Job Dekker

List of Publications by Citations

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166	41,406	76	203
papers	citations	h-index	g-index
221	51,536	21.6	7.46
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
166	Comprehensive mapping of long-range interactions reveals folding principles of the human genome. *Science*, **2009**, 326, 289-93	33.3	4993
165	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
164	Capturing chromosome conformation. *Science*, **2002**, 295, 1306-11	33.3	2589
163	The accessible chromatin landscape of the human genome. *Nature*, **2012**, 489, 75-82	50.4	1900
162	Spatial partitioning of the regulatory landscape of the X-inactivation centre. *Nature*, **2012**, 485, 381-5	50.4	1894
161	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. *Nature*, **2011**, 472, 120-4	50.4	1502
160	Mediator and cohesin connect gene expression and chromatin architecture. *Nature*, **2010**, 467, 430-5	50.4	1410
159	The long-range interaction landscape of gene promoters. *Nature*, **2012**, 489, 109-13	50.4	1066
158	Architectural protein subclasses shape 3D organization of genomes during lineage commitment. *Cell*, **2013**, 153, 1281-95	56.2	848
157	Targeted Degradation of CTCF Decouples Local Insulation of Chromosome Domains from Genomic Compartmentalization. *Cell*, **2017**, 169, 930-944.e22	56.2	845
156	Chromosome Conformation Capture Carbon Copy (5C): a massively parallel solution for mapping interactions between genomic elements. *Genome Research*, **2006**, 16, 1299-309	9.7	824
155	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. *Nature Methods*, **2012**, 9, 999-1003	21.6	822
154	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. *Genome Biology*, **2015**, 16, 259	18.3	811
153	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. *Nature Reviews Genetics*, **2013**, 14, 390-403	30.1	762
152	Organization of the mitotic chromosome. *Science*, **2013**, 342, 948-53	33.3	654
151	Activation of proto-oncogenes by disruption of chromosome neighborhoods. *Science*, **2016**, 351, 1454-1458	33.3	600
150	The 3D Genome as Moderator of Chromosomal Communication. *Cell*, **2016**, 164, 1110-1121	56.2	558

149	The hierarchy of the 3D genome. *Molecular Cell*, **2013**, 49, 773-82	17.6	512
148	Quantitative analysis of chromosome conformation capture assays (3C-qPCR). *Nature Protocols*, **2007**, 2, 1722-33	18.8	510
147	Condensin-driven remodelling of X chromosome topology during dosage compensation. *Nature*, **2015**, 523, 240-4	50.4	501
146	Defining functional DNA elements in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6131-8	11.5	490
145	Hi-C: a comprehensive technique to capture the conformation of genomes. *Methods*, **2012**, 58, 268-76	4.6	472
144	Proximity among distant regulatory elements at the beta-globin locus requires GATA-1 and FOG-1. *Molecular Cell*, **2005**, 17, 453-62	17.6	420
143	Spatial organization of the mouse genome and its role in recurrent chromosomal translocations. *Cell*, **2012**, 148, 908-21	56.2	411
142	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
141	A pathway for mitotic chromosome formation. *Science*, **2018**, 359,	33.3	352
140	Mapping Nucleosome Resolution Chromosome Folding in Yeast by Micro-C. *Cell*, **2015**, 162, 108-19	56.2	341
139	An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biology*, **2012**, 13, 418	18.3	340
138	The 4D nucleome project. *Nature*, **2017**, 549, 219-226	50.4	332
137	Predictive polymer modeling reveals coupled fluctuations in chromosome conformation and transcription. *Cell*, **2014**, 157, 950-63	56.2	321
136	Patterns of Growth and Decline in Lung Function in Persistent Childhood Asthma. *New England Journal of Medicine*, **2016**, 374, 1842-1852	59.2	312
135	Genome-wide maps of nuclear lamina interactions in single human cells. *Cell*, **2015**, 163, 134-47	56.2	291
134	The three SCSs of chromosome conformation capture: controls, controls, controls. *Nature Methods*, **2006**, 3, 17-21	21.6	290
133	Structural organization of the inactive X chromosome in the mouse. *Nature*, **2016**, 535, 575-9	50.4	261
132	Mechanisms that regulate localization of a DNA double-strand break to the nuclear periphery. *Genes and Development*, **2009**, 23, 912-27	12.6	240

131	A mechanical basis for chromosome function. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 12592-7	11.5	239
130	Heterochromatin drives compartmentalization of inverted and conventional nuclei. *Nature*, **2019**, 570, 395-399	50.4	236
129	Polycomb response elements mediate the formation of chromosome higher-order structures in the bithorax complex. *Nature Cell Biology*, **2007**, 9, 1167-74	23.4	235
128	Correlated alterations in genome organization, histone methylation, and DNA-lamin A/C interactions in Hutchinson-Gilford progeria syndrome. *Genome Research*, **2013**, 23, 260-9	9.7	234
127	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. *Genome Research*, **2013**, 23, 2066-77	9.7	232
126	The three-dimensional folding of the βglobin gene domain reveals formation of chromatin globules. *Nature Structural and Molecular Biology*, **2011**, 18, 107-14	17.6	232
125	Extensive Heterogeneity and Intrinsic Variation in Spatial Genome Organization. *Cell*, **2019**, 176, 1502-1515.e10	56.2	221
124	MORC family ATPases required for heterochromatin condensation and gene silencing. *Science*, **2012**, 336, 1448-51	33.3	220
123	The HitchhikerŠs guide to Hi-C analysis: practical guidelines. *Methods*, **2015**, 72, 65-75	4.6	209
122	The three-dimensional architecture of a bacterial genome and its alteration by genetic perturbation. *Molecular Cell*, **2011**, 44, 252-64	17.6	203
121	Cohesin-dependent globules and heterochromatin shape 3D genome architecture in S. pombe. *Nature*, **2014**, 516, 432-435	50.4	188
120	Structural and functional diversity of Topologically Associating Domains. *FEBS Letters*, **2015**, 589, 2877-84	3.8	186
119	Sister cohesion and structural axis components mediate homolog bias of meiotic recombination. *Cell*, **2010**, 143, 924-37	56.2	183
118	Gene regulation in the third dimension. *Science*, **2008**, 319, 1793-4	33.3	183
117	Polycomb Repressive Complex 1 Generates Discrete Compacted Domains that Change during Differentiation. *Molecular Cell*, **2017**, 65, 432-446.e5	17.6	180
116	Genomics tools for unraveling chromosome architecture. *Nature Biotechnology*, **2010**, 28, 1089-95	44.5	176
115	Progression of meiotic DNA replication is modulated by interchromosomal interaction proteins, negatively by Spo11p and positively by Rec8p. *Genes and Development*, **2000**, 14, 493-503	12.6	164
114	Mapping networks of physical interactions between genomic elements using 5C technology. *Nature Protocols*, **2007**, 2, 988-1002	18.8	163

113	Chemical genetic strategy identifies histone deacetylase 1 (HDAC1) and HDAC2 as therapeutic targets in sickle cell disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 12617-22	11.5	155
112	Condensin promotes the juxtaposition of DNA flanking its loading site in Bacillus subtilis. *Genes and Development*, **2015**, 29, 1661-75	12.6	150
111	Long-Range Chromatin Interactions. *Cold Spring Harbor Perspectives in Biology*, **2015**, 7, a019356	10.2	147
110	Long-range chromosomal interactions and gene regulation. *Molecular BioSystems*, **2008**, 4, 1046-57		147
109	Integrative detection and analysis of structural variation in cancer genomes. *Nature Genetics*, **2018**, 50, 1388-1398	36.3	147
108	Ultrastructural Details of Mammalian Chromosome Architecture. *Molecular Cell*, **2020**, 78, 554-565.e7	17.6	137
107	Segmental folding of chromosomes: a basis for structural and regulatory chromosomal neighborhoods?. *BioEssays*, **2013**, 35, 818-28	4.1	136
106	Hi-C 2.0: An optimized Hi-C procedure for high-resolution genome-wide mapping of chromosome conformation. *Methods*, **2017**, 123, 56-65	4.6	130
105	TAD disruption as oncogenic driver. *Current Opinion in Genetics and Development*, **2016**, 36, 34-40	4.9	127
104	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. *Genome Biology*, **2015**, 16, 214	18.3	123
103	High-throughput genome scaffolding from in vivo DNA interaction frequency. *Nature Biotechnology* , **2013**, 31, 1143-7	44.5	120
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101	Mapping in vivo chromatin interactions in yeast suggests an extended chromatin fiber with regional variation in compaction. *Journal of Biological Chemistry*, **2008**, 283, 34532-40	5.4	118
100	CTCF-mediated topological boundaries during development foster appropriate gene regulation. *Genes and Development*, **2016**, 30, 2657-2662	12.6	107
99	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. *Genome Research*, **2015**, 25, 504-13	9.7	106
98	Local Genome Topology Can Exhibit an Incompletely Rewired 3D-Folding State during Somatic Cell Reprogramming. *Cell Stem Cell*, **2016**, 18, 611-24	18	92
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96	The cluster is a dynamic and resilient TAD boundary controlling the segregation of antagonistic regulatory landscapes. *Genes and Development*, **2017**, 31, 2264-2281	12.6	90

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92	A chromosome folding intermediate at the condensin-to-cohesin transition during telophase. *Nature Cell Biology*, **2019**, 21, 1393-1402	23.4	82
91	Enhanced yeast one-hybrid assays for high-throughput gene-centered regulatory network mapping. *Nature Methods*, **2011**, 8, 1059-64	21.6	82
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89	My5C: web tools for chromosome conformation capture studies. *Nature Methods*, **2009**, 6, 690-1	21.6	74
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86	Mechanisms and Functions of Chromosome Compartmentalization. *Trends in Biochemical Sciences*, **2020**, 45, 385-396	10.3	67
85	C-BERST: defining subnuclear proteomic landscapes at genomic elements with dCas9-APEX2. *Nature Methods*, **2018**, 15, 433-436	21.6	67
84	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. *Genome Research*, **2016**, 26, 1188-201	9.7	64
83	Measuring the reproducibility and quality of Hi-C data. *Genome Biology*, **2019**, 20, 57	18.3	62
82	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
81	Two ways to fold the genome during the cell cycle: insights obtained with chromosome conformation capture. *Epigenetics and Chromatin*, **2014**, 7, 25	5.8	60
80	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in Drosophila. *Molecular Cell*, **2015**, 60, 146-62	17.6	58
79	CTCF sites display cell cycle-dependent dynamics in factor binding and nucleosome positioning. *Genome Research*, **2019**, 29, 236-249	9.7	58
78	Chromatin globules: a common motif of higher order chromosome structure?. *Current Opinion in Cell Biology*, **2011**, 23, 325-31	9	56

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76	The non-canonical SMC protein SmcHD1 antagonises TAD formation and compartmentalisation on the inactive X chromosome. *Nature Communications*, **2019**, 10, 30	17.4	56
75	The yeast genome undergoes significant topological reorganization in quiescence. *Nucleic Acids Research*, **2015**, 43, 8299-313	20.1	53
74	Evidence for transcript networks composed of chimeric RNAs in human cells. *PLoS ONE*, **2012**, 7, e28213	3.7	51
73	Integrating one-dimensional and three-dimensional maps of genomes. *Journal of Cell Science*, **2010**, 123, 1979-88	5.3	49
72	The active FMR1 promoter is associated with a large domain of altered chromatin conformation with embedded local histone modifications. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 12463-8	11.5	49
71	Cohesin Members Stag1 and Stag2 Display Distinct Roles in Chromatin Accessibility and Topological Control of HSC Self-Renewal and Differentiation. *Cell Stem Cell*, **2019**, 25, 682-696.e8	18	48
70	GC- and AT-rich chromatin domains differ in conformation and histone modification status and are differentially modulated by Rpd3p. *Genome Biology*, **2007**, 8, R116	18.3	47
69	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2016**, 1859, 1389-1397	6	43
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66	Mapping the 3D genome: Aiming for consilience. *Nature Reviews Molecular Cell Biology*, **2016**, 17, 741-742	48.7	40
65	Higher-Order Organization Principles of Pre-translational mRNPs. *Molecular Cell*, **2018**, 72, 715-726.e3	17.6	39
64	CBF□SMMHC Inhibition Triggers Apoptosis by Disrupting MYC Chromatin Dynamics in Acute Myeloid Leukemia. *Cell*, **2018**, 174, 172-186.e21	56.2	37
63	Transcriptional Silencers in Drosophila Serve a Dual Role as Transcriptional Enhancers in Alternate Cellular Contexts. *Molecular Cell*, **2020**, 77, 324-337.e8	17.6	35
62	Flexible ordering of antibody class switch and V(D)J joining during B-cell ontogeny. *Genes and Development*, **2013**, 27, 2439-44	12.6	34
61	From cells to chromatin: capturing snapshots of genome organization with 5C technology. *Methods*, **2012**, 58, 255-67	4.6	33
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59	Liquid chromatin Hi-C characterizes compartment-dependent chromatin interaction dynamics. *Nature Genetics*, **2021**, 53, 367-378	36.3	30
58	Highly structured homolog pairing reflects functional organization of the Drosophila genome. *Nature Communications*, **2019**, 10, 4485	17.4	26
57	Multi-contact 3C reveals that the human genome during interphase is largely not entangled. *Nature Structural and Molecular Biology*, **2020**, 27, 1105-1114	17.6	24
56	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. *Cell Reports*, **2015**, 13, 1855-67	10.6	23
55	ATP-independent DNA unwinding by the adenovirus single-stranded DNA binding protein requires a flexible DNA binding loop. *Journal of Molecular Biology*, **1998**, 277, 825-38	6.5	23
54	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. *Proceedings of the National Academy of Sciences of the United States of America* , **2014**, 111, E3366	11.5	22
53	Epigenetic characteristics of the mitotic chromosome in 1D and 3D. *Critical Reviews in Biochemistry and Molecular Biology*, **2017**, 52, 185-204	8.7	20
52	Heterochromatin drives organization of conventional and inverted nuclei		19
51	Genetics and Genomics of Longitudinal Lung Function Patterns in Individuals with Asthma. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 194, 1465-1474	10.2	18
50	Rapid Irreversible Transcriptional Reprogramming in Human Stem Cells Accompanied by Discordance between Replication Timing and Chromatin Compartment. *Stem Cell Reports*, **2019**, 13, 193-206	8	16
49	The genome-wide multi-layered architecture of chromosome pairing in early Drosophila embryos. *Nature Communications*, **2019**, 10, 4486	17.4	16
48	Genetic and spatial organization of the unusual chromosomes of the dinoflagellate Symbiodinium microadriaticum. *Nature Genetics*, **2021**, 53, 618-629	36.3	16
47	Cohesin mutations alter DNA damage repair and chromatin structure and create therapeutic vulnerabilities in MDS/AML. *JCI Insight*, **2021**, 6,	9.9	16
46	Hi-C in Budding Yeast. *Cold Spring Harbor Protocols*, **2015**, 2015, 649-61	1.2	14
45	Compartment-dependent chromatin interaction dynamics revealed by liquid chromatin Hi-C		14
44	Spatial organization of transcribed eukaryotic genes		11
43	Crystal structure of the DNA binding domain of the transcription factor T-bet suggests simultaneous recognition of distant genome sites. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E6572-E6581	11.5	11
42	Shelterin components mediate genome reorganization in response to replication stress. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 5479-5484	11.5	10

41	Chromosome Conformation Capture (3C) in Budding Yeast. *Cold Spring Harbor Protocols*, **2015**, 2015, 580-6	1.2	10
40	Mechanisms of Chromosome Folding and Nuclear Organization: Their Interplay and Open Questions. *Cold Spring Harbor Perspectives in Biology*, **2021**,	10.2	10
39	Detecting chromatin interactions between and along sister chromatids with SisterC. *Nature Methods*, **2020**, 17, 1002-1009	21.6	8
38	Systematic evaluation of chromosome conformation capture assays. *Nature Methods*, **2021**, 18, 1046-1055	21.6	8
37	Hi-C 3.0: Improved Protocol for Genome-Wide Chromosome Conformation Capture. *Current Protocols*, **2021**, 1, e198		7
36	Large domains of heterochromatin direct the formation of short mitotic chromosome loops. *ELife*, **2020**, 9,	8.9	6
35	CTCF and cohesin help neurons raise their self-awareness. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 8799-800	11.5	5
34	Systematic evaluation of chromosome conformation capture assays		5
33	Linker histone H1.8 inhibits chromatin binding of condensins and DNA topoisomerase II to tune chromosome length and individualization. *ELife*, **2021**, 10,	8.9	5
32	Chromosome Conformation Capture Carbon Copy (5C) in Budding Yeast. *Cold Spring Harbor Protocols*, **2015**, 2015, 593-8	1.2	4
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30	Clustering of strong replicators associated with active promoters is sufficient to establish an early-replicating domain. *EMBO Journal*, **2020**, 39, e99520	13	4
29	Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. *Nature Communications*, **2021**, 12, 6241	17.4	4
28	Biochemically distinct cohesin complexes mediate positioned loops between CTCF sites and dynamic loops within chromatin domains		4
27	Chromosome-scale assembly of the coral endosymbiont Symbiodinium microadriaticum genome provides insight into the unique biology of dinoflagellate chromosomes		3
26	The genome-wide, multi-layered architecture of chromosome pairing in early Drosophila embryos		3
25	A cohesin traffic pattern genetically linked to gene regulation		3
24	Measuring Chromatin Structure in Budding Yeast. *Cold Spring Harbor Protocols*, **2015**, 2015, 614-8	1.2	2

23	Nuclear biology: whatS been most surprising?. *Cell*, **2013**, 152, 1207-8	56.2	2
22	Translocation mapping exposes the risky lifestyle of B cells. *Cell*, **2011**, 147, 20-2	56.2	2
21	The non-canonical SMC protein SmcHD1 antagonises TAD formation on the inactive X chromosome		2
20	Chromosome-Level Assembly of the Atlantic Silverside Genome Reveals Extreme Levels of Sequence Diversity and Structural Genetic Variation. *Genome Biology and Evolution*, **2021**, 13,	3.9	2
19	A Guide to Packing Your DNA. *Cell*, **2016**, 165, 259-61	56.2	2
18	Heterochromatin diversity modulates genome compartmentalization and loop extrusion barriers		2
17	Multi-contact 3C data reveal that the human genome is largely unentangled		1
16	CTCF sites display cell cycle dependent dynamics in factor binding and nucleosome positioning		1
15	A chromosome folding intermediate at the condensin-to-cohesin transition during telophase		1
14	Detecting chromatin interactions along and between sister chromatids with SisterC		1
13	Chromosome-level assembly of the Atlantic silverside genome reveals extreme levels of sequence diversity and structural genetic variation		1
12	Higher-Order Organization Principles of Pre-translational mRNPs		1
11	Loops, TADs, Compartments, and Territories are Elastic and Robust to Dramatic Nuclear Volume Swelling		1
10	Spatial organization of transcribed eukaryotic genes.. *Nature Cell Biology*, **2022**,	23.4	1
9	Loops, topologically associating domains, compartments, and territories are elastic and robust to dramatic nuclear volume swelling.. *Scientific Reports*, **2022**, 12, 4721	4.9	1
8	Nutritional control regulates symbiont proliferation and life history in coral-dinoflagellate symbiosis.. *BMC Biology*, **2022**, 20, 103	7.3	1
7	Symbiodinium microadriaticum (coral microalgal endosymbiont). *Trends in Genetics*, **2021**, 37, 1044-1045	8.5	0
6	Three-Dimensional Architecture of Genomes **2011**, 211-234		

5	Inner Nuclear Protein Matrin-3 Coordinates Hematopoietic Cell Transcription and Differentiation By Stabilizing Chromatin Architecture. *Blood*, **2021**, 138, 285-285	2.2
4	GATA-1 Directly Induces Physical Proximity between the LCR and βGlobin Promoter in Erythroid Cells.. *Blood*, **2004**, 104, 1612-1612	2.2
3	Ikaros Drives Human Haemoglobin Switching by Facilitating Active Chromatin Hub Formation.. *Blood*, **2007**, 110, 1772-1772	2.2
2	CBFβSMMHC Inhibition Disrupts Enhancer Chromatin Dynamics and Represses MYC Transcriptional Program in Inv(16) Leukemia. *Blood*, **2017**, 130, 784-784	2.2
1	Integrating Structural and Functional Studies Leads to a New Model of βGlobin Activation That Suggests Distinct Initiation and Maintenance States. *Blood*, **2011**, 118, 349-349	2.2