

# Hui Jiang

## List of Publications by Citations

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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 | A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74   | 50.4 | 8599      |
| 74 | 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       |
| 73 | Statistical inferences for isoform expression in RNA-Seq. <i>Bioinformatics</i> , <b>2009</b> , 25, 1026-32  | 7.2  | 360       |
| 72 | SeqMap: mapping massive amount of oligonucleotides to the genome. <i>Bioinformatics</i> , <b>2008</b> , 24, 2395-6   | 7.2  | 354       |
| 71 | 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       |
| 70 | Diversity of the vaginal microbiome correlates with preterm birth. <i>Reproductive Sciences</i> , <b>2014</b> , 21, 32-40  | 3.5  | 183       |
| 69 | A Potent and Selective Small-Molecule Degradator of STAT3 Achieves Complete Tumor Regression In Vivo. <i>Cancer Cell</i> , <b>2019</b> , 36, 498-511.e17                                       | 24.3 | 181       |
| 68 | Modeling non-uniformity in short-read rates in RNA-Seq data. <i>Genome Biology</i> , <b>2010</b> , 11, R50   | 18.3 | 146       |
| 67 | 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       |
| 66 | 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       |
| 65 | 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       |
| 64 | Targeted Degradation of BET Proteins in Triple-Negative Breast Cancer. <i>Cancer Research</i> , <b>2017</b> , 77, 2476-2487  | 11.4 | 115       |
| 63 | 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        |
| 62 | 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        |
| 61 | 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        |
| 60 | The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <i>Nature Communications</i> , <b>2016</b> , 7, 11764  | 17.4 | 82        |
| 59 | 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        |

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|----|---|------|----|
| 58 | 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 |
| 57 | 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 |
| 56 | 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 |
| 55 | Statistical Modeling of RNA-Seq Data. <i>Statistical Science</i> , <b>2011</b> , 26,  | 2.4  | 53 |
| 54 | Identifiability of isoform deconvolution from junction arrays and RNA-Seq. <i>Bioinformatics</i> , <b>2009</b> , 25, 3056-9   | 6.9  | 51 |
| 53 | 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 |
| 52 | 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 |
| 51 | Fast and accurate read alignment for resequencing. <i>Bioinformatics</i> , <b>2012</b> , 28, 2366-73  | 7.2  | 37 |
| 50 | Label-free absolute protein quantification with data-independent acquisition. <i>Journal of Proteomics</i> , <b>2019</b> , 200, 51-59   | 3.9  | 32 |
| 49 | Cross-hybridization modeling on Affymetrix exon arrays. <i>Bioinformatics</i> , <b>2008</b> , 24, 2887-93   | 7.2  | 32 |
| 48 | 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 |
| 47 | 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 |
| 46 | 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 |
| 45 | CisGenome Browser: a flexible tool for genomic data visualization. <i>Bioinformatics</i> , <b>2010</b> , 26, 1781-2   | 7.2  | 31 |
| 44 | 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 |
| 43 | Multivariate Density Estimation by Bayesian Sequential Partitioning. <i>Journal of the American Statistical Association</i> , <b>2013</b> , 108, 1402-1410  | 2.8  | 26 |
| 42 | 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 |
| 41 | RNA-Seq accurately identifies cancer biomarker signatures to distinguish tissue of origin. <i>Neoplasia</i> , <b>2014</b> , 16, 918-27  | 6.4  | 25 |

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|----|---|-----|----|
| 40 | 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 |
| 39 | Gestalt-based feature similarity measure in trademark database. <i>Pattern Recognition</i> , <b>2006</b> , 39, 988-1001   | 7.7 | 22 |
| 38 | 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 |
| 37 | Programmed Death-ligand 1 Expression in Upper Tract Urothelial Carcinoma. <i>European Urology Focus</i> , <b>2017</b> , 3, 502-509  | 5.1 | 18 |
| 36 | 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 |
| 35 | 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 |
| 34 | Statistical properties of an early stopping rule for resampling-based multiple testing. <i>Biometrika</i> , <b>2012</b> , 99, 973-980   | 2   | 15 |
| 33 | 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 |
| 32 | 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 |
| 31 | 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 |
| 30 | 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 |
| 29 | 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 |
| 28 | 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 |
| 27 | 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 |
| 26 | 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 |
| 25 | A direct comparison of the KBBasercaller 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  |
| 24 | Identifying Interaction Clusters for MiRNA and MRNA Pairs in TCGA Network. <i>Genes</i> , <b>2019</b> , 10,   | 4.2 | 8  |
| 23 | 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  |

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|----|---|-----|---|
| 22 | 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 |
| 21 | 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 |
| 20 | 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 |
| 19 | 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 |
| 18 | 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 |
| 17 | An optimization algorithm for designing phase I cancer clinical trials. <i>Contemporary Clinical Trials</i> , <b>2008</b> , 29, 102-8   | 2.3 | 6 |
| 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 | 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 |
| 14 | 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 |
| 13 | False Discovery Rate Control in Cancer Biomarker Selection Using Knockoffs. <i>Cancers</i> , <b>2019</b> , 11,  | 6.6 | 5 |
| 12 | 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 |
| 11 | 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 |
| 10 | 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 |
| 9  | Computational Aspects of Optional Plya Tree. <i>Journal of Computational and Graphical Statistics</i> , <b>2016</b> , 25, 301-320   | 1.4 | 4 |
| 8  | 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 |
| 7  | 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 |
| 6  | 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 |
| 5  | Joint between-sample normalization and differential expression detection through $\ell_1$ -regularized regression. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 593  | 3.6 | 1 |

- 4 False discovery control for penalized variable selections with high-dimensional covariates. *Statistical Applications in Genetics and Molecular Biology*, **2018**, 17, 1.2 1
- 3 Advancement of PI3 Kinase Inhibitor Combination Therapies for PI3K-Aberrant Chordoma.. *Journal of Neurological Surgery, Part B: Skull Base*, **2022**, 83, 87-98 1.5 0
- 2 Differential Regulation of c-Myc/Lin28 Discriminates Subclasses of Rearranged MLL Leukemia. *Blood*, **2015**, 126, 163-163 2.2
- 1 Response to the Comments on "Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Proteomics Method". *Journal of Proteome Research*, **2019**, 18, 1458-1459<sup>5,6</sup>