

# Chia-Lin Wei

## List of Publications by Year in descending order

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75  
papers

24,821  
citations

53751

45  
h-index

74108

75  
g-index

78  
all docs

78  
docs citations

78  
times ranked

32378  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
2	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. <i>Cell</i> , 2008, 133, 1106-1117.	13.5	2,279
3	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006, 38, 431-440.	9.4	2,162
4	An oestrogen-receptor- $\hat{\pm}$ -bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64.	13.7	1,537
5	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	13.5	1,096
6	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. <i>Cell</i> , 2006, 124, 207-219.	13.5	1,060
7	Dynamic changes in the human methylome during differentiation. <i>Genome Research</i> , 2010, 20, 320-331.	2.4	930
8	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , 2015, 163, 1611-1627.	13.5	881
9	A Large Fraction of Extragenic RNA Pol II Transcription Sites Overlap Enhancers. <i>PLoS Biology</i> , 2010, 8, e1000384.	2.6	762
10	Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. <i>Nature Genetics</i> , 2010, 42, 53-61.	9.4	652
11	Identification and Characterization of Enhancers Controlling the Inflammatory Gene Expression Program in Macrophages. <i>Immunity</i> , 2010, 32, 317-328.	6.6	567
12	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638.	9.4	567
13	Whole-Genome Mapping of Histone H3 Lys4 and 27 Trimethylations Reveals Distinct Genomic Compartments in Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2007, 1, 286-298.	5.2	536
14	Evolution of the mammalian transcription factor binding repertoire via transposable elements. <i>Genome Research</i> , 2008, 18, 1752-1762.	2.4	501
15	Global mapping of c-Myc binding sites and target gene networks in human B cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17834-17839.	3.3	462
16	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , 2013, 504, 306-310.	13.7	405
17	Whole-Genome Cartography of Estrogen Receptor $\hat{\pm}$ Binding Sites. <i>PLoS Genetics</i> , 2007, 3, e87.	1.5	400
18	Activation and repression by oncogenic MYC shape tumour-specific gene expression profiles. <i>Nature</i> , 2014, 511, 483-487.	13.7	392

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19	Jmjd3 contributes to the control of gene expression in LPS-activated macrophages. <i>EMBO Journal</i> , 2009, 28, 3341-3352.	3.5	383
20	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. <i>Cell</i> , 2013, 155, 1507-1520.	13.5	299
21	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. <i>Genome Research</i> , 2009, 19, 521-532.	2.4	286
22	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	9.4	271
23	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010, 11, R22.	13.9	255
24	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005, 2, 105-111.	9.0	244
25	CHD7 Targets Active Gene Enhancer Elements to Modulate ES Cell-Specific Gene Expression. <i>PLoS Genetics</i> , 2010, 6, e1001023.	1.5	213
26	Sall4 Regulates Distinct Transcription Circuitries in Different Blastocyst-Derived Stem Cell Lineages. <i>Cell Stem Cell</i> , 2008, 3, 543-554.	5.2	209
27	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007, 17, 839-851.	2.4	191
28	Mapping of transcription factor binding regions in mammalian cells by ChIP: Comparison of array- and sequencing-based technologies. <i>Genome Research</i> , 2007, 17, 898-909.	2.4	181
29	Genome-wide Mapping of RELA(p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF- $\kappa$ B upon TLR4 Activation. <i>Molecular Cell</i> , 2007, 27, 622-635.	4.5	180
30	Multiplex chromatin interactions with single-molecule precision. <i>Nature</i> , 2019, 566, 558-562.	13.7	180
31	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. <i>PLoS Biology</i> , 2008, 6, e256.	2.6	172
32	The Major Protein of Messenger Ribonucleoprotein Particles in Somatic Cells Is a Member of the Y-box Binding Transcription Factor Family. <i>Journal of Biological Chemistry</i> , 1995, 270, 3186-3192.	1.6	163
33	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. <i>Cancer Cell</i> , 2021, 39, 694-707.e7.	7.7	115
34	Multiplex sequencing of paired-end ditags (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptomes and genomes. <i>Nucleic Acids Research</i> , 2006, 34, e84-e84.	6.5	111
35	Marine algae and land plants share conserved phytochrome signaling systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15827-15832.	3.3	108
36	Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. <i>Nature Genetics</i> , 2020, 52, 264-272.	9.4	104

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37	5' Long serial analysis of gene expression (LongSAGE) and 3' LongSAGE for transcriptome characterization and genome annotation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11701-11706.	3.3	103
38	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). Genome Research, 2007, 17, 828-838.	2.4	86
39	Picky comprehensively detects high-resolution structural variants in nanopore long reads. Nature Methods, 2018, 15, 455-460.	9.0	80
40	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. Genome Research, 2011, 21, 665-675.	2.4	74
41	Ecotopic viral integration site 1 (EV1) regulates multiple cellular processes important for cancer and is a synergistic partner for FOS protein in invasive tumors. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2168-2173.	3.3	74
42	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. BMC Genomics, 2016, 17, 267.	1.2	74
43	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765 <sup>T</sup> , <i>Desulfosporosinus youngiae</i> DSM17734 <sup>T</sup> , <i>Desulfosporosinus meridiei</i> DSM13257 <sup>T</sup> , and <i>Desulfosporosinus acidiphilus</i> DSM22704 <sup>T</sup> . Journal of Bacteriology, 2012, 194, 6300-6301.	1.0	73
44	Mapping the Global Chromatin Connectivity Network for Sox2 Function in Neural Stem Cell Maintenance. Cell Stem Cell, 2019, 24, 462-476.e6.	5.2	72
45	Target Gene Analysis by Microarrays and Chromatin Immunoprecipitation Identifies HEY Proteins as Highly Redundant bHLH Repressors. PLoS Genetics, 2012, 8, e1002728.	1.5	66
46	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. Plant Journal, 2015, 84, 800-815.	2.8	47
47	<i>DNA</i> methylation and gene expression regulation associated with vascularization in <i>Sorghum bicolor</i> . New Phytologist, 2017, 214, 1213-1229.	3.5	47
48	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23T. Standards in Genomic Sciences, 2013, 8, 375-388.	1.5	44
49	Characterization of Yeast Translation Initiation Factor 1A and Cloning of Its Essential Gene. Journal of Biological Chemistry, 1995, 270, 22788-22794.	1.6	43
50	Sox2 Controls Neural Stem Cell Self-Renewal Through a <i>Fos</i> -Centered Gene Regulatory Network. Stem Cells, 2021, 39, 1107-1119.	1.4	36
51	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. Standards in Genomic Sciences, 2013, 7, 449-468.	1.5	31
52	<i>Sox2</i> conditional mutation in mouse causes ataxic symptoms, cerebellar vermis hypoplasia, and postnatal defects of <i>Bergmann</i> glia. Glia, 2018, 66, 1929-1946.	2.5	28
53	Protein Synthesis Initiation Factor eIF-1A Is a Moderately Abundant RNA-binding Protein. Journal of Biological Chemistry, 1995, 270, 5764-5771.	1.6	27
54	Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. Nature Microbiology, 2018, 3, 781-790.	5.9	26

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55	Transcriptional responses of the marine green alga <i>Micromonas pusilla</i> and an infecting prasinovirus under different phosphate conditions. <i>Environmental Microbiology</i> , 2018, 20, 2898-2912.	1.8	25
56	Culture-independent analysis of liver abscess using nanopore sequencing. <i>PLoS ONE</i> , 2018, 13, e0190853.	1.1	22
57	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. <i>Science Advances</i> , 2020, 6, eaay2078.	4.7	22
58	Ultra-long Read Sequencing for Whole Genomic DNA Analysis. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	20
59	Discovery of photosynthesis genes through whole-genome sequencing of acetate-requiring mutants of <i>Chlamydomonas reinhardtii</i> . <i>PLoS Genetics</i> , 2021, 17, e1009725.	1.5	18
60	Reduced subgenomic RNA expression is a molecular indicator of asymptomatic SARS-CoV-2 infection. <i>Communications Medicine</i> , 2021, 1, .	1.9	13
61	A genome-wide map of adeno-associated virus-mediated human gene targeting. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 969-975.	3.6	12
62	Chromatin topology reorganization and transcription repression by PML-RAR $\alpha$ in acute promyeloid leukemia. <i>Genome Biology</i> , 2020, 21, 110.	3.8	12
63	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. <i>Standards in Genomic Sciences</i> , 2013, 9, 243-253.	1.5	10
64	Genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia sprentiae</i> strain WSM5005T. <i>Standards in Genomic Sciences</i> , 2013, 9, 385-394.	1.5	9
65	Genome sequence of the <i>Listia angolensis</i> microsymbiont <i>Microvirga lotononidis</i> strain WSM3557T. <i>Standards in Genomic Sciences</i> , 2013, 9, 540-550.	1.5	7
66	Sox2-Dependent 3D Chromatin Interactomes in Transcription, Neural Stem Cell Proliferation and Neurodevelopmental Diseases. <i>Journal of Experimental Neuroscience</i> , 2019, 13, 117906951986822.	2.3	7
67	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga <i>Micromonas pusilla</i> . <i>PLoS ONE</i> , 2016, 11, e0155839.	1.1	7
68	TGF $\beta$ -dependent gene expression shows that senescence correlates with abortive differentiation along several lineages in Myc-induced lymphomas. <i>Cell Cycle</i> , 2010, 9, 4622-4626.	1.3	6
69	Complex Microbiome in Brain Abscess Revealed by Whole-Genome Culture-Independent and Culture-Based Sequencing. <i>Journal of Clinical Medicine</i> , 2019, 8, 351.	1.0	6
70	Guilt by association: EcDNA as a mobile transactivator in cancer. <i>Trends in Cancer</i> , 2022, 8, 747-758.	3.8	5
71	Multiplex parallel pair-end tag sequencing approaches in system biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 224-234.	6.6	4
72	Genome sequence of the South American clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM597. <i>Standards in Genomic Sciences</i> , 2013, 9, 264-272.	1.5	4

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73	Genome sequence of the <i>Trifolium rueppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012.. <i>Standards in Genomic Sciences</i> , 2013, 9, 283-293.	1.5	3
74	Linked-read Sequencing Analysis Reveals Tumor-specific Genome Variation Landscapes in Neurofibromatosis Type 2 (NF2) Patients. <i>Otology and Neurotology</i> , 2019, 40, e150-e159.	0.7	3
75	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. <i>Standards in Genomic Sciences</i> , 2013, 9, 254-263.	1.5	0