

# Tao Liu

## 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.

57  
papers

16,053  
citations

30  
h-index

68  
g-index

68  
ext. papers

21,152  
ext. citations

14.5  
avg, IF

5.98  
L-index

#	Paper	IF	Citations
57	Model-based analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , <b>2008</b> , 9, R137	18.3	8406
56	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , <b>2012</b> , 22, 1813-31	9.7	1211
55	Identifying ChIP-seq enrichment using MACS. <i>Nature Protocols</i> , <b>2012</b> , 7, 1728-40	18.8	857
54	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , <b>2010</b> , 330, 1775-87	33.3	744
53	EZH2 oncogenic activity in castration-resistant prostate cancer cells is Polycomb-independent. <i>Science</i> , <b>2012</b> , 338, 1465-9	33.3	585
52	Differential chromatin marking of introns and expressed exons by H3K36me3. <i>Nature Genetics</i> , <b>2009</b> , 41, 376-81	36.3	509
51	A circadian rhythm orchestrated by histone deacetylase 3 controls hepatic lipid metabolism. <i>Science</i> , <b>2011</b> , 331, 1315-9	33.3	507
50	Cistrome: an integrative platform for transcriptional regulation studies. <i>Genome Biology</i> , <b>2011</b> , 12, R83	18.3	461
49	CEAS: cis-regulatory element annotation system. <i>Bioinformatics</i> , <b>2009</b> , 25, 2605-6	7.2	352
48	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , <b>2014</b> , 512, 449-52	50.4	265
47	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D658-D662	20.1	265
46	Broad chromosomal domains of histone modification patterns in <i>C. elegans</i> . <i>Genome Research</i> , <b>2011</b> , 21, 227-36	9.7	208
45	Practical guidelines for the comprehensive analysis of ChIP-seq data. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003326	5	166
44	Using MACS to identify peaks from ChIP-Seq data. <i>Current Protocols in Bioinformatics</i> , <b>2011</b> , Chapter 2, Unit 2.14	24.2	149
43	Use model-based Analysis of ChIP-Seq (MACS) to analyze short reads generated by sequencing protein-DNA interactions in embryonic stem cells. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1150, 81-95	1.4	119
42	Systematic evaluation of factors influencing ChIP-seq fidelity. <i>Nature Methods</i> , <b>2012</b> , 9, 609-14	21.6	112
41	NONCODE v2.0: decoding the non-coding. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D170-2	20.1	108

40	A comprehensive view of nuclear receptor cancer cistromes. <i>Cancer Research</i> , <b>2011</b> , 71, 6940-7	10.1	99
39	Polycomb-independent activity of EZH2 in castration resistant prostate cancer. <i>Epigenetics and Chromatin</i> , <b>2013</b> , 6,	5.8	78
38	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 404	3.6	72
37	Sources of artifact in measurements of 6mA and 4mC abundance in eukaryotic genomic DNA. <i>BMC Genomics</i> , <b>2019</b> , 20, 445	4.5	56
36	MicroRNA-encoding long non-coding RNAs. <i>BMC Genomics</i> , <b>2008</b> , 9, 236	4.5	53
35	TRANSCRIPTION. Recruitment of RNA polymerase II by the pioneer transcription factor PHA-4. <i>Science</i> , <b>2015</b> , 348, 1372-6	33.3	51
34	Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. <i>Genome Research</i> , <b>2007</b> , 17, 1471-7	9.7	49
33	Genome-wide identification and differential analysis of translational initiation. <i>Nature Communications</i> , <b>2017</b> , 8, 1749	17.4	47
32	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , <b>2006</b> , 440, 1194-8	50.4	43
31	Genome-wide map of nuclear protein degradation shows NCoR1 turnover as a key to mitochondrial gene regulation. <i>Cell</i> , <b>2013</b> , 155, 1380-95	56.2	40
30	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. <i>Genome Biology</i> , <b>2020</b> , 21, 198	18.3	38
29	Regional centromeres in the yeast <i>Candida lusitanae</i> lack pericentromeric heterochromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 12139-44	11.5	35
28	HMMRATAC: a Hidden Markov ModelER for ATAC-seq. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, e91	20.1	33
27	JMJD6 is a tumorigenic factor and therapeutic target in neuroblastoma. <i>Nature Communications</i> , <b>2019</b> , 10, 3319	17.4	29
26	CistromeMap: a knowledgebase and web server for ChIP-Seq and DNase-Seq studies in mouse and human. <i>Bioinformatics</i> , <b>2012</b> , 28, 1411-2	7.2	29
25	Profiling <i>Caenorhabditis elegans</i> non-coding RNA expression with a combined microarray. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 2976-83	20.1	29
24	An unusual haplotype structure on human chromosome 8p23 derived from the inversion polymorphism. <i>Human Mutation</i> , <b>2008</b> , 29, 1209-16	4.7	27
23	The histone methyltransferase DOT1L: regulatory functions and a cancer therapy target. <i>American Journal of Cancer Research</i> , <b>2015</b> , 5, 2823-37	4.4	27

22	Amelioration of autism-like social deficits by targeting histone methyltransferases EHMT1/2 in Shank3-deficient mice. <i>Molecular Psychiatry</i> , <b>2020</b> , 25, 2517-2533	15.1	26
21	Disease-Associated Single-Nucleotide Polymorphisms From Noncoding Regions in Juvenile Idiopathic Arthritis Are Located Within or Adjacent to Functional Genomic Elements of Human Neutrophils and CD4+ T Cells. <i>Arthritis and Rheumatology</i> , <b>2015</b> , 67, 1966-77	9.5	24
20	Computational methodology for ChIP-seq analysis. <i>Quantitative Biology</i> , <b>2013</b> , 1, 54-70	3.9	20
19	MM-ChIP enables integrative analysis of cross-platform and between-laboratory ChIP-chip or ChIP-seq data. <i>Genome Biology</i> , <b>2011</b> , 12, R11	18.3	18
18	CistromeFinder for ChIP-seq and DNase-seq data reuse. <i>Bioinformatics</i> , <b>2013</b> , 29, 1352-4	7.2	15
17	An amino terminal phosphorylation motif regulates intranuclear compartmentalization of Olig2 in neural progenitor cells. <i>Journal of Neuroscience</i> , <b>2014</b> , 34, 8507-18	6.6	13
16	Chromatin landscapes and genetic risk in systemic lupus. <i>Arthritis Research and Therapy</i> , <b>2016</b> , 18, 281	5.7	12
15	Single cell transcriptomics reveals lineage trajectory of retinal ganglion cells in wild-type and Atoh7-null retinas. <i>Nature Communications</i> , <b>2021</b> , 12, 1465	17.4	10
14	An ALYREF-MYCN coactivator complex drives neuroblastoma tumorigenesis through effects on USP3 and MYCN stability. <i>Nature Communications</i> , <b>2021</b> , 12, 1881	17.4	8
13	Chromatin landscapes and genetic risk for juvenile idiopathic arthritis. <i>Arthritis Research and Therapy</i> , <b>2017</b> , 19, 57	5.7	7
12	Computational dissection of Arabidopsis smRNAome leads to discovery of novel microRNAs and short interfering RNAs associated with transcription start sites. <i>Genomics</i> , <b>2011</b> , 97, 235-43	4.3	7
11	IDO1 Expression in Ovarian Cancer Induces PD-1 in T Cells Aryl Hydrocarbon Receptor Activation. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 678999	8.4	7
10	Activation of NF- $\kappa$ B and p300/CBP potentiates cancer chemoimmunotherapy through induction of MHC-I antigen presentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	5
9	Evolution of Distinct Responses to Low NAD Stress by Rewiring the Sir2 Deacetylase Network in Yeasts. <i>Genetics</i> , <b>2020</b> , 214, 855-868	4	4
8	Robust repression of tRNA gene transcription during stress requires protein arginine methylation. <i>Life Science Alliance</i> , <b>2019</b> , 2,	5.8	3
7	Helicobacter pylori-Induced Rev-erb $\beta$ Fosters Gastric Bacteria Colonization by Impairing Host Innate and Adaptive Defense. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , <b>2021</b> , 12, 395-425	7.9	3
6	A174: JIA-Associated SNPs From Non-Coding Regions Are Located Within or Adjacent to Functional Genomic Elements of Human Neutrophils. <i>Arthritis and Rheumatology</i> , <b>2014</b> , 66, S227-S227	9.5	2
5	MUC1-C Dictates JUN and BAF-mediated Chromatin Remodeling at Enhancer Signatures in Cancer Stem Cells.. <i>Molecular Cancer Research</i> , <b>2022</b> ,	6.6	2

4	MUC1-C integrates type II interferon and chromatin remodeling pathways in immunosuppression of prostate cancer.. <i>OncotImmunology</i> , <b>2022</b> , 11, 2029298	7.2	2
3	CD4+ T cells from children with active juvenile idiopathic arthritis show altered chromatin features associated with transcriptional abnormalities. <i>Scientific Reports</i> , <b>2021</b> , 11, 4011	4.9	2
2	Fast alignment and preprocessing of chromatin profiles with Chromap. <i>Nature Communications</i> , <b>2021</b> , 12, 6566	17.4	1
1	HMMRATAC: a Hidden Markov Modeler for ATAC-seq		1