8	19
43	Concurrent nuclear ERG and MYC protein overexpression defines a subset of locally advanced prostate cancer: Potential opportunities for synergistic targeted therapeutics. Prostate, 2016, 76, 845-853.	2.3	9
44	Clinical experience from Thailand: noninvasive prenatal testing as screening tests for trisomies 21, 18 and 13 in 4736 pregnancies. Prenatal Diagnosis, 2016, 36, 224-231.	2.3	18
45	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	12.8	114
46	Comparative analysis of circulating tumor DNA stability In K3EDTA, Streck, and CellSave blood collection tubes. Clinical Biochemistry, 2016, 49, 1354-1360.	1.9	175
47	First report of human salivirus/klassevirus in respiratory specimens of a child with fatal adenovirus infection. Virus Genes, 2016, 52, 620-624.	1.6	2
48	Dissecting the biological relationship between TCGA miRNA and mRNA sequencing data using MMiRNA-Viewer. BMC Bioinformatics, 2016, 17, 336.	2.6	10
49	Complete mitochondrial genome of the Saker falcon, Falco cherrug (Falco, Falconidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3226-3227.	0.7	3
50	Low-pass whole-genome sequencing in clinical cytogenetics: a validated approach. Genetics in Medicine, 2016, 18, 940-948.	2.4	138
51	Promoter targeted bisulfite sequencing reveals DNA methylation profiles associated with low sperm motility in asthenozoospermia. Human Reproduction, 2016, 31, 24-33.	0.9	47
52	Computational Aspects of Optional PÃ³lya Tree. Journal of Computational and Graphical Statistics, 2016, 25, 301-320.	1.7	4
53	Expression of PDL1 (B7-H1) Before and After Neoadjuvant Chemotherapy in Urothelial Carcinoma. European Urology Focus, 2016, 1, 265-268.	3.1	45
54	Performance Evaluation of NIPT in Detection of Chromosomal Copy Number Variants Using Low-Coverage Whole-Genome Sequencing of Plasma DNA. PLoS ONE, 2016, 11, e0159233.	2.5	42

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55	Novel cancer stem cell targets during epithelial to mesenchymal transition in PTEN-deficient trastuzumab-resistant breast cancer. Oncotarget, 2016, 7, 51408-51422.	1.8	37
56	Rapid diagnosis of Propionibacterium acnes infection in patient with hyperpyrexia after hematopoietic stem cell transplantation by next-generation sequencing: a case report. BMC Infectious Diseases, 2015, 16, 5.	2.9	18
57	Trastuzumab resistance induces EMT to transform HER2+ PTENâ¯ to a triple negative breast cancer that requires unique treatment options. Scientific Reports, 2015, 5, 15821.	3.3	50
58	Performance of lateral flow device and galactomannan for the detection of Aspergillus species in bronchoalveolar fluid of patients at risk for invasive pulmonary aspergillosis. Mycoses, 2015, 58, 368-374.	4.0	26
59	Clustering of Cancer Cell Lines Using A Promoter- Targeted Liquid Hybridization Capture-Based Bisulfite Sequencing Approach. Technology in Cancer Research and Treatment, 2015, 14, 383-394.	1.9	9
60	rSeqNP: a non-parametric approach for detecting differential expression and splicing from RNA-Seq data. Bioinformatics, 2015, 31, 2222-2224.	4.1	13
61	Correlating Bladder Cancer Risk Genes with Their Targeting MicroRNAs Using MMiRNA-Tar. Genomics, Proteomics and Bioinformatics, 2015, 13, 177-182.	6.9	8
62	An atypical form of AOA2 with myoclonus associated with mutations in SETX and AFG3L2. BMC Medical Genetics, 2015, 16, 16.	2.1	12
63	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
64	Clinicopathologic characteristics of anterior prostate cancer (APC), including correlation with previous biopsy pathology. Medical Oncology, 2015, 32, 249.	2.5	10
65	A penalized likelihood approach for robust estimation of isoform expression. Statistics and Its Interface, 2015, 8, 437-445.	0.3	11
66	Expansion of CTCs from early stage lung cancer patients using a microfluidic co-culture model. Oncotarget, 2014, 5, 12383-12397.	1.8	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. Neoplasia, 2014, 16, 1121-1127.	5.3	81
68	Frequent discordance betweenERGgene rearrangement and ERG protein expression in a rapid autopsy cohort of patients with lethal, metastatic, castration-resistant prostate cancer. Prostate, 2014, 74, 1199-1208.	2.3	33
69	RNA-Seq Accurately Identifies Cancer Biomarker Signatures to Distinguish Tissue of Origin. Neoplasia, 2014, 16, 918-927.	5.3	37
70	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. Reproductive Sciences, 2014, 21, 32-40.	2.5	259
71	A Robust Approach for Blind Detection of Balanced Chromosomal Rearrangements with Whole-Genome Low-Coverage Sequencing. Human Mutation, 2014, 35, 625-636.	2.5	65
72	PSCC: Sensitive and Reliable Population-Scale Copy Number Variation Detection Method Based on Low Coverage Sequencing. PLoS ONE, 2014, 9, e85096.	2.5	30

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73	Performance Comparison between Rapid Sequencing Platforms for Ultra-Low Coverage Sequencing Strategy. PLoS ONE, 2014, 9, e92192.	2.5	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.	10.3	88
75	Multivariate Density Estimation by Bayesian Sequential Partitioning. Journal of the American Statistical Association, 2013, 108, 1402-1410.	3.1	39
76	rSeqDiff: Detecting Differential Isoform Expression from RNA-Seq Data Using Hierarchical Likelihood Ratio Test. PLoS ONE, 2013, 8, e79448.	2.5	29
77	Statistical properties of an early stopping rule for resampling-based multiple testing. Biometrika, 2012, 99, 973-980.	2.4	17
78	Clinical application of massively parallel sequencingâ€based prenatal noninvasive fetal trisomy test for trisomies 21 and 18 in 11â€‰105 pregnancies with mixed risk factors. Prenatal Diagnosis, 2012, 32, 1225-1232.	2.3	197
79	Fast and accurate read alignment for resequencing. Bioinformatics, 2012, 28, 2366-2373.	4.1	48
80	Noninvasive prenatal genetic testing for fetal aneuploidy detects maternal trisomy X. Prenatal Diagnosis, 2012, 32, 1114-1116.	2.3	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.	1.5	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.	2.5	124
83	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	2.5	7
84	Using CisGenome to Analyze ChIPâ€chip and ChIPâ€seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
85	Statistical Modeling of RNA-Seq Data. Statistical Science, 2011, 26, .	2.8	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.	7.1	122
87	A direct comparison of the KBâ„¢ Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. BMC Research Notes, 2010, 3, 257.	1.4	9
88	CisGenome Browser: a flexible tool for genomic data visualization. Bioinformatics, 2010, 26, 1781-1782.	4.1	37
89	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	14.5	300
90	Modeling non-uniformity in short-read rates in RNA-Seq data. Genome Biology, 2010, 11, R50.	9.6	165

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91	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. Bioinformatics, 2009, 25, 3056-3059.	4.1	54
92	Statistical inferences for isoform expression in RNA-Seq. Bioinformatics, 2009, 25, 1026-1032.	4.1	405
93	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	17.5	662
94	An optimization algorithm for designing phase I cancer clinical trials. Contemporary Clinical Trials, 2008, 29, 102-108.	1.8	6
95	SeqMap: mapping massive amount of oligonucleotides to the genome. Bioinformatics, 2008, 24, 2395-2396.	4.1	459
96	Cross-hybridization modeling on Affymetrix exon arrays. Bioinformatics, 2008, 24, 2887-2893.	4.1	35
97	MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. Rna, 2008, 14, 1470-1479.	3.5	86
98	Gestalt-based feature similarity measure in trademark database. Pattern Recognition, 2006, 39, 988-1001.	8.1	32
99	Graph based image matching. , 2004, , .		0