

Wouter L De Laat

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

19,868
citations

14655

66
h-index

24982

109
g-index

117
all docs

117
docs citations

117
times ranked

21437
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of the cellular factor CTCF in the regulation of bovine leukemia virus latency and three-dimensional chromatin organization. <i>Nucleic Acids Research</i> , 2022, 50, 3190-3202.	14.5	5
2	Building regulatory landscapes reveals that an enhancer can recruit cohesin to create contact domains, engage CTCF sites and activate distant genes. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 563-574.	8.2	49
3	Novel orthogonal methods to uncover the complexity and diversity of nuclear architecture. <i>Current Opinion in Genetics and Development</i> , 2021, 67, 10-17.	3.3	6
4	Genetic Dissection of a Super Enhancer Controlling the <i>Nppa-Nppb</i> Cluster in the Heart. <i>Circulation Research</i> , 2021, 128, 115-129.	4.5	32
5	Robust detection of translocations in lymphoma FFPE samples using targeted locus capture-based sequencing. <i>Nature Communications</i> , 2021, 12, 3361.	12.8	19
6	Interplay between CTCF boundaries and a super enhancer controls cohesin extrusion trajectories and gene expression. <i>Molecular Cell</i> , 2021, 81, 3082-3095.e6.	9.7	29
7	A public-private partnership model for COVID-19 diagnostics. <i>Nature Biotechnology</i> , 2021, 39, 1182-1184.	17.5	4
8	4C-seq from beginning to end: A detailed protocol for sample preparation and data analysis. <i>Methods</i> , 2020, 170, 17-32.	3.8	107
9	Multi-contact 4C: long-molecule sequencing of complex proximity ligation products to uncover local cooperative and competitive chromatin topologies. <i>Nature Protocols</i> , 2020, 15, 364-397.	12.0	25
10	How chromosome topologies get their shape: views from proximity ligation and microscopy methods. <i>FEBS Letters</i> , 2020, 594, 3439-3449.	2.8	3
11	Recently Evolved Enhancers Emerge with High Interindividual Variability and Less Frequently Associate with Disease. <i>Cell Reports</i> , 2020, 31, 107799.	6.4	7
12	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e003085.	3.6	14
13	Epigenetic and Transcriptional Networks Underlying Atrial Fibrillation. <i>Circulation Research</i> , 2020, 127, 34-50.	4.5	48
14	Hominin-specific regulatory elements selectively emerged in oligodendrocytes and are disrupted in autism patients. <i>Nature Communications</i> , 2020, 11, 301.	12.8	37
15	Abstract PO-45: Robust detection of translocations in lymphoma FFPE samples using Targeted Locus Capture-based sequencing. , 2020, , .		2
16	An enhancer cluster controls gene activity and topology of the <i>SCN5A-SCN10A</i> locus in vivo. <i>Nature Communications</i> , 2019, 10, 4943.	12.8	24
17	Identification and Characterization of a Transcribed Distal Enhancer Involved in Cardiac <i>Kcnh2</i> Regulation. <i>Cell Reports</i> , 2019, 28, 2704-2714.e5.	6.4	15
18	DamC reveals principles of chromatin folding in vivo without crosslinking and ligation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 471-480.	8.2	71

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19	Chromatin Conformation Links Putative Enhancers in Intracranial Aneurysm-Associated Regions to Potential Candidate Genes. <i>Journal of the American Heart Association</i> , 2019, 8, e011201.	3.7	13
20	YAP Partially Reprograms Chromatin Accessibility to Directly Induce Adult Cardiogenesis In Vivo. <i>Developmental Cell</i> , 2019, 48, 765-779.e7.	7.0	171
21	peakC: a flexible, non-parametric peak calling package for 4C and Capture-C data. <i>Nucleic Acids Research</i> , 2018, 46, e91-e91.	14.5	63
22	Enhancer hubs and loop collisions identified from single-allele topologies. <i>Nature Genetics</i> , 2018, 50, 1151-1160.	21.4	189
23	Enhancer-Mediated Oncogenic Function of the Menin Tumor Suppressor in Breast Cancer. <i>Cell Reports</i> , 2017, 18, 2359-2372.	6.4	59
24	Can We Just Say: Transcription Second?. <i>Cell</i> , 2017, 169, 184-185.	28.9	10
25	Small chromosomal regions position themselves autonomously according to their chromatin class. <i>Genome Research</i> , 2017, 27, 922-933.	5.5	39
26	Sensitive Monogenic Noninvasive Prenatal Diagnosis by Targeted Haplotyping. <i>American Journal of Human Genetics</i> , 2017, 101, 326-339.	6.2	76
27	A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression. <i>Cell</i> , 2017, 170, 522-533.e15.	28.9	356
28	Transcription-factor-dependent enhancer transcription defines a gene regulatory network for cardiac rhythm. <i>ELife</i> , 2017, 6, .	6.0	36
29	Enhancers reside in a unique epigenetic environment during early zebrafish development. <i>Genome Biology</i> , 2016, 17, 146.	8.8	41
30	Polarized regulatory landscape and Wnt responsiveness underlie Hox activation in embryos. <i>Genes and Development</i> , 2016, 30, 1937-1942.	5.9	77
31	Regulation of disease-associated gene expression in the 3D genome. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 771-782.	37.0	294
32	The second decade of 3C technologies: detailed insights into nuclear organization. <i>Genes and Development</i> , 2016, 30, 1357-1382.	5.9	320
33	Epigenomic annotation of gene regulatory alterations during evolution of the primate brain. <i>Nature Neuroscience</i> , 2016, 19, 494-503.	14.8	113
34	Cause and Consequence of Tethering a SubTAD to Different Nuclear Compartments. <i>Molecular Cell</i> , 2016, 61, 461-473.	9.7	73
35	Cell-of-Origin-Specific 3D Genome Structure Acquired during Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2016, 18, 597-610.	11.1	187
36	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. <i>ELife</i> , 2016, 5, .	6.0	115

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37	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. <i>BMC Genomics</i> , 2015, 16, 982.	2.8	2
38	Local compartment changes and regulatory landscape alterations in histone H1-depleted cells. <i>Genome Biology</i> , 2015, 16, 289.	8.8	56
39	Characterization and dynamics of pericentromere-associated domains in mice. <i>Genome Research</i> , 2015, 25, 958-969.	5.5	70
40	Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. <i>Genome Biology</i> , 2015, 16, 149.	8.8	104
41	Architectural hallmarks of the pluripotent genome. <i>FEBS Letters</i> , 2015, 589, 2905-2913.	2.8	21
42	Genome-wide profiling of p53-regulated enhancer RNAs uncovers a subset of enhancers controlled by a lncRNA. <i>Nature Communications</i> , 2015, 6, 6520.	12.8	149
43	YAP Drives Growth by Controlling Transcriptional Pause Release from Dynamic Enhancers. <i>Molecular Cell</i> , 2015, 60, 328-337.	9.7	228
44	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.	9.7	70
45	Getting the genome in shape: the formation of loops, domains and compartments. <i>Genome Biology</i> , 2015, 16, 154.	8.8	103
46	CTCF Binding Polarity Determines Chromatin Looping. <i>Molecular Cell</i> , 2015, 60, 676-684.	9.7	537
47	A Long-Distance Chromatin Affair. <i>Cell</i> , 2015, 162, 942-943.	28.9	12
48	Transcription of Mammalian cis-Regulatory Elements Is Restrained by Actively Enforced Early Termination. <i>Molecular Cell</i> , 2015, 60, 460-474.	9.7	80
49	Large-Scale Identification of Coregulated Enhancer Networks in the Adult Human Brain. <i>Cell Reports</i> , 2014, 9, 767-779.	6.4	78
50	A Large Permissive Regulatory Domain Exclusively Controls Tbx3 Expression in the Cardiac Conduction System. <i>Circulation Research</i> , 2014, 115, 432-441.	4.5	44
51	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. <i>Nature Biotechnology</i> , 2014, 32, 1019-1025.	17.5	231
52	A Single Oncogenic Enhancer Rearrangement Causes Concomitant EVI1 and GATA2 Deregulation in Leukemia. <i>Cell</i> , 2014, 157, 369-381.	28.9	571
53	A common genetic variant within SCN10A modulates cardiac SCN5A expression. <i>Journal of Clinical Investigation</i> , 2014, 124, 1844-1852.	8.2	168
54	DNA methylation dynamics during intestinal stem cell differentiation reveals enhancers driving gene expression in the villus. <i>Genome Biology</i> , 2013, 14, R50.	9.6	109

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55	The pluripotent genome in three dimensions is shaped around pluripotency factors. <i>Nature</i> , 2013, 501, 227-231.	27.8	236
56	Flexible Long-Range Loops in the VH Gene Region of the Igh Locus Facilitate the Generation of a Diverse Antibody Repertoire. <i>Immunity</i> , 2013, 39, 229-244.	14.3	130
57	Topology of mammalian developmental enhancers and their regulatory landscapes. <i>Nature</i> , 2013, 502, 499-506.	27.8	463
58	CTCF: the protein, the binding partners, the binding sites and their chromatin loops. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120369.	4.0	191
59	Long-Range Chromatin Contacts in Embryonic Stem Cells Reveal a Role for Pluripotency Factors and Polycomb Proteins in Genome Organization. <i>Cell Stem Cell</i> , 2013, 13, 602-616.	11.1	246
60	For Genomes to Stay in Shape, Insulators Must Be up to PAR. <i>Cell</i> , 2013, 155, 15-16.	28.9	1
61	eRNAs Are Required for p53-Dependent Enhancer Activity and Gene Transcription. <i>Molecular Cell</i> , 2013, 49, 524-535.	9.7	484
62	Genome-wide analysis of FOXO3 mediated transcription regulation through RNA polymerase II profiling. <i>Molecular Systems Biology</i> , 2013, 9, 638.	7.2	104
63	Identical cells with different 3D genomes; cause and consequences?. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 191-196.	3.3	42
64	Allelic exclusion of the immunoglobulin heavy chain locus is independent of its nuclear localization in mature B cells. <i>Nucleic Acids Research</i> , 2013, 41, 6905-6916.	14.5	26
65	3D chromatin conformation correlates with replication timing and is conserved in resting cells. <i>Nucleic Acids Research</i> , 2012, 40, 9470-9481.	14.5	76
66	Determining long-range chromatin interactions for selected genomic sites using 4C-seq technology: From fixation to computation. <i>Methods</i> , 2012, 58, 221-230.	3.8	198
67	3C-based technologies to study the shape of the genome. <i>Methods</i> , 2012, 58, 189-191.	3.8	75
68	Robust 4C-seq data analysis to screen for regulatory DNA interactions. <i>Nature Methods</i> , 2012, 9, 969-972.	19.0	357
69	4C Technology: Protocols and Data Analysis. <i>Methods in Enzymology</i> , 2012, 513, 89-112.	1.0	203
70	Chromatin loops, gene positioning, and gene expression. <i>Frontiers in Genetics</i> , 2012, 3, 217.	2.3	83
71	A decade of 3C technologies: insights into nuclear organization. <i>Genes and Development</i> , 2012, 26, 11-24.	5.9	631
72	Diverse gene reprogramming events occur in the same spatial clusters of distal regulatory elements. <i>Genome Research</i> , 2011, 21, 697-706.	5.5	132

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73	An evolutionarily conserved three-dimensional structure in the vertebrate <i>Irx</i> clusters facilitates enhancer sharing and coregulation. <i>Nature Communications</i> , 2011, 2, 310.	12.8	73
74	A Regulatory Archipelago Controls Hox Genes Transcription in Digits. <i>Cell</i> , 2011, 147, 1132-1145.	28.9	454
75	Interactions among Polycomb Domains Are Guided by Chromosome Architecture. <i>PLoS Genetics</i> , 2011, 7, e1001343.	3.5	156
76	Genome organization influences partner selection for chromosomal rearrangements. <i>Trends in Genetics</i> , 2011, 27, 63-71.	6.7	43
77	Integrated Transcript and Genome Analyses Reveal NKX2-1 and MEF2C as Potential Oncogenes in T Cell Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2011, 19, 484-497.	16.8	322
78	The Dynamic Architecture of <i>Hox</i> Gene Clusters. <i>Science</i> , 2011, 334, 222-225.	12.6	370
79	Variegated gene expression caused by cell-specific long-range DNA interactions. <i>Nature Cell Biology</i> , 2011, 13, 944-951.	10.3	133
80	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.	5.9	278
81	The complex transcription regulatory landscape of our genome: control in three dimensions. <i>EMBO Journal</i> , 2011, 30, 4345-4355.	7.8	59
82	Tissue- and Expression Level-Specific Chromatin Looping at Maize <i>b1</i> Epialleles. <i>Plant Cell</i> , 2009, 21, 832-842.	6.6	126
83	High-resolution identification of balanced and complex chromosomal rearrangements by 4C technology. <i>Nature Methods</i> , 2009, 6, 837-842.	19.0	86
84	Studying physical chromatin interactions in plants using Chromosome Conformation Capture (3C). <i>Nature Protocols</i> , 2009, 4, 1216-1229.	12.0	85
85	Joining the loops: β -Globin gene regulation. <i>IUBMB Life</i> , 2008, 60, 824-833.	3.4	74
86	Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions. <i>Nature</i> , 2008, 453, 948-951.	27.8	1,658
87	FISH-eyed and genome-wide views on the spatial organisation of gene expression. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2008, 1783, 2052-2060.	4.1	25
88	Maintenance of Long-Range DNA Interactions after Inhibition of Ongoing RNA Polymerase II Transcription. <i>PLoS ONE</i> , 2008, 3, e1661.	2.5	114
89	Chapter 5 Three-Dimensional Organization of Gene Expression in Erythroid Cells. <i>Current Topics in Developmental Biology</i> , 2008, 82, 117-139.	2.2	75
90	Chapter 4 β -Globin Regulation and Long-Range Interactions. <i>Advances in Genetics</i> , 2008, 61, 107-142.	1.8	112

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91	Transcription and Chromatin Organization of a Housekeeping Gene Cluster Containing an Integrated $\hat{\nu}$ -Globin Locus Control Region. <i>PLoS Genetics</i> , 2008, 4, e1000016.	3.5	68
92	Inter-chromosomal gene regulation in the mammalian cell nucleus. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 456-464.	3.3	51
93	$\hat{\nu}$ -Globin Active Chromatin Hub Formation in Differentiating Erythroid Cells and in p45 NF-E2 Knock-out Mice. <i>Journal of Biological Chemistry</i> , 2007, 282, 16544-16552.	3.4	72
94	Reversible contraction by looping of the Tcra and Tcrb loci in rearranging thymocytes. <i>Nature Immunology</i> , 2007, 8, 378-387.	14.5	143
95	An evaluation of 3C-based methods to capture DNA interactions. <i>Nature Methods</i> , 2007, 4, 895-901.	19.0	274
96	Quantitative analysis of chromosome conformation capture assays (3C-qPCR). <i>Nature Protocols</i> , 2007, 2, 1722-1733.	12.0	620
97	Long-range DNA contacts: romance in the nucleus?. <i>Current Opinion in Cell Biology</i> , 2007, 19, 317-320.	5.4	28
98	CTCF mediates long-range chromatin looping and local histone modification in the beta-globin locus. <i>Genes and Development</i> , 2006, 20, 2349-2354.	5.9	643
99	Nuclear organization of active and inactive chromatin domains uncovered by chromosome conformation capture "on-chip" (4C). <i>Nature Genetics</i> , 2006, 38, 1348-1354.	21.4	1,219
100	Multiple interactions between regulatory regions are required to stabilize an active chromatin hub. <i>Genes and Development</i> , 2004, 18, 1495-1509.	5.9	157
101	The active spatial organization of the $\hat{\nu}$ -globin locus requires the transcription factor EKLF. <i>Genes and Development</i> , 2004, 18, 2485-2490.	5.9	321
102	Spatial organization of gene expression: the active chromatin hub. <i>Chromosome Research</i> , 2003, 11, 447-459.	2.2	336
103	The $\hat{\nu}$ -globin nuclear compartment in development and erythroid differentiation. <i>Nature Genetics</i> , 2003, 35, 190-194.	21.4	512
104	3C Technology: Analyzing the Spatial Organization of Genomic Loci In Vivo. <i>Methods in Enzymology</i> , 2003, 375, 493-507.	1.0	104
105	Looping and Interaction between Hypersensitive Sites in the Active $\hat{\nu}$ -globin Locus. <i>Molecular Cell</i> , 2002, 10, 1453-1465.	9.7	1,205
106	Novel Functional Interactions between Nucleotide Excision DNA Repair Proteins Influencing the Enzymatic Activities of TFIIH, XPG, and ERCC1-XPF. <i>Biochemistry</i> , 2001, 40, 160-165.	2.5	26
107	Mapping of interaction domains between human repair proteins ERCC1 and XPF. <i>Nucleic Acids Research</i> , 1998, 26, 4146-4152.	14.5	94
108	DNA Structural Elements Required for ERCC1-XPF Endonuclease Activity. <i>Journal of Biological Chemistry</i> , 1998, 273, 7835-7842.	3.4	198

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109	Xeroderma Pigmentosum Group F Caused by a Defect in a Structure-Specific DNA Repair Endonuclease. Cell, 1996, 86, 811-822.	28.9	492
110	Detailed Regulatory Interaction Map of the Human Heart Facilitates Gene Discovery for Cardiovascular Disease. SSRN Electronic Journal, 0, , .	0.4	1