

# Elzo de Wit

## List of Publications by Year in descending order

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Version: 2024-02-01

68  
papers

12,102  
citations

46918

47  
h-index

95083

68  
g-index

82  
all docs

82  
docs citations

82  
times ranked

16193  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Mediator-cohesin axis controls heterochromatin domain formation. <i>Nature Communications</i> , 2022, 13, 754.	5.8	17
2	Unexpected gene activation following CRISPR-Cas9-mediated genome editing. <i>EMBO Reports</i> , 2022, 23, e53902.	2.0	5
3	The cohesin acetylation cycle controls chromatin loop length through a PDS5A brake mechanism. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 586-591.	3.6	27
4	WAPL maintains a cohesin loading cycle to preserve cell-type-specific distal gene regulation. <i>Nature Genetics</i> , 2021, 53, 100-109.	9.4	101
5	Histone methyltransferase DOT1L controls state-specific identity during B cell differentiation. <i>EMBO Reports</i> , 2021, 22, e51184.	2.0	27
6	Hi-C analyses with GENOVA: a case study with cohesin variants. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab040.	1.5	59
7	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	6.0	132
8	Glucocorticoid receptor triggers a reversible drug-tolerant dormancy state with acquired therapeutic vulnerabilities in lung cancer. <i>Nature Communications</i> , 2021, 12, 4360.	5.8	35
9	TADs as the Caller Calls Them. <i>Journal of Molecular Biology</i> , 2020, 432, 638-642.	2.0	38
10	The histone methyltransferase DOT1L prevents antigen-independent differentiation and safeguards epigenetic identity of CD8 <sup>+</sup> T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20706-20716.	3.3	32
11	The structural basis for cohesin-CTCF-anchored loops. <i>Nature</i> , 2020, 578, 472-476.	13.7	278
12	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.	6.5	21
13	High-throughput identification of human SNPs affecting regulatory element activity. <i>Nature Genetics</i> , 2019, 51, 1160-1169.	9.4	157
14	Gene Regulation Knows Its Boundaries. <i>Trends in Genetics</i> , 2019, 35, 883-885.	2.9	2
15	Distinct Roles for Condensin's Two ATPase Sites in Chromosome Condensation. <i>Molecular Cell</i> , 2019, 76, 724-737.e5.	4.5	39
16	A transient absence of SMC-mediated loops after mitosis. <i>Nature Cell Biology</i> , 2019, 21, 1303-1304.	4.6	11
17	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. <i>Cell</i> , 2019, 178, 1437-1451.e14.	13.5	118
18	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.	9.4	60

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19	Developing landscapes: genome architecture during early embryogenesis. <i>Current Opinion in Genetics and Development</i> , 2019, 55, 39-45.	1.5	10
20	A natural WNT signaling variant potently synergizes with Cdkn2ab loss in skin carcinogenesis. <i>Nature Communications</i> , 2019, 10, 1425.	5.8	13
21	CTCF: a Swiss-army knife for genome organization and transcription regulation. <i>Essays in Biochemistry</i> , 2019, 63, 157-165.	2.1	87
22	LncRNA-OIS1 regulates DPP4 activation to modulate senescence induced by RAS. <i>Nucleic Acids Research</i> , 2018, 46, 4213-4227.	6.5	40
23	peakC: a flexible, non-parametric peak calling package for 4C and Capture-C data. <i>Nucleic Acids Research</i> , 2018, 46, e91-e91.	6.5	63
24	Systemic Loss and Gain of Chromatin Architecture throughout Zebrafish Development. <i>Cell Reports</i> , 2018, 24, 1-10.e4.	2.9	124
25	Enhancer hubs and loop collisions identified from single-allele topologies. <i>Nature Genetics</i> , 2018, 50, 1151-1160.	9.4	189
26	The Cohesin Release Factor WAPL Restricts Chromatin Loop Extension. <i>Cell</i> , 2017, 169, 693-707.e14.	13.5	636
27	Capturing heterogeneity: single-cell structures of the 3D genome. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 437-438.	3.6	8
28	Sensitive Monogenic Noninvasive Prenatal Diagnosis by Targeted Haplotyping. <i>American Journal of Human Genetics</i> , 2017, 101, 326-339.	2.6	76
29	Plasticity between Epithelial and Mesenchymal States Unlinks EMT from Metastasis-Enhancing Stem Cell Capacity. <i>Cell Reports</i> , 2016, 14, 2281-2288.	2.9	273
30	Cell-of-Origin-Specific 3D Genome Structure Acquired during Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2016, 18, 597-610.	5.2	187
31	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. <i>ELife</i> , 2016, 5, .	2.8	115
32	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. <i>BMC Genomics</i> , 2015, 16, 982.	1.2	2
33	InÂVivo Imaging Reveals Extracellular Vesicle-Mediated Phenocopying of Metastatic Behavior. <i>Cell</i> , 2015, 161, 1046-1057.	13.5	704
34	Characterization and dynamics of pericentromere-associated domains in mice. <i>Genome Research</i> , 2015, 25, 958-969.	2.4	70
35	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in <i>Drosophila</i> . <i>Molecular Cell</i> , 2015, 60, 146-162.	4.5	70
36	CTCF Binding Polarity Determines Chromatin Looping. <i>Molecular Cell</i> , 2015, 60, 676-684.	4.5	537

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37	Transcription of Mammalian cis-Regulatory Elements Is Restrained by Actively Enforced Early Termination. <i>Molecular Cell</i> , 2015, 60, 460-474.	4.5	80
38	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. <i>Nature Biotechnology</i> , 2014, 32, 1019-1025.	9.4	231
39	A Single Oncogenic Enhancer Rearrangement Causes Concomitant EVI1 and GATA2 Deregulation in Leukemia. <i>Cell</i> , 2014, 157, 369-381.	13.5	571
40	DNA methylation dynamics during intestinal stem cell differentiation reveals enhancers driving gene expression in the villus. <i>Genome Biology</i> , 2013, 14, R50.	13.9	109
41	The pluripotent genome in three dimensions is shaped around pluripotency factors. <i>Nature</i> , 2013, 501, 227-231.	13.7	236
42	eRNAs Are Required for p53-Dependent Enhancer Activity and Gene Transcription. <i>Molecular Cell</i> , 2013, 49, 524-535.	4.5	484
43	Genome-wide analysis of FOXO3 mediated transcription regulation through RNA polymerase II profiling. <i>Molecular Systems Biology</i> , 2013, 9, 638.	3.2	104
44	Determining long-range chromatin interactions for selected genomic sites using 4C-seq technology: From fixation to computation. <i>Methods</i> , 2012, 58, 221-230.	1.9	198
45	Robust 4C-seq data analysis to screen for regulatory DNA interactions. <i>Nature Methods</i> , 2012, 9, 969-972.	9.0	357
46	4C Technology: Protocols and Data Analysis. <i>Methods in Enzymology</i> , 2012, 513, 89-112.	0.4	203
47	A decade of 3C technologies: insights into nuclear organization. <i>Genes and Development</i> , 2012, 26, 11-24.	2.7	631
48	Variegated gene expression caused by cell-specific long-range DNA interactions. <i>Nature Cell Biology</i> , 2011, 13, 944-951.	4.6	133
49	The inactive X chromosome adopts a unique three-dimensional conformation that is dependent on Xist RNA. <i>Genes and Development</i> , 2011, 25, 1371-1383.	2.7	278
50	Small RNA expression and strain specificity in the rat. <i>BMC Genomics</i> , 2010, 11, 249.	1.2	71
51	Repertoire and evolution of miRNA genes in four divergent nematode species. <i>Genome Research</i> , 2009, 19, 2064-2074.	2.4	107
52	Chromatin domains in higher eukaryotes: insights from genome-wide mapping studies. <i>Chromosoma</i> , 2009, 118, 25-36.	1.0	49
53	Limitations and possibilities of small RNA digital gene expression profiling. <i>Nature Methods</i> , 2009, 6, 474-476.	9.0	280
54	Complete knockout of the nociceptin/orphanin FQ receptor in the rat does not induce compensatory changes in $\mu$ , $\kappa$ and $\delta$ opioid receptors. <i>Neuroscience</i> , 2009, 163, 308-315.	1.1	34

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55	Global Chromatin Domain Organization of the <i>Drosophila</i> Genome. <i>PLoS Genetics</i> , 2008, 4, e1000045.	1.5	72
56	High-Resolution Mapping Reveals Links of HP1 with Active and Inactive Chromatin Components. <i>PLoS Genetics</i> , 2007, 3, e38.	1.5	113
57	SUUR joins separate subsets of PcG, HP1 and B-type lamin targets in <i>Drosophila</i> . <i>Journal of Cell Science</i> , 2007, 120, 2344-2351.	1.2	54
58	HP1 controls genomic targeting of four novel heterochromatin proteins in <i>Drosophila</i> . <i>EMBO Journal</i> , 2007, 26, 741-751.	3.5	48
59	Prospero Acts as a Binary Switch between Self-Renewal and Differentiation in <i>Drosophila</i> Neural Stem Cells. <i>Developmental Cell</i> , 2006, 11, 775-789.	3.1	348
60	Genome-wide profiling of PRC1 and PRC2 Polycomb chromatin binding in <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2006, 38, 694-699.	9.4	335
61	Characterization of the <i>Drosophila melanogaster</i> genome at the nuclear lamina. <i>Nature Genetics</i> , 2006, 38, 1005-1014.	9.4	540
62	Nuclear organization of active and inactive chromatin domains uncovered by chromosome conformation capture "on-chip" (4C). <i>Nature Genetics</i> , 2006, 38, 1348-1354.	9.4	1,219
63	Human heterochromatin proteins form large domains containing KRAB-ZNF genes. <i>Genome Research</i> , 2006, 16, 1493-1504.	2.4	141
64	Hotspots of transcription factor colocalization in the genome of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12027-12032.	3.3	182
65	Chromosome-wide gene-specific targeting of the <i>Drosophila</i> dosage compensation complex. <i>Genes and Development</i> , 2006, 20, 858-870.	2.7	142
66	Genome-wide HP1 binding in <i>Drosophila</i> : Developmental plasticity and genomic targeting signals. <i>Genome Research</i> , 2005, 15, 1265-1273.	2.4	94
67	Quantitative comparison of cDNA-AFLP, microarrays, and genechip expression data in <i>Saccharomyces cerevisiae</i> . <i>Genomics</i> , 2003, 82, 606-618.	1.3	80
68	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, 2825-2838.	2.7	153