

Ting Wang

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

16,887
citations

57758

44
h-index

43889

91
g-index

110
all docs

110
docs citations

110
times ranked

31322
citing authors

#	ARTICLE	IF	CITATIONS
1	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. <i>Cell Genomics</i> , 2022, 2, 100085.	6.5	59
2	Whole-genome profiling of DNA methylation and hydroxymethylation identifies distinct regulatory programs among innate lymphocytes. <i>Nature Immunology</i> , 2022, 23, 619-631.	14.5	14
3	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	27.8	192
4	WashU Epigenome Browser update 2022. <i>Nucleic Acids Research</i> , 2022, 50, W774-W781.	14.5	62
5	A genome-wide CRISPR-Cas9 knockout screen identifies essential and growth-restricting genes in human trophoblast stem cells. <i>Nature Communications</i> , 2022, 13, 2548.	12.8	25
6	Epigenomic analysis reveals prevalent contribution of transposable elements to cis-regulatory elements, tissue-specific expression, and alternative promoters in zebrafish. <i>Genome Research</i> , 2022, 32, 1424-1436.	5.5	7
7	Epigenomic differences in the human and chimpanzee genomes are associated with structural variation. <i>Genome Research</i> , 2021, 31, 279-290.	5.5	7
8	The qBED track: a novel genome browser visualization for point processes. <i>Bioinformatics</i> , 2021, 37, 1168-1170.	4.1	4
9	CRISPRi screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer. <i>Nature Communications</i> , 2021, 12, 1781.	12.8	32
10	Research on the Species Difference of the Hepatotoxicity of Medicine Based on Transcriptome. <i>Frontiers in Pharmacology</i> , 2021, 12, 647084.	3.5	11
11	Common DNA methylation dynamics in endometrioid adenocarcinoma and glioblastoma suggest universal epigenomic alterations in tumorigenesis. <i>Communications Biology</i> , 2021, 4, 607.	4.4	9
12	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021, 56, 1238-1252.e5.	7.0	29
13	AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 641-651.	6.9	19
14	Differential usage of transcriptional repressor Zeb2 enhancers distinguishes adult and embryonic hematopoiesis. <i>Immunity</i> , 2021, 54, 1417-1432.e7.	14.3	17
15	The Need for a Human Pangenome Reference Sequence. <i>Annual Review of Genomics and Human Genetics</i> , 2021, 22, 81-102.	6.2	71
16	OCT4 cooperates with distinct ATP-dependent chromatin remodelers in naïve and primed pluripotent states in human. <i>Nature Communications</i> , 2021, 12, 5123.	12.8	17
17	Epigenetic Therapies in Ovarian Cancer Alter Repetitive Element Expression in a TP53-Dependent Manner. <i>Cancer Research</i> , 2021, 81, 5176-5189.	0.9	15
18	Transcript assembly improves expression quantification of transposable elements in single-cell RNA-seq data. <i>Genome Research</i> , 2021, 31, 88-100.	5.5	34

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19	A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development. <i>Cell</i> , 2021, 184, 5541-5558.e22.	28.9	52
20	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. <i>Genome Biology</i> , 2021, 22, 282.	8.8	8
21	Tissue-specific usage of transposable element-derived promoters in mouse development. <i>Genome Biology</i> , 2020, 21, 255.	8.8	55
22	Cell-type-specific 3D epigenomes in the developing human cortex. <i>Nature</i> , 2020, 587, 644-649.	27.8	110
23	Epigenomic programming in early fetal brain development. <i>Epigenomics</i> , 2020, 12, 1053-1070.	2.1	9
24	Requisite Chromatin Remodeling for Myeloid and Erythroid Lineage Differentiation from Erythromyeloid Progenitors. <i>Cell Reports</i> , 2020, 33, 108395.	6.4	6
25	A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020, 588, 337-343.	27.8	80
26	Exploring the coronavirus pandemic with the WashU Virus Genome Browser. <i>Nature Genetics</i> , 2020, 52, 986-991.	21.4	13
27	Cellular diversity of the regenerating caudal fin. <i>Science Advances</i> , 2020, 6, eaba2084.	10.3	34
28	A genomic and epigenomic atlas of prostate cancer in Asian populations. <i>Nature</i> , 2020, 580, 93-99.	27.8	183
29	Comparison of differential accessibility analysis strategies for ATAC-seq data. <i>Scientific Reports</i> , 2020, 10, 10150.	3.3	32
30	DeepH&M: Estimating single-CpG hydroxymethylation and methylation levels from enrichment and restriction enzyme sequencing methods. <i>Science Advances</i> , 2020, 6, .	10.3	8
31	Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. <i>BMC Biology</i> , 2020, 18, 80.	3.8	28
32	Regenerating zebrafish fin epigenome is characterized by stable lineage-specific DNA methylation and dynamic chromatin accessibility. <i>Genome Biology</i> , 2020, 21, 52.	8.8	44
33	Co-opted transposons help perpetuate conserved higher-order chromosomal structures. <i>Genome Biology</i> , 2020, 21, 16.	8.8	57
34	Derivation of trophoblast stem cells from naïve human pluripotent stem cells. <i>ELife</i> , 2020, 9, .	6.0	203
35	WashU Epigenome Browser update 2019. <i>Nucleic Acids Research</i> , 2019, 47, W158-W165.	14.5	223
36	Epigenetic dysregulation of enhancers in neurons is associated with Alzheimer's disease pathology and cognitive symptoms. <i>Nature Communications</i> , 2019, 10, 2246.	12.8	160

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37	FeatSNP: An Interactive Database for Brain-Specific Epigenetic Annotation of Human SNPs. <i>Frontiers in Genetics</i> , 2019, 10, 262.	2.3	7
38	Transposable elements drive widespread expression of oncogenes in human cancers. <i>Nature Genetics</i> , 2019, 51, 611-617.	21.4	253
39	The epigenomic landscape of transposable elements across normal human development and anatomy. <i>Nature Communications</i> , 2019, 10, 5640.	12.8	67
40	The NIEHS TaRGET II Consortium and environmental epigenomics. <i>Nature Biotechnology</i> , 2018, 36, 225-227.	17.5	79
41	Comprehensive Whole DNA Methylome Analysis by Integrating MeDIP-seq and MRE-seq. <i>Methods in Molecular Biology</i> , 2018, 1708, 209-246.	0.9	20
42	Transposable Element Mediated Innovation in Gene Regulatory Landscapes of Cells: Revisiting the "Gene-Battery" Model. <i>BioEssays</i> , 2018, 40, 1700155.	2.5	39
43	Genome-wide association study identifies a novel locus for cannabis dependence. <i>Molecular Psychiatry</i> , 2018, 23, 1293-1302.	7.9	39
44	A high-fat diet alters genome-wide DNA methylation and gene expression in SM/J mice. <i>BMC Genomics</i> , 2018, 19, 888.	2.8	34
45	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. <i>Genome Biology</i> , 2018, 19, 151.	8.8	393
46	Genome-wide DNA methylation profiling of primary colorectal laterally spreading tumors identifies disease-specific epimutations on common pathways. <i>International Journal of Cancer</i> , 2018, 143, 2488-2498.	5.1	18
47	Long-Term In Vitro Expansion of Epithelial Stem Cells Enabled by Pharmacological Inhibition of PAK1-ROCK-Myosin II and TGF- β Signaling. <i>Cell Reports</i> , 2018, 25, 598-610.e5.	6.4	70
48	Soluble inflammatory mediators induce transcriptional re-organization that is independent of dna methylation changes in cultured human chorionic villous trophoblasts. <i>Journal of Reproductive Immunology</i> , 2018, 128, 2-8.	1.9	3
49	Maternal high-fat diet associated with altered gene expression, DNA methylation, and obesity risk in mouse offspring. <i>PLoS ONE</i> , 2018, 13, e0192606.	2.5	95
50	Whole-Genome DNA Methylation Profiling Identifies Epigenetic Signatures of Uterine Carcinosarcoma. <i>Neoplasia</i> , 2017, 19, 100-111.	5.3	27
51	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. <i>Nature Genetics</i> , 2017, 49, 1052-1060.	21.4	235
52	EpiCompare: an online tool to define and explore genomic regions with tissue or cell type-specific epigenomic features. <i>Bioinformatics</i> , 2017, 33, 3268-3275.	4.1	17
53	Functional cis-regulatory modules encoded by mouse-specific endogenous retrovirus. <i>Nature Communications</i> , 2017, 8, 14550.	12.8	73
54	Online resources for studies of genome biology and epigenetics. <i>Current Opinion in Toxicology</i> , 2017, 6, 34-41.	5.0	0

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55	Uncovering the transcriptomic and epigenomic landscape of nicotinic receptor genes in non-neuronal tissues. <i>BMC Genomics</i> , 2017, 18, 439.	2.8	15
56	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. <i>BMC Genomics</i> , 2017, 18, 724.	2.8	71
57	DNA methyltransferase 3b regulates articular cartilage homeostasis by altering metabolism. <i>JCI Insight</i> , 2017, 2, .	5.0	55
58	Epigenomic annotation of noncoding mutations identifies mutated pathways in primary liver cancer. <i>PLoS ONE</i> , 2017, 12, e0174032.	2.5	9
59	Inhibition of DNA Methyltransferases Blocks Mutant Huntingtin-Induced Neurotoxicity. <i>Scientific Reports</i> , 2016, 6, 31022.	3.3	28
60	Integrated small copy number variations and epigenome maps of disorders of sex development. <i>Human Genome Variation</i> , 2016, 3, 16012.	0.7	20
61	Evolution of Epigenetic Regulation in Vertebrate Genomes. <i>Trends in Genetics</i> , 2016, 32, 269-283.	6.7	86
62	Mapping of Variable DNA Methylation Across Multiple Cell Types Defines a Dynamic Regulatory Landscape of the Human Genome. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 973-986.	1.8	41
63	Evidence of CNH3 involvement in opioid dependence. <i>Molecular Psychiatry</i> , 2016, 21, 608-614.	7.9	109
64	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	12.8	91
65	Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. <i>Nature Biotechnology</i> , 2015, 33, 345-346.	17.5	83
66	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
67	Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015, 6, 6351.	12.8	56
68	Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. <i>Nature Communications</i> , 2015, 6, 6315.	12.8	73
69	Induction of hematopoietic and endothelial cell program orchestrated by <i>ETS</i> transcription factor <i>ER</i> 71/ <i>ETV</i> 2. <i>EMBO Reports</i> , 2015, 16, 654-669.	4.5	95
70	Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. <i>Methods</i> , 2015, 72, 29-40.	3.8	93
71	Comparative DNA methylome analysis of endometrial carcinoma reveals complex and distinct deregulation of cancer promoters and enhancers. <i>BMC Genomics</i> , 2014, 15, 868.	2.8	49
72	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. <i>Nature Communications</i> , 2014, 5, 5442.	12.8	25

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73	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259
74	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
75	methylC Track: visual integration of single-base resolution DNA methylation data on the WashU EpiGenome Browser. <i>Bioinformatics</i> , 2014, 30, 2206-2207.	4.1	26
76	Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , 2014, 24, 1963-1976.	5.5	408
77	Recurrent epimutations activate gene body promoters in primary glioblastoma. <i>Genome Research</i> , 2014, 24, 761-774.	5.5	39
78	DNA unmethylome profiling by covalent capture of CpG sites. <i>Nature Communications</i> , 2013, 4, 2190.	12.8	53
79	Estimating absolute methylation levels at single-CpG resolution from methylation enrichment and restriction enzyme sequencing methods. <i>Genome Research</i> , 2013, 23, 1541-1553.	5.5	138
80	Exploring long-range genome interactions using the WashU Epigenome Browser. <i>Nature Methods</i> , 2013, 10, 375-376.	19.0	199
81	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013, 45, 836-841.	21.4	207
82	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. <i>Genome Research</i> , 2013, 23, 1522-1540.	5.5	162
83	Comparative Epigenomic Annotation of Regulatory DNA. <i>Cell</i> , 2012, 149, 1381-1392.	28.9	188
84	Using the Wash U Epigenome Browser to Examine Genome-wide Sequencing Data. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit10.10.	25.8	56
85	The Human Epigenome Browser at Washington University. <i>Nature Methods</i> , 2011, 8, 989-990.	19.0	302
86	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <i>Genome Research</i> , 2011, 21, 1757-1767.	5.5	449
87	Conserved role of intragenic DNA methylation in regulating alternative promoters. <i>Nature</i> , 2010, 466, 253-257.	27.8	1,568
88	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	17.5	647
89	Visualizing genomes: techniques and challenges. <i>Nature Methods</i> , 2010, 7, S5-S15.	19.0	146
90	Species-specific endogenous retroviruses shape the transcriptional network of the human tumor suppressor protein p53. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18613-18618.	7.1	364