

Elzo de Wit

List of Publications by Year in Descending Order

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

75
papers

9,160
citations

44
h-index

82
g-index

82
ext. papers

11,039
ext. citations

18.4
avg, IF

6.04
L-index

#	Paper	IF	Citations
75	A Mediator-cohesin axis controls heterochromatin domain formation.. <i>Nature Communications</i> , 2022 , 13, 754	17.4	2
74	Hi-C analyses with GENOVA: a case study with cohesin variants. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab040	3.7	6
73	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021 , 372, 984-989	33.3	33
72	WAPL maintains a cohesin loading cycle to preserve cell-type-specific distal gene regulation. <i>Nature Genetics</i> , 2021 , 53, 100-109	36.3	29
71	Histone methyltransferase DOT1L controls state-specific identity during B cell differentiation. <i>EMBO Reports</i> , 2021 , 22, e51184	6.5	8
70	Glucocorticoid receptor triggers a reversible drug-tolerant dormancy state with acquired therapeutic vulnerabilities in lung cancer. <i>Nature Communications</i> , 2021 , 12, 4360	17.4	4
69	Unexpected gene activation following CRISPR-Cas9-mediated genome editing.. <i>EMBO Reports</i> , 2021 , e53902	6.5	0
68	The structural basis for cohesin-CTCF-anchored loops. <i>Nature</i> , 2020 , 578, 472-476	50.4	119
67	The histone methyltransferase DOT1L prevents antigen-independent differentiation and safeguards epigenetic identity of CD8 T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 20706-20716	11.5	16
66	TADs as the Caller Calls Them. <i>Journal of Molecular Biology</i> , 2020 , 432, 638-642	6.5	26
65	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. <i>Cell</i> , 2019 , 178, 1437-1451.e14	56.2	46
64	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. <i>Nature Genetics</i> , 2019 , 51, 1024-1034	36.3	37
63	Developing landscapes: genome architecture during early embryogenesis. <i>Current Opinion in Genetics and Development</i> , 2019 , 55, 39-45	4.9	3
62	A natural WNT signaling variant potently synergizes with Cdkn2ab loss in skin carcinogenesis. <i>Nature Communications</i> , 2019 , 10, 1425	17.4	6
61	CTCF: a Swiss-army knife for genome organization and transcription regulation. <i>Essays in Biochemistry</i> , 2019 , 63, 157-165	7.6	41
60	A CRISPR-Cas9 screen identifies essential CTCF anchor sites for estrogen receptor-driven breast cancer cell proliferation. <i>Nucleic Acids Research</i> , 2019 , 47, 9557-9572	20.1	8
59	High-throughput identification of human SNPs affecting regulatory element activity. <i>Nature Genetics</i> , 2019 , 51, 1160-1169	36.3	87

58	Gene Regulation Knows Its Boundaries. <i>Trends in Genetics</i> , 2019 , 35, 883-885	8.5	2
57	Distinct Roles for Condensin's Two ATPase Sites in Chromosome Condensation. <i>Molecular Cell</i> , 2019 , 76, 724-737.e5	17.6	20
56	A transient absence of SMC-mediated loops after mitosis. <i>Nature Cell Biology</i> , 2019 , 21, 1303-1304	23.4	9
55	LncRNA-OIS1 regulates DPP4 activation to modulate senescence induced by RAS. <i>Nucleic Acids Research</i> , 2018 , 46, 4213-4227	20.1	28
54	Enhancer hubs and loop collisions identified from single-allele topologies. <i>Nature Genetics</i> , 2018 , 50, 1151-1160	36.3	113
53	peakC: a flexible, non-parametric peak calling package for 4C and Capture-C data. <i>Nucleic Acids Research</i> , 2018 , 46, e91	20.1	33
52	Systemic Loss and Gain of Chromatin Architecture throughout Zebrafish Development. <i>Cell Reports</i> , 2018 , 24, 1-10.e4	10.6	82
51	The Cohesin Release Factor WAPL Restricts Chromatin Loop Extension. <i>Cell</i> , 2017 , 169, 693-707.e14	56.2	407
50	Capturing heterogeneity: single-cell structures of the 3D genome. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 437-438	17.6	3
49	Sensitive Monogenic Noninvasive Prenatal Diagnosis by Targeted Haplotyping. <i>American Journal of Human Genetics</i> , 2017 , 101, 326-339	11	50
48	Plasticity between Epithelial and Mesenchymal States Unlinks EMT from Metastasis-Enhancing Stem Cell Capacity. <i>Cell Reports</i> , 2016 , 14, 2281-8	10.6	221
47	Cell-of-Origin-Specific 3D Genome Structure Acquired during Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2016 , 18, 597-610	18	151
46	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. <i>ELife</i> , 2016 , 5,	8.9	64
45	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in Drosophila. <i>Molecular Cell</i> , 2015 , 60, 146-62	17.6	58
44	CTCF Binding Polarity Determines Chromatin Looping. <i>Molecular Cell</i> , 2015 , 60, 676-84	17.6	381
43	Transcription of Mammalian cis-Regulatory Elements Is Restrained by Actively Enforced Early Termination. <i>Molecular Cell</i> , 2015 , 60, 460-74	17.6	53
42	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. <i>BMC Genomics</i> , 2015 , 16, 982	4.5	2
41	InVivo imaging reveals extracellular vesicle-mediated phenocopying of metastatic behavior. <i>Cell</i> , 2015 , 161, 1046-1057	56.2	546

40	Characterization and dynamics of pericentromere-associated domains in mice. <i>Genome Research</i> , 2015 , 25, 958-69	9.7	54
39	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. <i>Nature Biotechnology</i> , 2014 , 32, 1019-25	44.5	152
38	A single oncogenic enhancer rearrangement causes concomitant EVI1 and GATA2 deregulation in leukemia. <i>Cell</i> , 2014 , 157, 369-381	56.2	419
37	DNA methylation dynamics during intestinal stem cell differentiation reveals enhancers driving gene expression in the villus. <i>Genome Biology</i> , 2013 , 14, R50	18.3	78
36	The pluripotent genome in three dimensions is shaped around pluripotency factors. <i>Nature</i> , 2013 , 501, 227-31	50.4	208
35	eRNAs are required for p53-dependent enhancer activity and gene transcription. <i>Molecular Cell</i> , 2013 , 49, 524-35	17.6	399
34	Genome-wide analysis of FOXO3 mediated transcription regulation through RNA polymerase II profiling. <i>Molecular Systems Biology</i> , 2013 , 9, 638	12.2	88
33	Determining long-range chromatin interactions for selected genomic sites using 4C-seq technology: from fixation to computation. <i>Methods</i> , 2012 , 58, 221-30	4.6	167
32	Robust 4C-seq data analysis to screen for regulatory DNA interactions. <i>Nature Methods</i> , 2012 , 9, 969-72	21.6	278
31	4C technology: protocols and data analysis. <i>Methods in Enzymology</i> , 2012 , 513, 89-112	1.7	150
30	A decade of 3C technologies: insights into nuclear organization. <i>Genes and Development</i> , 2012 , 26, 11-24	12.6	543
29	Variegated gene expression caused by cell-specific long-range DNA interactions. <i>Nature Cell Biology</i> , 2011 , 13, 944-51	23.4	125
28	The inactive X chromosome adopts a unique three-dimensional conformation that is dependent on Xist RNA. <i>Genes and Development</i> , 2011 , 25, 1371-83	12.6	238
27	Small RNA expression and strain specificity in the rat. <i>BMC Genomics</i> , 2010 , 11, 249	4.5	61
26	Repertoire and evolution of miRNA genes in four divergent nematode species. <i>Genome Research</i> , 2009 , 19, 2064-74	9.7	94
25	Chromatin domains in higher eukaryotes: insights from genome-wide mapping studies. <i>Chromosoma</i> , 2009 , 118, 25-36	2.8	45
24	Limitations and possibilities of small RNA digital gene expression profiling. <i>Nature Methods</i> , 2009 , 6, 474-6	21.6	244
23	Complete knockout of the nociceptin/orphanin FQ receptor in the rat does not induce compensatory changes in mu, delta and kappa opioid receptors. <i>Neuroscience</i> , 2009 , 163, 308-15	3.9	29

22	Global chromatin domain organization of the Drosophila genome. <i>PLoS Genetics</i> , 2008 , 4, e1000045	6	70
21	HP1 controls genomic targeting of four novel heterochromatin proteins in Drosophila. <i>EMBO Journal</i> , 2007 , 26, 741-51	13	41
20	High-resolution mapping reveals links of HP1 with active and inactive chromatin components. <i>PLoS Genetics</i> , 2007 , 3, e38	6	98
19	SUUR joins separate subsets of PcG, HP1 and B-type lamin targets in Drosophila. <i>Journal of Cell Science</i> , 2007 , 120, 2344-51	5.3	47
18	Human heterochromatin proteins form large domains containing KRAB-ZNF genes. <i>Genome Research</i> , 2006 , 16, 1493-504	9.7	122
17	Hotspots of transcription factor colocalization in the genome of Drosophila melanogaster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12027-32	11.5	159
16	Chromosome-wide gene-specific targeting of the Drosophila dosage compensation complex. <i>Genes and Development</i> , 2006 , 20, 858-70	12.6	134
15	Prospero acts as a binary switch between self-renewal and differentiation in Drosophila neural stem cells. <i>Developmental Cell</i> , 2006 , 11, 775-89	10.2	300
14	Genome-wide profiling of PRC1 and PRC2 Polycomb chromatin binding in Drosophila melanogaster. <i>Nature Genetics</i> , 2006 , 38, 694-9	36.3	302
13	Characterization of the Drosophila melanogaster genome at the nuclear lamina. <i>Nature Genetics</i> , 2006 , 38, 1005-14	36.3	474
12	Nuclear organization of active and inactive chromatin domains uncovered by chromosome conformation capture-on-chip (4C). <i>Nature Genetics</i> , 2006 , 38, 1348-54	36.3	1021
11	Genome-wide HP1 binding in Drosophila: developmental plasticity and genomic targeting signals. <i>Genome Research</i> , 2005 , 15, 1265-73	9.7	83
10	Distinct HP1 and Su(var)3-9 complexes bind to sets of developmentally coexpressed genes depending on chromosomal location. <i>Genes and Development</i> , 2003 , 17, 2825-38	12.6	139
9	Quantitative comparison of cDNA-AFLP, microarrays, and GeneChip expression data in <i>Saccharomyces cerevisiae</i> . <i>Genomics</i> , 2003 , 82, 606-18	4.3	77
8	Condensin ATPase Machinery Drives and Dampens Mitotic Chromosome Condensation		4
7	Systematic identification of human SNPs affecting regulatory element activity		4
6	WAPL maintains dynamic cohesin to preserve lineage specific distal gene regulation		3
5	Glucocorticoids regulate cancer cell dormancy		3

4	Histone methyltransferase DOT1L controls state-specific identity during B cell differentiation	1
3	Perturbations in 3D genome organization can promote acquired drug resistance	3
2	Rapid depletion of CTCF and cohesin proteins reveals dynamic features of chromosome architecture	2
1	Hi-C Analyses with GENOVA: a case study with cohesin variants	4