Tao Liu

List of Publications by Year in Descending Order

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	MUC1-C Dictates JUN and BAF-mediated Chromatin Remodeling at Enhancer Signatures in Cancer Stem Cells.. *Molecular Cancer Research*, **2022**,	6.6	2
56	MUC1-C integrates type II interferon and chromatin remodeling pathways in immunosuppression of prostate cancer.. *OncoImmunology*, **2022**, 11, 2029298	7.2	2
55	Fast alignment and preprocessing of chromatin profiles with Chromap. *Nature Communications*, **2021**, 12, 6566	17.4	1
54	Single cell transcriptomics reveals lineage trajectory of retinal ganglion cells in wild-type and Atoh7-null retinas. *Nature Communications*, **2021**, 12, 1465	17.4	10
53	An ALYREF-MYCN coactivator complex drives neuroblastoma tumorigenesis through effects on USP3 and MYCN stability. *Nature Communications*, **2021**, 12, 1881	17.4	8
52	IDO1 Expression in Ovarian Cancer Induces PD-1 in T Cells Aryl Hydrocarbon Receptor Activation. *Frontiers in Immunology*, **2021**, 12, 678999	8.4	7
51	Helicobacter pylori-Induced Rev-erbꭇFosters Gastric Bacteria Colonization by Impairing Host Innate and Adaptive Defense. *Cellular and Molecular Gastroenterology and Hepatology*, **2021**, 12, 395-425	7.9	3
50	Activation of NF-ꞵB and p300/CBP potentiates cancer chemoimmunotherapy through induction of MHC-I antigen presentation. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	5
49	CD4+ T cells from children with active juvenile idiopathic arthritis show altered chromatin features associated with transcriptional abnormalities. *Scientific Reports*, **2021**, 11, 4011	4.9	2
48	Evolution of Distinct Responses to Low NAD Stress by Rewiring the Sir2 Deacetylase Network in Yeasts. *Genetics*, **2020**, 214, 855-868	4	4
47	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. *Genome Biology*, **2020**, 21, 198	18.3	38
46	Amelioration of autism-like social deficits by targeting histone methyltransferases EHMT1/2 in Shank3-deficient mice. *Molecular Psychiatry*, **2020**, 25, 2517-2533	15.1	26
45	HMMRATAC: a Hidden Markov ModeleR for ATAC-seq. *Nucleic Acids Research*, **2019**, 47, e91	20.1	33
44	Sources of artifact in measurements of 6mA and 4mC abundance in eukaryotic genomic DNA. *BMC Genomics*, **2019**, 20, 445	4.5	56
43	JMJD6 is a tumorigenic factor and therapeutic target in neuroblastoma. *Nature Communications*, **2019**, 10, 3319	17.4	29
42	Robust repression of tRNA gene transcription during stress requires protein arginine methylation. *Life Science Alliance*, **2019**, 2,	5.8	3
41	Chromatin landscapes and genetic risk for juvenile idiopathic arthritis. *Arthritis Research and Therapy*, **2017**, 19, 57	5.7	7

40	Genome-wide identification and differential analysis of translational initiation. *Nature Communications*, **2017**, 8, 1749	17.4	47
39	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. *Nucleic Acids Research*, **2017**, 45, D658-D662	20.1	265
38	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. *BMC Bioinformatics*, **2016**, 17, 404	3.6	72
37	Chromatin landscapes and genetic risk in systemic lupus. *Arthritis Research and Therapy*, **2016**, 18, 281	5.7	12
36	TRANSCRIPTION. Recruitment of RNA polymerase II by the pioneer transcription factor PHA-4. *Science*, **2015**, 348, 1372-6	33.3	51
35	Regional centromeres in the yeast Candida lusitaniae lack pericentromeric heterochromatin. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 12139-44	11.5	35
34	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. *Arthritis and Rheumatology*, **2015**, 67, 1966-77	9.5	24
33	The histone methyltransferase DOT1L: regulatory functions and a cancer therapy target. *American Journal of Cancer Research*, **2015**, 5, 2823-37	4.4	27
32	A174: JIA-Associated SNPs From Non-Coding Regions Are Located Within or Adjacent to Functional Genomic Elements of Human Neutrophils. *Arthritis and Rheumatology*, **2014**, 66, S227-S227	9.5	2
31	Comparative analysis of metazoan chromatin organization. *Nature*, **2014**, 512, 449-52	50.4	265
30	An amino terminal phosphorylation motif regulates intranuclear compartmentalization of Olig2 in neural progenitor cells. *Journal of Neuroscience*, **2014**, 34, 8507-18	6.6	13
29	Use model-based Analysis of ChIP-Seq (MACS) to analyze short reads generated by sequencing protein-DNA interactions in embryonic stem cells. *Methods in Molecular Biology*, **2014**, 1150, 81-95	1.4	119
28	Polycomb-independent activity of EZH2 in castration resistant prostate cancer. *Epigenetics and Chromatin*, **2013**, 6,	5.8	78
27	Computational methodology for ChIP-seq analysis. *Quantitative Biology*, **2013**, 1, 54-70	3.9	20
26	Genome-wide map of nuclear protein degradation shows NCoR1 turnover as a key to mitochondrial gene regulation. *Cell*, **2013**, 155, 1380-95	56.2	40
25	Practical guidelines for the comprehensive analysis of ChIP-seq data. *PLoS Computational Biology*, **2013**, 9, e1003326	5	166
24	CistromeFinder for ChIP-seq and DNase-seq data reuse. *Bioinformatics*, **2013**, 29, 1352-4	7.2	15
23	EZH2 oncogenic activity in castration-resistant prostate cancer cells is Polycomb-independent. *Science*, **2012**, 338, 1465-9	33.3	585

22	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. *Genome Research*, **2012**, 22, 1813-31	9.7	1211
21	CistromeMap: a knowledgebase and web server for ChIP-Seq and DNase-Seq studies in mouse and human. *Bioinformatics*, **2012**, 28, 1411-2	7.2	29
20	Identifying ChIP-seq enrichment using MACS. *Nature Protocols*, **2012**, 7, 1728-40	18.8	857
19	Systematic evaluation of factors influencing ChIP-seq fidelity. *Nature Methods*, **2012**, 9, 609-14	21.6	112
18	Using MACS to identify peaks from ChIP-Seq data. *Current Protocols in Bioinformatics*, **2011**, Chapter 2, Unit 2.14	24.2	149
17	Cistrome: an integrative platform for transcriptional regulation studies. *Genome Biology*, **2011**, 12, R83	18.3	461
16	MM-ChIP enables integrative analysis of cross-platform and between-laboratory ChIP-chip or ChIP-seq data. *Genome Biology*, **2011**, 12, R11	18.3	18
15	Computational dissection of Arabidopsis smRNAome leads to discovery of novel microRNAs and short interfering RNAs associated with transcription start sites. *Genomics*, **2011**, 97, 235-43	4.3	7
14	A circadian rhythm orchestrated by histone deacetylase 3 controls hepatic lipid metabolism. *Science*, **2011**, 331, 1315-9	33.3	507
13	Broad chromosomal domains of histone modification patterns in C. elegans. *Genome Research*, **2011**, 21, 227-36	9.7	208
12	A comprehensive view of nuclear receptor cancer cistromes. *Cancer Research*, **2011**, 71, 6940-7	10.1	99
11	Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project. *Science*, **2010**, 330, 1775-87	33.3	744
10	CEAS: cis-regulatory element annotation system. *Bioinformatics*, **2009**, 25, 2605-6	7.2	352
9	Differential chromatin marking of introns and expressed exons by H3K36me3. *Nature Genetics*, **2009**, 41, 376-81	36.3	509
8	MicroRNA-encoding long non-coding RNAs. *BMC Genomics*, **2008**, 9, 236	4.5	53
7	Model-based analysis of ChIP-Seq (MACS). *Genome Biology*, **2008**, 9, R137	18.3	8406
6	An unusual haplotype structure on human chromosome 8p23 derived from the inversion polymorphism. *Human Mutation*, **2008**, 29, 1209-16	4.7	27
5	NONCODE v2.0: decoding the non-coding. *Nucleic Acids Research*, **2008**, 36, D170-2	20.1	108

List of Publications

4	Mapping the C. elegans noncoding transcriptome with a whole-genome tiling microarray. *Genome Research*, **2007**, 17, 1471-7	9.7	49
3	Profiling Caenorhabditis elegans non-coding RNA expression with a combined microarray. *Nucleic Acids Research*, **2006**, 34, 2976-83	20.1	29
2	The DNA sequence, annotation and analysis of human chromosome 3. *Nature*, **2006**, 440, 1194-8	50.4	43
1	HMMRATAC: a Hidden Markov ModeleR for ATAC-seq		1