

# Chia-Lin Wei

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/870774/chia-lin-wei-publications-by-year.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. <i>Cancer Cell</i> , <b>2021</b> , 39, 694-707.e7	24.3	22
75	Discovery of photosynthesis genes through whole-genome sequencing of acetate-requiring mutants of <i>Chlamydomonas reinhardtii</i> . <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009725	6	4
74	Reduced subgenomic RNA expression is a molecular indicator of asymptomatic SARS-CoV-2 infection. <i>Communications Medicine</i> , <b>2021</b> , 1,		3
73	Sox2 controls neural stem cell self-renewal through a Fos-centered gene regulatory network. <i>Stem Cells</i> , <b>2021</b> , 39, 1107-1119	5.8	12
72	Chromatin topology reorganization and transcription repression by PML-RAR $\alpha$ in acute promyeloid leukemia. <i>Genome Biology</i> , <b>2020</b> , 21, 110	18.3	5
71	Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. <i>Nature Genetics</i> , <b>2020</b> , 52, 264-272	36.3	37
70	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. <i>Science Advances</i> , <b>2020</b> , 6, eaay2078	14.3	6
69	Complex Microbiome in Brain Abscess Revealed by Whole-Genome Culture-Independent and Culture-Based Sequencing. <i>Journal of Clinical Medicine</i> , <b>2019</b> , 8,	5.1	4
68	Mapping the Global Chromatin Connectivity Network for Sox2 Function in Neural Stem Cell Maintenance. <i>Cell Stem Cell</i> , <b>2019</b> , 24, 462-476.e6	18	41
67	Ultra-long Read Sequencing for Whole Genomic DNA Analysis. <i>Journal of Visualized Experiments</i> , <b>2019</b> ,	1.6	9
66	Sox2-Dependent 3D Chromatin Interactomes in Transcription, Neural Stem Cell Proliferation and Neurodevelopmental Diseases. <i>Journal of Experimental Neuroscience</i> , <b>2019</b> , 13, 1179069519868224	3.6	4
65	Multiplex chromatin interactions with single-molecule precision. <i>Nature</i> , <b>2019</b> , 566, 558-562	50.4	98
64	Linked-read Sequencing Analysis Reveals Tumor-specific Genome Variation Landscapes in Neurofibromatosis Type 2 (NF2) Patients. <i>Otology and Neurotology</i> , <b>2019</b> , 40, e150-e159	2.6	2
63	Picky comprehensively detects high-resolution structural variants in nanopore long reads. <i>Nature Methods</i> , <b>2018</b> , 15, 455-460	21.6	50
62	Sox2 conditional mutation in mouse causes ataxic symptoms, cerebellar vermis hypoplasia, and postnatal defects of Bergmann glia. <i>Glia</i> , <b>2018</b> , 66, 1929-1946	9	16
61	Culture-independent analysis of liver abscess using nanopore sequencing. <i>PLoS ONE</i> , <b>2018</b> , 13, e0190853,7	3.7	15
60	Transcriptional responses of the marine green alga <i>Micromonas pusilla</i> and an infecting prasinovirus under different phosphate conditions. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 2898-2912	5.2	16

59	Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. <i>Nature Microbiology</i> , <b>2018</b> , 3, 781-790	26.6	18
58	DNA methylation and gene expression regulation associated with vascularization in Sorghum bicolor. <i>New Phytologist</i> , <b>2017</b> , 214, 1213-1229	9.8	20
57	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga Micromonas pusilla. <i>PLoS ONE</i> , <b>2016</b> , 11, e0155839	3.7	6
56	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , <b>2016</b> , 17, 267	4.5	52
55	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , <b>2015</b> , 84, 800-15	6.9	33
54	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , <b>2015</b> , 163, 1611-27	56.2	585
53	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , <b>2014</b> , 46, 558-66	36.3	203
52	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> , <b>2014</b> , 111, 15827-32	11.5	87
51	A genome-wide map of adeno-associated virus-mediated human gene targeting. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 969-75	17.6	9
50	Activation and repression by oncogenic MYC shape tumour-specific gene expression profiles. <i>Nature</i> , <b>2014</b> , 511, 483-7	50.4	302
49	Genome sequence of the <i>Listia angolensis</i> microsymbiont <i>Microvirga lotononidis</i> strain WSM3557(T.). <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 540-50		4
48	Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. <i>Cell</i> , <b>2013</b> , 155, 1507-20	56.2	255
47	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , <b>2013</b> , 504, 306-310	50.4	313
46	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> , <b>2013</b> , 9, 283-93		3
45	<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> , <b>2013</b> , 7, 449-68		22
44	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23(T.). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 375-88		34
43	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 243-53		8
42	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 254-63		

41	Genome sequence of the South American clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM597. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 264-72		3
40	Genome sequence of the <i>Lebeckia ambigua</i> -nodulating " <i>Burkholderia sprentiae</i> " strain WSM5005(T.). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 385-94		6
39	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , <b>2012</b> , 148, 84-98	56.2	882
38	Target gene analysis by microarrays and chromatin immunoprecipitation identifies HEY proteins as highly redundant bHLH repressors. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002728	6	56
37	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> , <b>2012</b> , 194, 6300-1	3.5	46
36	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> , <b>2012</b> , 109, 2168-73	11.5	61
35	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , <b>2011</b> , 43, 630-8	36.3	503
34	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , <b>2011</b> , 21, 665-75	9.7	68
33	Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. <i>Nature Genetics</i> , <b>2010</b> , 42, 53-61	36.3	547
32	A large fraction of extragenic RNA pol II transcription sites overlap enhancers. <i>PLoS Biology</i> , <b>2010</b> , 8, e1000384	9.7	617
31	TGF $\beta$ -dependent gene expression shows that senescence correlates with abortive differentiation along several lineages in Myc-induced lymphomas. <i>Cell Cycle</i> , <b>2010</b> , 9, 4622-6	4.7	6
30	Dynamic changes in the human methylome during differentiation. <i>Genome Research</i> , <b>2010</b> , 20, 320-31	9.7	772
29	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , <b>2010</b> , 11, R22	18.3	199
28	Identification and characterization of enhancers controlling the inflammatory gene expression program in macrophages. <i>Immunity</i> , <b>2010</b> , 32, 317-28	32.3	497
27	Multiplex parallel pair-end-ditag sequencing approaches in system biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2010</b> , 2, 224-234	6.6	3
26	CHD7 targets active gene enhancer elements to modulate ES cell-specific gene expression. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001023	6	188
25	Jmjd3 contributes to the control of gene expression in LPS-activated macrophages. <i>EMBO Journal</i> , <b>2009</b> , 28, 3341-52	13	332
24	An oestrogen-receptor-alpha-bound human chromatin interactome. <i>Nature</i> , <b>2009</b> , 462, 58-64	50.4	1243

23	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. <i>Genome Research</i> , <b>2009</b> , 19, 521-32	9.7	252
22	Sall4 regulates distinct transcription circuitries in different blastocyst-derived stem cell lineages. <i>Cell Stem Cell</i> , <b>2008</b> , 3, 543-54	18	171
21	Integration of external signaling pathways with the core transcriptional network in embryonic stem cells. <i>Cell</i> , <b>2008</b> , 133, 1106-17	56.2	1978
20	Evolution of the mammalian transcription factor binding repertoire via transposable elements. <i>Genome Research</i> , <b>2008</b> , 18, 1752-62	9.7	378
19	REST regulates distinct transcriptional networks in embryonic and neural stem cells. <i>PLoS Biology</i> , <b>2008</b> , 6, e256	9.7	155
18	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
17	Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies. <i>Genome Research</i> , <b>2007</b> , 17, 898-909	9.7	164
16	Whole-genome cartography of estrogen receptor alpha binding sites. <i>PLoS Genetics</i> , <b>2007</b> , 3, e87	6	352
15	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). <i>Genome Research</i> , <b>2007</b> , 17, 828-38	9.7	80
14	Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , <b>2007</b> , 17, 839-51	9.7	158
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> , <b>2007</b> , 1, 286-98	18	489
12	Genome-wide mapping of RELA(p65) binding identifies E2F1 as a transcriptional activator recruited by NF-kappaB upon TLR4 activation. <i>Molecular Cell</i> , <b>2007</b> , 27, 622-35	17.6	149
11	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> , <b>2006</b> , 103, 17834-9	11.5	411
10	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> , <b>2006</b> , 34, e84	20.1	96
9	A global map of p53 transcription-factor binding sites in the human genome. <i>Cell</i> , <b>2006</b> , 124, 207-19	56.2	958
8	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , <b>2006</b> , 38, 431-40	36.3	1920
7	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , <b>2005</b> , 2, 105-11	21.6	218
6	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> , <b>2004</b> , 101, 11701-6	11.5	90

5	Protein synthesis initiation factor eIF-1A is a moderately abundant RNA-binding protein. <i>Journal of Biological Chemistry</i> , <b>1995</b> , 270, 5764-71	5-4	22
4	Characterization of yeast translation initiation factor 1A and cloning of its essential gene. <i>Journal of Biological Chemistry</i> , <b>1995</b> , 270, 22788-94	5-4	37
3	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> , <b>1995</b> , 270, 3186-92	5-4	146
2	Sox2 controls neural stem cell self-renewal through a Fos-centered gene regulatory network		1
1	Subgenomic RNAs as molecular indicators of asymptomatic SARS-CoV-2 infection		4