

# Hui Jiang

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75  
papers

12,701  
citations

31  
h-index

80  
g-index

80  
ext. papers

17,003  
ext. citations

8  
avg, IF

5.51  
L-index

#	Paper	IF	Citations
75	Advancement of PI3 Kinase Inhibitor Combination Therapies for PI3K-Aberrant Chordoma.. <i>Journal of Neurological Surgery, Part B: Skull Base</i> , <b>2022</b> , 83, 87-98	1.5	0
74	Genetic analysis of sinonasal undifferentiated carcinoma discovers recurrent SWI/SNF alterations and a novel PGAP3-SRPK1 fusion gene. <i>BMC Cancer</i> , <b>2021</b> , 21, 636	4.8	1
73	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> , <b>2020</b> , 295, 12188-12202	5.4	6
72	Single-Cell Transcriptomics Analysis Identifies Nuclear Protein 1 as a Regulator of Docetaxel Resistance in Prostate Cancer Cells. <i>Molecular Cancer Research</i> , <b>2020</b> , 18, 1290-1301	6.6	8
71	Variability in protein cargo detection in technical and biological replicates of exosome-enriched extracellular vesicles. <i>PLoS ONE</i> , <b>2020</b> , 15, e0228871	3.7	4
70	Genome-wide pQTL analysis of protein expression regulatory networks in the human liver. <i>BMC Biology</i> , <b>2020</b> , 18, 97	7.3	11
69	Identifying Interaction Clusters for MiRNA and MRNA Pairs in TCGA Network. <i>Genes</i> , <b>2019</b> , 10,	4.2	8
68	False Discovery Rate Control in Cancer Biomarker Selection Using Knockoffs. <i>Cancers</i> , <b>2019</b> , 11,	6.6	5
67	The molecular landscape of the University of Michigan laryngeal squamous cell carcinoma cell line panel. <i>Head and Neck</i> , <b>2019</b> , 41, 3114-3124	4.2	14
66	Label-free absolute protein quantification with data-independent acquisition. <i>Journal of Proteomics</i> , <b>2019</b> , 200, 51-59	3.9	32
65	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> , <b>2019</b> , 95, 528-536	4.3	11
64	A Potent and Selective Small-Molecule Degradar of STAT3 Achieves Complete Tumor Regression In Vivo. <i>Cancer Cell</i> , <b>2019</b> , 36, 498-511.e17	24.3	181
63	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> , <b>2019</b> , 116, 23618-23624	11.5	50
62	Joint between-sample normalization and differential expression detection through Regularized regression. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 593	3.6	1
61	Response to the Comments on "Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Proteomics Method". <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 1458-1459 <sup>5.6</sup>	5.6	5.6
60	Accurate and efficient estimation of small P-values with the cross-entropy method: applications in genomic data analysis. <i>Bioinformatics</i> , <b>2019</b> , 35, 2441-2448	7.2	4
59	Minimizing Sum of Truncated Convex Functions and Its Applications. <i>Journal of Computational and Graphical Statistics</i> , <b>2019</b> , 28, 1-10	1.4	13

58	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> , <b>2019</b> , 16, 442-454	3	8
57	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> , <b>2018</b> , 33, 133-140	2.2	30
56	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> , <b>2018</b> , 61, 4-10	5.2	11
55	Comprehensive multi-center assessment of small RNA-seq methods for quantitative miRNA profiling. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 746-757	44.5	85
54	Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Based Proteomics Method. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 3606-3612	5.6	14
53	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. <i>Bayesian Analysis</i> , <b>2018</b> , 13, 411-436	2.3	5
52	Fast approximation of small p-values in permutation tests by partitioning the permutations. <i>Biometrics</i> , <b>2018</b> , 74, 196-206	1.8	8
51	False discovery control for penalized variable selections with high-dimensional covariates. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2018</b> , 17,	1.2	1
50	The genomic landscape of UM-SCC oral cavity squamous cell carcinoma cell lines. <i>Oral Oncology</i> , <b>2018</b> , 87, 144-151	4.4	16
49	Targeting LRP8 inhibits breast cancer stem cells in triple-negative breast cancer. <i>Cancer Letters</i> , <b>2018</b> , 438, 165-173	9.9	16
48	Analysis of the androgen receptor-regulated lncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. <i>Nature Genetics</i> , <b>2018</b> , 50, 814-824	36.3	124
47	Programmed Death-ligand 1 Expression in Upper Tract Urothelial Carcinoma. <i>European Urology Focus</i> , <b>2017</b> , 3, 502-509	5.1	18
46	Targeted Degradation of BET Proteins in Triple-Negative Breast Cancer. <i>Cancer Research</i> , <b>2017</b> , 77, 2476-2487	6.2	115
45	Development of Peptidomimetic Inhibitors of the ERG Gene Fusion Product in Prostate Cancer. <i>Cancer Cell</i> , <b>2017</b> , 31, 532-548.e7	24.3	57
44	Unit-Free and Robust Detection of Differential Expression from RNA-Seq Data. <i>Statistics in Biosciences</i> , <b>2017</b> , 9, 178-199	1.5	3
43	Dissecting the biological relationship between TCGA miRNA and mRNA sequencing data using MMiRNA-Viewer. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 336	3.6	8
42	Computational Aspects of Optional Pliya Tree. <i>Journal of Computational and Graphical Statistics</i> , <b>2016</b> , 25, 301-320	1.4	4
41	Expression of PDL1 (B7-H1) Before and After Neoadjuvant Chemotherapy in Urothelial Carcinoma. <i>European Urology Focus</i> , <b>2016</b> , 1, 265-268	5.1	31

40	Novel cancer stem cell targets during epithelial to mesenchymal transition in PTEN-deficient trastuzumab-resistant breast cancer. <i>Oncotarget</i> , <b>2016</b> , 7, 51408-51422	3.3	32
39	Differential regulation of the c-Myc/Lin28 axis discriminates subclasses of rearranged MLL leukemia. <i>Oncotarget</i> , <b>2016</b> , 7, 25208-23	3.3	15
38	Concurrent nuclear ERG and MYC protein overexpression defines a subset of locally advanced prostate cancer: Potential opportunities for synergistic targeted therapeutics. <i>Prostate</i> , <b>2016</b> , 76, 845-53	4.2	6
37	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <i>Nature Communications</i> , <b>2016</b> , 7, 11764	17.4	82
36	Comparative analysis of circulating tumor DNA stability in KEDTA, Streck, and CellSave blood collection tubes. <i>Clinical Biochemistry</i> , <b>2016</b> , 49, 1354-1360	3.5	141
35	rSeqNP: a non-parametric approach for detecting differential expression and splicing from RNA-Seq data. <i>Bioinformatics</i> , <b>2015</b> , 31, 2222-4	7.2	11
34	Correlating bladder cancer risk genes with their targeting microRNAs using MMiRNA-Tar. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2015</b> , 13, 177-82	6.5	7
33	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
32	Clinicopathologic characteristics of anterior prostate cancer (APC), including correlation with previous biopsy pathology. <i>Medical Oncology</i> , <b>2015</b> , 32, 249	3.7	5
31	Trastuzumab resistance induces EMT to transform HER2(+) PTEN(-) to a triple negative breast cancer that requires unique treatment options. <i>Scientific Reports</i> , <b>2015</b> , 5, 15821	4.9	43
30	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> , <b>2015</b> , 58, 368-74	5.2	22
29	A penalized likelihood approach for robust estimation of isoform expression. <i>Statistics and Its Interface</i> , <b>2015</b> , 8, 437-445	0.4	6
28	Differential Regulation of c-Myc/Lin28 Discriminates Subclasses of Rearranged MLL Leukemia. <i>Blood</i> , <b>2015</b> , 126, 163-163	2.2	
27	Diversity of the vaginal microbiome correlates with preterm birth. <i>Reproductive Sciences</i> , <b>2014</b> , 21, 32-40	3	183
26	Expansion of CTCs from early stage lung cancer patients using a microfluidic co-culture model. <i>Oncotarget</i> , <b>2014</b> , 5, 12383-97	3.3	134
25	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> , <b>2014</b> , 16, 1121-7	6.4	71
24	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> , <b>2014</b> , 74, 1199-208	4.2	25
23	RNA-Seq accurately identifies cancer biomarker signatures to distinguish tissue of origin. <i>Neoplasia</i> , <b>2014</b> , 16, 918-27	6.4	25

22	Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 1244-52	23.4	69
21	Multivariate Density Estimation by Bayesian Sequential Partitioning. <i>Journal of the American Statistical Association</i> , <b>2013</b> , 108, 1402-1410	2.8	26
20	rSeqDiff: detecting differential isoform expression from RNA-Seq data using hierarchical likelihood ratio test. <i>PLoS ONE</i> , <b>2013</b> , 8, e79448	3.7	21
19	The dynamics of the vaginal microbiome during infertility therapy with in vitro fertilization-embryo transfer. <i>Journal of Assisted Reproduction and Genetics</i> , <b>2012</b> , 29, 105-15	3.4	94
18	Fast and accurate read alignment for resequencing. <i>Bioinformatics</i> , <b>2012</b> , 28, 2366-73	7.2	37
17	Statistical properties of an early stopping rule for resampling-based multiple testing. <i>Biometrika</i> , <b>2012</b> , 99, 973-980	2	15
16	Knowledge-based reconstruction of mRNA transcripts with short sequencing reads for transcriptome research. <i>PLoS ONE</i> , <b>2012</b> , 7, e31440	3.7	6
15	Using CisGenome to analyze CHIP-chip and CHIP-seq data. <i>Current Protocols in Bioinformatics</i> , <b>2011</b> , Chapter 2, Unit2.13	24.2	31
14	Statistical Modeling of RNA-Seq Data. <i>Statistical Science</i> , <b>2011</b> , 26,	2.4	53
13	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 3707-12	11.5	91
12	CisGenome Browser: a flexible tool for genomic data visualization. <i>Bioinformatics</i> , <b>2010</b> , 26, 1781-2	7.2	31
11	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 4570-8	20.1	255
10	Modeling non-uniformity in short-read rates in RNA-Seq data. <i>Genome Biology</i> , <b>2010</b> , 11, R50	18.3	146
9	A direct comparison of the K&B;B;Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. <i>BMC Research Notes</i> , <b>2010</b> , 3, 257	2.3	9
8	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. <i>Bioinformatics</i> , <b>2009</b> , 25, 3056-9	7.9	51
7	Statistical inferences for isoform expression in RNA-Seq. <i>Bioinformatics</i> , <b>2009</b> , 25, 1026-32	7.2	360
6	An integrated software system for analyzing CHIP-chip and CHIP-seq data. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 1293-300	44.5	604
5	An optimization algorithm for designing phase I cancer clinical trials. <i>Contemporary Clinical Trials</i> , <b>2008</b> , 29, 102-8	2.3	6

4	SeqMap: mapping massive amount of oligonucleotides to the genome. <i>Bioinformatics</i> , <b>2008</b> , 24, 2395-6	7.2	354
3	Cross-hybridization modeling on Affymetrix exon arrays. <i>Bioinformatics</i> , <b>2008</b> , 24, 2887-93	7.2	32
2	MADS: a new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. <i>Rna</i> , <b>2008</b> , 14, 1470-9	5.8	78
1	Gestalt-based feature similarity measure in trademark database. <i>Pattern Recognition</i> , <b>2006</b> , 39, 988-1001	7.7	22