

# Bas van Steensel

## List of Publications by Year in descending order

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Version: 2024-02-01

92  
papers

19,259  
citations

28190

55  
h-index

46693

89  
g-index

108  
all docs

108  
docs citations

108  
times ranked

19397  
citing authors

#	ARTICLE	IF	CITATIONS
1	Easy quantitative assessment of genome editing by sequence trace decomposition. <i>Nucleic Acids Research</i> , 2014, 42, e168-e168.	6.5	1,838
2	Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions. <i>Nature</i> , 2008, 453, 948-951.	13.7	1,658
3	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
4	Molecular Maps of the Reorganization of Genome-Nuclear Lamina Interactions during Differentiation. <i>Molecular Cell</i> , 2010, 38, 603-613.	4.5	916
5	Systematic Protein Location Mapping Reveals Five Principal Chromatin Types in <i>Drosophila</i> Cells. <i>Cell</i> , 2010, 143, 212-224.	13.5	854
6	Lamina-Associated Domains: Links with Chromosome Architecture, Heterochromatin, and Gene Repression. <i>Cell</i> , 2017, 169, 780-791.	13.5	798
7	Genome Architecture: Domain Organization of Interphase Chromosomes. <i>Cell</i> , 2013, 152, 1270-1284.	13.5	659
8	The Cohesin Release Factor WAPL Restricts Chromatin Loop Extension. <i>Cell</i> , 2017, 169, 693-707.e14.	13.5	636
9	Single-Cell Dynamics of Genome-Nuclear Lamina Interactions. <i>Cell</i> , 2013, 153, 178-192.	13.5	609
10	Identification of in vivo DNA targets of chromatin proteins using tethered Dam methyltransferase. <i>Nature Biotechnology</i> , 2000, 18, 424-428.	9.4	544
11	Characterization of the <i>Drosophila melanogaster</i> genome at the nuclear lamina. <i>Nature Genetics</i> , 2006, 38, 1005-1014.	9.4	540
12	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. <i>Cell</i> , 2015, 163, 134-147.	13.5	399
13	Constitutive nuclear lamina“genome interactions are highly conserved and associated with A/T-rich sequence. <i>Genome Research</i> , 2013, 23, 270-280.	2.4	377
14	Genomic binding by the <i>Drosophila</i> Myc, Max, Mad/Mnt transcription factor network. <i>Genes and Development</i> , 2003, 17, 1101-1114.	2.7	352
15	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
16	Detection of in vivo protein“DNA interactions using DamID in mammalian cells. <i>Nature Protocols</i> , 2007, 2, 1467-1478.	5.5	341
17	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
18	Genome-wide DNA replication profile for <i>Drosophila melanogaster</i> : a link between transcription and replication timing. <i>Nature Genetics</i> , 2002, 32, 438-442.	9.4	310

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19	Chromatin profiling using targeted DNA adenine methyltransferase. <i>Nature Genetics</i> , 2001, 27, 304-308.	9.4	303
20	Domains of genome-wide gene expression dysregulation in Downâ€™s syndrome. <i>Nature</i> , 2014, 508, 345-350.	13.7	298
21	Chromatin Position Effects Assayed by Thousands of Reporters Integrated in Parallel. <i>Cell</i> , 2013, 154, 914-927.	13.5	283
22	Mapping 3D genome organization relative to nuclear compartments using TSA-Seq as a cytological ruler. <i>Journal of Cell Biology</i> , 2018, 217, 4025-4048.	2.3	275
23	Genomics tools for unraveling chromosome architecture. <i>Nature Biotechnology</i> , 2010, 28, 1089-1095.	9.4	202
24	Kinetics and Fidelity of the Repair of Cas9-Induced Double-Strand DNA Breaks. <i>Molecular Cell</i> , 2018, 70, 801-813.e6.	4.5	194
25	The role of transcription in shaping the spatial organization of the genome. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 327-337.	16.1	188
26	Nonlinear control of transcription through enhancerâ€™promoter interactions. <i>Nature</i> , 2022, 604, 571-577.	13.7	187
27	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
28	Genomeâ€™nuclear lamina interactions and gene regulation. <i>Current Opinion in Cell Biology</i> , 2010, 22, 320-325.	2.6	176
29	High-throughput identification of human SNPs affecting regulatory element activity. <i>Nature Genetics</i> , 2019, 51, 1160-1169.	9.4	157
30	Interactions among Polycomb Domains Are Guided by Chromosome Architecture. <i>PLoS Genetics</i> , 2011, 7, e1001343.	1.5	156
31	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
32	Easy quantification of template-directed CRISPR/Cas9 editing. <i>Nucleic Acids Research</i> , 2018, 46, e58-e58.	6.5	147
33	In search of the determinants of enhancerâ€™promoter interaction specificity. <i>Trends in Cell Biology</i> , 2014, 24, 695-702.	3.6	142
34	Human heterochromatin proteins form large domains containing KRAB-ZNF genes. <i>Genome Research</i> , 2006, 16, 1493-1504.	2.4	141
35	Chromatin: constructing the big picture. <i>EMBO Journal</i> , 2011, 30, 1885-1895.	3.5	141
36	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

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37	[16] DamID: Mapping of In Vivo Protein–Genome Interactions Using Tethered DNA Adenine Methyltransferase. <i>Methods in Enzymology</i> , 2006, 410, 342-359.	0.4	115
38	Genomewide analysis of <i>Drosophila</i> GAGA factor target genes reveals context-dependent DNA binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2580-2585.	3.3	114
39	High-Resolution Mapping Reveals Links of HP1 with Active and Inactive Chromatin Components. <i>PLoS Genetics</i> , 2007, 3, e38.	1.5	113
40	Mapping of genetic and epigenetic regulatory networks using microarrays. <i>Nature Genetics</i> , 2005, 37, S18-S24.	9.4	110
41	The Genomic Landscape of the Somatic Linker Histone Subtypes H1.1 to H1.5 in Human Cells. <i>Cell Reports</i> , 2013, 3, 2142-2154.	2.9	110
42	Promoter-Intrinsic and Local Chromatin Features Determine Gene Repression in LADs. <i>Cell</i> , 2019, 177, 852-864.e14.	13.5	108
43	Impact of chromatin context on Cas9-induced DNA double-strand break repair pathway balance. <i>Molecular Cell</i> , 2021, 81, 2216-2230.e10.	4.5	106
44	Mechanisms and dynamics of nuclear lamina–genome interactions. <i>Current Opinion in Cell Biology</i> , 2014, 28, 61-68.	2.6	103
45	Nuclear lamins are not required for lamina-associated domain organization in mouse embryonic stem cells. <i>EMBO Reports</i> , 2015, 16, 610-617.	2.0	98
46	Histone H1 binding is inhibited by histone variant H3.3. <i>EMBO Journal</i> , 2009, 28, 3635-3645.	3.5	97
47	Genome-wide mapping of autonomous promoter activity in human cells. <i>Nature Biotechnology</i> , 2017, 35, 145-153.	9.4	97
48	The Insulator Protein SU(HW) Fine-Tunes Nuclear Lamina Interactions of the <i>Drosophila</i> Genome. <i>PLoS ONE</i> , 2010, 5, e15013.	1.1	95
49	A single double-strand break system reveals repair dynamics and mechanisms in heterochromatin and euchromatin. <i>Genes and Development</i> , 2016, 30, 1645-1657.	2.7	95
50	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
51	Mapping of lamin A- and progerin-interacting genome regions. <i>Chromosoma</i> , 2012, 121, 447-464.	1.0	86
52	Rapid Quantitative Evaluation of CRISPR Genome Editing by TIDE and TIDER. <i>Methods in Molecular Biology</i> , 2019, 1961, 29-44.	0.4	83
53	Stochastic genome-nuclear lamina interactions. <i>Nucleus</i> , 2014, 5, 124-130.	0.6	79
54	Cell cycle dynamics of lamina-associated DNA. <i>EMBO Reports</i> , 2020, 21, e50636.	2.0	74

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55	Protein-DNA interaction mapping using genomic tiling path microarrays in <i>Drosophila</i> . Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9428-9433.	3.3	73
56	Global Chromatin Domain Organization of the <i>Drosophila</i> Genome. PLoS Genetics, 2008, 4, e1000045.	1.5	72
57	Massive reshaping of genomeâ€™nuclear lamina interactions during oncogene-induced senescence. Genome Research, 2017, 27, 1634-1644.	2.4	66
58	SPIN reveals genome-wide landscape of nuclear compartmentalization. Genome Biology, 2021, 22, 36.	3.8	61
59	The inner nuclear membrane proteins Man1 and Ima1 link to two different types of chromatin at the nuclear periphery in <i>S. pombe</i> . Nucleus, 2012, 3, 77-87.	0.6	60
60	Local rewiring of genomeâ€™nuclear lamina interactions by transcription. EMBO Journal, 2020, 39, e103159.	3.5	59
61	A Network Model of the Molecular Organization of Chromatin in <i>Drosophila</i> . Molecular Cell, 2013, 49, 759-771.	4.5	58
62	Epigenomic profiling using microarrays. BioTechniques, 2003, 35, 346-357.	0.8	57
63	SUIR joins separate subsets of PcG, HP1 and B-type lamin targets in <i>Drosophila</i> . Journal of Cell Science, 2007, 120, 2344-2351.	1.2	54
64	Chromatin domains in higher eukaryotes: insights from genome-wide mapping studies. Chromosoma, 2009, 118, 25-36.	1.0	49
65	HP1 controls genomic targeting of four novel heterochromatin proteins in <i>Drosophila</i> . EMBO Journal, 2007, 26, 741-751.	3.5	48
66	Bayesian network analysis of targeting interactions in chromatin. Genome Research, 2010, 20, 190-200.	2.4	48
67	Systematic analysis of intrinsic enhancer-promoter compatibility in the mouse genome. Molecular Cell, 2022, 82, 2519-2531.e6.	4.5	47
68	Clustering of <i>Drosophila</i> housekeeping promoters facilitates their expression. Genome Research, 2017, 27, 1153-1161.	2.4	46
69	High-resolution mapping of heterochromatin redistribution in a <i>Drosophila</i> position-effect variegation model. Epigenetics and Chromatin, 2009, 2, 1.	1.8	45
70	Inducible DamID systems for genomic mapping of chromatin proteins in <i>Drosophila</i> . Nucleic Acids Research, 2016, 44, 5646-5657.	6.5	42
71	Small chromosomal regions position themselves autonomously according to their chromatin class. Genome Research, 2017, 27, 922-933.	2.4	39
72	Using TRIP for genome-wide position effect analysis in cultured cells. Nature Protocols, 2014, 9, 1255-1281.	5.5	34

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73	Lamina-associated domains: Tethers and looseners. <i>Current Opinion in Cell Biology</i> , 2022, 74, 80-87.	2.6	34
74	Whole-genome views of chromatin structure. <i>Chromosome Research</i> , 2005, 13, 289-298.	1.0	28
75	Genome-wide nuclear lamina interactions: from cell populations to single cells. <i>Current Opinion in Genetics and Development</i> , 2017, 43, 67-72.	1.5	28
76	The large fraction of heterochromatin in <i>Drosophila</i> neurons is bound by both B-type lamin and HP1a. <i>Epigenetics and Chromatin</i> , 2018, 11, 65.	1.8	26
77	CHRAC/ACF contribute to the repressive ground state of chromatin. <i>Life Science Alliance</i> , 2018, 1, e201800024.	1.3	26
78	Comprehensive analysis of nucleocytoplasmic dynamics of mRNA in <i>Drosophila</i> cells. <i>PLoS Genetics</i> , 2017, 13, e1006929.	1.5	23
79	Enhanced processivity of Dnmt1 by monoubiquitinated histone H3. <i>Genes To Cells</i> , 2020, 25, 22-32.	0.5	18
80	High-throughput assessment of context-dependent effects of chromatin proteins. <i>Epigenetics and Chromatin</i> , 2016, 9, 43.	1.8	13
81	Deciphering Gene Regulation Using Massively Parallel Reporter Assays. <i>Trends in Biochemical Sciences</i> , 2020, 45, 90-91.	3.7	11
82	DamID profiling of dynamic Polycomb-binding sites in <i>Drosophila</i> imaginal disc development and tumorigenesis. <i>Epigenetics and Chromatin</i> , 2018, 11, 27.	1.8	9
83	Hox in space. <i>Nucleus</i> , 2012, 3, 118-122.	0.6	8
84	The Spatial Architecture of Chromosomes. , 2013, , 137-151.		8
85	Chromatin-dependent negative regulation of Dnmt1 by nucleosome structure and histone tails. <i>FEBS Journal</i> , 2017, 284, 3455-3469.	2.2	8
86	A HUSH for transgene expression. <i>Science</i> , 2015, 348, 1433-1434.	6.0	7
87	A short guide to technology development in cell biology. <i>Journal of Cell Biology</i> , 2015, 208, 655-657.	2.3	2
88	Functional Enhancer Screening in Single Cells. <i>Molecular Cell</i> , 2017, 66, 167-168.	4.5	1
89	Phosphorylated Lamins in Euchromatin: New Clues to Progeria. <i>Developmental Cell</i> , 2020, 52, 676-678.	3.1	1
90	Genome-Wide Mapping and Microscopy Visualization of Protein-DNA Interactions by pA-DamID. <i>Methods in Molecular Biology</i> , 2022, 2458, 215-229.	0.4	1

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91	Protocol: A Multiplexed Reporter Assay to Study Effects of Chromatin Context on DNA Double-Strand Break Repair. <i>Frontiers in Genetics</i> , 2021, 12, 785947.	1.1	1
92	Scientific honesty and publicly shared lab notebooks. <i>EMBO Reports</i> , 2018, 19, .	2.0	0