

Job Dekker

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

166
papers

41,406
citations

76
h-index

203
g-index

221
ext. papers

51,536
ext. citations

21.6
avg, IF

7.46
L-index

#	Paper	IF	Citations
166	Spatial organization of transcribed eukaryotic genes.. <i>Nature Cell Biology</i> , 2022 ,	23.4	1
165	Loops, topologically associating domains, compartments, and territories are elastic and robust to dramatic nuclear volume swelling.. <i>Scientific Reports</i> , 2022 , 12, 4721	4.9	1
164	Nutritional control regulates symbiont proliferation and life history in coral-dinoflagellate symbiosis.. <i>BMC Biology</i> , 2022 , 20, 103	7.3	1
163	Inner Nuclear Protein Matrin-3 Coordinates Hematopoietic Cell Transcription and Differentiation By Stabilizing Chromatin Architecture. <i>Blood</i> , 2021 , 138, 285-285	2.2	
162	Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. <i>Nature Communications</i> , 2021 , 12, 6241	17.4	4
161	Genetic and spatial organization of the unusual chromosomes of the dinoflagellate <i>Symbiodinium microadriaticum</i> . <i>Nature Genetics</i> , 2021 , 53, 618-629	36.3	16
160	Chromosome-Level Assembly of the Atlantic Silverside Genome Reveals Extreme Levels of Sequence Diversity and Structural Genetic Variation. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	2
159	Hi-C 3.0: Improved Protocol for Genome-Wide Chromosome Conformation Capture. <i>Current Protocols</i> , 2021 , 1, e198		7
158	Liquid chromatin Hi-C characterizes compartment-dependent chromatin interaction dynamics. <i>Nature Genetics</i> , 2021 , 53, 367-378	36.3	30
157	Cohesin mutations alter DNA damage repair and chromatin structure and create therapeutic vulnerabilities in MDS/AML. <i>JCI Insight</i> , 2021 , 6,	9.9	16
156	Linker histone H1.8 inhibits chromatin binding of condensins and DNA topoisomerase II to tune chromosome length and individualization. <i>ELife</i> , 2021 , 10,	8.9	5
155	Mechanisms of Chromosome Folding and Nuclear Organization: Their Interplay and Open Questions. <i>Cold Spring Harbor Perspectives in Biology</i> , 2021 ,	10.2	10
154	<i>Symbiodinium microadriaticum</i> (coral microalgal endosymbiont). <i>Trends in Genetics</i> , 2021 , 37, 1044-1045	5.5	0
153	Systematic evaluation of chromosome conformation capture assays. <i>Nature Methods</i> , 2021 , 18, 1046-1055	5.6	8
152	Ultrastructural Details of Mammalian Chromosome Architecture. <i>Molecular Cell</i> , 2020 , 78, 554-565	17.6	137
151	Mechanisms and Functions of Chromosome Compartmentalization. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 385-396	10.3	67
150	Clustering of strong replicators associated with active promoters is sufficient to establish an early-replicating domain. <i>EMBO Journal</i> , 2020 , 39, e99520	13	4

149	Large domains of heterochromatin direct the formation of short mitotic chromosome loops. <i>ELife</i> , 2020 , 9,	8.9	6
148	SPEN integrates transcriptional and epigenetic control of X-inactivation. <i>Nature</i> , 2020 , 578, 455-460	50.4	73
147	Transcriptional Silencers in Drosophila Serve a Dual Role as Transcriptional Enhancers in Alternate Cellular Contexts. <i>Molecular Cell</i> , 2020 , 77, 324-337.e8	17.6	35
146	Detecting chromatin interactions between and along sister chromatids with SisterC. <i>Nature Methods</i> , 2020 , 17, 1002-1009	21.6	8
145	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
144	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	50.4	360
143	Multi-contact 3C reveals that the human genome during interphase is largely not entangled. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 1105-1114	17.6	24
142	Cohesin Members Stag1 and Stag2 Display Distinct Roles in Chromatin Accessibility and Topological Control of HSC Self-Renewal and Differentiation. <i>Cell Stem Cell</i> , 2019 , 25, 682-696.e8	18	48
141	Highly structured homolog pairing reflects functional organization of the Drosophila genome. <i>Nature Communications</i> , 2019 , 10, 4485	17.4	26
140	Rapid Irreversible Transcriptional Reprogramming in Human Stem Cells Accompanied by Discordance between Replication Timing and Chromatin Compartment. <i>Stem Cell Reports</i> , 2019 , 13, 193-206	8	16
139	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , 2019 , 570, 395-399	50.4	236
138	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019 , 20, 57	18.3	62
137	Extensive Heterogeneity and Intrinsic Variation in Spatial Genome Organization. <i>Cell</i> , 2019 , 176, 1502-1515.e10	15.2	121
136	The genome-wide multi-layered architecture of chromosome pairing in early Drosophila embryos. <i>Nature Communications</i> , 2019 , 10, 4486	17.4	16
135	A chromosome folding intermediate at the condensin-to-cohesin transition during telophase. <i>Nature Cell Biology</i> , 2019 , 21, 1393-1402	23.4	82
134	The non-canonical SMC protein SmcHD1 antagonises TAD formation and compartmentalisation on the inactive X chromosome. <i>Nature Communications</i> , 2019 , 10, 30	17.4	56
133	CTCF sites display cell cycle-dependent dynamics in factor binding and nucleosome positioning. <i>Genome Research</i> , 2019 , 29, 236-249	9.7	58
132	A pathway for mitotic chromosome formation. <i>Science</i> , 2018 , 359,	33.3	352

131	C-BERST: defining subnuclear proteomic landscapes at genomic elements with dCas9-APEX2. <i>Nature Methods</i> , 2018 , 15, 433-436	21.6	67
130	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , 2018 , 72, 715-726.e3	17.6	39
129	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. <i>Nature Genetics</i> , 2018 , 50, 1744-1751	36.3	90
128	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018 , 50, 1388-1398	36.3	147
127	CBF β MMHC Inhibition Triggers Apoptosis by Disrupting MYC Chromatin Dynamics in Acute Myeloid Leukemia. <i>Cell</i> , 2018 , 174, 172-186.e21	56.2	37
126	Polycomb Repressive Complex 1 Generates Discrete Compacted Domains that Change during Differentiation. <i>Molecular Cell</i> , 2017 , 65, 432-446.e5	17.6	180
125	Epigenetic characteristics of the mitotic chromosome in 1D and 3D. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017 , 52, 185-204	8.7	20
124	Hi-C 2.0: An optimized Hi-C procedure for high-resolution genome-wide mapping of chromosome conformation. <i>Methods</i> , 2017 , 123, 56-65	4.6	130
123	Shelterin components mediate genome reorganization in response to replication stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 5479-5484	11.5	10
122	Targeted Degradation of CTCF Decouples Local Insulation of Chromosome Domains from Genomic Compartmentalization. <i>Cell</i> , 2017 , 169, 930-944.e22	56.2	845
121	SMC complexes differentially compact mitotic chromosomes according to genomic context. <i>Nature Cell Biology</i> , 2017 , 19, 1071-1080	23.4	87
120	The 4D nucleome project. <i>Nature</i> , 2017 , 549, 219-226	50.4	332
119	The cluster is a dynamic and resilient TAD boundary controlling the segregation of antagonistic regulatory landscapes. <i>Genes and Development</i> , 2017 , 31, 2264-2281	12.6	90
118	CBF β MMHC Inhibition Disrupts Enhancer Chromatin Dynamics and Represses MYC Transcriptional Program in Inv(16) Leukemia. <i>Blood</i> , 2017 , 130, 784-784	2.2	
117	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 1389-1397	6	43
116	Mapping the 3D genome: Aiming for consilience. <i>Nature Reviews Molecular Cell Biology</i> , 2016 , 17, 741-7428.7	48.7	40
115	Structural organization of the inactive X chromosome in the mouse. <i>Nature</i> , 2016 , 535, 575-9	50.4	261
114	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. <i>Genome Research</i> , 2016 , 26, 1188-201	9.7	64

113	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016 , 351, 1454-1458	358	600
112	The 3D Genome as Moderator of Chromosomal Communication. <i>Cell</i> , 2016 , 164, 1110-1121	56.2	558
111	Invariant TAD Boundaries Constrain Cell-Type-Specific Looping Interactions between Promoters and Distal Elements around the CFTR Locus. <i>American Journal of Human Genetics</i> , 2016 , 98, 185-201	11	91
110	Genetics and Genomics of Longitudinal Lung Function Patterns in Individuals with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016 , 194, 1465-1474	10.2	18
109	Crystal structure of the DNA binding domain of the transcription factor T-bet suggests simultaneous recognition of distant genome sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E6572-E6581	11.5	11
108	CTCF-mediated topological boundaries during development foster appropriate gene regulation. <i>Genes and Development</i> , 2016 , 30, 2657-2662	12.6	107
107	A Guide to Packing Your DNA. <i>Cell</i> , 2016 , 165, 259-61	56.2	2
106	Extremely Long-Range Chromatin Loops Link Topological Domains to Facilitate a Diverse Antibody Repertoire. <i>Cell Reports</i> , 2016 , 14, 896-906	10.6	41
105	Local Genome Topology Can Exhibit an Incompletely Rewired 3D-Folding State during Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2016 , 18, 611-24	18	92
104	TAD disruption as oncogenic driver. <i>Current Opinion in Genetics and Development</i> , 2016 , 36, 34-40	4.9	127
103	Patterns of Growth and Decline in Lung Function in Persistent Childhood Asthma. <i>New England Journal of Medicine</i> , 2016 , 374, 1842-1852	59.2	312
102	Condensin promotes the juxtaposition of DNA flanking its loading site in <i>Bacillus subtilis</i> . <i>Genes and Development</i> , 2015 , 29, 1661-75	12.6	150
101	Hi-C in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 649-61	1.2	14
100	Measuring Chromatin Structure in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 614-8	1.2	2
99	Chromosome Conformation Capture Carbon Copy (5C) in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 593-8	1.2	4
98	Randomized ligation control for chromosome conformation capture. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 587-92	1.2	4
97	Mapping Nucleosome Resolution Chromosome Folding in Yeast by Micro-C. <i>Cell</i> , 2015 , 162, 108-19	56.2	341
96	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, 146-62	17.6	58

95	Long-Range Chromatin Interactions. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015 , 7, a019356	10.2	147
94	The yeast genome undergoes significant topological reorganization in quiescence. <i>Nucleic Acids Research</i> , 2015 , 43, 8299-313	20.1	53
93	Chromosome Conformation Capture (3C) in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 580-6	1.2	10
92	Genome-wide maps of nuclear lamina interactions in single human cells. <i>Cell</i> , 2015 , 163, 134-47	56.2	291
91	Structural and functional diversity of Topologically Associating Domains. <i>FEBS Letters</i> , 2015 , 589, 2877-848	3.4	186
90	The Hitchhiker's guide to Hi-C analysis: practical guidelines. <i>Methods</i> , 2015 , 72, 65-75	4.6	209
89	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. <i>Cell Reports</i> , 2015 , 13, 1855-67	10.6	23
88	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. <i>Genome Biology</i> , 2015 , 16, 214	18.3	123
87	Condensin-driven remodelling of X chromosome topology during dosage compensation. <i>Nature</i> , 2015 , 523, 240-4	50.4	501
86	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. <i>Genome Biology</i> , 2015 , 16, 259	18.3	811
85	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. <i>Genome Research</i> , 2015 , 25, 504-13	9.7	106
84	Predictive polymer modeling reveals coupled fluctuations in chromosome conformation and transcription. <i>Cell</i> , 2014 , 157, 950-63	56.2	321
83	Cohesin-dependent globules and heterochromatin shape 3D genome architecture in <i>S. pombe</i> . <i>Nature</i> , 2014 , 516, 432-435	50.4	188
82	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3366	11.5	22
81	Two ways to fold the genome during the cell cycle: insights obtained with chromosome conformation capture. <i>Epigenetics and Chromatin</i> , 2014 , 7, 25	5.8	60
80	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6131-8	11.5	490
79	Segmental folding of chromosomes: a basis for structural and regulatory chromosomal neighborhoods?. <i>BioEssays</i> , 2013 , 35, 818-28	4.1	136
78	Organization of the mitotic chromosome. <i>Science</i> , 2013 , 342, 948-53	33.3	654

77	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013 , 23, 2066-77	9.7	232
76	Flexible ordering of antibody class switch and V(D)J joining during B-cell ontogeny. <i>Genes and Development</i> , 2013 , 27, 2439-44	12.6	34
75	High-throughput genome scaffolding from in vivo DNA interaction frequency. <i>Nature Biotechnology</i> , 2013 , 31, 1143-7	44.5	120
74	Correlated alterations in genome organization, histone methylation, and DNA-lamin A/C interactions in Hutchinson-Gilford progeria syndrome. <i>Genome Research</i> , 2013 , 23, 260-9	9.7	234
73	The hierarchy of the 3D genome. <i>Molecular Cell</i> , 2013 , 49, 773-82	17.6	512
72	Nuclear biology: what's been most surprising?. <i>Cell</i> , 2013 , 152, 1207-8	56.2	2
71	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. <i>Nature Reviews Genetics</i> , 2013 , 14, 390-403	30.1	762
70	Architectural protein subclasses shape 3D organization of genomes during lineage commitment. <i>Cell</i> , 2013 , 153, 1281-95	56.2	848
69	Hi-C: a comprehensive technique to capture the conformation of genomes. <i>Methods</i> , 2012 , 58, 268-76	4.6	472
68	From cells to chromatin: capturing snapshots of genome organization with 5C technology. <i>Methods</i> , 2012 , 58, 255-67	4.6	33
67	The long-range interaction landscape of gene promoters. <i>Nature</i> , 2012 , 489, 109-13	50.4	1066
66	Spatial organization of the mouse genome and its role in recurrent chromosomal translocations. <i>Cell</i> , 2012 , 148, 908-21	56.2	411
65	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012 , 9, 999-1003	21.6	822
64	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012 , 489, 75-82	50.4	1900
63	Evidence for transcript networks composed of chimeric RNAs in human cells. <i>PLoS ONE</i> , 2012 , 7, e28213	3.7	51
62	Spatial partitioning of the regulatory landscape of the X-inactivation centre. <i>Nature</i> , 2012 , 485, 381-5	50.4	1894
61	CTCF and cohesin help neurons raise their self-awareness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 8799-800	11.5	5
60	MORC family ATPases required for heterochromatin condensation and gene silencing. <i>Science</i> , 2012 , 336, 1448-51	33.3	220

59	HiTC: exploration of high-throughput χ Sexperiments. <i>Bioinformatics</i> , 2012 , 28, 2843-4	7.2	119
58	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012 , 13, 418	18.3	340
57	Translocation mapping exposes the risky lifestyle of B cells. <i>Cell</i> , 2011 , 147, 20-2	56.2	2
56	The three-dimensional architecture of a bacterial genome and its alteration by genetic perturbation. <i>Molecular Cell</i> , 2011 , 44, 252-64	17.6	203
55	Three-Dimensional Architecture of Genomes 2011 , 211-234		
54	The three-dimensional folding of the β globin gene domain reveals formation of chromatin globules. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 107-14	17.6	232
53	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011 , 472, 120-4	50.4	1502
52	Chromatin globules: a common motif of higher order chromosome structure?. <i>Current Opinion in Cell Biology</i> , 2011 , 23, 325-31	9	56
51	Enhanced yeast one-hybrid assays for high-throughput gene-centered regulatory network mapping. <i>Nature Methods</i> , 2011 , 8, 1059-64	21.6	82
50	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011 , 8, 1050-2	21.6	41
49	Integrating Structural and Functional Studies Leads to a New Model of β Globin Activation That Suggests Distinct Initiation and Maintenance States. <i>Blood</i> , 2011 , 118, 349-349	2.2	
48	Mediator and cohesin connect gene expression and chromatin architecture. <i>Nature</i> , 2010 , 467, 430-5	50.4	1410
47	Genomics tools for unraveling chromosome architecture. <i>Nature Biotechnology</i> , 2010 , 28, 1089-95	44.5	176
46	Cell-type-specific long-range looping interactions identify distant regulatory elements of the CFTR gene. <i>Nucleic Acids Research</i> , 2010 , 38, 4325-36	20.1	84
45	Chemical genetic strategy identifies histone deacetylase 1 (HDAC1) and HDAC2 as therapeutic targets in sickle cell disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 12617-22	11.5	155
44	Integrating one-dimensional and three-dimensional maps of genomes. <i>Journal of Cell Science</i> , 2010 , 123, 1979-88	5.3	49
43	Sister cohesion and structural axis components mediate homolog bias of meiotic recombination. <i>Cell</i> , 2010 , 143, 924-37	56.2	183
42	Disease-causing 7.4 kb cis-regulatory deletion disrupting conserved non-coding sequences and their interaction with the FOXL2 promoter: implications for mutation screening. <i>PLoS Genetics</i> , 2009 , 5, e1000522	6	76

41	My5C: web tools for chromosome conformation capture studies. <i>Nature Methods</i> , 2009 , 6, 690-1	21.6	74
40	Comprehensive mapping of long-range interactions reveals folding principles of the human genome. <i>Science</i> , 2009 , 326, 289-93	33.3	4993
39	Mechanisms that regulate localization of a DNA double-strand break to the nuclear periphery. <i>Genes and Development</i> , 2009 , 23, 912-27	12.6	240
38	Yeast silent mating type loci form heterochromatic clusters through silencer protein-dependent long-range interactions. <i>PLoS Genetics</i> , 2009 , 5, e1000478	6	73
37	A mechanism for Ikaros regulation of human globin gene switching. <i>British Journal of Haematology</i> , 2008 , 141, 398-406	4.5	30
36	Gene regulation in the third dimension. <i>Science</i> , 2008 , 319, 1793-4	33.3	183
35	Long-range chromosomal interactions and gene regulation. <i>Molecular BioSystems</i> , 2008 , 4, 1046-57		147
34	Mapping in vivo chromatin interactions in yeast suggests an extended chromatin fiber with regional variation in compaction. <i>Journal of Biological Chemistry</i> , 2008 , 283, 34532-40	5.4	118
33	Polycomb response elements mediate the formation of chromosome higher-order structures in the bithorax complex. <i>Nature Cell Biology</i> , 2007 , 9, 1167-74	23.4	235
32	Mapping networks of physical interactions between genomic elements using 5C technology. <i>Nature Protocols</i> , 2007 , 2, 988-1002	18.8	163
31	Quantitative analysis of chromosome conformation capture assays (3C-qPCR). <i>Nature Protocols</i> , 2007 , 2, 1722-33	18.8	510
30	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
29	GC- and AT-rich chromatin domains differ in conformation and histone modification status and are differentially modulated by Rpd3p. <i>Genome Biology</i> , 2007 , 8, R116	18.3	47
28	Ikaros Drives Human Haemoglobin Switching by Facilitating Active Chromatin Hub Formation.. <i>Blood</i> , 2007 , 110, 1772-1772	2.2	
27	The active FMR1 promoter is associated with a large domain of altered chromatin conformation with embedded local histone modifications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12463-8	11.5	49
26	Chromosome Conformation Capture Carbon Copy (5C): a massively parallel solution for mapping interactions between genomic elements. <i>Genome Research</i> , 2006 , 16, 1299-309	9.7	824
25	The three 5Cs of chromosome conformation capture: controls, controls, controls. <i>Nature Methods</i> , 2006 , 3, 17-21	21.6	290
24	Proximity among distant regulatory elements at the beta-globin locus requires GATA-1 and FOG-1. <i>Molecular Cell</i> , 2005 , 17, 453-62	17.6	420

23	A mechanical basis for chromosome function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 12592-7	11.5	239
22	GATA-1 Directly Induces Physical Proximity between the LCR and β Globin Promoter in Erythroid Cells.. <i>Blood</i> , 2004 , 104, 1612-1612	2.2	
21	A closer look at long-range chromosomal interactions. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 277-80	10.3	56
20	Capturing chromosome conformation. <i>Science</i> , 2002 , 295, 1306-11	33.3	2589
19	Progression of meiotic DNA replication is modulated by interchromosomal interaction proteins, negatively by Spo11p and positively by Rec8p. <i>Genes and Development</i> , 2000 , 14, 493-503	12.6	164
18	ATP-independent DNA unwinding by the adenovirus single-stranded DNA binding protein requires a flexible DNA binding loop. <i>Journal of Molecular Biology</i> , 1998 , 277, 825-38	6.5	23
17	Multi-contact 3C data reveal that the human genome is largely unentangled		1
16	The non-canonical SMC protein SmcHD1 antagonises TAD formation on the inactive X chromosome		2
15	CTCF sites display cell cycle dependent dynamics in factor binding and nucleosome positioning		1
14	A chromosome folding intermediate at the condensin-to-cohesin transition during telophase		1
13	Detecting chromatin interactions along and between sister chromatids with SisterC		1
12	Spatial organization of transcribed eukaryotic genes		11
11	Chromosome-scale assembly of the coral endosymbiont <i>Symbiodinium microadriaticum</i> genome provides insight into the unique biology of dinoflagellate chromosomes		3
10	Chromosome-level assembly of the Atlantic silverside genome reveals extreme levels of sequence diversity and structural genetic variation		1
9	Systematic evaluation of chromosome conformation capture assays		5
8	Heterochromatin drives organization of conventional and inverted nuclei		19
7	Higher-Order Organization Principles of Pre-translational mRNPs		1
6	The genome-wide, multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos		3

5	Compartment-dependent chromatin interaction dynamics revealed by liquid chromatin Hi-C	14
4	A cohesin traffic pattern genetically linked to gene regulation	3
3	Biochemically distinct cohesin complexes mediate positioned loops between CTCF sites and dynamic loops within chromatin domains	4
2	Loops, TADs, Compartments, and Territories are Elastic and Robust to Dramatic Nuclear Volume Swelling	1
1	Heterochromatin diversity modulates genome compartmentalization and loop extrusion barriers	2