

Job Dekker

List of Articles by Year in descending order

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157

PR articles

39,297

PR citations

6980

74

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7960

147

g-index

181

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62327

citing authors

#	ARTICLE	IF	CITATIONS
1	TOP2B is required for compartment strength changes upon retinoic acid treatment in SH-SY5Y cells. <i>Chromosome Research</i> , 2025, 33, .	2.2	0
2	Rules of engagement for condensins and cohesins guide mitotic chromosome formation. <i>Science</i> , 2025, 388, .	36.2	37
3	Mitotic chromosomes harbor cell type- and species-specific structural features within a universal loop array conformation. <i>Genome Research</i> , 2025, 35, 1733-1744.	4.6	3
4	Enhancer-driven 3D chromatin domain folding modulates transcription in human mammary tumor cells. <i>Life Science Alliance</i> , 2024, 7, e202302154.	2.6	5
5	Chromosome evolution screens recapitulate tissue-specific tumor aneuploidy patterns. <i>Nature Genetics</i> , 2024, 56, 900-912.	25.2	46
6	Mitotic chromosomes are self-entangled and disentangle through a topoisomerase-II-dependent two-stage exit from mitosis. <i>Molecular Cell</i> , 2024, 84, 1422-1441.e14.	13.3	38
7	Polymer Physics Models Reveal Structural Folding Features of Single-Molecule Gene Chromatin Conformations. <i>International Journal of Molecular Sciences</i> , 2024, 25, 10215.	4.4	3
8	The chromosome folding problem and how cells solve it. <i>Cell</i> , 2024, 187, 6424-6450.	33.7	76
9	The little skate genome and the evolutionary emergence of wing-like fins. <i>Nature</i> , 2023, 616, 495-503.	37.9	63
10	Mechanisms of insertions at a DNA double-strand break. <i>Molecular Cell</i> , 2023, 83, 2434-2448.e7.	13.3	20
11	Multi-omics comparison of malignant and normal uveal melanocytes reveals molecular features of uveal melanoma. <i>Cell Reports</i> , 2023, 42, 113132.	6.3	18
12	RNA-mediated symmetry breaking enables singular olfactory receptor choice. <i>Nature</i> , 2023, 625, 181-188.	37.9	40
13	Revisiting chromatin packaging in mouse sperm. <i>Genome Research</i> , 2023, 33, 2079-2093.	4.6	30
14	Mechanisms of Chromosome Folding and Nuclear Organization: Their Interplay and Open Questions. <i>Cold Spring Harbor Perspectives in Biology</i> , 2022, 14, a040147.	7.2	108
15	Spatial organization of transcribed eukaryotic genes. <i>Nature Cell Biology</i> , 2022, 24, 327-339.	16.3	111
16	Loops, topologically associating domains, compartments, and territories are elastic and robust to dramatic nuclear volume swelling. <i>Scientific Reports</i> , 2022, 12, .	3.4	23
17	Chromosome-Level Reference Genomes for Two Strains of <i>Caenorhabditis briggsae</i> : An Improved Platform for Comparative Genomics. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.4	36
18	Nutritional control regulates symbiont proliferation and life history in coral-dinoflagellate symbiosis. <i>BMC Biology</i> , 2022, 20, .	3.9	32

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19	Cohesin-mediated loop anchors confine the locations of human replication origins. <i>Nature</i> , 2022, 606, 812-819.	37.9	114
20	CTCF–CTCF loops and intra-TAD interactions show differential dependence on cohesin ring integrity. <i>Nature Cell Biology</i> , 2022, 24, 1516-1527.	16.3	59
21	Regulation of the mitotic chromosome folding machines. <i>Biochemical Journal</i> , 2022, 479, 2153-2173.	3.8	8
22	Multiscale reorganization of the genome following DNA damage facilitates chromosome translocations via nuclear actin polymerization. <i>Nature Structural and Molecular Biology</i> , 2022, 30, 99-106.	8.8	64
23	A cohesin traffic pattern genetically linked to gene regulation. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 1239-1251.	8.8	74
24	Diverse silent chromatin states modulate genome compartmentalization and loop extrusion barriers. <i>Nature Structural and Molecular Biology</i> , 2022, 30, 38-51.	8.8	116
25	Liquid chromatin Hi-C characterizes compartment-dependent chromatin interaction dynamics. <i>Nature Genetics</i> , 2021, 53, 367-378.	25.2	126
26	Cohesin mutations alter DNA damage repair and chromatin structure and create therapeutic vulnerabilities in MDS/AML. <i>JCI Insight</i> , 2021, 6, .	5.4	79
27	Genetic and spatial organization of the unusual chromosomes of the dinoflagellate <i>Symbiodinium microadriaticum</i> . <i>Nature Genetics</i> , 2021, 53, 618-629.	25.2	80
28	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, .	2.4	36
29	<i>Symbiodinium microadriaticum</i> (coral microalgal endosymbiont). <i>Trends in Genetics</i> , 2021, 37, 1044-1045.	9.8	6
30	Systematic evaluation of chromosome conformation capture assays. <i>Nature Methods</i> , 2021, 18, 1046-1055.	24.6	227
31	Inner nuclear protein MatrIn-3 coordinates cell differentiation by stabilizing chromatin architecture. <i>Nature Communications</i> , 2021, 12, .	13.7	41
32	Transcriptional Silencers in <i>Drosophila</i> Serve a Dual Role as Transcriptional Enhancers in Alternate Cellular Contexts. <i>Molecular Cell</i> , 2020, 77, 324-337.e8.	13.3	120
33	Detecting chromatin interactions between and along sister chromatids with SisterC. <i>Nature Methods</i> , 2020, 17, 1002-1009.	24.6	48
34	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	37.9	2,189
35	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.	8.8	86
36	rad21 Is Involved in Corneal Stroma Development by Regulating Neural Crest Migration. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7807.	4.4	5

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37	Ultrastructural Details of Mammalian Chromosome Architecture. <i>Molecular Cell</i> , 2020, 78, 554-565.e7.	13.3	571
38	Mechanisms and Functions of Chromosome Compartmentalization. <i>Trends in Biochemical Sciences</i> , 2020, 45, 385-396.	6.7	269
39	SPEN integrates transcriptional and epigenetic control of X-inactivation. <i>Nature</i> , 2020, 578, 455-460.	37.9	193
40	Clustering of strong replicators associated with active promoters is sufficient to establish an early replicating domain. <i>EMBO Journal</i> , 2020, 39, .	7.3	13
41	The genome-wide multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos. <i>Nature Communications</i> , 2019, 10, .	13.7	56
42	A chromosome folding intermediate at the condensin-to-cohesin transition during telophase. <i>Nature Cell Biology</i> , 2019, 21, 1393-1402.	16.3	203
43	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.	16.4	151
44	Highly structured homolog pairing reflects functional organization of the <i>Drosophila</i> genome. <i>Nature Communications</i> , 2019, 10, .	13.7	69
45	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.	4.4	33
46	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , 2019, 570, 395-399.	37.9	640
47	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019, 20, .	8.1	169
48	Extensive Heterogeneity and Intrinsic Variation in Spatial Genome Organization. <i>Cell</i> , 2019, 176, 1502-1515.e10.	33.7	453
49	The non-canonical SMC protein SmcHD1 antagonises TAD formation and compartmentalisation on the inactive X chromosome. <i>Nature Communications</i> , 2019, 10, .	13.7	110
50	CTCF sites display cell cycle-dependent dynamics in factor binding and nucleosome positioning. <i>Genome Research</i> , 2019, 29, 236-249.	4.6	137
51	A pathway for mitotic chromosome formation. <i>Science</i> , 2018, 359, .	36.2	757
52	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , 2018, 72, 715-726.e3.	13.3	78
53	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018, 50, 1388-1398.	25.2	347
54	3C-Based Chromatin Interaction Analyses. <i>Cold Spring Harbor Protocols</i> , 2018, 2018, pdb.top097832.	0.3	13

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55	CBF $\hat{2}$ -SMMHC Inhibition Triggers Apoptosis by Disrupting MYC Chromatin Dynamics in Acute Myeloid Leukemia. <i>Cell</i> , 2018, 174, 172-186.e21.	33.7	83
56	C-BERST: defining subnuclear proteomic landscapes at genomic elements with dCas9 \hat{A} APEX2. <i>Nature Methods</i> , 2018, 15, 433-436.	24.6	144
57	Polycomb Repressive Complex 1 Generates Discrete Compacted Domains that Change during Differentiation. <i>Molecular Cell</i> , 2017, 65, 432-446.e5.	13.3	331
58	Epigenetic characteristics of the mitotic chromosome in 1D and 3D. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017, 52, 185-204.	6.7	31
59	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.	3.5	301
60	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.	7.5	17
61	Targeted Degradation of CTCF Decouples Local Insulation of Chromosome Domains from Genomic Compartmentalization. <i>Cell</i> , 2017, 169, 930-944.e22.	33.7	1,732
62	SMC complexes differentially compact mitotic chromosomes according to genomic context. <i>Nature Cell Biology</i> , 2017, 19, 1071-1080.	16.3	154
63	The HoxD cluster is a dynamic and resilient TAD boundary controlling the segregation of antagonistic regulatory landscapes. <i>Genes and Development</i> , 2017, 31, 2264-2281.	4.6	179
64	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.	8.9	23
65	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, .	7.5	26
66	CTCF-mediated topological boundaries during development foster appropriate gene regulation. <i>Genes and Development</i> , 2016, 30, 2657-2662.	4.6	181
67	A Guide to Packing Your DNA. <i>Cell</i> , 2016, 165, 259-261.	33.7	2
68	Extremely Long-Range Chromatin Loops Link Topological Domains to Facilitate a Diverse Antibody Repertoire. <i>Cell Reports</i> , 2016, 14, 896-906.	6.3	86
69	Local Genome Topology Can Exhibit an Incompletely Rewired 3D-Folding State during Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2016, 18, 611-624.	16.4	131
70	TAD disruption as oncogenic driver. <i>Current Opinion in Genetics and Development</i> , 2016, 36, 34-40.	3.2	252
71	Patterns of Growth and Decline in Lung Function in Persistent Childhood Asthma. <i>New England Journal of Medicine</i> , 2016, 374, 1842-1852.	34.6	554
72	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.	2.4	73

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73	Structural organization of the inactive X chromosome in the mouse. <i>Nature</i> , 2016, 535, 575-579.	37.9	423
74	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. <i>Genome Research</i> , 2016, 26, 1188-1201.	4.6	106
75	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.	6.5	147
76	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. <i>Cell Reports</i> , 2015, 13, 1855-1867.	6.3	42
77	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. <i>Genome Biology</i> , 2015, 16, .	8.1	239
78	Condensin-driven remodelling of X chromosome topology during dosage compensation. <i>Nature</i> , 2015, 523, 240-244.	37.9	972
79	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. <i>Genome Research</i> , 2015, 25, 504-513.	4.6	161
80	Condensin promotes the juxtaposition of DNA flanking its loading site in <i>Bacillus subtilis</i> . <i>Genes and Development</i> , 2015, 29, 1661-1675.	4.6	260
81	Hi-C in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot085209.	0.3	22
82	Measuring Chromatin Structure in Budding Yeast: Figure 1.. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.top077552.	0.3	4
83	Chromosome Conformation Capture Carbon Copy (5C) in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot085191.	0.3	5
84	Randomized Ligation Control for Chromosome Conformation Capture. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot085183.	0.3	4
85	Mapping Nucleosome Resolution Chromosome Folding in Yeast by Micro-C. <i>Cell</i> , 2015, 162, 108-119.	33.7	738
86	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.	13.3	84
87	Long-Range Chromatin Interactions. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a019356.	7.2	258
88	The yeast genome undergoes significant topological reorganization in quiescence. <i>Nucleic Acids Research</i> , 2015, 43, 8299-8313.	15.5	81
89	Chromosome Conformation Capture (3C) in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot085175.	0.3	12
90	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. <i>Cell</i> , 2015, 163, 134-147.	33.7	476

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91	Structural and functional diversity of Topologically Associating Domains. <i>FEBS Letters</i> , 2015, 589, 2877-2884.	2.7	313
92	The Hitchhiker's guide to Hi-C analysis: Practical guidelines. <i>Methods</i> , 2015, 72, 65-75.	3.5	406
93	Two ways to fold the genome during the cell cycle: insights obtained with chromosome conformation capture. <i>Epigenetics and Chromatin</i> , 2014, 7, .	3.2	73
94	Predictive Polymer Modeling Reveals Coupled Fluctuations in Chromosome Conformation and Transcription. <i>Cell</i> , 2014, 157, 950-963.	33.7	451
95	Cohesin-dependent globules and heterochromatin shape 3D genome architecture in <i>S. pombe</i> . <i>Nature</i> , 2014, 516, 432-435.	37.9	289
96	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, .	7.5	25
97	Segmental folding of chromosomes: A basis for structural and regulatory chromosomal neighborhoods?. <i>BioEssays</i> , 2013, 35, 818-828.	2.1	172
98	Organization of the Mitotic Chromosome. <i>Science</i> , 2013, 342, 948-953.	36.2	1,027
99	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013, 23, 2066-2077.	4.6	299
100	Flexible ordering of antibody class switch and V(D)J joining during B-cell ontogeny. <i>Genes and Development</i> , 2013, 27, 2439-2444.	4.6	47
101	High-throughput genome scaffolding from in vivo DNA interaction frequency. <i>Nature Biotechnology</i> , 2013, 31, 1143-1147.	29.8	197
102	Correlated alterations in genome organization, histone methylation, and DNA-lamin A/C interactions in Hutchinson-Gilford progeria syndrome. <i>Genome Research</i> , 2013, 23, 260-269.	4.6	307
103	The Hierarchy of the 3D Genome. <i>Molecular Cell</i> , 2013, 49, 773-782.	13.3	693
104	Nuclear Biology: What's Been Most Surprising?. <i>Cell</i> , 2013, 152, 1207-1208.	33.7	3
105	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. <i>Nature Reviews Genetics</i> , 2013, 14, 390-403.	47.0	1,052
106	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. <i>Cell</i> , 2013, 153, 1281-1295.	33.7	1,160
107	HiTC: exploration of high-throughput Hi-C experiments. <i>Bioinformatics</i> , 2012, 28, 2843-2844.	4.7	198
108	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, .	8.1	437

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109	Hi-C: A comprehensive technique to capture the conformation of genomes. <i>Methods</i> , 2012, 58, 268-276.	3.5	1,142
110	From cells to chromatin: Capturing snapshots of genome organization with 5C technology. <i>Methods</i> , 2012, 58, 255-267.	3.5	44
111	Analysis of long-range chromatin interactions using Chromosome Conformation Capture. <i>Methods</i> , 2012, 58, 192-203.	3.5	154
112	The long-range interaction landscape of gene promoters. <i>Nature</i> , 2012, 489, 109-113.	37.9	1,420
113	Spatial Organization of the Mouse Genome and Its Role in Recurrent Chromosomal Translocations. <i>Cell</i> , 2012, 148, 908-921.	33.7	523
114	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012, 9, 999-1003.	24.6	1,420
115	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	37.9	2,636
116	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	2.3	62
117	The context of gene expression regulation. <i>F1000 Biology Reports</i> , 2012, 4, .	2.2	24
118	Spatial partitioning of the regulatory landscape of the X-inactivation centre. <i>Nature</i> , 2012, 485, 381-385.	37.9	2,977
119	Enhanced yeast one-hybrid assays for high-throughput gene-centered regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1059-1064.	24.6	134
120	The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation. <i>Molecular Cell</i> , 2011, 44, 252-264.	13.3	267
121	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011, 472, 120-124.	37.9	1,883
122	Chromatin globules: a common motif of higher order chromosome structure?. <i>Current Opinion in Cell Biology</i> , 2011, 23, 325-331.	3.9	65
123	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1050-1052.	24.6	51
124	Integrating Structural and Functional Studies Leads to a New Model of β^2 -Globin Activation That Suggests Distinct Initiation and Maintenance States. <i>Blood</i> , 2011, 118, 349-349.	4.2	0
125	Hi-C: A Method to Study the Three-dimensional Architecture of Genomes.. <i>Journal of Visualized Experiments</i> , 2010, , .	0.3	359
126	Mediator and cohesin connect gene expression and chromatin architecture. <i>Nature</i> , 2010, 467, 430-435.	37.9	1,846

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127	Genomics tools for unraveling chromosome architecture. <i>Nature Biotechnology</i> , 2010, 28, 1089-1095.	29.8	210
128	Cell-type-specific long-range looping interactions identify distant regulatory elements of the CFTR gene. <i>Nucleic Acids Research</i> , 2010, 38, 4325-4336.	15.5	101
129	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, 12617-12622.	7.5	195
130	Sister Cohesion and Structural Axis Components Mediate Homolog Bias of Meiotic Recombination. <i>Cell</i> , 2010, 143, 924-937.	33.7	274
131	Disease-Causing 7.4 kb Cis-Regulatory Deletion Disrupting Conserved Non-Coding Sequences and Their Interaction with the FOXL2 Promotor: Implications for Mutation Screening. <i>PLoS Genetics</i> , 2009, 5, e1000522.	3.2	85
132	Gene dates, parties and galas. <i>EMBO Reports</i> , 2009, 10, 689-693.	5.2	3
133	My5C: web tools for chromosome conformation capture studies. <i>Nature Methods</i> , 2009, 6, 690-691.	24.6	87
134	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. <i>Science</i> , 2009, 326, 289-293.	36.2	8,581
135	Mechanisms that regulate localization of a DNA double-strand break to the nuclear periphery. <i>Genes and Development</i> , 2009, 23, 912-927.	4.6	304
136	Yeast Silent Mating Type Loci Form Heterochromatic Clusters through Silencer Protein-Dependent Long-Range Interactions. <i>PLoS Genetics</i> , 2009, 5, e1000478.	3.2	94
137	A mechanism for Ikaros regulation of human globin gene switching. <i>British Journal of Haematology</i> , 2008, 141, 398-406.	2.7	36
138	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, 34532-34540.	2.2	147
139	Chromosome Conformation Capture Carbon Copy Technology. <i>Current Protocols in Molecular Biology</i> , 2007, 80, .	0.0	40
140	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.	12.2	67
141	Polycomb response elements mediate the formation of chromosome higher-order structures in the bithorax complex. <i>Nature Cell Biology</i> , 2007, 9, 1167-1174.	16.3	277
142	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	37.9	4,877
143	Ikaros Drives Human Haemoglobin Switching by Facilitating Active Chromatin Hub Formation.. <i>Blood</i> , 2007, 110, 1772-1772.	4.2	0
144	Chromosome Conformation Capture Carbon Copy (5C): A massively parallel solution for mapping interactions between genomic elements. <i>Genome Research</i> , 2006, 16, 1299-1309.	4.6	1,110

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145	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, 12463-12468.	7.5	52
146	Proximity among Distant Regulatory Elements at the β -Globin Locus Requires GATA-1 and FOG-1. Molecular Cell, 2005, 17, 453-462.	13.3	467
147	A mechanical basis for chromosome function. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12592-12597.	7.5	306
148	A closer look at long-range chromosomal interactions. Trends in Biochemical Sciences, 2003, 28, 277-280.	6.7	57
149	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.	4.6	215
150	ATP-independent DNA unwinding by the adenovirus single-stranded DNA binding protein requires a flexible DNA binding loop 1 Edited by M. Yaniv. Journal of Molecular Biology, 1998, 277, 825-838.	4.1	23
151	Multimerization of the adenovirus DNA-binding protein is the driving force for ATP-independent DNA unwinding during strand displacement synthesis. EMBO Journal, 1997, 16, 1455-1463.	7.3	47
152	Linker histone H1.8 inhibits chromatin binding of condensins and DNA topoisomerase II to tune chromosome length and individualization. ELife, 0, 10, .	1.6	44
153	Large domains of heterochromatin direct the formation of short mitotic chromosome loops. ELife, 0, 9, .	1.6	12
154	Mitotic chromosomes scale to nuclear-cytoplasmic ratio and cell size in Xenopus. ELife, 0, 12, .	1.6	17
155	mRNA initiation and termination are spatially coordinated. Science, 0, 390, .	36.2	4
156	An integrated view of the structure and function of the human 4D nucleome. Nature, 0, 649, 759-776.	37.9	2
157	Interphase chromosome conformation is specified by distinct folding programmes inherited through mitotic chromosomes or the cytoplasm. Nature Cell Biology, 0, 28, 82-97.	16.3	3