

Chia-Lin Wei

List of Publications by Year in descending order

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75
papers

24,821
citations

53751

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74108

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g-index

78
all docs

78
docs citations

78
times ranked

32378
citing authors

#	ARTICLE	IF	CITATIONS
1	Guilt by association: EcDNA as a mobile transactivator in cancer. <i>Trends in Cancer</i> , 2022, 8, 747-758.	3.8	5
2	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. <i>Cancer Cell</i> , 2021, 39, 694-707.e7.	7.7	115
3	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
4	Reduced subgenomic RNA expression is a molecular indicator of asymptomatic SARS-CoV-2 infection. <i>Communications Medicine</i> , 2021, 1, .	1.9	13
5	Sox2 Controls Neural Stem Cell Self-Renewal Through a <sc>Fos</sc>-Centered Gene Regulatory Network. <i>Stem Cells</i> , 2021, 39, 1107-1119.	1.4	36
6	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. <i>Science Advances</i> , 2020, 6, eaay2078.	4.7	22
7	Chromatin topology reorganization and transcription repression by PML-RAR $\hat{\pm}$ in acute promyeloid leukemia. <i>Genome Biology</i> , 2020, 21, 110.	3.8	12
8	Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. <i>Nature Genetics</i> , 2020, 52, 264-272.	9.4	104
9	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
10	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
11	Mapping the Global Chromatin Connectivity Network for Sox2 Function in Neural Stem Cell Maintenance. <i>Cell Stem Cell</i> , 2019, 24, 462-476.e6.	5.2	72
12	Ultra-long Read Sequencing for Whole Genomic DNA Analysis. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	20
13	Multiplex chromatin interactions with single-molecule precision. <i>Nature</i> , 2019, 566, 558-562.	13.7	180
14	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
15	Picky comprehensively detects high-resolution structural variants in nanopore long reads. <i>Nature Methods</i> , 2018, 15, 455-460.	9.0	80
16	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
17	Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. <i>Nature Microbiology</i> , 2018, 3, 781-790.	5.9	26
18	<sc>S</sc>x2 conditional mutation in mouse causes ataxic symptoms, cerebellar vermis hypoplasia, and postnatal defects of <sc>B</sc>ergmann glia. <i>Glia</i> , 2018, 66, 1929-1946.	2.5	28

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19	Culture-independent analysis of liver abscess using nanopore sequencing. PLoS ONE, 2018, 13, e0190853.	1.1	22
20	<scp>DNA</scp> methylation and gene expression regulation associated with vascularization in <i>Sorghum bicolor</i>. New Phytologist, 2017, 214, 1213-1229.	3.5	47
21	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. BMC Genomics, 2016, 17, 267.	1.2	74
22	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga <i>Micromonas pusilla</i> . PLoS ONE, 2016, 11, e0155839.	1.1	7
23	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. Plant Journal, 2015, 84, 800-815.	2.8	47
24	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. Cell, 2015, 163, 1611-1627.	13.5	881
25	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. Nature Genetics, 2014, 46, 558-566.	9.4	271
26	Marine algae and land plants share conserved phytochrome signaling systems. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15827-15832.	3.3	108
27	A genome-wide map of adeno-associated virus-mediated human gene targeting. Nature Structural and Molecular Biology, 2014, 21, 969-975.	3.6	12
28	Activation and repression by oncogenic MYC shape tumour-specific gene expression profiles. Nature, 2014, 511, 483-487.	13.7	392
29	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. Cell, 2013, 155, 1507-1520.	13.5	299
30	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. Nature, 2013, 504, 306-310.	13.7	405
31	Genome sequence of the <i>Trifolium rueppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012.. Standards in Genomic Sciences, 2013, 9, 283-293.	1.5	3
32	Genome sequence of the <i>Listia angolensis</i> microsymbiont <i>Microvirga lotononidis</i> strain WSM3557T. Standards in Genomic Sciences, 2013, 9, 540-550.	1.5	7
33	<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
34	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23T. Standards in Genomic Sciences, 2013, 8, 375-388.	1.5	44
35	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. Standards in Genomic Sciences, 2013, 9, 243-253.	1.5	10
36	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. Standards in Genomic Sciences, 2013, 9, 254-263.	1.5	0

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37	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
38	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
39	Target Gene Analysis by Microarrays and Chromatin Immunoprecipitation Identifies HEY Proteins as Highly Redundant bHLH Repressors. <i>PLoS Genetics</i> , 2012, 8, e1002728.	1.5	66
40	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765 ^T , <i>Desulfosporosinus youngiae</i> DSM17734 ^T , <i>Desulfosporosinus meridiei</i> DSM13257 ^T , and <i>Desulfosporosinus acidiphilus</i> DSM22704 ^T . <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301.	1.0	73
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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2168-2173.	3.3	74
42	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	13.5	1,096
43	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638.	9.4	567
44	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011, 21, 665-675.	2.4	74
45	Identification and Characterization of Enhancers Controlling the Inflammatory Gene Expression Program in Macrophages. <i>Immunity</i> , 2010, 32, 317-328.	6.6	567
46	Multiplex parallel paired-end tag sequencing approaches in system biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 224-234.	6.6	4
47	Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. <i>Nature Genetics</i> , 2010, 42, 53-61.	9.4	652
48	A Large Fraction of Extragenic RNA Pol II Transcription Sites Overlap Enhancers. <i>PLoS Biology</i> , 2010, 8, e1000384.	2.6	762
49	TGF β 2-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
50	Dynamic changes in the human methylome during differentiation. <i>Genome Research</i> , 2010, 20, 320-331.	2.4	930
51	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010, 11, R22.	13.9	255
52	CHD7 Targets Active Gene Enhancer Elements to Modulate ES Cell-Specific Gene Expression. <i>PLoS Genetics</i> , 2010, 6, e1001023.	1.5	213
53	<i>Jmjd3</i> contributes to the control of gene expression in LPS-activated macrophages. <i>EMBO Journal</i> , 2009, 28, 3341-3352.	3.5	383
54	An oestrogen-receptor-bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64.	13.7	1,537

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55	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
56	Sall4 Regulates Distinct Transcription Circuitries in Different Blastocyst-Derived Stem Cell Lineages. <i>Cell Stem Cell</i> , 2008, 3, 543-554.	5.2	209
57	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
58	Evolution of the mammalian transcription factor binding repertoire via transposable elements. <i>Genome Research</i> , 2008, 18, 1752-1762.	2.4	501
59	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. <i>PLoS Biology</i> , 2008, 6, e256.	2.6	172
60	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
61	Whole-Genome Cartography of Estrogen Receptor α Binding Sites. <i>PLoS Genetics</i> , 2007, 3, e87.	1.5	400
62	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). <i>Genome Research</i> , 2007, 17, 828-838.	2.4	86
63	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007, 17, 839-851.	2.4	191
64	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
65	Genome-wide Mapping of RELA(p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF- κ B upon TLR4 Activation. <i>Molecular Cell</i> , 2007, 27, 622-635.	4.5	180
66	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
67	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. <i>Cell</i> , 2006, 124, 207-219.	13.5	1,060
68	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
69	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
70	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
71	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005, 2, 105-111.	9.0	244
72	5' Long serial analysis of gene expression (LongSAGE) and 3' LongSAGE for transcriptome characterization and genome annotation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11701-11706.	3.3	103

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73	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
74	Protein Synthesis Initiation Factor eIF-1A Is a Moderately Abundant RNA-binding Protein. <i>Journal of Biological Chemistry</i> , 1995, 270, 5764-5771.	1.6	27
75	Characterization of Yeast Translation Initiation Factor 1A and Cloning of Its Essential Gene. <i>Journal of Biological Chemistry</i> , 1995, 270, 22788-22794.	1.6	43