

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	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
2	Lamina-associated domains: Tethers and looseners. <i>Current Opinion in Cell Biology</i> , 2022, 74, 80-87.	2.6	34
3	Nonlinear control of transcription through enhancer-promoter interactions. <i>Nature</i> , 2022, 604, 571-577.	13.7	187
4	Systematic analysis of intrinsic enhancer-promoter compatibility in the mouse genome. <i>Molecular Cell</i> , 2022, 82, 2519-2531.e6.	4.5	47
5	SPIN reveals genome-wide landscape of nuclear compartmentalization. <i>Genome Biology</i> , 2021, 22, 36.	3.8	61
6	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
7	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
8	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
9	Enhanced processivity of Dnmt1 by monoubiquitinated histone H3. <i>Genes To Cells</i> , 2020, 25, 22-32.	0.5	18
10	Deciphering Gene Regulation Using Massively Parallel Reporter Assays. <i>Trends in Biochemical Sciences</i> , 2020, 45, 90-91.	3.7	11
11	Local rewiring of genome-nuclear lamina interactions by transcription. <i>EMBO Journal</i> , 2020, 39, e103159.	3.5	59
12	Phosphorylated Lamins in Euchromatin: New Clues to Progeria. <i>Developmental Cell</i> , 2020, 52, 676-678.	3.1	1
13	Cell cycle dynamics of lamina-associated DNA. <i>EMBO Reports</i> , 2020, 21, e50636.	2.0	74
14	High-throughput identification of human SNPs affecting regulatory element activity. <i>Nature Genetics</i> , 2019, 51, 1160-1169.	9.4	157
15	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
16	Rapid Quantitative Evaluation of CRISPR Genome Editing by TIDE and TIDER. <i>Methods in Molecular Biology</i> , 2019, 1961, 29-44.	0.4	83
17	Promoter-Intrinsic and Local Chromatin Features Determine Gene Repression in LADs. <i>Cell</i> , 2019, 177, 852-864.e14.	13.5	108
18	Easy quantification of template-directed CRISPR/Cas9 editing. <i>Nucleic Acids Research</i> , 2018, 46, e58-e58.	6.5	147

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19	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
20	Scientific honesty and publicly shared lab notebooks. <i>EMBO Reports</i> , 2018, 19, .	2.0	0
21	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
22	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
23	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
24	CHRAC/ACF contribute to the repressive ground state of chromatin. <i>Life Science Alliance</i> , 2018, 1, e201800024.	1.3	26
25	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
26	Functional Enhancer Screening in Single Cells. <i>Molecular Cell</i> , 2017, 66, 167-168.	4.5	1
27	Clustering of <i>Drosophila</i> housekeeping promoters facilitates their expression. <i>Genome Research</i> , 2017, 27, 1153-1161.	2.4	46
28	The Cohesin Release Factor WAPL Restricts Chromatin Loop Extension. <i>Cell</i> , 2017, 169, 693-707.e14.	13.5	636
29	Lamina-Associated Domains: Links with Chromosome Architecture, Heterochromatin, and Gene Repression. <i>Cell</i> , 2017, 169, 780-791.	13.5	798
30	Small chromosomal regions position themselves autonomously according to their chromatin class. <i>Genome Research</i> , 2017, 27, 922-933.	2.4	39
31	Genome-wide mapping of autonomous promoter activity in human cells. <i>Nature Biotechnology</i> , 2017, 35, 145-153.	9.4	97
32	Independent negative regulation of Dnmt1 by nucleosome structure and histone tails. <i>FEBS Journal</i> , 2017, 284, 3455-3469.	2.2	8
33	Massive reshaping of genome-wide nuclear lamina interactions during oncogene-induced senescence. <i>Genome Research</i> , 2017, 27, 1634-1644.	2.4	66
34	Comprehensive analysis of nucleocytoplasmic dynamics of mRNA in <i>Drosophila</i> cells. <i>PLoS Genetics</i> , 2017, 13, e1006929.	1.5	23
35	High-throughput assessment of context-dependent effects of chromatin proteins. <i>Epigenetics and Chromatin</i> , 2016, 9, 43.	1.8	13
36	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

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37	Inducible DamID systems for genomic mapping of chromatin proteins in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2016, 44, 5646-5657.	6.5	42
38	A HUSH for transgene expression. <i>Science</i> , 2015, 348, 1433-1434.	6.0	7
39	A short guide to technology development in cell biology. <i>Journal of Cell Biology</i> , 2015, 208, 655-657.	2.3	2
40	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
41	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. <i>Cell</i> , 2015, 163, 134-147.	13.5	399
42	Stochastic genome-nuclear lamina interactions. <i>Nucleus</i> , 2014, 5, 124-130.	0.6	79
43	Easy quantitative assessment of genome editing by sequence trace decomposition. <i>Nucleic Acids Research</i> , 2014, 42, e168-e168.	6.5	1,838
44	Mechanisms and dynamics of nuclear lamina-genome interactions. <i>Current Opinion in Cell Biology</i> , 2014, 28, 61-68.	2.6	103
45	Domains of genome-wide gene expression dysregulation in Down's syndrome. <i>Nature</i> , 2014, 508, 345-350.	13.7	298
46	In search of the determinants of enhancer-promoter interaction specificity. <i>Trends in Cell Biology</i> , 2014, 24, 695-702.	3.6	142
47	Using TRIP for genome-wide position effect analysis in cultured cells. <i>Nature Protocols</i> , 2014, 9, 1255-1281.	5.5	34
48	Chromatin Position Effects Assayed by Thousands of Reporters Integrated in Parallel. <i>Cell</i> , 2013, 154, 914-927.	13.5	283
49	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
50	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
51	The Spatial Architecture of Chromosomes. , 2013, , 137-151.		8
52	Genome Architecture: Domain Organization of Interphase Chromosomes. <i>Cell</i> , 2013, 152, 1270-1284.	13.5	659
53	A Network Model of the Molecular Organization of Chromatin in <i>Drosophila</i> . <i>Molecular Cell</i> , 2013, 49, 759-771.	4.5	58
54	Single-Cell Dynamics of Genome-Nuclear Lamina Interactions. <i>Cell</i> , 2013, 153, 178-192.	13.5	609

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55	Hox in space. <i>Nucleus</i> , 2012, 3, 118-122.	0.6	8
56	The inner nuclear membrane proteins Man1 and Ima1 link to two different types of chromatin at the nuclear periphery in <i>S. pombe</i> . <i>Nucleus</i> , 2012, 3, 77-87.	0.6	60
57	Mapping of lamin A- and progerin-interacting genome regions. <i>Chromosoma</i> , 2012, 121, 447-464.	1.0	86
58	Interactions among Polycomb Domains Are Guided by Chromosome Architecture. <i>PLoS Genetics</i> , 2011, 7, e1001343.	1.5	156
59	Chromatin: constructing the big picture. <i>EMBO Journal</i> , 2011, 30, 1885-1895.	3.5	141
60	Genome-wide nuclear lamina interactions and gene regulation. <i>Current Opinion in Cell Biology</i> , 2010, 22, 320-325.	2.6	176
61	Genomics tools for unraveling chromosome architecture. <i>Nature Biotechnology</i> , 2010, 28, 1089-1095.	9.4	202
62	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
63	Bayesian network analysis of targeting interactions in chromatin. <i>Genome Research</i> , 2010, 20, 190-200.	2.4	48
64	Molecular Maps of the Reorganization of Genome-Nuclear Lamina Interactions during Differentiation. <i>Molecular Cell</i> , 2010, 38, 603-613.	4.5	916
65	Systematic Protein Location Mapping Reveals Five Principal Chromatin Types in <i>Drosophila</i> Cells. <i>Cell</i> , 2010, 143, 212-224.	13.5	854
66	Chromatin domains in higher eukaryotes: insights from genome-wide mapping studies. <i>Chromosoma</i> , 2009, 118, 25-36.	1.0	49
67	High-resolution mapping of heterochromatin redistribution in a <i>Drosophila</i> position-effect variegation model. <i>Epigenetics and Chromatin</i> , 2009, 2, 1.	1.8	45
68	Histone H1 binding is inhibited by histone variant H3.3. <i>EMBO Journal</i> , 2009, 28, 3635-3645.	3.5	97
69	Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions. <i>Nature</i> , 2008, 453, 948-951.	13.7	1,658
70	Global Chromatin Domain Organization of the <i>Drosophila</i> Genome. <i>PLoS Genetics</i> , 2008, 4, e1000045.	1.5	72
71	High-Resolution Mapping Reveals Links of HP1 with Active and Inactive Chromatin Components. <i>PLoS Genetics</i> , 2007, 3, e38.	1.5	113
72	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

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73	Detection of in vivo protein-DNA interactions using DamID in mammalian cells. <i>Nature Protocols</i> , 2007, 2, 1467-1478.	5.5	341
74	HP1 controls genomic targeting of four novel heterochromatin proteins in <i>Drosophila</i> . <i>EMBO Journal</i> , 2007, 26, 741-751.	3.5	48
75	[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
76	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
77	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
78	Characterization of the <i>Drosophila melanogaster</i> genome at the nuclear lamina. <i>Nature Genetics</i> , 2006, 38, 1005-1014.	9.4	540
79	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
80	Human heterochromatin proteins form large domains containing KRAB-ZNF genes. <i>Genome Research</i> , 2006, 16, 1493-1504.	2.4	141
81	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
82	Mapping of genetic and epigenetic regulatory networks using microarrays. <i>Nature Genetics</i> , 2005, 37, S18-S24.	9.4	110
83	Whole-genome views of chromatin structure. <i>Chromosome Research</i> , 2005, 13, 289-298.	1.0	28
84	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
85	Protein-DNA interaction mapping using genomic tiling path microarrays in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9428-9433.	3.3	73
86	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
87	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
88	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
89	Epigenomic profiling using microarrays. <i>BioTechniques</i> , 2003, 35, 346-357.	0.8	57
90	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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91	Chromatin profiling using targeted DNA adenine methyltransferase. <i>Nature Genetics</i> , 2001, 27, 304-308.	9.4	303
92	Identification of in vivo DNA targets of chromatin proteins using tethered Dam methyltransferase. <i>Nature Biotechnology</i> , 2000, 18, 424-428.	9.4	544