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	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	17.5	662
3	SeqMap: mapping massive amount of oligonucleotides to the genome. Bioinformatics, 2008, 24, 2395-2396.	4.1	459
4	Statistical inferences for isoform expression in RNA-Seq. Bioinformatics, 2009, 25, 1026-1032.	4.1	405
5	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	14.5	300
6	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. Reproductive Sciences, 2014, 21, 32-40.	2.5	259
7	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
8	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
9	Expansion of CTCs from early stage lung cancer patients using a microfluidic co-culture model. Oncotarget, 2014, 5, 12383-12397.	1.8	175
10	Comparative analysis of circulating tumor DNA stability In K3EDTA, Streck, and CellSave blood collection tubes. Clinical Biochemistry, 2016, 49, 1354-1360.	1.9	175
11	Targeted Degradation of BET Proteins in Triple-Negative Breast Cancer. Cancer Research, 2017, 77, 2476-2487.	0.9	173
12	Modeling non-uniformity in short-read rates in RNA-Seq data. Genome Biology, 2010, 11, R50.	9.6	165
13	Low-pass whole-genome sequencing in clinical cytogenetics: a validated approach. Genetics in Medicine, 2016, 18, 940-948.	2.4	138
14	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 2017, 6, 1-13.	6.4	137
15	Comprehensive multi-center assessment of small RNA-seq methods for quantitative miRNA profiling. Nature Biotechnology, 2018, 36, 746-757.	17.5	134
16	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
17	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
18	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	12.8	114

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19	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
20	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
21	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
22	MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. Rna, 2008, 14, 1470-1479.	3.5	86
23	Development of Peptidomimetic Inhibitors of the ERG Gene Fusion Product in Prostate Cancer. Cancer Cell, 2017, 31, 532-548.e7.	16.8	85
24	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
25	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
26	Statistical Modeling of RNA-Seq Data. Statistical Science, 2011, 26, .	2.8	64
27	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
28	Label-free absolute protein quantification with data-independent acquisition. Journal of Proteomics, 2019, 200, 51-59.	2.4	60
29	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. Bioinformatics, 2009, 25, 3056-3059.	4.1	54
30	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
31	Noninvasive prenatal genetic testing for fetal aneuploidy detects maternal trisomy X. Prenatal Diagnosis, 2012, 32, 1114-1116.	2.3	51
32	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
33	Fast and accurate read alignment for resequencing. Bioinformatics, 2012, 28, 2366-2373.	4.1	48
34	Promoter targeted bisulfite sequencing reveals DNA methylation profiles associated with low sperm motility in asthenozoospermia. Human Reproduction, 2016, 31, 24-33.	0.9	47
35	Expression of PDL1 (B7-H1) Before and After Neoadjuvant Chemotherapy in Urothelial Carcinoma. European Urology Focus, 2016, 1, 265-268.	3.1	45
36	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

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37	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
38	Multivariate Density Estimation by Bayesian Sequential Partitioning. Journal of the American Statistical Association, 2013, 108, 1402-1410.	3.1	39
39	CisGenome Browser: a flexible tool for genomic data visualization. Bioinformatics, 2010, 26, 1781-1782.	4.1	37
40	RNA-Seq Accurately Identifies Cancer Biomarker Signatures to Distinguish Tissue of Origin. Neoplasia, 2014, 16, 918-927.	5.3	37
41	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
42	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
43	Cross-hybridization modeling on Affymetrix exon arrays. Bioinformatics, 2008, 24, 2887-2893.	4.1	35
44	Using CisGenome to Analyze ChIPâ€chip and ChIPâ€seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
45	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
46	Gestalt-based feature similarity measure in trademark database. Pattern Recognition, 2006, 39, 988-1001.	8.1	32
47	PSCC: Sensitive and Reliable Population-Scale Copy Number Variation Detection Method Based on Low Coverage Sequencing. PLoS ONE, 2014, 9, e85096.	2.5	30
48	rSeqDiff: Detecting Differential Isoform Expression from RNA-Seq Data Using Hierarchical Likelihood Ratio Test. PLoS ONE, 2013, 8, e79448.	2.5	29
49	Targeting LRP8 inhibits breast cancer stem cells in triple-negative breast cancer. Cancer Letters, 2018, 438, 165-173.	7.2	28
50	The genomic landscape of UM-SCC oral cavity squamous cell carcinoma cell lines. Oral Oncology, 2018, 87, 144-151.	1.5	27
51	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
52	Programmed Death-ligand 1 Expression in Upper Tract Urothelial Carcinoma. European Urology Focus, 2017, 3, 502-509.	3.1	25
53	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
54	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

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55	Performance Comparison between Rapid Sequencing Platforms for Ultra-Low Coverage Sequencing Strategy. PLoS ONE, 2014, 9, e92192.	2.5	23
56	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
57	Differential regulation of the c-Myc/Lin28 axis discriminates subclasses of rearranged MLL leukemia. Oncotarget, 2016, 7, 25208-25223.	1.8	19
58	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
59	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
60	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
61	Statistical properties of an early stopping rule for resampling-based multiple testing. Biometrika, 2012, 99, 973-980.	2.4	17
62	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
63	Minimizing Sum of Truncated Convex Functions and Its Applications. Journal of Computational and Graphical Statistics, 2019, 28, 1-10.	1.7	17
64	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
65	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
66	Fast Approximation of Small P-values in Permutation Tests by Partitioning the Permutations. Biometrics, 2018, 74, 196-206.	1.4	15
67	Variability in protein cargo detection in technical and biological replicates of exosome-enriched extracellular vesicles. PLoS ONE, 2020, 15, e0228871.	2.5	14
68	rSeqNP: a non-parametric approach for detecting differential expression and splicing from RNA-Seq data. Bioinformatics, 2015, 31, 2222-2224.	4.1	13
69	Identifying Interaction Clusters for MiRNA and MRNA Pairs in TCGA Network. Genes, 2019, 10, 702.	2.4	13
70	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
71	An atypical form of AOA2 with myoclonus associated with mutations in SETX and AFG3L2. BMC Medical Genetics, 2015, 16, 16.	2.1	12
72	False Discovery Rate Control in Cancer Biomarker Selection Using Knockoffs. Cancers, 2019, 11, 744.	3.7	12

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73	A penalized likelihood approach for robust estimation of isoform expression. Statistics and Its Interface, 2015, 8, 437-445.	0.3	11
74	Clinicopathologic characteristics of anterior prostate cancer (APC), including correlation with previous biopsy pathology. Medical Oncology, 2015, 32, 249.	2.5	10
75	Dissecting the biological relationship between TCGA miRNA and mRNA sequencing data using MMiRNA-Viewer. BMC Bioinformatics, 2016, 17, 336.	2.6	10
76	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
77	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
78	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
79	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
80	Correlating Bladder Cancer Risk Genes with Their Targeting MicroRNAs Using MMiRNA-Tar. Genomics, Proteomics and Bioinformatics, 2015, 13, 177-182.	6.9	8
81	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	2.5	7
82	An optimization algorithm for designing phase I cancer clinical trials. Contemporary Clinical Trials, 2008, 29, 102-108.	1.8	6
83	Identification of gene pairs through penalized regression subject to constraints. BMC Bioinformatics, 2017, 18, 466.	2.6	6
84	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
85	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. Bayesian Analysis, 2018, 13, 411-436.	3.0	5
86	Computational Aspects of Optional PÃ³lya Tree. Journal of Computational and Graphical Statistics, 2016, 25, 301-320.	1.7	4
87	Unit-Free and Robust Detection of Differential Expression from RNA-Seq Data. Statistics in Biosciences, 2017, 9, 178-199.	1.2	4
88	Microbe-Mediated Activation of Toll-like Receptor 2 Drives PDL1 Expression in HNSCC. Cancers, 2021, 13, 4782.	3.7	4
89	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
90	P-splines with an ell_{1} penalty for repeated measures. Electronic Journal of Statistics, 2018, 12, .	0.7	3

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91	A Two-Part Mixed Model for Differential Expression Analysis in Single-Cell High-Throughput Gene Expression Data. Genes, 2022, 13, 377.	2.4	3
92	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
93	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
94	False discovery control for penalized variable selections with high-dimensional covariates. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	1
95	Statistics in the Genomic Era. Genes, 2020, 11, 443.	2.4	1
96	Collaborative Multilabel Classification. Journal of the American Statistical Association, 2023, 118, 913-924.	3.1	1
97	Graph based image matching. , 2004, , .		0
98	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
99	A Cross-Validation Statistical Framework for Asymmetric Data Integration. Biometrics, 2023, 79, 1280-1292.	1.4	0