

Chia-Lin Wei

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76
papers

20,680
citations

42
h-index

78
g-index

78
ext. papers

23,274
ext. citations

18.6
avg, IF

5.46
L-index

#	Paper	IF	Citations
76	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
75	Integration of external signaling pathways with the core transcriptional network in embryonic stem cells. <i>Cell</i> , 2008 , 133, 1106-17	56.2	1978
74	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006 , 38, 431-40	36.3	1920
73	An oestrogen-receptor-alpha-bound human chromatin interactome. <i>Nature</i> , 2009 , 462, 58-64	50.4	1243
72	A global map of p53 transcription-factor binding sites in the human genome. <i>Cell</i> , 2006 , 124, 207-19	56.2	958
71	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
70	Dynamic changes in the human methylome during differentiation. <i>Genome Research</i> , 2010 , 20, 320-31	9.7	772
69	A large fraction of extragenic RNA pol II transcription sites overlap enhancers. <i>PLoS Biology</i> , 2010 , 8, e1000384	9.7	617
68	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , 2015 , 163, 1611-27	56.2	585
67	Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. <i>Nature Genetics</i> , 2010 , 42, 53-61	36.3	547
66	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011 , 43, 630-8	36.3	503
65	Identification and characterization of enhancers controlling the inflammatory gene expression program in macrophages. <i>Immunity</i> , 2010 , 32, 317-28	32.3	497
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, 286-98	18	489
63	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, 17834-9	11.5	411
62	Evolution of the mammalian transcription factor binding repertoire via transposable elements. <i>Genome Research</i> , 2008 , 18, 1752-62	9.7	378
61	Whole-genome cartography of estrogen receptor alpha binding sites. <i>PLoS Genetics</i> , 2007 , 3, e87	6	352
60	Jmjd3 contributes to the control of gene expression in LPS-activated macrophages. <i>EMBO Journal</i> , 2009 , 28, 3341-52	13	332

59	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , 2013 , 504, 306-310	50.4	313
58	Activation and repression by oncogenic MYC shape tumour-specific gene expression profiles. <i>Nature</i> , 2014 , 511, 483-7	50.4	302
57	Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. <i>Cell</i> , 2013 , 155, 1507-20	56.2	255
56	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. <i>Genome Research</i> , 2009 , 19, 521-32	9.7	252
55	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005 , 2, 105-11	21.6	218
54	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014 , 46, 558-66	36.3	203
53	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010 , 11, R22	18.3	199
52	CHD7 targets active gene enhancer elements to modulate ES cell-specific gene expression. <i>PLoS Genetics</i> , 2010 , 6, e1001023	6	188
51	Sall4 regulates distinct transcription circuitries in different blastocyst-derived stem cell lineages. <i>Cell Stem Cell</i> , 2008 , 3, 543-54	18	171
50	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	9.7	164
49	Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007 , 17, 839-51	9.7	158
48	REST regulates distinct transcriptional networks in embryonic and neural stem cells. <i>PLoS Biology</i> , 2008 , 6, e256	9.7	155
47	Genome-wide mapping of RELA(p65) binding identifies E2F1 as a transcriptional activator recruited by NF-kappaB upon TLR4 activation. <i>Molecular Cell</i> , 2007 , 27, 622-35	17.6	149
46	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, 3186-92	5.4	146
45	Multiplex chromatin interactions with single-molecule precision. <i>Nature</i> , 2019 , 566, 558-562	50.4	98
44	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	20.1	96
43	5S Long serial analysis of gene expression (LongSAGE) and 3S LongSAGE for transcriptome characterization and genome annotation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 11701-6	11.5	90
42	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, 15827-32	11.5	87

41	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). <i>Genome Research</i> , 2007 , 17, 828-38	9.7	80
40	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011 , 21, 665-75	9.7	68
39	Ecotopic viral integration site 1 (EVI1) 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, 2168-73	11.5	61
38	Target gene analysis by microarrays and chromatin immunoprecipitation identifies HEY proteins as highly redundant bHLH repressors. <i>PLoS Genetics</i> , 2012 , 8, e1002728	6	56
37	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016 , 17, 267	4.5	52
36	Picky comprehensively detects high-resolution structural variants in nanopore long reads. <i>Nature Methods</i> , 2018 , 15, 455-460	21.6	50
35	Complete genome sequences of <i>Desulfosporosinus orientis</i> DSM765T, <i>Desulfosporosinus youngiae</i> DSM17734T, <i>Desulfosporosinus meridiei</i> DSM13257T, and <i>Desulfosporosinus acidiphilus</i> DSM22704T. <i>Journal of Bacteriology</i> , 2012 , 194, 6300-1	3.5	46
34	Mapping the Global Chromatin Connectivity Network for Sox2 Function in Neural Stem Cell Maintenance. <i>Cell Stem Cell</i> , 2019 , 24, 462-476.e6	18	41
33	Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. <i>Nature Genetics</i> , 2020 , 52, 264-272	36.3	37
32	Characterization of yeast translation initiation factor 1A and cloning of its essential gene. <i>Journal of Biological Chemistry</i> , 1995 , 270, 22788-94	5.4	37
31	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23(T.). <i>Standards in Genomic Sciences</i> , 2013 , 8, 375-88		34
30	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015 , 84, 800-15	6.9	33
29	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , 2013 , 7, 449-68		22
28	Protein synthesis initiation factor eIF-1A is a moderately abundant RNA-binding protein. <i>Journal of Biological Chemistry</i> , 1995 , 270, 5764-71	5.4	22
27	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. <i>Cancer Cell</i> , 2021 , 39, 694-707.e7	24.3	22
26	DNA methylation and gene expression regulation associated with vascularization in Sorghum bicolor. <i>New Phytologist</i> , 2017 , 214, 1213-1229	9.8	20
25	Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. <i>Nature Microbiology</i> , 2018 , 3, 781-790	26.6	18
24	Sox2 conditional mutation in mouse causes ataxic symptoms, cerebellar vermis hypoplasia, and postnatal defects of Bergmann glia. <i>Glia</i> , 2018 , 66, 1929-1946	9	16

23	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	5.2	16
22	Culture-independent analysis of liver abscess using nanopore sequencing. <i>PLoS ONE</i> , 2018 , 13, e0190853	3.7	15
21	Sox2 controls neural stem cell self-renewal through a Fos-centered gene regulatory network. <i>Stem Cells</i> , 2021 , 39, 1107-1119	5.8	12
20	Ultra-long Read Sequencing for Whole Genomic DNA Analysis. <i>Journal of Visualized Experiments</i> , 2019 ,	1.6	9
19	A genome-wide map of adeno-associated virus-mediated human gene targeting. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 969-75	17.6	9
18	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. <i>Standards in Genomic Sciences</i> , 2013 , 9, 243-53		8
17	Genome sequence of the <i>Lebeckia ambigua</i> -nodulating " <i>Burkholderia sprentiae</i> " strain WSM5005(T.). <i>Standards in Genomic Sciences</i> , 2013 , 9, 385-94		6
16	TGF β -dependent gene expression shows that senescence correlates with abortive differentiation along several lineages in Myc-induced lymphomas. <i>Cell Cycle</i> , 2010 , 9, 4622-6	4.7	6
15	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	3.7	6
14	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. <i>Science Advances</i> , 2020 , 6, eaay2078	14.3	6
13	Chromatin topology reorganization and transcription repression by PML-RAR α in acute promyeloid leukemia. <i>Genome Biology</i> , 2020 , 21, 110	18.3	5
12	Complex Microbiome in Brain Abscess Revealed by Whole-Genome Culture-Independent and Culture-Based Sequencing. <i>Journal of Clinical Medicine</i> , 2019 , 8,	5.1	4
11	Sox2-Dependent 3D Chromatin Interactomes in Transcription, Neural Stem Cell Proliferation and Neurodevelopmental Diseases. <i>Journal of Experimental Neuroscience</i> , 2019 , 13, 1179069519868224	3.6	4
10	Genome sequence of the <i>Listia angolensis</i> microsymbiont <i>Microvirga lotononidis</i> strain WSM3557(T.). <i>Standards in Genomic Sciences</i> , 2014 , 9, 540-50		4
9	Subgenomic RNAs as molecular indicators of asymptomatic SARS-CoV-2 infection		4
8	Discovery of photosynthesis genes through whole-genome sequencing of acetate-requiring mutants of <i>Chlamydomonas reinhardtii</i> . <i>PLoS Genetics</i> , 2021 , 17, e1009725	6	4
7	Genome sequence of the <i>Trifolium ruppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012. <i>Standards in Genomic Sciences</i> , 2013 , 9, 283-93		3
6	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, 264-72		3

5	Multiplex parallel pair-end-ditag sequencing approaches in system biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010 , 2, 224-234	6.6	3
4	Reduced subgenomic RNA expression is a molecular indicator of asymptomatic SARS-CoV-2 infection. <i>Communications Medicine</i> , 2021 , 1,		3
3	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	2.6	2
2	Sox2 controls neural stem cell self-renewal through a Fos-centered gene regulatory network		1
1	Genome sequence of the Ornithopus/Lupinus-nodulating Bradyrhizobium sp. strain WSM471. <i>Standards in Genomic Sciences</i> , 2013 , 9, 254-63		