

# 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  | Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.  | 27.8 | 5,653     |
| 2  | Conserved role of intragenic DNA methylation in regulating alternative promoters. <i>Nature</i> , 2010, 466, 253-257.  | 27.8 | 1,568     |
| 3  | A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.  | 27.8 | 1,444     |
| 4  | 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       |
| 5  | 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       |
| 6  | Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , 2014, 24, 1963-1976.  | 5.5  | 408       |
| 7  | 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       |
| 8  | 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       |
| 9  | The Human Epigenome Browser at Washington University. <i>Nature Methods</i> , 2011, 8, 989-990.  | 19.0 | 302       |
| 10 | Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.   | 27.8 | 259       |
| 11 | Transposable elements drive widespread expression of oncogenes in human cancers. <i>Nature Genetics</i> , 2019, 51, 611-617.   | 21.4 | 253       |
| 12 | 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       |
| 13 | WashU Epigenome Browser update 2019. <i>Nucleic Acids Research</i> , 2019, 47, W158-W165.  | 14.5 | 223       |
| 14 | DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013, 45, 836-841.  | 21.4 | 207       |
| 15 | Derivation of trophoblast stem cells from naïve human pluripotent stem cells. <i>ELife</i> , 2020, 9, .  | 6.0  | 203       |
| 16 | Exploring long-range genome interactions using the WashU Epigenome Browser. <i>Nature Methods</i> , 2013, 10, 375-376.   | 19.0 | 199       |
| 17 | The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.   | 27.8 | 192       |
| 18 | Comparative Epigenomic Annotation of Regulatory DNA. <i>Cell</i> , 2012, 149, 1381-1392.   | 28.9 | 188       |

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|----|--|------|-----------|
| 19 | A genomic and epigenomic atlas of prostate cancer in Asian populations. <i>Nature</i> , 2020, 580, 93-99.  | 27.8 | 183       |
| 20 | 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       |
| 21 | 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       |
| 22 | Visualizing genomes: techniques and challenges. <i>Nature Methods</i> , 2010, 7, S5-S15.   | 19.0 | 146       |
| 23 | 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       |
| 24 | Cell-type-specific 3D epigenomes in the developing human cortex. <i>Nature</i> , 2020, 587, 644-649.   | 27.8 | 110       |
| 25 | Evidence of CNH3 involvement in opioid dependence. <i>Molecular Psychiatry</i> , 2016, 21, 608-614.  | 7.9  | 109       |
| 26 | 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        |
| 27 | 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        |
| 28 | Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. <i>Methods</i> , 2015, 72, 29-40.  | 3.8  | 93        |
| 29 | Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.  | 12.8 | 91        |
| 30 | Evolution of Epigenetic Regulation in Vertebrate Genomes. <i>Trends in Genetics</i> , 2016, 32, 269-283.   | 6.7  | 86        |
| 31 | Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. <i>Nature Biotechnology</i> , 2015, 33, 345-346.  | 17.5 | 83        |
| 32 | A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020, 588, 337-343.  | 27.8 | 80        |
| 33 | The NIEHS TaRGET II Consortium and environmental epigenomics. <i>Nature Biotechnology</i> , 2018, 36, 225-227.   | 17.5 | 79        |
| 34 | Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. <i>Nature Communications</i> , 2015, 6, 6315.   | 12.8 | 73        |
| 35 | Functional cis-regulatory modules encoded by mouse-specific endogenous retrovirus. <i>Nature Communications</i> , 2017, 8, 14550.  | 12.8 | 73        |
| 36 | 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        |

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|----|--|------|-----------|
| 37 | The Need for a Human Pangenome Reference Sequence. <i>Annual Review of Genomics and Human Genetics</i> , 2021, 22, 81-102.   | 6.2  | 71        |
| 38 | Long-Term InÂVitro Expansion of Epithelial Stem Cells Enabled by Pharmacological Inhibition of PAK1-ROCK-Myosin II and TGF-Î² Signaling. <i>Cell Reports</i> , 2018, 25, 598-610.e5. | 6.4  | 70        |
| 39 | The epigenomic landscape of transposable elements across normal human development and anatomy. <i>Nature Communications</i> , 2019, 10, 5640.  | 12.8 | 67        |
| 40 | WashU Epigenome Browser update 2022. <i>Nucleic Acids Research</i> , 2022, 50, W774-W781.  | 14.5 | 62        |
| 41 | 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        |
| 42 | Co-opted transposons help perpetuate conserved higher-order chromosomal structures. <i>Genome Biology</i> , 2020, 21, 16.  | 8.8  | 57        |
| 43 | 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        |
| 44 | Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015, 6, 6351.   | 12.8 | 56        |
| 45 | Tissue-specific usage of transposable element-derived promoters in mouse development. <i>Genome Biology</i> , 2020, 21, 255.   | 8.8  | 55        |
| 46 | DNA methyltransferase 3b regulates articular cartilage homeostasis by altering metabolism. <i>JCI Insight</i> , 2017, 2, .   | 5.0  | 55        |
| 47 | DNA unmethylome profiling by covalent capture of CpG sites. <i>Nature Communications</i> , 2013, 4, 2190.  | 12.8 | 53        |
| 48 | A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development. <i>Cell</i> , 2021, 184, 5541-5558.e22.   | 28.9 | 52        |
| 49 | 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        |
| 50 | 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        |
| 51 | 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        |
| 52 | Recurrent epimutations activate gene body promoters in primary glioblastoma. <i>Genome Research</i> , 2014, 24, 761-774.   | 5.5  | 39        |
| 53 | Transposable Element Mediated Innovation in Gene Regulatory Landscapes of Cells: Re-Visiting the "Gene-Battery" Model. <i>BioEssays</i> , 2018, 40, 1700155.                         | 2.5  | 39        |
| 54 | Genome-wide association study identifies a novel locus for cannabis dependence. <i>Molecular Psychiatry</i> , 2018, 23, 1293-1302.   | 7.9  | 39        |

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|----|--|------|-----------|
| 55 | A high-fat diet alters genome-wide DNA methylation and gene expression in SM/J mice. BMC Genomics, 2018, 19, 888.  | 2.8  | 34        |
| 56 | Cellular diversity of the regenerating caudal fin. Science Advances, 2020, 6, eaba2084.  | 10.3 | 34        |
| 57 | Transcript assembly improves expression quantification of transposable elements in single-cell RNA-seq data. Genome Research, 2021, 31, 88-100.  | 5.5  | 34        |
| 58 | Comparison of differential accessibility analysis strategies for ATAC-seq data. Scientific Reports, 2020, 10, 10150.   | 3.3  | 32        |
| 59 | CRISPRi screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer. Nature Communications, 2021, 12, 1781.  | 12.8 | 32        |
| 60 | Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. Developmental Cell, 2021, 56, 1238-1252.e5.  | 7.0  | 29        |
| 61 | Inhibition of DNA Methyltransferases Blocks Mutant Huntingtin-Induced Neurotoxicity. Scientific Reports, 2016, 6, 31022.   | 3.3  | 28        |
| 62 | Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. BMC Biology, 2020, 18, 80.  | 3.8  | 28        |
| 63 | Whole-Genome DNA Methylation Profiling Identifies Epigenetic Signatures of Uterine Carcinosarcoma. Neoplasia, 2017, 19, 100-111.   | 5.3  | 27        |
| 64 | methylC Track: visual integration of single-base resolution DNA methylation data on the WashU EpiGenome Browser. Bioinformatics, 2014, 30, 2206-2207.  | 4.1  | 26        |
| 65 | Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. Nature Communications, 2014, 5, 5442.   | 12.8 | 25        |
| 66 | A genome-wide CRISPR-Cas9 knockout screen identifies essential and growth-restricting genes in human trophoblast stem cells. Nature Communications, 2022, 13, 2548.  | 12.8 | 25        |
| 67 | Integrated small copy number variations and epigenome maps of disorders of sex development. Human Genome Variation, 2016, 3, 16012.  | 0.7  | 20        |
| 68 | Comprehensive Whole DNA Methylome Analysis by Integrating MeDIP-seq and MRE-seq. Methods in Molecular Biology, 2018, 1708, 209-246.  | 0.9  | 20        |
| 69 | AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 641-651.  | 6.9  | 19        |
| 70 | Genome-wide DNA methylation profiling of primary colorectal laterally spreading tumors identifies disease-specific epimutations on common pathways. International Journal of Cancer, 2018, 143, 2488-2498. | 5.1  | 18        |
| 71 | EpiCompare: an online tool to define and explore genomic regions with tissue or cell type-specific epigenomic features. Bioinformatics, 2017, 33, 3268-3275.   | 4.1  | 17        |
| 72 | Differential usage of transcriptional repressor Zeb2 enhancers distinguishes adult and embryonic hematopoiesis. Immunity, 2021, 54, 1417-1432.e7.  | 14.3 | 17        |

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|----|--|------|-----------|
| 73 | 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        |
| 74 | Uncovering the transcriptomic and epigenomic landscape of nicotinic receptor genes in non-neuronal tissues. <i>BMC Genomics</i> , 2017, 18, 439.   | 2.8  | 15        |
| 75 | 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        |
| 76 | 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        |
| 77 | Exploring the coronavirus pandemic with the WashU Virus Genome Browser. <i>Nature Genetics</i> , 2020, 52, 986-991.  | 21.4 | 13        |
| 78 | Research on the Species Difference of the Hepatotoxicity of Medicine Based on Transcriptome. <i>Frontiers in Pharmacology</i> , 2021, 12, 647084.  | 3.5  | 11        |
| 79 | Epigenomic programming in early fetal brain development. <i>Epigenomics</i> , 2020, 12, 1053-1070.   | 2.1  | 9         |
| 80 | 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         |
| 81 | Epigenomic annotation of noncoding mutations identifies mutated pathways in primary liver cancer. <i>PLoS ONE</i> , 2017, 12, e0174032.  | 2.5  | 9         |
| 82 | 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         |
| 83 | Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. <i>Genome Biology</i> , 2021, 22, 282.  | 8.8  | 8         |
| 84 | FeatSNP: An Interactive Database for Brain-Specific Epigenetic Annotation of Human SNPs. <i>Frontiers in Genetics</i> , 2019, 10, 262.   | 2.3  | 7         |
| 85 | Epigenomic differences in the human and chimpanzee genomes are associated with structural variation. <i>Genome Research</i> , 2021, 31, 279-290.   | 5.5  | 7         |
| 86 | 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         |
| 87 | Requisite Chromatin Remodeling for Myeloid and Erythroid Lineage Differentiation from Erythromyeloid Progenitors. <i>Cell Reports</i> , 2020, 33, 108395.  | 6.4  | 6         |
| 88 | The qBED track: a novel genome browser visualization for point processes. <i>Bioinformatics</i> , 2021, 37, 1168-1170.   | 4.1  | 4         |
| 89 | 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         |
| 90 | Online resources for studies of genome biology and epigenetics. <i>Current Opinion in Toxicology</i> , 2017, 6, 34-41.   | 5.0  | 0         |