

Tao Liu

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

24,172
citations

136740

32
h-index

143772

57
g-index

68
all docs

68
docs citations

68
times ranked

41952
citing authors

#	ARTICLE	IF	CITATIONS
1	Model-based Analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , 2008, 9, R137.	13.9	13,517
2	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	2.4	1,708
3	Identifying ChIP-seq enrichment using MACS. <i>Nature Protocols</i> , 2012, 7, 1728-1740.	5.5	1,471
4	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
5	EZH2 Oncogenic Activity in Castration-Resistant Prostate Cancer Cells Is Polycomb-Independent. <i>Science</i> , 2012, 338, 1465-1469.	6.0	748
6	Cistrome: an integrative platform for transcriptional regulation studies. <i>Genome Biology</i> , 2011, 12, R83.	13.9	598
7	A Circadian Rhythm Orchestrated by Histone Deacetylase 3 Controls Hepatic Lipid Metabolism. <i>Science</i> , 2011, 331, 1315-1319.	6.0	596
8	Differential chromatin marking of introns and expressed exons by H3K36me3. <i>Nature Genetics</i> , 2009, 41, 376-381.	9.4	592
9	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. <i>Nucleic Acids Research</i> , 2017, 45, D658-D662.	6.5	451
10	CEAS: <i>cis</i> -regulatory element annotation system. <i>Bioinformatics</i> , 2009, 25, 2605-2606.	1.8	415
11	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	13.7	363
12	Broad chromosomal domains of histone modification patterns in <i>C. elegans</i> . <i>Genome Research</i> , 2011, 21, 227-236.	2.4	256
13	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> , 2014, 1150, 81-95.	0.4	222
14	Practical Guidelines for the Comprehensive Analysis of ChIP-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003326.	1.5	221
15	Using MACS to Identify Peaks from ChIP-Seq Data. <i>Current Protocols in Bioinformatics</i> , 2011, 34, Unit 2.14.	25.8	203
16	Systematic evaluation of factors influencing ChIP-seq fidelity. <i>Nature Methods</i> , 2012, 9, 609-614.	9.0	156
17	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. <i>Genome Biology</i> , 2020, 21, 198.	3.8	126
18	Sources of artifact in measurements of 6mA and 4mC abundance in eukaryotic genomic DNA. <i>BMC Genomics</i> , 2019, 20, 445.	1.2	120

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19	A Comprehensive View of Nuclear Receptor Cancer Cistromes. <i>Cancer Research</i> , 2011, 71, 6940-6947.	0.4	118
20	NONCODE v2.0: decoding the non-coding. <i>Nucleic Acids Research</i> , 2007, 36, D170-D172.	6.5	115
21	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404.	1.2	100
22	Genome-wide identification and differential analysis of translational initiation. <i>Nature Communications</i> , 2017, 8, 1749.	5.8	100
23	HMMRATAC: a Hidden Markov Modeler for ATAC-seq. <i>Nucleic Acids Research</i> , 2019, 47, e91-e91.	6.5	67
24	Recruitment of RNA polymerase II by the pioneer transcription factor PHA-4. <i>Science</i> , 2015, 348, 1372-1376.	6.0	65
25	JMJD6 is a tumorigenic factor and therapeutic target in neuroblastoma. <i>Nature Communications</i> , 2019, 10, 3319.	5.8	63
26	MicroRNA-encoding long non-coding RNAs. <i>BMC Genomics</i> , 2008, 9, 236.	1.2	60
27	Amelioration of autism-like social deficits by targeting histone methyltransferases EHMT1/2 in Shank3-deficient mice. <i>Molecular Psychiatry</i> , 2020, 25, 2517-2533.	4.1	57
28	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	13.7	53
29	Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. <i>Genome Research</i> , 2007, 17, 1471-1477.	2.4	53
30	Activation of NF- κ 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> , 2021, 118, .	3.3	47
31	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> , 2015, 112, 12139-12144.	3.3	46
32	Genome-wide Map of Nuclear Protein Degradation Shows NCoR1 Turnover as a Key to Mitochondrial Gene Regulation. <i>Cell</i> , 2013, 155, 1380-1395.	13.5	45
33	Single cell transcriptomics reveals lineage trajectory of retinal ganglion cells in wild-type and Atoh7-null retinas. <i>Nature Communications</i> , 2021, 12, 1465.	5.8	41
34	IDO1 Expression in Ovarian Cancer Induces PD-1 in T Cells via Aryl Hydrocarbon Receptor Activation. <i>Frontiers in Immunology</i> , 2021, 12, 678999.	2.2	40
35	Fast alignment and preprocessing of chromatin profiles with Chromap. <i>Nature Communications</i> , 2021, 12, 6566.	5.8	39
36	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> , 2015, 67, 1966-1977.	2.9	38

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37	CistromeMap: a knowledgebase and web server for ChIP-Seq and DNase-Seq studies in mouse and human. <i>Bioinformatics</i> , 2012, 28, 1411-1412.	1.8	35
38	An ALYREF-MYCN coactivator complex drives neuroblastoma tumorigenesis through effects on USP3 and MYCN stability. <i>Nature Communications</i> , 2021, 12, 1881.	5.8	31
39	Profiling <i>Caenorhabditis elegans</i> non-coding RNA expression with a combined microarray. <i>Nucleic Acids Research</i> , 2006, 34, 2976-2983.	6.5	30
40	An unusual haplotype structure on human chromosome 8p23 derived from the inversion polymorphism. <i>Human Mutation</i> , 2008, 29, 1209-1216.	1.1	30
41	The histone methyltransferase DOT1L: regulatory functions and a cancer therapy target. <i>American Journal of Cancer Research</i> , 2015, 5, 2823-37.	1.4	27
42	Computational methodology for ChIP-seq analysis. <i>Quantitative Biology</i> , 2013, 1, 54-70.	0.3	24
43	MM-ChIP enables integrative analysis of cross-platform and between-laboratory ChIP-chip or ChIP-seq data. <i>Genome Biology</i> , 2011, 12, R11.	13.9	22
44	An Amino Terminal Phosphorylation Motif Regulates Intranuclear Compartmentalization of Olig2 in Neural Progenitor Cells. <i>Journal of Neuroscience</i> , 2014, 34, 8507-8518.	1.7	21
45	CistromeFinder for ChIP-seq and DNase-seq data reuse. <i>Bioinformatics</i> , 2013, 29, 1352-1354.	1.8	18
46	Chromatin landscapes and genetic risk in systemic lupus. <i>Arthritis Research and Therapy</i> , 2016, 18, 281.	1.6	18
47	MUC1-C Dictates JUN and BAF-Mediated Chromatin Remodeling at Enhancer Signatures in Cancer Stem Cells. <i>Molecular Cancer Research</i> , 2022, 20, 556-567.	1.5	17
48	MUC1-C integrates type II interferon and chromatin remodeling pathways in immunosuppression of prostate cancer. <i>Oncolmmunology</i> , 2022, 11, 2029298.	2.1	17
49	Chromatin landscapes and genetic risk for juvenile idiopathic arthritis. <i>Arthritis Research and Therapy</i> , 2017, 19, 57.	1.6	15
50	Computational dissection of Arabidopsis smRNAome leads to discovery of novel microRNAs and short interfering RNAs associated with transcription start sites. <i>Genomics</i> , 2011, 97, 235-243.	1.3	8
51	<i>Helicobacter pylori</i> Induced Rev-erb β Fosters Gastric Bacteria Colonization by Impairing Host Innate and Adaptive Defense. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 395-425.	2.3	8
52	Evolution of Distinct Responses to Low NAD ⁺ Stress by Rewiring the Sir2 Deacetylase Network in Yeasts. <i>Genetics</i> , 2020, 214, 855-868.	1.2	6
53	CD4 ⁺ T cells from children with active juvenile idiopathic arthritis show altered chromatin features associated with transcriptional abnormalities. <i>Scientific Reports</i> , 2021, 11, 4011.	1.6	5
54	Robust repression of tRNA gene transcription during stress requires protein arginine methylation. <i>Life Science Alliance</i> , 2019, 2, e201800261.	1.3	5

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55	Conservation of a DNA Replication Motif among Phylogenetically Distant Budding Yeast Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
56	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> , 2014, 66, S227-S227.	2.9	2
57	Polycomb-independent activity of EZH2 in castration resistant prostate cancer. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0
58	FRI0002â€¦THE JUVENILE IDIOPATHIC ARTHRITIS-ASSOCIATED IL2RA HAPLOTYPE CONTAINS AN INTRONIC ENHANCER WHOSE FUNCTION IS DIMINISHED BY JIA-ASSOCIATED GENETIC VARIANTS. , 2019, , .		0