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**Comprehensive mapping of long-range interactions reveals folding principles of the human genome**

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2211	Current world literature. <b>2010</b> , 17, 568-80		
2210	Intra- and inter-chromosomal interactions correlate with CTCF binding genome wide. <b>2010</b> , 6, 426		85
2209	Next generation sequencing: advances in characterizing the methylome. <b>2010</b> , 1, 143-65		3
2208	Mapping chromatin conformation. <b>2010</b> , 2,		5
2207	Hi-C: a method to study the three-dimensional architecture of genomes. <b>2010</b> ,		212
2206	Early Career Research Award Lecture. Structure, evolution and dynamics of transcriptional regulatory networks. <b>2010</b> , 38, 1155-78		18
2205	FRACTALS WITH POINT IMPACT IN FUNCTIONAL LINEAR REGRESSION. <b>2010</b> , 38, 2559-2586		26
2204	Chromatin dynamics. <b>2010</b> , 39, 471-89		125

2203	Space and time in the nucleus: developmental control of replication timing and chromosome architecture. <b>2010</b> , 75, 143-53	79
2202	Window into the complexities of chromosome interactomes. <b>2010</b> , 75, 493-500	5
2201	In junk we trust: repetitive DNA, epigenetics and facioscapulohumeral muscular dystrophy. <b>2010</b> , 2, 271-87	24
2200	DNA curvature and flexibility in vitro and in vivo. <b>2010</b> , 43, 23-63	177
2199	Evolutionary origin of the cell nucleus and its functional architecture. <b>2010</b> , 48, 1-24	20
2198	Summary: The nucleus--a close-knit community of dynamic structures. <b>2010</b> , 75, 607-15	3
2197	Codon populations in single-stranded whole human genome DNA Are fractal and fine-tuned by the Golden Ratio 1.618. <b>2010</b> , 2, 228-40	23
2196	Interchromosomal association and gene regulation in trans. <b>2010</b> , 26, 188-97	72
2195	Genome3D: a viewer-model framework for integrating and visualizing multi-scale epigenomic information within a three-dimensional genome. <b>2010</b> , 11, 444	27
2194	Epigenetic domains found in mouse embryonic stem cells via a hidden Markov model. <b>2010</b> , 11, 557	14
2193	Human transcriptional interactome of chromatin contribute to gene co-expression. <b>2010</b> , 11, 704	18
2192	Fractal dimension of chromatin is an independent prognostic factor for survival in melanoma. <b>2010</b> , 10, 260	55
2191	Nature or nurture: let food be your epigenetic medicine in chronic inflammatory disorders. <b>2010</b> , 80, 1816-32	106
2190	Genome architecture and the role of transcription. <b>2010</b> , 22, 271-6	41
2189	Yeast chromosomal interactions and nuclear architecture. <b>2010</b> , 22, 298-304	3
2188	Genomic neighbourhood and the regulation of gene expression. <b>2010</b> , 22, 326-33	43
2187	3D shortcuts to gene regulation. <b>2010</b> , 22, 305-13	28
2186	Genomic Pangea: coordinate gene regulation and cell-specific chromosomal topologies. <b>2010</b> , 22, 314-9	8

2185	Binding of the Rett syndrome protein, MeCP2, to methylated and unmethylated DNA and chromatin. <b>2010</b> , 62, 732-8	73
2184	Genome size, self-organization and DNA's dark matter. <b>2010</b> , 16, 20-23	106
2183	Form and function of dosage-compensated chromosomes--a chicken-and-egg relationship. <b>2010</b> , 32, 709-17	8
2182	Conformational and Dynamical Properties of the Isolated, Three-Dimensional Single- and Double-Tethered Polymer Chain on an Infinite Surface. <b>2010</b> , 19, 440-448	5
2181	Maintaining cell identity through global control of genomic organization. <b>2010</b> , 33, 12-24	156
2180	Regulation of the Ifng locus in the context of T-lineage specification and plasticity. <b>2010</b> , 238, 216-32	43
2179	Advances in the understanding of haemoglobin switching. <b>2010</b> , 149, 181-94	153
2178	Fractal geometry in the nucleus. <b>2010</b> , 29, 2-3	38
2177	A three-dimensional model of the yeast genome. <b>2010</b> , 465, 363-7	722
2176	GREAT improves functional interpretation of cis-regulatory regions. <b>2010</b> , 28, 495-501	2532
2175	Genomics tools for unraveling chromosome architecture. <b>2010</b> , 28, 1089-95	176
2174	Tackling the epigenome: challenges and opportunities for collaboration. <b>2010</b> , 28, 1039-44	73
2173	Epigenomics reveals a functional genome anatomy and a new approach to common disease. <b>2010</b> , 28, 1049-52	92
2172	Getting connected in the globin interactome. <b>2010</b> , 42, 16-7	2
2171	Mapping genomes in 3D. <b>2010</b> , 7, 35-35	3
2170	Next-generation genomics: an integrative approach. <b>2010</b> , 11, 476-86	488
2169	Annotating non-coding regions of the genome. <b>2010</b> , 11, 559-71	303
2168	Triggers for genomic rearrangements: insights into genomic, cellular and environmental influences. <b>2010</b> , 11, 819-29	106

2167	The nuclear pore complex: bridging nuclear transport and gene regulation. <b>2010</b> , 11, 490-501	382
2166	Principles for the post-GWAS functional characterisation of risk loci. <b>2010</b> ,	1
2165	Differential DNA methylation correlates with differential expression of angiogenic factors in human heart failure. <b>2010</b> , 5, e8564	153
2164	Stable morphology, but dynamic internal reorganisation, of interphase human chromosomes in living cells. <b>2010</b> , 5, e11560	51
2163	Diffusion-driven looping provides a consistent framework for chromatin organization. <b>2010</b> , 5, e12218	135
2162	Analysis of $\beta$ globin chromatin micro-environment using a novel 3C variant, 4Cv. <b>2010</b> , 5, e13045	4
2161	A non-coding RNA within the Rasgrf1 locus in mouse is imprinted and regulated by its homologous chromosome in trans. <b>2010</b> , 5, e13784	12
2160	Nuclear architecture in stem cells. <b>2010</b> , 695, 14-25	2
2159	Epigenetics in humans: an overview. <b>2010</b> , 17, 493-9	26
2158	Distance between homologous chromosomes results from chromosome positioning constraints. <b>2010</b> , 123, 4063-75	53
2157	Functional nuclear organization of transcription and DNA replication: a topographical marriage between chromatin domains and the interchromatin compartment. <b>2010</b> , 75, 475-92	116
2156	G2 phase chromatin lacks determinants of replication timing. <b>2010</b> , 189, 967-80	33
2155	The effect of translocation-induced nuclear reorganization on gene expression. <b>2010</b> , 20, 554-64	78
2154	Into the unknown: expression profiling without genome sequence information in CHO by next generation sequencing. <b>2010</b> , 38, 3999-4010	90
2153	Changes in chromatin fiber density as a marker for pluripotency. <b>2010</b> , 75, 245-9	27
2152	Impact of nuclear organization and dynamics on epigenetic regulation in the central nervous system: implications for neurological disease states. <b>2010</b> , 1204 Suppl, E20-37	18
2151	Identification of $\beta$ -catenin binding regions in colon cancer cells using ChIP-Seq. <b>2010</b> , 38, 5735-45	129
2150	Cell-type-specific long-range looping interactions identify distant regulatory elements of the CFTR gene. <b>2010</b> , 38, 4325-36	84

2149	RNA dust: where are the genes?. <b>2010</b> , 17, 51-9	55
2148	The role of mechanistic factors in promoting chromosomal translocations found in lymphoid and other cancers. <b>2010</b> , 106, 93-133	97
2147	Matrix elasticity, cytoskeletal forces and physics of the nucleus: how deeply do cells 'feel' outside and in?. <b>2010</b> , 123, 297-308	307
2146	Vibrational shortcut to the mean-first-passage-time problem. <b>2010</b> , 81, 040103	17
2145	Histone modifications and chromatin organization in prostate cancer. <b>2010</b> , 2, 551-60	57
2144	Topological interactions between ring polymers: Implications for chromatin loops. <b>2010</b> , 132, 044904	57
2143	4D Chromatin dynamics in cycling cells. <b>2010</b> , 1, 284-297	67
2142	Upregulation of c-MYC in cis through a large chromatin loop linked to a cancer risk-associated single-nucleotide polymorphism in colorectal cancer cells. <b>2010</b> , 30, 1411-20	218
2141	Selection upon genome architecture: conservation of functional neighborhoods with changing genes. <b>2010</b> , 6, e1000953	42
2140	Polymorphic cis- and trans-regulation of human gene expression. <b>2010</b> , 8, e1000480	120
2139	Chromatin conformation signatures: ideal human disease biomarkers?. <b>2010</b> , 4, 611-29	34
2138	An in vitro model for Pelger-Huë anomaly: stable knockdown of lamin B receptor in HL-60 cells. <b>2010</b> , 1, 506-12	25
2137	Epigenetic remedies by dietary phytochemicals against inflammatory skin disorders: myth or reality?. <b>2010</b> , 11, 436-50	7
2136	Cell-survival probability at large doses: an alternative to the linear-quadratic model. <b>2010</b> , 55, 4687-702	38
2135	Cell fate transitions and the replication timing decision point. <b>2010</b> , 191, 899-903	26
2134	Nucleosome positioning, gene regulation and disease. <b>2010</b> , 2, 351-4	1
2133	Chromosome conformation by crosslinking: polymer physics matters. <b>2010</b> , 1, 37-9	8
2132	Next-generation sequencing techniques for eukaryotic microorganisms: sequencing-based solutions to biological problems. <b>2010</b> , 9, 1300-10	106

2131	ERG rearrangement is specific to prostate cancer and does not occur in any other common tumor. <b>2010</b> , 23, 1061-7	97
2130	Active RNA polymerases: mobile or immobile molecular machines?. <b>2010</b> , 8, e1000419	76
2129	Spatial epigenetics: linking nuclear structure and function in higher eukaryotes. <b>2010</b> , 48, 25-43	7
2128	Comparative analysis of DNA replication timing reveals conserved large-scale chromosomal architecture. <b>2010</b> , 6, e1001011	124
2127	Looping probabilities in model interphase chromosomes. <b>2010</b> , 98, 2410-9	90
2126	Networking the nucleus. <b>2010</b> , 6, 395	14
2125	Chromatin folding: from linear chromosomes to the 4D nucleus. <b>2010</b> , 75, 461-73	7
2124	Fractal dimension of chromatin and cancer prognosis. <b>2010</b> , 2, 601-4	37
2123	Chromatin higher-order structure and dynamics. <b>2010</b> , 2, a000596	238
2122	Scaling properties and fractality in the distribution of coding segments in eukaryotic genomes revealed through a block entropy approach. <b>2010</b> , 82, 051917	8
2121	The role of transcription factories-mediated interchromosomal contacts in the organization of nuclear architecture. <b>2010</b> , 38, 7410-21	26
2120	Integrating one-dimensional and three-dimensional maps of genomes. <b>2010</b> , 123, 1979-88	49
2119	Epigenome mapping in normal and disease States. <b>2010</b> , 107, 327-39	124
2118	Regulatory regions in DNA: promoters, enhancers, silencers, and insulators. <b>2010</b> , 674, 33-42	62
2117	4D chromatin dynamics in cycling cells: Theodor Boveri's hypotheses revisited. <b>2010</b> , 1, 284-97	69
2116	Analysis of active and inactive X chromosome architecture reveals the independent organization of 30 nm and large-scale chromatin structures. <b>2010</b> , 40, 397-409	57
2115	The transcriptional interactome: gene expression in 3D. <b>2010</b> , 20, 127-33	120
2114	Epimutations and cancer predisposition: importance and mechanisms. <b>2010</b> , 20, 290-8	51

2113	Differentiation and large scale spatial organization of the genome. <b>2010</b> , 20, 562-9	58
2112	Origin of chromosomal translocations in lymphoid cancer. <b>2010</b> , 141, 27-38	226
2111	Regulation of replication termination by Reb1 protein-mediated action at a distance. <b>2010</b> , 142, 868-78	20
2110	The silence of the LADs: dynamic genome-lamina interactions during ESC differentiation. <b>2010</b> , 6, 495-7	7
2109	Multiple, interconvertible states of human pluripotent stem cells. <b>2010</b> , 6, 497-9	13
2108	The epigenetic role of non-coding RNA transcription and nuclear organization in immunoglobulin repertoire generation. <b>2010</b> , 22, 353-61	22
2107	Enhancers: the abundance and function of regulatory sequences beyond promoters. <b>2010</b> , 339, 250-7	142
2106	Insights into interphase large-scale chromatin structure from analysis of engineered chromosome regions. <b>2010</b> , 75, 453-60	19
2105	A CTCF-independent role for cohesin in tissue-specific transcription. <b>2010</b> , 20, 578-88	286
2104	Gene positioning. <b>2010</b> , 2, a000588	54
2103	Genome organization and function: a view from yeast and Arabidopsis. <b>2010</b> , 3, 678-90	23
2102	Mapping of long-range associations throughout the fission yeast genome reveals global genome organization linked to transcriptional regulation. <b>2010</b> , 38, 8164-77	188
2101	Evolutionarily conserved replication timing profiles predict long-range chromatin interactions and distinguish closely related cell types. <b>2010</b> , 20, 761-70	417
2100	Anomalous diffusion in the interphase cell nucleus: the effect of spatial correlations of chromatin. <b>2010</b> , 133, 025101	26
2099	Chromosome territories. <b>2010</b> , 2, a003889	753
2098	Functional nuclear architecture studied by microscopy: present and future. <b>2010</b> , 282, 1-90	79
2097	Physical plasticity of the nucleus and its manipulation. <b>2010</b> , 98, 207-20	11
2096	The Genomic HyperBrowser: inferential genomics at the sequence level. <b>2010</b> , 11, R121	70

2095	Capturing the dynamic epigenome. <b>2010</b> , 11, 218	39
2094	The Cell Biology of Stem Cells. <b>2010</b> ,	2
2093	Genetic and epigenetic dysregulation of imprinted genes in the brain. <b>2010</b> , 2, 743-63	15
2092	Genomics of long-range regulatory elements. <b>2010</b> , 11, 1-23	121
2091	The nucleus introduced. <b>2011</b> , 3,	26
2090	Harnessing cloud computing with Galaxy Cloud. <b>2011</b> , 29, 972-4	85
2089	The real cost of sequencing: higher than you think!. <b>2011</b> , 12, 125	247
2088	Identification of cis-regulatory sequence variations in individual genome sequences. <b>2011</b> , 3, 65	13
2087	Transcriptional regulation by miRNA mimics that target sequences downstream of gene termini. <b>2011</b> , 7, 2383-8	25
2086	Local and global epigenetic regulation of V(D)J recombination. <b>2012</b> , 356, 65-89	12
2085	Facilitated diffusion of proteins on chromatin. <b>2011</b> , 106, 038102	55
2084	Intermittent search strategies. <b>2011</b> , 83, 81-129	450
2083	Epigenetic signatures distinguish multiple classes of enhancers with distinct cellular functions. <b>2011</b> , 21, 1273-83	402
2082	Nuclear architecture in developmental biology and cell specialisation. <b>2011</b> , 23, 94-106	17
2081	Pathogenesis of chagas' disease: parasite persistence and autoimmunity. <b>2011</b> , 24, 592-630	148
2080	Simulation analysis of the temperature dependence of lignin structure and dynamics. <b>2011</b> , 133, 20277-87	100
2079	Diverse gene reprogramming events occur in the same spatial clusters of distal regulatory elements. <b>2011</b> , 21, 697-706	117
2078	Light-scattering technologies for field carcinogenesis detection: a modality for endoscopic prescreening. <b>2011</b> , 140, 35-41	38

2077	Control of eukaryotic gene expression: gene loops and transcriptional memory. <b>2011</b> , 51, 118-25	66
2076	Reprogramming to pluripotency: stepwise resetting of the epigenetic landscape. <b>2011</b> , 21, 486-501	137
2075	The Mitotic Chromosome: Structure and Mechanics. <b>2011</b> , 449-485	6
2074	Universality classes of first-passage-time distribution in confined media. <b>2011</b> , 83, 051116	36
2073	Thinking Holistically About Gene Transcription. <b>2011</b> , 189-205	
2072	Loops determine the mechanical properties of mitotic chromosomes. <b>2011</b> , 6, e29225	19
2071	Confinement driven spatial organization of semiflexible ring polymers: Implications for biopolymer packaging. <b>2011</b> , 7, 6906	22
2070	Innate structure of DNA foci restricts the mixing of DNA from different chromosome territories. <b>2011</b> , 6, e27527	11
2069	Crowding-induced structural alterations of random-loop chromosome model. <b>2011</b> , 106, 168102	47
2068	Nuclear visions enhanced: chromatin structure, organization and dynamics. <b>2011</b> , 12, 748-50	
2067	Large-scale nuclear architecture and transcriptional control. <b>2011</b> , 52, 279-95	4
2066	Meet the neighbours: tools to dissect nuclear structure and function. <b>2011</b> , 10, 11-7	9
2065	A Handbook of Transcription Factors. <b>2011</b> ,	11
2064	Mechanics of the nucleus. <b>2011</b> , 1, 783-807	100
2063	A transposon in tb1 drove maize domestication. <b>2011</b> , 43, 1048-50	12
2062	The influence of chromosome density variations on the increase in nuclear disorder strength in carcinogenesis. <b>2011</b> , 8, 015004	27
2061	Nuclear mechanics in disease. <b>2011</b> , 13, 397-428	97
2060	Modulated contact frequencies at gene-rich loci support a statistical helix model for mammalian chromatin organization. <b>2011</b> , 12, R42	19

2059	Mechanosignaling to the cell nucleus and gene regulation. <b>2011</b> , 40, 361-78	128
2058	High-resolution genome-wide mapping of the primary structure of chromatin. <b>2011</b> , 144, 175-86	129
2057	Functional and mechanistic diversity of distal transcription enhancers. <b>2011</b> , 144, 327-39	598
2056	Genome-wide translocation sequencing reveals mechanisms of chromosome breaks and rearrangements in B cells. <b>2011</b> , 147, 107-19	353
2055	Translocation mapping exposes the risky lifestyle of B cells. <b>2011</b> , 147, 20-2	2
2054	Epstein-Barr virus exploits intrinsic B-lymphocyte transcription programs to achieve immortal cell growth. <b>2011</b> , 108, 14902-7	146
2053	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. <b>2011</b> , 29, 1109-13	162
2052	Epigenetics in Male Reproduction: A Practical Introduction to the Informatics of Next Generation Sequencing. <b>2011</b> , 231-258	
2051	Enhancer-promoter communication and transcriptional regulation of Igh. <b>2011</b> , 32, 532-9	32
2050	Activation-induced cytidine deaminase induces reproducible DNA breaks at many non-Ig Loci in activated B cells. <b>2011</b> , 41, 232-42	75
2049	Direct interactions of OCA-B and TFII-I regulate immunoglobulin heavy-chain gene transcription by facilitating enhancer-promoter communication. <b>2011</b> , 42, 342-55	47
2048	Insulators organize chromatin: emerging rules of the game. <b>2011</b> , 44, 1-2	17
2047	The three-dimensional architecture of a bacterial genome and its alteration by genetic perturbation. <b>2011</b> , 44, 252-64	203
2046	Decoding the genome beyond sequencing: the new phase of genomic research. <b>2011</b> , 98, 242-52	73
2045	Distant cis-regulatory elements in human skeletal muscle differentiation. <b>2011</b> , 98, 401-11	10
2044	A novel application of pattern recognition for accurate SNP and indel discovery from high-throughput data: targeted resequencing of the glucocorticoid receptor co-chaperone FKBP5 in a Caucasian population. <b>2011</b> , 104, 457-69	13
2043	Androgen receptor-driven chromatin looping in prostate cancer. <b>2011</b> , 22, 474-80	38
2042	Mechanisms of specificity in neuronal activity-regulated gene transcription. <b>2011</b> , 94, 259-95	140

2041	Cell surface as a fractal: normal and cancerous cervical cells demonstrate different fractal behavior of surface adhesion maps at the nanoscale. <b>2011</b> , 107, 028101	62
2040	Regulatory variation within and between species. <b>2011</b> , 12, 327-46	52
2039	Electrostatic interactions in biological DNA-related systems. <b>2011</b> , 13, 9942-68	119
2038	Introduction and Historical Overview of DNA Sequencing. <b>2011</b> , 96, 7.0.1	1
2037	Three-Dimensional Architecture of Genomes. <b>2011</b> , 211-234	
2036	Higher Order Chromatin Organization and Dynamics. <b>2011</b> , 417-447	3
2035	The new landscape of protein ubiquitination. <b>2011</b> , 29, 1098-100	24
2034	An integrated strategy for identification of both sharp and broad peaks from next-generation sequencing data. <b>2011</b> , 12, 120	3
2033	DNA replication timing and long-range DNA interactions predict mutational landscapes of cancer genomes. <b>2011</b> , 29, 1103-8	129
2032	Interactions among Polycomb domains are guided by chromosome architecture. <b>2011</b> , 7, e1001343	133
2031	Capturing the essence of folding and functions of biomolecules using coarse-grained models. <b>2011</b> , 2, 487	174
2030	Associated chromosome trap for identifying long-range DNA interactions. <b>2011</b> ,	2
2029	Genetic, Epigenetic and Molecular Changes in Melanoma: A New Paradigm for Biological Classification. <b>2011</b> ,	
2028	Principles for the post-GWAS functional characterisation of risk loci. <b>2011</b> ,	
2027	High-order chromatin architecture determines the landscape of chromosomal alterations in cancer. <b>2011</b> ,	0
2026	. <b>2011</b> ,	0
2025	Replication Timing: Evolution, Nuclear Organization and Relevance for Human Disease. <b>2011</b> ,	
2024	Phytochemicals and Cancer Chemoprevention: Epigenetic Friends or Foe?. <b>2011</b> ,	1

2023	Physiological environment induces quick response - slow exhaustion reactions. <b>2011</b> , 2, 50	10
2022	Gene duplication and ectopic gene conversion in <i>Drosophila</i> . <b>2011</b> , 2, 131-51	8
2021	Chromatin Organization by Repetitive Elements (CORE): A Genomic Principle for the Higher-Order Structure of Chromosomes. <b>2011</b> , 2, 502-15	25
2020	Repulsive forces between looping chromosomes induce entropy-driven segregation. <b>2011</b> , 6, e14428	34
2019	Fractal characteristics of May-Grünwald-Giemsa stained chromatin are independent prognostic factors for survival in multiple myeloma. <b>2011</b> , 6, e20706	43
2018	Interplay between SIN3A and STAT3 mediates chromatin conformational changes and GFAP expression during cellular differentiation. <b>2011</b> , 6, e22018	41
2017	Shaping the Genome with Non-Coding RNAs. <b>2011</b> , 12, 307-21	37
2016	Abstracts of Albany 2011, the 17th Conversation. June 14-18 2011. Albany, New York, USA. <b>2011</b> , 28, 975-1170	1
2015	THE STRUCTURE AND FUNCTION OF CHROMATIN AND CHROMOSOMES. <b>2011</b> ,	
2014	Human genetics and genomics a decade after the release of the draft sequence of the human genome. <b>2011</b> , 5, 577-622	65
2013	From nucleosome to chromosome: a dynamic organization of genetic information. <b>2011</b> , 66, 4-17	70
2012	Chromatin architecture and the regulation of nuclear receptor inducible transcription. <b>2011</b> , 23, 94-106	13
2011	A physical approach to segregation and folding of the <i>Caulobacter crescentus</i> genome. <b>2011</b> , 82, 1311-5	8
2010	At the edge of translation - materials to program cells for directed differentiation. <b>2011</b> , 17, 241-51	14
2009	Association of a functional variant downstream of TNFAIP3 with systemic lupus erythematosus. <b>2011</b> , 43, 253-8	208
2008	Protein folding: To knot or not to knot?. <b>2011</b> , 10, 84-6	15
2007	Material witness: Carbon tailoring. <b>2011</b> , 10, 86	2
2006	Points of view: the overview figure. <b>2011</b> , 8, 365	8

2005	Charting histone modifications and the functional organization of mammalian genomes. <b>2011</b> , 12, 7-18	852
2004	The three-dimensional folding of the $\beta$ globin gene domain reveals formation of chromatin globules. <b>2011</b> , 18, 107-14	232
2003	Mapping of INS promoter interactions reveals its role in long-range regulation of SYT8 transcription. <b>2011</b> , 18, 372-8	49
2002	The inner life of the genome. <b>2011</b> , 304, 66-73	18
2001	Chromatin: constructing the big picture. <b>2011</b> , 30, 1885-95	111
2000	The genomic complexity of primary human prostate cancer. <b>2011</b> , 470, 214-20	984
1999	9p21 DNA variants associated with coronary artery disease impair interferon- $\beta$ signalling response. <b>2011</b> , 470, 264-8	490
1998	Initial impact of the sequencing of the human genome. <b>2011</b> , 470, 187-97	750
1997	Genomics: Genomes in three dimensions. <b>2011</b> , 470, 289-94	20
1996	Compartmentalization of the nucleus. <b>2011</b> , 21, 701-8	70
1995	Living without 30nm chromatin fibers. <b>2011</b> , 36, 1-6	150
1994	Genome-wide approaches for cancer gene discovery. <b>2011</b> , 29, 558-68	25
1993	Genome organization influences partner selection for chromosomal rearrangements. <b>2011</b> , 27, 63-71	37
1992	Genome-wide transcription factor binding: beyond direct target regulation. <b>2011</b> , 27, 141-8	168
1991	Genome organization in and around the nucleolus. <b>2011</b> , 27, 149-56	152
1990	Polycomb group proteins: repression in 3D. <b>2011</b> , 27, 454-64	100
1989	Genome cartography: charting the apicomplexan genome. <b>2011</b> , 27, 345-54	29
1988	Condensed DNA: condensing the concepts. <b>2011</b> , 105, 208-22	189

1987	Occupancy of chromatin organizers in the Epstein-Barr virus genome. <b>2011</b> , 415, 1-5	32
1986	Identifying elemental genomic track types and representing them uniformly. <b>2011</b> , 12, 494	16
1985	MotifMap: integrative genome-wide maps of regulatory motif sites for model species. <b>2011</b> , 12, 495	113
1984	Perioperative genomics. <b>2011</b> , 25, 549-55	4
1983	Transcription and recombination factories: common features?. <b>2011</b> , 23, 318-24	29
1982	Nuclear organization: taking a position on gene expression. <b>2011</b> , 23, 354-9	70
1981	Chromatin globules: a common motif of higher order chromosome structure?. <b>2011</b> , 23, 325-31	56
1980	Physical nuclear organization: loops and entropy. <b>2011</b> , 23, 332-7	34
1979	Probabilistic modeling of Hi-C contact maps eliminates systematic biases to characterize global chromosomal architecture. <b>2011</b> , 43, 1059-65	451
1978	Understanding Genome Function: Quantitative Modeling of Chromatin Folding and Chromatin-Associated Processes. <b>2011</b> , 535-555	2
1977	Epigenomics of human embryonic stem cells and induced pluripotent stem cells: insights into pluripotency and implications for disease. <b>2011</b> , 3, 36	39
1976	CTCF, cohesin, and histone variants: connecting the genome. <b>2011</b> , 89, 505-13	39
1975	Roles of lineage-determining transcription factors in establishing open chromatin: lessons from high-throughput studies. <b>2012</b> , 356, 1-15	30
1974	Epigenetic regulation of retinal development and disease. <b>2011</b> , 4, 121-36	9
1973	Nano- and microscales in genetic material organization: On the issue of Lima-de-Faria "chromosome fields". <b>2011</b> , 436, 5-7	
1972	Conformational dynamics and internal friction in homopolymer globules: equilibrium vs. non-equilibrium simulations. <b>2011</b> , 34, 1-16	14
1971	The dynamic architecture of Hox gene clusters. <i>Science</i> , <b>2011</b> , 334, 222-5	33:3 305
1970	CTCF-mediated functional chromatin interactome in pluripotent cells. <b>2011</b> , 43, 630-8	503

1969	A genome-wide view of mutation rate co-variation using multivariate analyses. <b>2011</b> , 12, R27	30
1968	DNA methylation topology: potential of a chromatin landmark for epigenetic drug toxicology. <b>2011</b> , 3, 761-70	15
1967	Translocation-capture sequencing reveals the extent and nature of chromosomal rearrangements in B lymphocytes. <b>2011</b> , 147, 95-106	286
1966	Chromatin folding--from biology to polymer models and back. <b>2011</b> , 124, 839-45	81
1965	Chromosomal haplotypes by genetic phasing of human families. <b>2011</b> , 89, 382-97	52
1964	Structure determination of genomic domains by satisfaction of spatial restraints. <b>2011</b> , 19, 25-35	35
1963	Chromosome dynamics, molecular crowding, and diffusion in the interphase cell nucleus: a Monte Carlo lattice simulation study. <b>2011</b> , 19, 63-81	33
1962	Nuclear proteins: finding and binding target sites in chromatin. <b>2011</b> , 19, 83-98	41
1961	The fractal globule as a model of chromatin architecture in the cell. <b>2011</b> , 19, 37-51	366
1960	Similar rye A and B chromosome organization in meristematic and differentiated interphase nuclei. <b>2011</b> , 19, 645-55	8
1959	Nuclear positioning, higher-order folding, and gene expression of Mmu15 sequences are refractory to chromosomal translocation. <b>2011</b> , 120, 61-71	4
1958	Modeling of chromosome intermingling by partially overlapping uniform random polygons. <b>2011</b> , 62, 371-89	11
1957	Chromosomal organization at the level of gene complexes. <b>2011</b> , 68, 977-90	10
1956	3C-based methods to detect long-range chromatin interactions. <b>2011</b> , 6, 76-81	2
1955	Identification and regulation of c-Myb target genes in MCF-7 cells. <b>2011</b> , 11, 30	62
1954	Clustered ChIP-Seq-defined transcription factor binding sites and histone modifications map distinct classes of regulatory elements. <b>2011</b> , 9, 80	25
1953	The self-organizing fractal theory as a universal discovery method: the phenomenon of life. <b>2011</b> , 8, 4	38
1952	Hierarchies in eukaryotic genome organization: Insights from polymer theory and simulations. <b>2011</b> , 4, 8	11

1951	Three-dimensional modeling of chromatin structure from interaction frequency data using Markov chain Monte Carlo sampling. <b>2011</b> , 12, 414	115
1950	Close 3D proximity of evolutionary breakpoints argues for the notion of spatial synteny. <b>2011</b> , 12, 303	31
1949	Refinement of <i>Bos taurus</i> sequence assembly based on BAC-FISH experiments. <b>2011</b> , 12, 639	10
1948	Advances in analysis of transcriptional regulatory networks. <b>2011</b> , 3, 21-35	27
1947	Layers of epistasis: genome-wide regulatory networks and network approaches to genome-wide association studies. <b>2011</b> , 3, 513-26	31
1946	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <b>2011</b> , 112, 2218-21	15
1945	Genom-Entschlüsselung mit Hochgeschwindigkeitsverfahren: Bedeutung für Wissenschaft und Medizin. <b>2011</b> , 123, 12612-12616	5
1944	Decoding genomes at high speed: implications for science and medicine. <b>2011</b> , 50, 12406-10	10
1943	Challenges in studying genomic structural variant formation mechanisms: the short-read dilemma and beyond. <b>2011</b> , 33, 840-50	30
1942	Long non-coding RNA modifies chromatin: epigenetic silencing by long non-coding RNAs. <b>2011</b> , 33, 830-9	148
1941	Spreading chromatin into chemical biology. <b>2011</b> , 12, 264-79	56
1940	Multi-scale coding of genomic information: From DNA sequence to genome structure and function. <b>2011</b> , 498, 45-188	91
1939	Polymers with spatial or topological constraints: Theoretical and computational results. <b>2011</b> , 504, 1-73	167
1938	Evolutionary trends of GC/AT distribution patterns in promoters. <b>2011</b> , 60, 228-35	13
1937	Transcription factor interactions in genomic nuclear receptor function. <b>2011</b> , 3, 471-85	19
1936	The nuclear envelope as a chromatin organizer. <b>2011</b> , 2, 339-49	75
1935	Visual representation of scientific information. <b>2011</b> , 4, pt1	3
1934	Epigenome sequencing comes of age in development, differentiation and disease mechanism research. <b>2011</b> , 3, 207-20	5

1933	Anomalous structure and scaling of ring polymer brushes. <b>2011</b> , 95, 28003	22
1932	Chromatin landscape: methylation beyond transcription. <b>2011</b> , 6, 9-15	81
1931	Roles of chromatin insulator proteins in higher-order chromatin organization and transcription regulation. <b>2011</b> , 2, 358-69	36
1930	A top-down analysis of X <sub>a</sub> - and X <sub>i</sub> -territories reveals differences of higher order structure at 120 Mb genomic length scales. <b>2011</b> , 2, 465-77	46
1929	Genomic approaches for the discovery of CFTR regulatory elements. <b>2011</b> , 2, 23-7	4
1928	Cohesin and related coiled-coil domain-containing complexes physically and functionally connect the dots across the genome. <b>2011</b> , 10, 2669-82	24
1927	Culturomics: Word play. <b>2011</b> , 474, 436-40	5
1926	Multiscale entanglement in ring polymers under spherical confinement. <b>2011</b> , 107, 188302	43
1925	Transcription factor search for a DNA promoter in a three-state model. <b>2011</b> , 84, 020901	27
1924	Ring polymers in melts and solutions: scaling and crossover. <b>2011</b> , 106, 167802	78
1923	Scale-free duplication dynamics: a model for ultraduplication. <b>2011</b> , 84, 061919	9
1922	Modeling and small-angle neutron scattering spectra of chromatin supernucleosomal structures at genome scale. <b>2011</b> , 110, 102217	2
1921	Transcriptional gene network inference from a massive dataset elucidates transcriptome organization and gene function. <b>2011</b> , 39, 8677-88	88
1920	On the role of DNA biomechanics in the regulation of gene expression. <b>2011</b> , 8, 1673-81	19
1919	The inactive X chromosome adopts a unique three-dimensional conformation that is dependent on Xist RNA. <b>2011</b> , 25, 1371-83	238
1918	On emerging nuclear order. <b>2011</b> , 192, 711-21	106
1917	Ectopic gene expression and organogenesis in Arabidopsis mutants missing BRU1 required for genome maintenance. <b>2011</b> , 189, 83-95	13
1916	Genome-wide analysis of the relationships between DNaseI HS, histone modifications and gene expression reveals distinct modes of chromatin domains. <b>2011</b> , 39, 7428-43	46

1915	Genome-wide profiling of forum domains in <i>Drosophila melanogaster</i> . <b>2011</b> , 39, 3667-85	15
1914	Integrative analysis of genomic, functional and protein interaction data predicts long-range enhancer-target gene interactions. <b>2011</b> , 39, 2492-502	18
1913	Transcription factories in the context of the nuclear and genome organization. <b>2011</b> , 39, 9085-92	46
1912	Distinct epigenomic features in end-stage failing human hearts. <b>2011</b> , 124, 2411-22	196
1911	Principles of chromosomal organization: lessons from yeast. <b>2011</b> , 192, 723-33	104
1910	Symmetry in the Language of Gene Expression: A Survey of Gene Promoter Networks in Multiple Bacterial Species and Non-Regulons. <b>2011</b> , 3, 750-766	6
1909	Transcription-induced DNA double strand breaks: both oncogenic force and potential therapeutic target?. <b>2011</b> , 17, 3858-64	72
1908	Unraveling the Tangled Complexity of DNA: Combining Mathematical Modeling and Experimental Biology to Understand Replication, Recombination and Repair. <b>2011</b> , 6, 108-135	1
1907	An epichromatin epitope: Persistence in the cell cycle and conservation in evolution. <b>2011</b> , 2, 47-60	22
1906	Dynamics and control of state-dependent networks for probing genomic organization. <b>2011</b> , 108, 17257-62	45
1905	GE Prize essay. Zoom!. <i>Science</i> , <b>2011</b> , 334, 1222-3	33.3 2
1904	The complex transcription regulatory landscape of our genome: control in three dimensions. <b>2011</b> , 30, 4345-55	51
1903	Genomic rearrangement in three dimensions. <b>2011</b> , 29, 1096-8	3
1902	More to Hi-C than meets the eye. <b>2011</b> , 43, 1047-8	2
1901	Molecular dynamics simulation study of nonconcatenated ring polymers in a melt. I. Statics. <b>2011</b> , 134, 204904	225
1900	The Cell Nucleus: Biogenesis, Structure, and Function. <b>2011</b> ,	
1899	Predicting promoter activities of primary human DNA sequences. <b>2011</b> , 39, e75	8
1898	Next-generation insights into regulatory T cells: expression profiling and FoxP3 occupancy in Human. <b>2011</b> , 39, 7946-60	71

1897	Trypanosoma cruzi in the chicken model: Chagas-like heart disease in the absence of parasitism. <b>2011</b> , 5, e1000	21
1896	A dynamical model reveals gene co-localizations in nucleus. <b>2011</b> , 7, e1002094	29
1895	Genomes, proteomes, and the central dogma. <b>2011</b> , 4, 576	21
1894	ESR1 is co-expressed with closely adjacent uncharacterised genes spanning a breast cancer susceptibility locus at 6q25.1. <b>2011</b> , 7, e1001382	46
1893	Bridging the resolution gap in structural modeling of 3D genome organization. <b>2011</b> , 7, e1002125	63
1892	The Vitamin D Receptor: Biochemical, Molecular, Biological, and Genomic Era Investigations. <b>2011</b> , 97-135	6
1891	CTCFBSDB 2.0: a database for CTCF-binding sites and genome organization. <b>2013</b> , 41, D188-94	109
1890	Cohesin protects genes against H2AX Induced by DNA double-strand breaks. <b>2012</b> , 8, e1002460	91
1889	Cohesin is required for expression of the estrogen receptor-alpha (ESR1) gene. <b>2012</b> , 5, 13	19
1888	Replication fork polarity gradients revealed by megabase-sized U-shaped replication timing domains in human cell lines. <b>2012</b> , 8, e1002443	54
1887	Tackling skeletal muscle cells epigenome in the next-generation sequencing era. <b>2012</b> , 2012, 979168	2
1886	Shape-based alignment of genomic landscapes in multi-scale resolution. <b>2012</b> , 40, 6435-48	5
1885	Tissue-specific regulation of chromatin insulator function. <b>2012</b> , 8, e1003069	36
1884	Spatial simulations in systems biology: from molecules to cells. <b>2012</b> , 13, 7798-827	43
1883	Genomic hallmarks of genes involved in chromosomal translocations in hematological cancer. <b>2012</b> , 8, e1002797	21
1882	Tools for mapping high-throughput sequencing data. <b>2012</b> , 28, 3169-77	211
1881	A genome-wide screen identifies genes that affect somatic homolog pairing in Drosophila. <b>2012</b> , 2, 731-40	28
1880	A fractal model for nuclear organization: current evidence and biological implications. <b>2012</b> , 40, 8783-92	82

1879	Galactose repressor mediated intersegmental chromosomal connections in Escherichia coli. <b>2012</b> , 109, 11336-41	26
1878	The spectrum of filament entanglement complexity and an entanglement phase transition. <b>2012</b> , 468, 4024-4040	6
1877	Breaking free from the chains of pathway annotation: de novo pathway discovery for the analysis of disease processes. <b>2012</b> , 13, 1967-78	6
1876	Cell type-specific genomics of Drosophila neurons. <b>2012</b> , 40, 9691-704	114
1875	Nuclear colocalization of transcription factor target genes strengthens coregulation in yeast. <b>2012</b> , 40, 27-36	27
1874	Chromosomes without a 30-nm chromatin fiber. <b>2012</b> , 3, 404-10	109
1873	Back to the origin: reconsidering replication, transcription, epigenetics, and cell cycle control. <b>2012</b> , 3, 678-96	14
1872	Hox in space: gene cluster regulation linked to folding of chromatin. <b>2012</b> , 3, 118-22	7
1871	Novel roles for KLF1 in erythropoiesis revealed by mRNA-seq. <b>2012</b> , 22, 2385-98	65
1870	Kinetic lattice Monte Carlo simulation of viscoelastic subdiffusion. <b>2012</b> , 137, 064114	8
1869	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. <b>2012</b> , 21, 322-33	91
1868	The 'sequence everything' approach and personalized clinical decision challenges. <b>2012</b> , 12, 319-22	
1867	Did the modulation of expression noise shape the evolution of three dimensional genome organizations in eukaryotes?. <b>2012</b> , 3, 286-9	2
1866	Developmental control of replication timing defines a new breed of chromosomal domains with a novel mechanism of chromatin unfolding. <b>2012</b> , 3, 500-7	16
1865	Mapping enhancer and promoter interactions. <b>2012</b> , 22, 789-90	5
1864	Dynamic structure factor of vibrating fractals: proteins as a case study. <b>2012</b> , 85, 011906	15
1863	Statistics and geometrical picture of ring polymer melts and solutions. <b>2012</b> , 85, 021806	25
1862	Dynamic structure factor of vibrating fractals. <b>2012</b> , 108, 068101	17

1861	Measuring chromosome conformation with degenerate labels. <b>2012</b> , 86, 011918	0
1860	Analyzing the association of SCNA boundaries with replication timing. <b>2012</b> , 30, 1043-5; author reply 1045-6	2
1859	A model for Escherichia coli chromosome packaging supports transcription factor-induced DNA domain formation. <b>2012</b> , 40, 972-80	68
1858	Actin-related protein BAF53 is essential for the formation of replication foci. <b>2012</b> , 16, 183-189	2
1857	The chromatin fingerprint of gene enhancer elements. <b>2012</b> , 287, 30888-96	65
1856	Uncovering transcription factor modules using one- and three-dimensional analyses. <b>2012</b> , 287, 30914-21	5
1855	Integration of Hi-C and ChIP-seq data reveals distinct types of chromatin linkages. <b>2012</b> , 40, 7690-704	76
1854	Oncogene-mediated alterations in chromatin conformation. <b>2012</b> , 109, 9083-8	110
1853	Identification of functionally active, low frequency copy number variants at 15q21.3 and 12q21.31 associated with prostate cancer risk. <b>2012</b> , 109, 6686-91	42
1852	3D chromatin conformation correlates with replication timing and is conserved in resting cells. <b>2012</b> , 40, 9470-81	62
1851	Genome-scale technology driven advances to research into normal and malignant haematopoiesis. <b>2012</b> , 2012, 437956	
1850	Human mitotic chromosomes consist predominantly of irregularly folded nucleosome fibres without a 30-nm chromatin structure. <b>2012</b> , 31, 1644-53	223
1849	HiTC: exploration of high-throughput 'C' experiments. <b>2012</b> , 28, 2843-4	119
1848	On the assessment of statistical significance of three-dimensional colocalization of sets of genomic elements. <b>2012</b> , 40, 3849-55	37
1847	Chromosome positioning and the clustering of functionally related loci in yeast is driven by chromosomal interactions. <b>2012</b> , 3, 370-83	51
1846	Spatio-temporal organization of replication in bacteria and eukaryotes (nucleoids and nuclei). <b>2012</b> , 4, a010389	22
1845	SIRT1 deacetylates SATB1 to facilitate MAR HS2-MAR interaction and promote H $\beta$ globin expression. <b>2012</b> , 40, 4804-15	17
1844	Self-organization of domain structures by DNA-loop-extruding enzymes. <b>2012</b> , 40, 11202-12	331

1843	Disordered proteins and network disorder in network descriptions of protein structure, dynamics and function: hypotheses and a comprehensive review. <b>2012</b> , 13, 19-33	44
1842	On the limitations of biological knowledge. <b>2012</b> , 13, 574-87	11
1841	Zooming in on genome organization. <b>2012</b> , 9, 961-3	1
1840	TNF $\beta$ signals through specialized factories where responsive coding and miRNA genes are transcribed. <b>2012</b> , 31, 4404-14	93
1839	Epigenomics of cancer - emerging new concepts. <b>2012</b> , 94, 2219-30	53
1838	Interpreting noncoding genetic variation in complex traits and human disease. <b>2012</b> , 30, 1095-106	347
1837	Genome-wide analysis of replication timing in mammalian cells: troubleshooting problems encountered when comparing different cell types. <b>2012</b> , 57, 165-9	6
1836	Lattice animal model of chromosome organization. <b>2012</b> , 86, 011911	17
1835	The expanding scope of DNA sequencing. <b>2012</b> , 30, 1084-94	237
1834	ChIA-PET analysis of transcriptional chromatin interactions. <b>2012</b> , 58, 289-99	69
1833	Chromatin structure, epigenetic mechanisms and long-range interactions in the human insulin locus. <b>2012</b> , 14 Suppl 3, 1-11	15
1832	DNA damage defines sites of recurrent chromosomal translocations in B lymphocytes. <b>2012</b> , 484, 69-74	159
1831	Order from chaos in the nucleus. <b>2012</b> , 48, 327-8	2
1830	Epigenetic regulation of gene expression in keratinocytes. <b>2012</b> , 132, 2505-21	95
1829	Hi-C: a comprehensive technique to capture the conformation of genomes. <b>2012</b> , 58, 268-76	472
1828	Pluripotency in 3D: genome organization in pluripotent cells. <b>2012</b> , 24, 793-801	15
1827	Genome-wide studies of CCCTC-binding factor (CTCF) and cohesin provide insight into chromatin structure and regulation. <b>2012</b> , 287, 30906-13	74
1826	Determining long-range chromatin interactions for selected genomic sites using 4C-seq technology: from fixation to computation. <b>2012</b> , 58, 221-30	167

1825	From cells to chromatin: capturing snapshots of genome organization with 5C technology. <b>2012</b> , 58, 255-67	33
1824	Chromosome conformation capture assays in bacteria. <b>2012</b> , 58, 212-20	6
1823	Super-resolution imaging reveals three-dimensional folding dynamics of the $\beta$ globin locus upon gene activation. <b>2012</b> , 125, 4630-9	27
1822	Detecting long-range chromatin interactions using the chromosome conformation capture sequencing (4C-seq) method. <b>2012</b> , 786, 211-25	38
1821	Chromosome conformation capture on chip in single <i>Drosophila melanogaster</i> tissues. <b>2012</b> , 58, 231-42	5
1820	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <b>2012</b> , 13, R48	194
1819	Multiple layers of complexity in cis-regulatory regions of developmental genes. <b>2012</b> , 241, 1857-66	23
1818	Visualization of the spatial positioning of the SNRPN, UBE3A, and GABRB3 genes in the normal human nucleus by three-color 3D fluorescence in situ hybridization. <b>2012</b> , 20, 659-72	12
1817	Large-scale functional organization of long-range chromatin interaction networks. <b>2012</b> , 2, 1207-19	84
1816	Features of endogenous cardiomyocyte chromatin revealed by super-resolution STED microscopy. <b>2012</b> , 53, 552-8	28
1815	Genome structure determination via 3C-based data integration by the Integrative Modeling Platform. <b>2012</b> , 58, 300-6	68
1814	A model for the 3D chromatin architecture of pro and eukaryotes. <b>2012</b> , 58, 307-14	15
1813	Visualising chromosomal replication sites and replicons in mammalian cells. <b>2012</b> , 57, 140-8	19
1812	3C Technologies in plants. <b>2012</b> , 58, 204-11	11
1811	A genome-wide 3C-method for characterizing the three-dimensional architectures of genomes. <b>2012</b> , 58, 277-88	26
1810	Analysis of long-range chromatin interactions using Chromosome Conformation Capture. <b>2012</b> , 58, 192-203	104
1809	3C-based technologies to study the shape of the genome. <b>2012</b> , 58, 189-91	66
1808	Close proximity to <i>Igh</i> is a contributing factor to AID-mediated translocations. <b>2012</b> , 47, 873-85	48

1807	Pharmacogene regulatory elements: from discovery to applications. <b>2012</b> , 4, 45	16
1806	Computational model of chromosome aberration yield induced by high- and low-LET radiation exposures. <b>2012</b> , 177, 727-37	20
1805	Physical tethering and volume exclusion determine higher-order genome organization in budding yeast. <b>2012</b> , 22, 1295-305	157
1804	Versatile design and synthesis platform for visualizing genomes with Oligopaint FISH probes. <b>2012</b> , 109, 21301-6	280
1803	Dopaminergic neurons for Parkinson's therapy. <b>2012</b> , 30, 56-8	25
1802	Characterization of genome-wide enhancer-promoter interactions reveals co-expression of interacting genes and modes of higher order chromatin organization. <b>2012</b> , 22, 490-503	169
1801	Bioinformatics applied to gene transcription regulation. <b>2012</b> , 49, R51-9	1
1800	Histone H2A variants in nucleosomes and chromatin: more or less stable?. <b>2012</b> , 40, 10719-41	199
1799	Unravelling global genome organization by 3C-seq. <b>2012</b> , 23, 213-21	12
1798	Noncoding transcription at enhancers: general principles and functional models. <b>2012</b> , 46, 1-19	290
1797	Technical considerations for functional sequencing assays. <b>2012</b> , 13, 802-7	32
1796	Nuclear organization and genome function. <b>2012</b> , 28, 163-87	82
1795	Single-tube linear DNA amplification for genome-wide studies using a few thousand cells. <b>2012</b> , 7, 328-38	30
1794	The long-range interaction landscape of gene promoters. <b>2012</b> , 489, 109-13	1066
1793	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. <b>2012</b> , 13, 667-72	215
1792	Mechanisms and impacts of chromosomal translocations in cancers. <b>2012</b> , 6, 263-74	15
1791	Development: segmentation by sequestration. <b>2012</b> , 13, 595	
1790	Drosophila CTCF tandemly aligns with other insulator proteins at the borders of H3K27me3 domains. <b>2012</b> , 22, 2176-87	94

1789	How two meters of DNA fit into a cell nucleus: Polymer models with topological constraints and experimental data. <b>2012</b> , 54, 1-10	25
1788	Structural variation and its effect on expression. <b>2012</b> , 838, 173-86	20
1787	Complexity of chromatin folding is captured by the strings and binders switch model. <b>2012</b> , 109, 16173-8	343
1786	Genetic and epigenetic contribution to complex traits. <b>2012</b> , 21, R24-8	55
1785	Robust 4C-seq data analysis to screen for regulatory DNA interactions. <b>2012</b> , 9, 969-72	278
1784	A predictive computational model of the dynamic 3D interphase yeast nucleus. <b>2012</b> , 22, 1881-90	117
1783	Methods for identifying higher-order chromatin structure. <b>2012</b> , 13, 59-82	60
1782	Packaging the fly genome: domains and dynamics. <b>2012</b> , 11, 347-55	12
1781	HiCNorm: removing biases in Hi-C data via Poisson regression. <b>2012</b> , 28, 3131-3	176
1780	Sensitive detection of chromatin coassociations using enhanced chromosome conformation capture on chip. <b>2012</b> , 7, 1335-50	33
1779	The radial nuclear positioning of genes correlates with features of megabase-sized chromatin domains. <b>2012</b> , 20, 735-52	27
1778	Chromatin insulator elements: establishing barriers to set heterochromatin boundaries. <b>2012</b> , 4, 67-80	51
1777	Regulation of mouse Cyp24a1 expression via promoter-proximal and downstream-distal enhancers highlights new concepts of 1,25-dihydroxyvitamin D(3) action. <b>2012</b> , 523, 2-8	34
1776	Independence of repressive histone marks and chromatin compaction during senescent heterochromatic layer formation. <b>2012</b> , 47, 203-14	213
1775	Discovering genome regulation with 3C and 3C-related technologies. <b>2012</b> , 1819, 401-10	31
1774	Nuclear organization and chromatin dynamics in yeast: biophysical models or biologically driven interactions?. <b>2012</b> , 1819, 468-81	12
1773	Chromatin domains, insulators, and the regulation of gene expression. <b>2012</b> , 1819, 644-51	88
1772	Intra-nuclear mobility and target search mechanisms of transcription factors: a single-molecule perspective on gene expression. <b>2012</b> , 1819, 482-93	33

1771	Genetic and epigenetic determinants of neurogenesis and myogenesis. <b>2012</b> , 22, 721-35	89
1770	Three-dimensional folding and functional organization principles of the Drosophila genome. <b>2012</b> , 148, 458-72	1335
1769	Spatial organization of the mouse genome and its role in recurrent chromosomal translocations. <b>2012</b> , 148, 908-21	411
1768	SnapShot: Chromosome confirmation capture. <b>2012</b> , 148, 1068.e1-2	38
1767	Enhancer and promoter interactions-long distance calls. <b>2012</b> , 22, 79-85	155
1766	Nuclear architecture by RNA. <b>2012</b> , 22, 179-87	54
1765	Chromosome organization in the nucleus - charting new territory across the Hi-Cs. <b>2012</b> , 22, 125-31	48
1764	Higher-order chromatin structure: bridging physics and biology. <b>2012</b> , 22, 115-24	125
1763	Transcription factories: genetic programming in three dimensions. <b>2012</b> , 22, 110-4	102
1762	New and Xisting regulatory mechanisms of X chromosome inactivation. <b>2012</b> , 22, 62-71	83
1761	Widespread occurrence of power-law distributions in inter-repeat distances shaped by genome dynamics. <b>2012</b> , 499, 88-98	10
1760	Arrangement of nuclear structures is not transmitted through mitosis but is identical in sister cells. <b>2012</b> , 113, 3313-29	10
1759	Linking the DNA strand asymmetry to the spatio-temporal replication program: II. Accounting for neighbor-dependent substitution rates. <b>2012</b> , 35, 123	11
1758	GeSICA: genome segmentation from intra-chromosomal associations. <b>2012</b> , 13, 164	5
1757	Transcription factor co-localization patterns affect human cell type-specific gene expression. <b>2012</b> , 13, 263	10
1756	Normalization of a chromosomal contact map. <b>2012</b> , 13, 436	142
1755	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. <b>2012</b> , 13, 566	33
1754	What's in a loop?. <b>2012</b> , 10, 31	3

1753	Electric oscillation and coupling of chromatin regulate chromosome packaging and transcription in eukaryotic cells. <b>2012</b> , 9, 27	10
1752	Gene density, transcription, and insulators contribute to the partition of the Drosophila genome into physical domains. <b>2012</b> , 48, 471-84	374
1751	4C technology: protocols and data analysis. <b>2012</b> , 513, 89-112	150
1750	Stress-associated H3K4 methylation accumulates during postnatal development and aging of rhesus macaque brain. <b>2012</b> , 11, 1055-64	36
1749	Condensin II promotes the formation of chromosome territories by inducing axial compaction of polyploid interphase chromosomes. <b>2012</b> , 8, e1002873	84
1748	Introduction to genome biology: features, processes, and structures. <b>2012</b> , 855, 3-49	1
1747	Chromosome Territory Organization within the Nucleus. <b>2012</b> ,	4
1746	Disentangling the many layers of eukaryotic transcriptional regulation. <b>2012</b> , 46, 43-68	150
1745	Analysis of interactions between genomic loci through Chromosome Conformation Capture (3C). <b>2012</b> , Chapter 22, Unit22.15	12
1744	ChIP-seq and beyond: new and improved methodologies to detect and characterize protein-DNA interactions. <b>2012</b> , 13, 840-52	524
1743	SANS spectra of the fractal supernucleosomal chromatin structure models. <b>2012</b> , 351, 012007	8
1742	What does our genome encode?. <b>2012</b> , 22, 1602-11	87
1741	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <b>2012</b> , 9, 999-1003	822
1740	Chromatin topology and the regulation of antigen receptor assembly. <b>2012</b> , 30, 337-56	71
1739	Global changes in the nuclear positioning of genes and intra- and interdomain genomic interactions that orchestrate B cell fate. <b>2012</b> , 13, 1196-204	206
1738	Memories from the polycomb group proteins. <b>2012</b> , 46, 561-89	129
1737	Open and closed domains in the mouse genome are configured as 10-nm chromatin fibres. <b>2012</b> , 13, 992-6	125
1736	Dynamical modeling of three-dimensional genome organization in interphase budding yeast. <b>2012</b> , 102, 296-304	62

1735	Geometry-induced bursting dynamics in gene expression. <b>2012</b> , 102, 2186-91	26
1734	Replication timing and its emergence from stochastic processes. <b>2012</b> , 28, 374-81	64
1733	Resolving Spatial Inconsistencies in Chromosome Conformation Data. <b>2012</b> , 288-300	1
1732	Computational models for large-scale simulations of facilitated diffusion. <b>2012</b> , 8, 2815-27	16
1731	Oncogenic transcription factors as master regulators of chromatin topology: a new role for ERG in prostate cancer. <b>2012</b> , 11, 3380-3	12
1730	Epigenetic regulation of condensin-mediated genome organization during the cell cycle and upon DNA damage through histone H3 lysine 56 acetylation. <b>2012</b> , 48, 532-46	65
1729	CTCF-mediated transcriptional regulation through cell type-specific chromosome organization in the <i>Eg</i> locus. <b>2012</b> , 40, 7718-27	34
1728	Epigenetic Regulation of Lymphocyte Development. <b>2012</b> ,	
1727	A Torrent of data: mapping chromatin organization using 5C and high-throughput sequencing. <b>2012</b> , 513, 113-41	20
1726	Gene Regulatory Networks. <b>2012</b> ,	2
1725	Chromatin in the Cell Nucleus: Higher-order Organisation. <b>2012</b> ,	1
1724	Chromatin landscape and endocrine response in breast cancer. <b>2012</b> , 4, 675-83	12
1723	Predicting expression-related features of chromosomal domain organization with network-structured analysis of gene expression and chromosomal location. <b>2012</b> ,	2
1722	Epigenomics Impact for Drug Safety Sciences. <b>2012</b> , 365-385	3
1721	How do you find transcription factors? Computational approaches to compile and annotate repertoires of regulators for any genome. <b>2012</b> , 786, 3-19	6
1720	Physical descriptions of the bacterial nucleoid at large scales, and their biological implications. <b>2012</b> , 75, 076602	51
1719	Graph rigidity reveals well-constrained regions of chromosome conformation embeddings. <b>2012</b> , 13, 241	
1718	Spatial proximity and similarity of the epigenetic state of genome domains. <b>2012</b> , 7, e33947	12

1717	Organizational heterogeneity of vertebrate genomes. <b>2012</b> , 7, e32076	5
1716	Expression-dependent folding of interphase chromatin. <b>2012</b> , 7, e37525	24
1715	Segment-wise genome-wide association analysis identifies a candidate region associated with schizophrenia in three independent samples. <b>2012</b> , 7, e38828	6
1714	Pairing of homologous regions in the mouse genome is associated with transcription but not imprinting status. <b>2012</b> , 7, e38983	20
1713	AID-targeting and hypermutation of non-immunoglobulin genes does not correlate with proximity to immunoglobulin genes in germinal center B cells. <b>2012</b> , 7, e39601	5
1712	Regulation of DNA replication timing on human chromosome by a cell-type specific DNA binding protein SATB1. <b>2012</b> , 7, e42375	10
1711	Three-dimensional genome architecture influences partner selection for chromosomal translocations in human disease. <b>2012</b> , 7, e44196	87
1710	Multi-edge gene set networks reveal novel insights into global relationships between biological themes. <b>2012</b> , 7, e45211	7
1709	Comprehensive human transcription factor binding site map for combinatorial binding motifs discovery. <b>2012</b> , 7, e49086	5
1708	A Model of Repetitive-DNA-Organized Chromatin Network of Interphase Chromosomes. <b>2012</b> , 3, 167-75	6
1707	The genetic and epigenetic journey of embryonic stem cells into mature neural cells. <b>2012</b> , 3, 81	39
1706	Transcription factor binding at enhancers: shaping a genomic regulatory landscape in flux. <b>2012</b> , 3, 195	29
1705	Chromatin loops, gene positioning, and gene expression. <b>2012</b> , 3, 217	63
1704	Genetics and Genomics in Cardiovascular Gene Discovery. <b>2012</b> , 231-259	2
1703	Fruitfly genome mapped in three dimensions. <b>2012</b> ,	
1702	Unique for human centromeric regions of interphase chromatin homing (CENTRICH) govern dynamic features of chromatin fractal globules. <b>2012</b> ,	
1701	Organ genomics: what can we learn?. <b>2012</b> , 01,	
1700	Modeling and experimental methods to probe the link between global transcription and spatial organization of chromosomes. <b>2012</b> , 7, e46628	22

1699	The context of gene expression regulation. <b>2012</b> , 4, 8	19
1698	Enhancers and silencers: an integrated and simple model for their function. <b>2012</b> , 5, 1	87
1697	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <b>2012</b> , 485, 376-80	4098
1696	Transcriptional and epigenetic control of T helper cell specification: molecular mechanisms underlying commitment and plasticity. <b>2012</b> , 30, 707-31	256
1695	Spatial partitioning of the regulatory landscape of the X-inactivation centre. <b>2012</b> , 485, 381-5	1894
1694	Chromatin replication and epigenome maintenance. <b>2012</b> , 13, 153-67	423
1693	Human mitotic chromosome structure: what happened to the 30-nm fibre?. <b>2012</b> , 31, 1621-3	32
1692	Protective effects of <i>Echinops echinatus</i> on testosterone-induced prostatic hyperplasia in rats. <b>2012</b> , 4, e177-e185	16
1691	Cohesin-mediated chromatin interactions--into the third dimension of gene regulation. <b>2012</b> , 11, 205-16	14
1690	Genome architectures revealed by tethered chromosome conformation capture and population-based modeling. <b>2011</b> , 30, 90-8	447
1689	A decade of 3C technologies: insights into nuclear organization. <b>2012</b> , 26, 11-24	543
1688	Chromatin organization is a major influence on regional mutation rates in human cancer cells. <b>2012</b> , 488, 504-7	451
1687	Navigating the epigenetic landscape of pluripotent stem cells. <b>2012</b> , 13, 524-35	90
1686	Chromatin-interaction compartment switch at developmentally regulated chromosomal domains reveals an unusual principle of chromatin folding. <b>2012</b> , 109, 12574-9	49
1685	Abnormal developmental control of replication-timing domains in pediatric acute lymphoblastic leukemia. <b>2012</b> , 22, 1833-44	72
1684	Landscapes and archipelagos: spatial organization of gene regulation in vertebrates. <b>2012</b> , 22, 347-54	31
1683	Third-generation sequencing techniques and applications to drug discovery. <b>2012</b> , 7, 231-43	42
1682	Calculating transcription factor binding maps for chromatin. <b>2012</b> , 13, 187-201	18

1681	Comparing enhancer action in cis and in trans. <b>2012</b> , 191, 1143-55	37
1680	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. <b>2011</b> , 44, 40-6	474
1679	Characterization of enhancer function from genome-wide analyses. <b>2012</b> , 13, 29-57	80
1678	Base-Calling for Bioinformaticians. <b>2012</b> , 67-83	2
1677	Transcription factors: from enhancer binding to developmental control. <b>2012</b> , 13, 613-26	1156
1676	The potential of 3D-FISH and super-resolution structured illumination microscopy for studies of 3D nuclear architecture: 3D structured illumination microscopy of defined chromosomal structures visualized by 3D (immuno)-FISH opens new perspectives for studies of nuclear architecture. <b>2012</b> , 31, 112-26	107
1675	First annual meeting of the EpiGeneSys Network of Excellence: moving epigenetics towards systems biology. <b>2012</b> , 34, 620-5	
1674	The genome in space and time: does form always follow function? How does the spatial and temporal organization of a eukaryotic genome reflect and influence its functions?. <b>2012</b> , 34, 800-10	19
1673	Genomic approaches towards finding cis-regulatory modules in animals. <b>2012</b> , 13, 469-83	156
1672	Parallel genome universes. <b>2012</b> , 30, 55-6	6
1671	Global identification of transcriptional regulators of pluripotency and differentiation in embryonic stem cells. <b>2012</b> , 40, 8199-209	8
1670	DNA-binding factor CTCF and long-range gene interactions in V(D)J recombination and oncogene activation. <b>2012</b> , 119, 6209-18	29
1669	A map of the cis-regulatory sequences in the mouse genome. <b>2012</b> , 488, 116-20	1019
1668	MORC family ATPases required for heterochromatin condensation and gene silencing. <i>Science</i> , <b>2012</b> , 336, 1448-51	333 220
1667	Different patterns of Robertsonian fusion pairing in Bovidae and the house mouse: the relationship between chromosome size and nuclear territories. <b>2012</b> , 94, 97-111	5
1666	Cohesin regulates tissue-specific expression by stabilizing highly occupied cis-regulatory modules. <b>2012</b> , 22, 2163-75	117
1665	Classes of fast and specific search mechanisms for proteins on DNA. <b>2012</b> , 75, 026601	92
1664	Higher-order genomic organization in pluripotent stem cells. <b>2012</b> , 3, 483-6	4

1663	Throwing transcription for a loop: expression of the genome in the 3D nucleus. <b>2012</b> , 121, 107-16	20
1662	Interphase chromatin organisation in Arabidopsis nuclei: constraints versus randomness. <b>2012</b> , 121, 369-87	49
1661	Dosage compensation in Drosophila melanogaster: epigenetic fine-tuning of chromosome-wide transcription. <b>2012</b> , 13, 123-34	173
1660	Polycomb: a paradigm for genome organization from one to three dimensions. <b>2012</b> , 24, 405-14	36
1659	Revisiting higher-order and large-scale chromatin organization. <b>2012</b> , 24, 359-66	50
1658	Bivalent histone modifications in early embryogenesis. <b>2012</b> , 24, 374-86	200
1657	Interrogating genomic and epigenomic data to understand prostate cancer. <b>2012</b> , 1825, 186-96	12
1656	Resolving the variable genome and epigenome in human disease. <b>2012</b> , 271, 379-91	13
1655	Changes in fractal dimension and lacunarity as early markers of UV-induced apoptosis. <b>2012</b> , 303, 87-92	34
1654	Impact of chromatin structure on PR signaling: transition from local to global analysis. <b>2012</b> , 357, 30-6	18
1653	Enhancers as information integration hubs in development: lessons from genomics. <b>2012</b> , 28, 276-84	178
1652	Mapping mouse hemangioblast maturation from headfold stages. <b>2012</b> , 365, 1-13	9
1651	Mitotic chromosome structure. <b>2012</b> , 318, 1381-5	2
1650	Chromosomal architecture changes upon cell differentiation. <b>2013</b> , 6,	78
1649	Polymer models of yeast <i>S. cerevisiae</i> genome organization. <b>2013</b> , 6,	78
1648	Imaging heterochromatin in human embryonic stem cells with light-sheet Bayesian microscopy. <b>2013</b> , 6, P109	78
1647	<i>S. cerevisiae</i> genome as a confined equilibrium polymer brush. <b>2013</b> , 6,	78
1646	Genomic positions of co-expressed genes: echoes of chromosome organisation in gene expression data. <b>2013</b> , 6, 229	9

1645	Physical chemistry of nucleic acids and their complexes. <b>2013</b> , 99, 910-5	3
1644	Short-term memory of danger signals and environmental stimuli in immune cells. <b>2013</b> , 14, 777-84	59
1643	Zinc finger proteins and the 3D organization of chromosomes. <b>2013</b> , 90, 67-117	8
1642	53BP1 alters the landscape of DNA rearrangements and suppresses AID-induced B cell lymphoma. <b>2013</b> , 49, 623-31	31
1641	The evolutionary potential of paramutation: a population-epigenetic model. <b>2013</b> , 88, 9-19	14
1640	The pluripotent genome in three dimensions is shaped around pluripotency factors. <b>2013</b> , 501, 227-31	208
1639	The spatial organization of the human genome. <b>2013</b> , 14, 67-84	267
1638	CNVs of noncoding cis-regulatory elements in human disease. <b>2013</b> , 23, 249-56	35
1637	Segmental folding of chromosomes: a basis for structural and regulatory chromosomal neighborhoods?. <b>2013</b> , 35, 818-28	136
1636	Something silent this way forms: the functional organization of the repressive nuclear compartment. <b>2013</b> , 29, 241-70	73
1635	Nuclear organization in the nematode <i>C. elegans</i> . <b>2013</b> , 25, 395-402	4
1634	Comparative analysis of 4C-Seq data generated from enzyme-based and sonication-based methods. <b>2013</b> , 14, 345	11
1633	Gene promoters show chromosome-specificity and reveal chromosome territories in humans. <b>2013</b> , 14, 278	13
1632	The genomic signature of trait-associated variants. <b>2013</b> , 14, 108	37
1631	Genome-wide analysis uncovers high frequency, strong differential chromosomal interactions and their associated epigenetic patterns in E2-mediated gene regulation. <b>2013</b> , 14, 70	27
1630	Open questions: Chromosome condensation - why does a chromosome look like a chromosome?. <b>2013</b> , 11, 9	4
1629	Polymer physics, scaling and heterogeneity in the spatial organisation of chromosomes in the cell nucleus. <b>2013</b> , 9, 8631	14
1628	Single-cell sequencing-based technologies will revolutionize whole-organism science. <b>2013</b> , 14, 618-30	779

1627	Amplification of distant estrogen response elements deregulates target genes associated with tamoxifen resistance in breast cancer. <b>2013</b> , 24, 197-212	42
1626	3-D DNA methylation phenotypes correlate with cytotoxicity levels in prostate and liver cancer cell models. <b>2013</b> , 14, 11	15
1625	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <b>2013</b> , 1, 156-174	22
1624	Computational methodology for ChIP-seq analysis. <b>2013</b> , 1, 54-70	20
1623	Algorithms in Bioinformatics. <b>2013</b> ,	1
1622	Correlative microscopy of individual cells: sequential application of microscopic systems with increasing resolution to study the nuclear landscape. <b>2013</b> , 1042, 299-336	16
1621	Systems Biology. <b>2013</b> ,	8
1620	53 2D to 3D: interaction frequency maps to chromatin higher-order folded conformations. <b>2013</b> , 31, 33-33	
1619	Chromatin in a marine picoeukaryote is a disordered assemblage of nucleosomes. <b>2013</b> , 122, 377-86	41
1618	Computer simulation of stiff-chain polymers. <b>2013</b> , 55, 4-22	13
1617	Functional Genomics, Proteomics, Metabolomics and Bioinformatics for Systems Biology. <b>2013</b> , 3-41	4
1616	Chromatin position effects assayed by thousands of reporters integrated in parallel. <b>2013</b> , 154, 914-27	219
1615	Identification of novel imprinted differentially methylated regions by global analysis of human-parthenogenetic-induced pluripotent stem cells. <b>2013</b> , 1, 79-89	26
1614	Micro- and nanoscale devices for the investigation of epigenetics and chromatin dynamics. <b>2013</b> , 8, 709-18	47
1613	New insights into the dynamics of plant cell nuclei and chromosomes. <b>2013</b> , 305, 253-301	25
1612	DNA loop domain organization as revealed by single-cell gel electrophoresis. <b>2013</b> , 1833, 3237-3244	17
1611	Classification of topological domains based on gene expression and regulation. <b>2013</b> , 56, 415-23	2
1610	A high-resolution map of the three-dimensional chromatin interactome in human cells. <b>2013</b> , 503, 290-4	861

1609	Chromosomal contact permits transcription between coregulated genes. <b>2013</b> , 155, 606-20	135
1608	Heart Proteomics. <b>2013</b> ,	2
1607	Topology of mammalian developmental enhancers and their regulatory landscapes. <b>2013</b> , 502, 499-506	355
1606	A Correction to the Research Article Titled: "Mucosal Imprinting of Vaccine-Induced CD8+ T Cells Is Crucial to Inhibit the Growth of Mucosal Tumors" by F. Sandoval, M. Terme, M. Nizard, C. Badoual, M.-F. Bureau, L. Freyburger, O. Clement, E. Marcheteau, A. Gey, G. Fraisse, C. Bouguin, N. Merillon, E. Dransart, T. Tran, F. Quintin-Colonna, G. Autret, M. Thiebaud, M. Suleman, S. Riffault, T.-C. Wu, O.	1
1605	Whole-genome haplotype reconstruction using proximity-ligation and shotgun sequencing. <b>2013</b> , 5, 178er2-178er3 31, 1111-8	196
1604	Chromosome-scale scaffolding of de novo genome assemblies based on chromatin interactions. <b>2013</b> , 31, 1119-25	650
1603	From simple bacterial and archaeal replicons to replication N/U-domains. <b>2013</b> , 425, 4673-89	27
1602	Organization of the mitotic chromosome. <i>Science</i> , <b>2013</b> , 342, 948-53	33.3 654
1601	High-resolution mapping of the spatial organization of a bacterial chromosome. <i>Science</i> , <b>2013</b> , 342, 731-4	33.3 389
1600	Mitochondrial fusion directs cardiomyocyte differentiation via calcineurin and Notch signaling. <i>Science</i> , <b>2013</b> , 342, 734-7	33.3 232
1599	DNA replication timing and higher-order nuclear organization determine single-nucleotide substitution patterns in cancer genomes. <b>2013</b> , 4, 1502	82
1598	Relating mammalian replication program to large-scale chromatin folding. <b>2013</b> ,	
1597	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <b>2013</b> , 23, 2066-77	232
1596	Dynamic transcriptomes of human myeloid leukemia cells. <b>2013</b> , 102, 250-6	26
1595	Bubble-seq analysis of the human genome reveals distinct chromatin-mediated mechanisms for regulating early- and late-firing origins. <b>2013</b> , 23, 1774-88	65
1594	A novel family of space-filling curves in their relation to chromosome conformation in eukaryotes. <b>2013</b> , 392, 6375-6388	17
1593	Nonspecific bridging-induced attraction drives clustering of DNA-binding proteins and genome organization. <b>2013</b> , 110, E3605-11	145
1592	The landscape of microsatellite instability in colorectal and endometrial cancer genomes. <b>2013</b> , 155, 858-68	247

1591	Cancer biology and the nuclear envelope: a convoluted relationship. <b>2013</b> , 23, 125-37	58
1590	Pan-cancer patterns of somatic copy number alteration. <b>2013</b> , 45, 1134-40	1198
1589	Chromatin dynamics at the replication fork: there's more to life than histones. <b>2013</b> , 23, 140-6	23
1588	Chromatin architecture, CCCTC-binding factor, and V(D)J recombination: managing long-distance relationships at antigen receptor loci. <b>2013</b> , 190, 4915-21	30
1587	CytoHiC: a cytoscape plugin for visual comparison of Hi-C networks. <b>2013</b> , 29, 1206-7	16
1586	Genome assembly and haplotyping with Hi-C. <b>2013</b> , 31, 1099-101	40
1585	High-throughput genome scaffolding from in vivo DNA interaction frequency. <b>2013</b> , 31, 1143-7	120
1584	High-throughput chromatin motion tracking in living yeast reveals the flexibility of the fiber throughout the genome. <b>2013</b> , 23, 1829-38	146
1583	Chromothripsis and beyond: rapid genome evolution from complex chromosomal rearrangements. <b>2013</b> , 27, 2513-30	174
1582	3D chromosome modeling with semi-definite programming and Hi-C data. <b>2013</b> , 20, 831-46	86
1581	Epigenetic alterations in oncogenesis. Preface. <b>2013</b> , 754, v-vii	7
1580	CTCF: the protein, the binding partners, the binding sites and their chromatin loops. <b>2013</b> , 368, 20120369	124
1579	Chromatin structure, pluripotency and differentiation. <b>2013</b> , 238, 259-70	22
1578	Understanding the regulatory and transcriptional complexity of the genome through structure. <b>2013</b> , 23, 1081-8	55
1577	Chromatin organization and global regulation of Hox gene clusters. <b>2013</b> , 368, 20120367	53
1576	Biological implications and regulatory mechanisms of long-range chromosomal interactions. <b>2013</b> , 288, 22369-77	17
1575	Fractal globule as a molecular machine. <b>2013</b> , 98, 242-246	14
1574	Analysis of genome-wide contacts of forum terminus in Drosophila S2 cells. <b>2013</b> , 452, 259-63	1

1573	Mapping genome-wide transcription factor binding sites in frozen tissues. <b>2013</b> , 6, 30	25
1572	Spatial compartmentalization at the nuclear periphery characterized by genome-wide mapping. <b>2013</b> , 14, 591	29
1571	Characterization of constitutive CTCF/cohesin loci: a possible role in establishing topological domains in mammalian genomes. <b>2013</b> , 14, 553	54
1570	Screening in silico predicted remotely acting NF1 gene regulatory elements for mutations in patients with neurofibromatosis type 1. <b>2013</b> , 7, 18	4
1569	Murine esBAF chromatin remodeling complex subunits BAF250a and Brg1 are necessary to maintain and reprogram pluripotency-specific replication timing of select replication domains. <b>2013</b> , 6, 42	23
1568	Light-sheet Bayesian microscopy enables deep-cell super-resolution imaging of heterochromatin in live human embryonic stem cells. <b>2013</b> , 2,	47
1567	Kinetics of Diffusing Polymer Encounter in Confined Cellular Microdomains. <b>2013</b> , 153, 1107-1131	3
1566	Condensins and 3D Organization of the Interphase Nucleus. <b>2013</b> , 1, 219-229	12
1565	Revealing long-range interconnected hubs in human chromatin interaction data using graph theory. <b>2013</b> , 111, 118102	29
1564	The regulation of Hox gene expression during animal development. <b>2013</b> , 140, 3951-63	200
1563	Long-range chromatin contacts in embryonic stem cells reveal a role for pluripotency factors and polycomb proteins in genome organization. <b>2013</b> , 13, 602-16	197
1562	Environmental Epigenomics in Health and Disease. <b>2013</b> ,	2
1561	Poly(ADP-ribosyl)ation regulates insulator function and intrachromosomal interactions in <i>Drosophila</i> . <b>2013</b> , 155, 148-59	56
1560	Ionizing radiation and genetic risks. XVII. Formation mechanisms underlying naturally occurring DNA deletions in the human genome and their potential relevance for bridging the gap between induced DNA double-strand breaks and deletions in irradiated germ cells. <b>2013</b> , 753, 114-130	16
1559	Cycles in spatial and temporal chromosomal organization driven by the circadian clock. <b>2013</b> , 20, 1206-13	86
1558	Single-cell Hi-C reveals cell-to-cell variability in chromosome structure. <b>2013</b> , 502, 59-64	994
1557	Biological techniques: Chromosomes captured one by one. <b>2013</b> , 502, 45-6	11
1556	Mapping human epigenomes. <b>2013</b> , 155, 39-55	405

1555	Changes in the organization of the genome during the mammalian cell cycle. <b>2013</b> , 14, 142	7
1554	Research in Computational Molecular Biology. <b>2013</b> ,	9
1553	54 DNA conformation and energy in nucleosome core: a theoretical approach. <b>2013</b> , 31, 33-34	0
1552	Dynamic changes of the epigenetic landscape during cellular differentiation. <b>2013</b> , 5, 701-13	12
1551	Regulation of AID, the B-cell genome mutator. <b>2013</b> , 27, 1-17	94
1550	Genome conformation capture reveals that the Escherichia coli chromosome is organized by replication and transcription. <b>2013</b> , 41, 6058-71	93
1549	Phenotypic impact of genomic structural variation: insights from and for human disease. <b>2013</b> , 14, 125-38	340
1548	DNA replication timing, genome stability and cancer: late and/or delayed DNA replication timing is associated with increased genomic instability. <b>2013</b> , 23, 80-9	78
1547	Spatial congregation of STAT binding directs selective nuclear architecture during T-cell functional differentiation. <b>2013</b> , 23, 462-72	38
1546	Regulation of a viral proteinase by a peptide and DNA in one-dimensional space: IV. viral proteinase slides along DNA to locate and process its substrates. <b>2013</b> , 288, 2092-102	40
1545	How glucocorticoid receptors modulate the activity of other transcription factors: a scope beyond tethering. <b>2013</b> , 380, 41-54	267
1544	Chromatin organization and transcriptional regulation. <b>2013</b> , 23, 89-95	121
1543	Genome-wide chromatin state transitions associated with developmental and environmental cues. <b>2013</b> , 152, 642-54	400
1542	Multiscale analysis of genome-wide replication timing profiles using a wavelet-based signal-processing algorithm. <b>2013</b> , 8, 98-110	36
1541	Chromatin organization: form to function. <b>2013</b> , 23, 185-90	37
1540	The Human Genome: A Window on Human Genetics, Biology, and Medicine. <b>2013</b> , 4-27	1
1539	Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes. <b>2013</b> , 23, 217-27	111
1538	Methods for cancer epigenome analysis. <b>2013</b> , 754, 313-38	21

1537	The Plant Nucleus at War and Peace: Genome Organization in the Interphase Nucleus. <b>2013</b> , 13-31	2
1536	Organization and segregation of bacterial chromosomes. <b>2013</b> , 14, 191-203	204
1535	Multiplexed chromosome conformation capture sequencing for rapid genome-scale high-resolution detection of long-range chromatin interactions. <b>2013</b> , 8, 509-24	116
1534	Chromatin structure outside and inside the nucleus. <b>2013</b> , 99, 225-32	20
1533	Exploring the effects of polymorphisms on cis-regulatory signal transduction response. <b>2013</b> , 19, 99-107	12
1532	Physical origin of the contact frequency in chromosome conformation capture data. <b>2013</b> , 105, 1786-95	5
1531	Nuclear location and the control of developmental progression. <b>2013</b> , 23, 104-8	3
1530	Response to Casellas et al. <b>2013</b> , 51, 277-8	2
1529	Chromatin Structure and Human Genome Evolution. <b>2013</b> ,	
1528	Exploring long-range genome interactions using the WashU Epigenome Browser. <b>2013</b> , 10, 375-6	167
1527	A tiered hidden Markov model characterizes multi-scale chromatin states. <b>2013</b> , 102, 1-7	7
1526	Complex genomic interactions in the dynamic regulation of transcription by the glucocorticoid receptor. <b>2013</b> , 380, 16-24	43
1525	2012 William Allan Award: Adventures in cytogenetics. <b>2013</b> , 92, 325-37	2
1524	Cancer genome sequencing: understanding malignancy as a disease of the genome, its conformation, and its evolution. <b>2013</b> , 340, 152-60	16
1523	The origin of B cell recurrent chromosomal translocations: proximity versus DNA damage. <b>2013</b> , 51, 275-6	5
1522	Transcription factories, chromatin loops, and the dysregulation of gene expression in malignancy. <b>2013</b> , 23, 65-71	34
1521	High-throughput sequencing for biology and medicine. <b>2013</b> , 9, 640	186
1520	Genome-wide distribution of DNA methylation and DNA demethylation and related chromatin regulators in cancer. <b>2013</b> , 1835, 155-63	17

1519	Correlated alterations in genome organization, histone methylation, and DNA-lamin A/C interactions in Hutchinson-Gilford progeria syndrome. <b>2013</b> , 23, 260-9	234
1518	Relationship between DNA replication and the nuclear matrix. <b>2013</b> , 18, 17-31	48
1517	Transcription regulatory codes of eukaryotic genomes. <b>2013</b> , 49, 29-45	8
1516	The Spatial Architecture of Chromosomes. <b>2013</b> , 137-151	6
1515	The RNA Pol II elongation factor Ell3 marks enhancers in ES cells and primes future gene activation. <b>2013</b> , 152, 144-56	73
1514	Structure and dynamics of molecular networks: a novel paradigm of drug discovery: a comprehensive review. <b>2013</b> , 138, 333-408	604
1513	The hierarchy of the 3D genome. <b>2013</b> , 49, 773-82	512
1512	Nuclear organization of RNA polymerase II transcription. <b>2013</b> , 91, 22-30	8
1511	CTCF and cohesin: linking gene regulatory elements with their targets. <b>2013</b> , 152, 1285-97	280
1510	Genome architecture: domain organization of interphase chromosomes. <b>2013</b> , 152, 1270-84	522
1509	"Seq-ing" insights into the epigenetics of neuronal gene regulation. <b>2013</b> , 77, 606-23	67
1508	A subset of Drosophila Myc sites remain associated with mitotic chromosomes colocalized with insulator proteins. <b>2013</b> , 4, 1464	47
1507	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <b>2013</b> , 45, 478-86	558
1506	Chromatin structure and organization: the relation with gene expression during development and disease. <b>2013</b> , 61, 373-96	6
1505	High Resolution Modeling of Chromatin Interactions. <b>2013</b> , 186-198	1
1504	A model of the large-scale organization of chromatin. <b>2013</b> , 41, 508-12	17
1503	The origin of recurrent translocations in recombining lymphocytes: a balance between break frequency and nuclear proximity. <b>2013</b> , 25, 365-71	11
1502	Chromatin looping and organization at developmentally regulated gene loci. <b>2013</b> , 2, 615-30	13

1501	Identical cells with different 3D genomes; cause and consequences?. <b>2013</b> , 23, 191-6	37
1500	Divergence of mammalian higher order chromatin structure is associated with developmental loci. <b>2013</b> , 9, e1003017	32
1499	Remodeling of three-dimensional organization of the nucleus during terminal keratinocyte differentiation in the epidermis. <b>2013</b> , 133, 2191-201	47
1498	Chromosomal domains: epigenetic contexts and functional implications of genomic compartmentalization. <b>2013</b> , 23, 197-203	52
1497	Transcription factories: genome organization and gene regulation. <b>2013</b> , 113, 8683-705	157
1496	Mechanisms of epigenetic regulation of leukemia onset and progression. <b>2013</b> , 117, 1-38	20
1495	Structural variations, the regulatory landscape of the genome and their alteration in human disease. <b>2013</b> , 35, 533-43	49
1494	Translocations in normal B cells and cancers: insights from new technical approaches. <b>2013</b> , 117, 39-71	3
1493	Systems proteomics of healthy and diseased chromatin. <b>2013</b> , 1005, 77-93	1
1492	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. <b>2013</b> , 14, 390-403	762
1491	Resolving spatial inconsistencies in chromosome conformation measurements. <b>2013</b> , 8, 8	7
1490	The replication domain model: regulating replicon firing in the context of large-scale chromosome architecture. <b>2013</b> , 425, 4690-5	27
1489	Genome organization and long-range regulation of gene expression by enhancers. <b>2013</b> , 25, 387-94	118
1488	Epigenetic control of cytokine gene expression: regulation of the TNF/LT locus and T helper cell differentiation. <b>2013</b> , 118, 37-128	51
1487	Architectural protein subclasses shape 3D organization of genomes during lineage commitment. <b>2013</b> , 153, 1281-95	848
1486	Chromatin insulators: linking genome organization to cellular function. <b>2013</b> , 50, 461-74	151
1485	Structure-driven homology pairing of chromatin fibers: the role of electrostatics and protein-induced bridging. <b>2013</b> , 39, 363-85	25
1484	Nucleotide resolution analysis of TMPRSS2 and ERG rearrangements in prostate cancer. <b>2013</b> , 230, 174-83	31

1483	Epigenetic layers and players underlying neurodevelopment. <b>2013</b> , 36, 460-70	66
1482	Klf4 organizes long-range chromosomal interactions with the oct4 locus in reprogramming and pluripotency. <b>2013</b> , 13, 36-47	157
1481	A polymer model explains the complexity of large-scale chromatin folding. <b>2013</b> , 4, 267-73	29
1480	Communication of genome regulatory elements in a folded chromosome. <b>2013</b> , 587, 1840-7	34
1479	Effect of nuclear architecture on the efficiency of double-strand break repair. <b>2013</b> , 15, 694-9	88
1478	Inference of Gene Regulatory Networks in Breast and Ovarian Cancer by Integrating Different Genomic Data. <b>2013</b> , 153-171	
1477	Genome-wide chromatin interactions of the Nanog locus in pluripotency, differentiation, and reprogramming. <b>2013</b> , 12, 699-712	161
1476	Successive gain of insulator proteins in arthropod evolution. <b>2013</b> , 67, 2945-56	21
1475	Mapping the Functional Genome. <b>2013</b> , 28-40	1
1474	Bridging epigenomics and complex disease: the basics. <b>2013</b> , 70, 1609-21	29
1473	Functional roles of enhancer RNAs for oestrogen-dependent transcriptional activation. <b>2013</b> , 498, 516-20	682
1472	Epigenetic Changes in Prostate Cancer. <b>2013</b> , 169-179	
1471	Chromatin meets its organizers. <b>2013</b> , 153, 1187-9	3
1470	The Xist lncRNA exploits three-dimensional genome architecture to spread across the X chromosome. <i>Science</i> , <b>2013</b> , 341, 1237973	333 695
1469	How next-generation sequencing is transforming complex disease genetics. <b>2013</b> , 29, 23-30	57
1468	Taking into account nucleosomes for predicting gene expression. <b>2013</b> , 62, 26-38	19
1467	On the stability of fractal globules. <b>2013</b> , 138, 224901	36
1466	Disclosure of a structural milieu for the proximity ligation reveals the elusive nature of an active chromatin hub. <b>2013</b> , 41, 3563-75	72

1465	P-value-based regulatory motif discovery using positional weight matrices. <b>2013</b> , 23, 181-94	51
1464	Interplay between chromatin modifications and paused RNA polymerase II in dynamic transition between stalled and activated genes. <b>2013</b> , 88, 40-8	19
1463	Fractal dimension of chromatin: potential molecular diagnostic applications for cancer prognosis. <b>2013</b> , 13, 719-35	54
1462	The genomic landscape of cohesin-associated chromatin interactions. <b>2013</b> , 23, 1224-34	85
1461	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. <b>2013</b> , 23, 228-35	109
1460	Chromatin and epigenetic features of long-range gene regulation. <b>2013</b> , 41, 7185-99	87
1459	Comparing the results of lattice and off-lattice simulations for the melt of nonconcatenated rings. <b>2013</b> , 46, 065002	21
1458	Nuclear Organization, Chromatin Structure, and Gene Silencing. <b>2013</b> , 314-317	
1457	Function and regulation of AUTS2, a gene implicated in autism and human evolution. <b>2013</b> , 9, e1003221	99
1456	Connecting chromatin modifying factors to DNA damage response. <b>2013</b> , 14, 2355-69	12
1455	Colocalization of coregulated genes: a steered molecular dynamics study of human chromosome 19. <b>2013</b> , 9, e1003019	40
1454	Topological constraints and chromosome organization in eukaryotes: a physical point of view. <b>2013</b> , 41, 612-5	8
1453	The links between chromatin spatial organization and biological function. <b>2013</b> , 41, 1634-9	5
1452	Cohesin-mediated interactions organize chromosomal domain architecture. <b>2013</b> , 32, 3119-29	303
1451	Human genome replication proceeds through four chromatin states. <b>2013</b> , 9, e1003233	46
1450	Drosophila functional elements are embedded in structurally constrained sequences. <b>2013</b> , 9, e1003512	10
1449	Deletion of an X-inactivation boundary disrupts adjacent gene silencing. <b>2013</b> , 9, e1003952	27
1448	A complex network framework for unbiased statistical analyses of DNA-DNA contact maps. <b>2013</b> , 41, 701-10	31

1447	High-resolution analysis of cis-acting regulatory networks at the $\beta$ -globin locus. <b>2013</b> , 368, 20120361	11
1446	Spatial localization of co-regulated genes exceeds genomic gene clustering in the <i>Saccharomyces cerevisiae</i> genome. <b>2013</b> , 41, 2191-201	40
1445	The statistical-mechanics of chromosome conformation capture. <b>2013</b> , 4, 390-8	35
1444	Epigenetic control by plant Polycomb proteins: new perspectives and emerging roles in stress response. <b>2013</b> , 31-48	0
1443	Chromatin reorganization through mitosis. <b>2013</b> , 90, 179-224	13
1442	Functional genomics of the inflammatory response: where are we now?. <b>2013</b> , 12, 483-8	7
1441	Centromeric motion facilitates the mobility of interphase genomic regions in fission yeast. <b>2013</b> , 126, 5271-83	16
1440	Transcription factor and chromatin features predict genes associated with eQTLs. <b>2013</b> , 41, 1450-63	22
1439	Space exploration by the promoter of a long human gene during one transcription cycle. <b>2013</b> , 41, 2216-27	21
1438	Estrogen represses gene expression through reconfiguring chromatin structures. <b>2013</b> , 41, 8061-71	13
1437	Micron-scale coherence in interphase chromatin dynamics. <b>2013</b> , 110, 15555-60	155
1436	DNA double-strand-break complexity levels and their possible contributions to the probability for error-prone processing and repair pathway choice. <b>2013</b> , 41, 7589-605	184
1435	A quality control system for profiles obtained by ChIP sequencing. <b>2013</b> , 41, e196	29
1434	Enhancer networks revealed by correlated DNase hypersensitivity states of enhancers. <b>2013</b> , 41, 6828-38	19
1433	The nucleolus: a raft adrift in the nuclear sea or the keystone in nuclear structure?. <b>2013</b> , 4, 277-86	14
1432	Detecting DNA-protein interactions in living cells--ChIP approach. <b>2013</b> , 91, 101-33	4
1431	Recovering ensembles of chromatin conformations from contact probabilities. <b>2013</b> , 41, 63-75	62
1430	An autonomous chromatin/DNA-PK mechanism for localized DNA damage signaling in mammalian cells. <b>2013</b> , 41, 2894-906	7

1429	The sequencing bias relaxed characteristics of Hi-C derived data and implications for chromatin 3D modeling. <b>2013</b> , 41, e183	38
1428	Combining Hi-C data with phylogenetic correlation to predict the target genes of distal regulatory elements in human genome. <b>2013</b> , 41, 10391-402	15
1427	The epigenetics of early lymphocyte development. <b>2013</b> , 78, 43-9	
1426	Genomic Architecture may Influence Recurrent Chromosomal Translocation Frequency in the Igh Locus. <b>2013</b> , 4, 500	4
1425	High-throughput identification of long-range regulatory elements and their target promoters in the human genome. <b>2013</b> , 41, 4835-46	23
1424	Topological properties of chromosome conformation graphs reflect spatial proximities within chromatin. <b>2013</b> ,	4
1423	Polymer model with long-range interactions: analysis and applications to the chromatin structure. <b>2013</b> , 88, 052604	36
1422	Handling realistic assumptions in hypothesis testing of 3D co-localization of genomic elements. <b>2013</b> , 41, 5164-74	21
1421	Maintenance of interphase chromosome compaction and homolog pairing in <i>Drosophila</i> is regulated by the condensin cap-h2 and its partner Mrg15. <b>2013</b> , 195, 127-46	26
1420	Diffusing polymers in confined microdomains and estimation of chromosomal territory sizes from chromosome capture data. <b>2013</b> , 110, 248105	25
1419	Genome-wide profiling of chromosome interactions in <i>Plasmodium falciparum</i> characterizes nuclear architecture and reconfigurations associated with antigenic variation. <b>2013</b> , 90, 519-37	37
1418	DNA replication timing. <b>2013</b> , 5, a010132	197
1417	Mechanisms of eukaryotic transcription: A meeting report. <b>2013</b> , 4, 273-285	
1416	How to build a yeast nucleus. <b>2013</b> , 4, 361-6	16
1415	Conserved chromosome 2q31 conformations are associated with transcriptional regulation of GAD1 GABA synthesis enzyme and altered in prefrontal cortex of subjects with schizophrenia. <b>2013</b> , 33, 11839-51	50
1414	Functional sub-division of the <i>Drosophila</i> genome via chromatin looping: the emerging importance of CP190. <b>2013</b> , 4, 115-22	19
1413	Genome organization by Klf4 regulates transcription in pluripotent stem cells. <b>2013</b> , 12, 3351-2	6
1412	Using chimaeric expression sequence tag as the reference to identify three-dimensional chromosome contacts. <b>2013</b> , 20, 45-53	2

1411	The shared genomic architecture of human nucleolar organizer regions. <b>2013</b> , 23, 2003-12	75
1410	Genome-wide prediction of nucleosome occupancy in maize reveals plant chromatin structural features at genes and other elements at multiple scales. <b>2013</b> , 162, 1127-41	24
1409	High-order chromatin structure and the epigenome in SAHFs. <b>2013</b> , 4, 23-8	46
1408	UpSET-ting the balance: modulating open chromatin features in metazoan genomes. <b>2013</b> , 7, 153-60	2
1407	Epigenetic regulation of the human genome: coherence between promoter activity and large-scale chromatin environment. <b>2013</b> , 7, 44-62	7
1406	Computational detection of abundant long-range nucleotide covariation in Drosophila genomes. <b>2013</b> , 19, 1171-82	5
1405	DNA looping in prokaryotes: experimental and theoretical approaches. <b>2013</b> , 195, 1109-19	54
1404	r3Cseq: an R/Bioconductor package for the discovery of long-range genomic interactions from chromosome conformation capture and next-generation sequencing data. <b>2013</b> , 41, e132	67
1403	Caulobacter chromosome in vivo configuration matches model predictions for a supercoiled polymer in a cell-like confinement. <b>2013</b> , 110, 1674-9	21
1402	Massively parallel sequencing: the new frontier of hematologic genomics. <b>2013</b> , 122, 3268-75	17
1401	Characterization of chromosomal architecture in Arabidopsis by chromosome conformation capture. <b>2013</b> , 14, R129	64
1400	DNA sequencing methods in human genetics and disease research. <b>2013</b> , 5, 34	6
1399	The interactomes of POU5F1 and SOX2 enhancers in human embryonic stem cells. <b>2013</b> , 3, 1588	27
1398	A quantitative model of ERK MAP kinase phosphorylation in crowded media. <b>2013</b> , 3, 1541	37
1397	Non-linear dynamics of chromosome condensation induced by colcemid. <b>2013</b> , 56, 85-92	4
1396	[Three-dimensional genome organization: a lesson from the Polycomb-Group proteins]. <b>2013</b> , 207, 19-31	
1395	G+C Content Evolution in the Human Genome. <b>2013</b> ,	6
1394	Genomic interaction profiles in breast cancer reveal altered chromatin architecture. <b>2013</b> , 8, e73974	30

1393	From genes to milk: genomic organization and epigenetic regulation of the mammary transcriptome. <b>2013</b> , 8, e75030	14
1392	NuChart: an R package to study gene spatial neighbourhoods with multi-omics annotations. <b>2013</b> , 8, e75146	26
1391	The network architecture of the <i>Saccharomyces cerevisiae</i> genome. <b>2013</b> , 8, e81972	9
1390	Polymer models of chromatin organization. <b>2013</b> , 4, 113	12
1389	Do chromatin changes around a nascent double strand DNA break spread spherically into linearly non-adjacent chromatin?. <b>2013</b> , 4, 139	2
1388	Chromatin structure and transposable elements in organismal aging. <b>2013</b> , 4, 274	80
1387	Understanding the Dynamics of Gene Regulatory Systems; Characterisation and Clinical Relevance of cis-Regulatory Polymorphisms. <b>2013</b> , 2, 64-84	7
1386	Insights into chromatin structure and dynamics in plants. <b>2013</b> , 2, 1378-410	22
1385	Locus-specific biochemical epigenetics/chromatin biochemistry by insertional chromatin immunoprecipitation. <b>2013</b> , 2013, 913273	15
1384	DNA.EXE: A Sequence Comparison between the Human Genome and Computer Code. <b>2013</b> ,	3
1383	visPIG--a web tool for producing multi-region, multi-track, multi-scale plots of genetic data. <b>2014</b> , 9, e107497	36
1382	The influence of promoter architectures and regulatory motifs on gene expression in <i>Escherichia coli</i> . <b>2014</b> , 9, e114347	21
1381	Single-molecule tracking in live cells reveals distinct target-search strategies of transcription factors in the nucleus. <b>2014</b> , 3,	196
1380	Mechanisms and proteins involved in long-distance interactions. <b>2014</b> , 5, 28	53
1379	Genetic anchoring of whole-genome shotgun assemblies. <b>2014</b> , 5, 208	40
1378	Insights from space: potential role of diet in the spatial organization of chromosomes. <b>2014</b> , 6, 5724-39	4
1377	A statistical approach for inferring the 3D structure of the genome. <b>2014</b> , 30, i26-33	149
1376	The Epithelial-to-Mesenchymal Transition (EMT), a Particular Case. <b>2014</b> , 1, e960770	4

1375	Physical mechanisms behind the large scale features of chromatin organization. <b>2014</b> , 5, e28447	7
1374	Are genes switched on when they kiss?. <b>2014</b> , 5, 103-12	6
1373	Retrotransposon Alu is enriched in the epichromatin of HL-60 cells. <b>2014</b> , 5, 237-46	17
1372	Approaches for establishing the function of regulatory genetic variants involved in disease. <b>2014</b> , 6, 92	31
1371	RNA polymerase II forms transcription networks in rye and Arabidopsis nuclei and its amount increases with endopolyploidy. <b>2014</b> , 143, 69-77	20
1370	lncRNA and gene looping: what's the connection?. <b>2014</b> , 5, e28658	21
1369	Functional chromatin features are associated with structural mutations in cancer. <b>2014</b> , 15, 1013	6
1368	Two ways to fold the genome during the cell cycle: insights obtained with chromosome conformation capture. <b>2014</b> , 7, 25	60
1367	De novo prediction of cis-regulatory elements and modules through integrative analysis of a large number of ChIP datasets. <b>2014</b> , 15, 1047	9
1366	Dynamics of double strand breaks and chromosomal translocations. <b>2014</b> , 13, 249	33
1365	Reprogramming of fibroblast nuclei in cloned bovine embryos involves major structural remodeling with both striking similarities and differences to nuclear phenotypes of in vitro fertilized embryos. <b>2014</b> , 5, 555-89	37
1364	The clustering of CpG islands may constitute an important determinant of the 3D organization of interphase chromosomes. <b>2014</b> , 9, 951-63	13
1363	Functions of noncoding sequences in mammalian genomes. <b>2014</b> , 79, 1442-69	37
1362	Functional redundancy in the nuclear compartmentalization of the late-replicating genome. <b>2014</b> , 5, 626-35	28
1361	Open chromatin in plant genomes. <b>2014</b> , 143, 18-27	15
1360	Nuclear architecture and chromatin dynamics in interphase nuclei of Arabidopsis thaliana. <b>2014</b> , 143, 28-50	19
1359	Biased, non-equivalent gene-proximal and -distal binding motifs of orphan nuclear receptor TR4 in primary human erythroid cells. <b>2014</b> , 10, e1004339	6
1358	Effects of supercoiling on enhancer-promoter contacts. <b>2014</b> , 42, 10425-32	27

1357	The bone-specific Runx2-P1 promoter displays conserved three-dimensional chromatin structure with the syntenic Supt3h promoter. <b>2014</b> , 42, 10360-72	20
1356	Assembly and characterization of novel inserts detected from next-generation sequencing data. <b>2014</b> , 4, 1-7	3
1355	Decoding the role of chromatin architecture in development: coming closer to the end of the tunnel. <b>2014</b> , 5, 374	3
1354	Chromatin associations in Arabidopsis interphase nuclei. <b>2014</b> , 5, 389	22
1353	Depletion of the chromatin looping proteins CTCF and cohesin causes chromatin compaction: insight into chromatin folding by polymer modelling. <b>2014</b> , 10, e1003877	49
1352	metaseq: a Python package for integrative genome-wide analysis reveals relationships between chromatin insulators and associated nuclear mRNA. <b>2014</b> , 42, 9158-70	21
1351	Cell type specific alterations in interchromosomal networks across the cell cycle. <b>2014</b> , 10, e1003857	14
1350	A Study of Fractality and Long-Range Order in the Distribution of Transposable Elements in Eukaryotic Genomes Using the Scaling Properties of Block Entropy and Box-Counting. <b>2014</b> , 16, 1860-1882	3
1349	Functional organization and dynamics of the cell nucleus. <b>2014</b> , 5, 378	22
1348	p53 binding to human genome: crowd control navigation in chromatin context. <b>2014</b> , 5, 447	5
1347	A Journey Through Genetics [Part II]. <b>2014</b> , 3, 1-71	
1346	High-quality genome (re)assembly using chromosomal contact data. <b>2014</b> , 5, 5695	104
1345	Three-dimensional eukaryotic genomic organization is strongly correlated with codon usage expression and function. <b>2014</b> , 5, 5876	19
1344	Epigenetic targeting of activation-induced cytidine deaminase. <b>2014</b> , 111, 18667-72	37
1343	B cell super-enhancers and regulatory clusters recruit AID tumorigenic activity. <b>2014</b> , 159, 1524-37	186
1342	Investigation of the spatial genome organization of mouse sperm and fibroblasts by the Hi-C method. <b>2014</b> , 4, 556-560	1
1341	Mapping of long-range INS promoter interactions reveals a role for calcium-activated chloride channel ANO1 in insulin secretion. <b>2014</b> , 111, 16760-5	24
1340	A statistical model of ChIA-PET data for accurate detection of chromatin 3D interactions. <b>2014</b> , 42, e143	38

1339	Ring polymers in the melt state: the physics of crumpling. <b>2014</b> , 112, 118302	117
1338	A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. <b>2014</b> , 159, 1665-80	3824
1337	The epigenomic tool kit. <b>2014</b> , 12, 27-33	
1336	A Systems Biology Approach to Blood. <b>2014</b> ,	2
1335	Answering the demands of digital genomics. <b>2014</b> , 26, 917-928	1
1334	The future of neuroepigenetics in the human brain. <b>2014</b> , 128, 199-228	10
1333	Probing transient protein-mediated DNA linkages using nanoconfinement. <b>2014</b> , 8, 034113	11
1332	Cell transcriptional state alters genomic patterns of DNA double-strand break repair in human astrocytes. <b>2014</b> , 5, 5799	9
1331	Genomic occupancy of Runx2 with global expression profiling identifies a novel dimension to control of osteoblastogenesis. <b>2014</b> , 15, R52	95
1330	From the chromatin interaction network to the organization of the human genome into replication N/U-domains. <b>2014</b> , 16, 115014	8
1329	Single cell correlation fractal dimension of chromatin: a framework to interpret 3D single molecule super-resolution. <b>2014</b> , 5, 75-84	30
1328	Distance-based assessment of the localization of functional annotations in 3D genome reconstructions. <b>2014</b> , 15, 992	10
1327	Nanoscale changes in chromatin organization represent the initial steps of tumorigenesis: a transmission electron microscopy study. <b>2014</b> , 14, 189	57
1326	Deletions of chromosomal regulatory boundaries are associated with congenital disease. <b>2014</b> , 15, 423	108
1325	Models that include supercoiling of topological domains reproduce several known features of interphase chromosomes. <b>2014</b> , 42, 2848-55	90
1324	IgH class switching exploits a general property of two DNA breaks to be joined in cis over long chromosomal distances. <b>2014</b> , 111, 2644-9	30
1323	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. <b>2014</b> , 111, 14631-6	28
1322	Higher-order chromatin domains link eQTLs with the expression of far-away genes. <b>2014</b> , 42, 87-96	37

1321	Collaboration between CpG sites is needed for stable somatic inheritance of DNA methylation states. <b>2014</b> , 42, 2235-44	54
1320	Hox in motion: tracking HoxA cluster conformation during differentiation. <b>2014</b> , 42, 1524-40	38
1319	Control of VEGF-A transcriptional programs by pausing and genomic compartmentalization. <b>2014</b> , 42, 12570-84	34
1318	Chromosome positioning from activity-based segregation. <b>2014</b> , 42, 4145-59	81
1317	Two-dimensional segmentation for analyzing Hi-C data. <b>2014</b> , 30, i386-92	99
1316	Quantitative analysis of genomic element interactions by molecular colony technique. <b>2014</b> , 42, e36	21
1315	Estrogen receptor coregulators and pioneer factors: the orchestrators of mammary gland cell fate and development. <b>2014</b> , 2, 34	54
1314	Exploring genomes with a game engine. <b>2014</b> , 169, 443-53	6
1313	Crowding-induced formation and structural alteration of nuclear compartments: insights from computer simulations. <b>2014</b> , 307, 73-108	13
1312	Transcriptional Control of Lineage Differentiation in Immune Cells. <b>2014</b> ,	
1311	Chromatin without the 30-nm fiber: constrained disorder instead of hierarchical folding. <b>2014</b> , 9, 653-7	35
1310	Nucleosome eviction and multiple co-factor binding predict estrogen-receptor-alpha-associated long-range interactions. <b>2014</b> , 42, 6935-44	9
1309	fourSig: a method for determining chromosomal interactions in 4C-Seq data. <b>2014</b> , 42, e68	32
1308	HiBrowse: multi-purpose statistical analysis of genome-wide chromatin 3D organization. <b>2014</b> , 30, 1620-2	33
1307	Modeling epigenome folding: formation and dynamics of topologically associated chromatin domains. <b>2014</b> , 42, 9553-61	247
1306	Characterization of human chromosomal material exchange with regard to the chromosome translocations using next-generation sequencing data. <b>2014</b> , 6, 3015-24	2
1305	Folded genome as a platform for the functional compartmentalization of the eukaryotic cell nucleus. <b>2014</b> , 30, 83-89	3
1304	CTCF and ncRNA Regulate the Three-Dimensional Structure of Antigen Receptor Loci to Facilitate V(D)J Recombination. <b>2014</b> , 5, 49	29

1303	CTCF induces histone variant incorporation, erases the H3K27me3 histone mark and opens chromatin. <b>2014</b> , 42, 11941-51	29
1302	Species-level deconvolution of metagenome assemblies with Hi-C-based contact probability maps. <b>2014</b> , 4, 1339-46	120
1301	Spatial confinement is a major determinant of the folding landscape of human chromosomes. <b>2014</b> , 42, 8223-30	43
1300	Chromosome conformation maps in fission yeast reveal cell cycle dependent sub nuclear structure. <b>2014</b> , 42, 12585-99	20
1299	Finite-Size Conformational Transitions: A Unifying Concept Underlying Chromosome Dynamics. <b>2014</b> , 62, 607-616	10
1298	Correlations of three-dimensional motion of chromosomal loci in yeast revealed by the double-helix point spread function microscope. <b>2014</b> , 25, 3619-29	46
1297	Spatial genome organization: contrasting views from chromosome conformation capture and fluorescence in situ hybridization. <b>2014</b> , 28, 2778-91	197
1296	Estrogen receptor-mediated long-range chromatin interactions and transcription in breast cancer. <b>2014</b> , 382, 624-632	25
1295	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. <b>2014</b> ,	
1294	Navigating and mining modENCODE data. <b>2014</b> , 68, 38-47	14
1293	Evolution of Alu elements toward enhancers. <b>2014</b> , 7, 376-385	81
1292	From first-passage times of random walks in confinement to geometry-controlled kinetics. <b>2014</b> , 539, 225-284	146
1291	The biology of boundary conditions: cellular reconstitution in one, two, and three dimensions. <b>2014</b> , 26, 60-8	22
1290	Three-dimensional modeling of the <i>P. falciparum</i> genome during the erythrocytic cycle reveals a strong connection between genome architecture and gene expression. <b>2014</b> , 24, 974-88	147
1289	Transcriptional enhancers: from properties to genome-wide predictions. <b>2014</b> , 15, 272-86	820
1288	Filling annotation gaps in yeast genomes using genome-wide contact maps. <b>2014</b> , 30, 2105-13	31
1287	Detection and replication of epistasis influencing transcription in humans. <b>2014</b> , 508, 249-53	149
1286	3D view of chromosomes, DNA damage, and translocations. <b>2014</b> , 25, 118-25	8

1285	The role of DNA methylation in stress-related psychiatric disorders. <b>2014</b> , 80, 115-32	207
1284	Fungal Genomics. <b>2014</b> ,	0
1283	Sex differences in the incidence of chronic myeloid leukemia. <b>2014</b> , 53, 55-63	22
1282	Long non-coding RNA in health and disease. <b>2014</b> , 92, 337-46	172
1281	Disruption of long-range gene regulation in human genetic disease: a kaleidoscope of general principles, diverse mechanisms and unique phenotypic consequences. <b>2014</b> , 133, 815-45	25
1280	Obesity-associated variants within FTO form long-range functional connections with IRX3. <b>2014</b> , 507, 371-5	835
1279	Laying a solid foundation for Manhattan--'setting the functional basis for the post-GWAS era'. <b>2014</b> , 30, 140-9	68
1278	Gathering around Firre. <b>2014</b> , 21, 207-8	8
1277	DNA double-strand breaks: linking gene expression to chromosome morphology and mobility. <b>2014</b> , 123, 103-15	12
1276	The dynamic architectural and epigenetic nuclear landscape: developing the genomic almanac of biology and disease. <b>2014</b> , 229, 711-27	11
1275	Transcription in the context of the 3D nucleus. <b>2014</b> , 25, 62-7	28
1274	Epigenetics, plasticity, and evolution: How do we link epigenetic change to phenotype?. <b>2014</b> , 322, 208-20	142
1273	Complex correlations: replication timing and mutational landscapes during cancer and genome evolution. <b>2014</b> , 25, 93-100	55
1272	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. <b>2014</b> , 24, 1053-63	147
1271	Helper T cell plasticity: impact of extrinsic and intrinsic signals on transcriptomes and epigenomes. <b>2014</b> , 381, 279-326	36
1270	Transcriptional control of a whole chromosome: emerging models for dosage compensation. <b>2014</b> , 21, 118-25	42
1269	Wide-scale alterations in interchromosomal organization in breast cancer cells: defining a network of interacting chromosomes. <b>2014</b> , 23, 5133-46	20
1268	Network types and their application in natural variation studies in plants. <b>2014</b> , 18, 80-6	8

1267	Models of chromosome structure. <b>2014</b> , 28, 90-5	76
1266	p63 and Brg1 control developmentally regulated higher-order chromatin remodelling at the epidermal differentiation complex locus in epidermal progenitor cells. <b>2014</b> , 141, 101-11	61
1265	Manipulating nuclear architecture. <b>2014</b> , 25, 1-7	21
1264	Epigenetic landscape for initiation of DNA replication. <b>2014</b> , 123, 183-99	16
1263	Fractals in the Neurosciences, Part I: General Principles and Basic Neurosciences. <b>2014</b> , 20, 403-417	101
1262	Annealed lattice animal model and Flory theory for the melt of non-concatenated rings: towards the physics of crumpling. <b>2014</b> , 10, 560-5	84
1261	Co-expressed genes prepositioned in spatial neighborhoods stochastically associate with SC35 speckles and RNA polymerase II factories. <b>2014</b> , 71, 1741-59	37
1260	A Crowdsourced nucleus: understanding nuclear organization in terms of dynamically networked protein function. <b>2014</b> , 1839, 178-90	4
1259	From a melt of rings to chromosome territories: the role of topological constraints in genome folding. <b>2014</b> , 77, 022601	180
1258	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. <b>2014</b> , 46, 205-12	331
1257	Histone variants: the tricksters of the chromatin world. <b>2014</b> , 25, 8-14,138	36
1256	Chromosomes: now in 3D!. <b>2014</b> , 15, 6	6
1255	Chromatin immunoprecipitation indirect peaks highlight long-range interactions of insulator proteins and Pol II pausing. <b>2014</b> , 53, 672-81	68
1254	Fundamentals of vitamin D hormone-regulated gene expression. <b>2014</b> , 144 Pt A, 5-11	86
1253	How chromatin looping and nuclear envelope attachment affect genome organization in eukaryotic cell nuclei. <b>2014</b> , 307, 351-81	17
1252	Relevance and limitations of crowding, fractal, and polymer models to describe nuclear architecture. <b>2014</b> , 307, 443-79	27
1251	Distal enhancers: new insights into heart development and disease. <b>2014</b> , 24, 294-302	32
1250	The genome in three dimensions: a new frontier in human brain research. <b>2014</b> , 75, 961-9	45

1249	CTCF and cohesin cooperate to organize the 3D structure of the mammalian genome. <b>2014</b> , 111, 889-90	17
1248	Message control in developmental transitions; deciphering chromatin's role using zebrafish genomics. <b>2014</b> , 13, 106-20	
1247	Subtelomeres. <b>2014</b> ,	6
1246	Polycomb silencing: from linear chromatin domains to 3D chromosome folding. <b>2014</b> , 25, 30-7	68
1245	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. <b>2014</b> , 24, 14-24	371
1244	Closing the (nuclear) envelope on the genome: how nuclear lamins interact with promoters and modulate gene expression. <b>2014</b> , 36, 75-83	41
1243	Surviving an identity crisis: a revised view of chromatin insulators in the genomics era. <b>2014</b> , 1839, 203-14	36
1242	Heterochromatin structure: lessons from the budding yeast. <b>2014</b> , 66, 657-66	8
1241	Large replication skew domains delimit GC-poor gene deserts in human. <b>2014</b> , 53 Pt A, 153-65	3
1240	Large-scale reconstruction of 3D structures of human chromosomes from chromosomal contact data. <b>2014</b> , 42, e52	52
1239	Cohesin-dependent globules and heterochromatin shape 3D genome architecture in <i>S. pombe</i> . <b>2014</b> , 516, 432-435	188
1238	Analytical tools and current challenges in the modern era of neuroepigenomics. <b>2014</b> , 17, 1476-90	75
1237	Polymer models of interphase chromosomes. <b>2014</b> , 5, 376-90	23
1236	Fractal globules: a new approach to artificial molecular machines. <b>2014</b> , 107, 2361-8	8
1235	Beyond modules and hubs: the potential of gene coexpression networks for investigating molecular mechanisms of complex brain disorders. <b>2014</b> , 13, 13-24	172
1234	Crumpled globule formation during collapse of a long flexible and semiflexible polymer in poor solvent. <b>2014</b> , 141, 134903	19
1233	Evidence for local regulatory control of escape from imprinted X chromosome inactivation. <b>2014</b> , 197, 715-23	13
1232	Nuclear matrix and structural and functional compartmentalization of the eucaryotic cell nucleus. <b>2014</b> , 79, 608-18	8

1231	Predicting interactome network perturbations in human cancer: application to gene fusions in acute lymphoblastic leukemia. <b>2014</b> , 25, 3973-85	11
1230	Decoding neural transcriptomes and epigenomes via high-throughput sequencing. <b>2014</b> , 17, 1463-75	42
1229	DNA clustering and genome complexity. <b>2014</b> , 53 Pt A, 71-8	6
1228	Functional gene groups are concentrated within chromosomes, among chromosomes and in the nuclear space of the human genome. <b>2014</b> , 42, 9854-61	63
1227	A large permissive regulatory domain exclusively controls Tbx3 expression in the cardiac conduction system. <b>2014</b> , 115, 432-41	32
1226	Retrieving the intracellular topology from multi-scale protein mobility mapping in living cells. <b>2014</b> , 5, 4494	100
1225	Generalized time-dependent model of radiation-induced chromosomal aberrations in normal and repair-deficient human cells. <b>2014</b> , 181, 284-92	9
1224	Nuclear physics (of the cell, not the atom). <b>2014</b> , 25, 3466-9	5
1223	Telomere position effect: regulation of gene expression with progressive telomere shortening over long distances. <b>2014</b> , 28, 2464-76	178
1222	Combining a wavelet change point and the Bayes factor for analysing chromosomal interaction data. <b>2014</b> , 10, 1576-85	25
1221	Unusual size-dependence of effective interactions between collapsed polymers in crowded environments. <b>2014</b> , 10, 9098-104	5
1220	Stem cell senescence in diabetes: forgetting the sweet old memories. <b>2014</b> , 63, 1841-3	5
1219	Distinct structural transitions of chromatin topological domains correlate with coordinated hormone-induced gene regulation. <b>2014</b> , 28, 2151-62	201
1218	pENCODE: a plant encyclopedia of DNA elements. <b>2014</b> , 48, 49-70	28
1217	Transcription as a force partitioning the eukaryotic genome. <b>2014</b> , 395, 1301-5	7
1216	Geometry of the nucleus: a perspective on gene expression regulation. <b>2014</b> , 20, 112-9	42
1215	Genome-wide map of regulatory interactions in the human genome. <b>2014</b> , 24, 1905-17	197
1214	FisHiCal: an R package for iterative FISH-based calibration of Hi-C data. <b>2014</b> , 30, 3120-2	25

1213	Computational models of large-scale genome architecture. <b>2014</b> , 307, 275-349	51
1212	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. <b>2014</b> , 24, 1854-68	168
1211	Genome-wide Hi-C analyses in wild-type and mutants reveal high-resolution chromatin interactions in Arabidopsis. <b>2014</b> , 55, 694-707	216
1210	3D trajectories adopted by coding and regulatory DNA elements: first-passage times for genomic interactions. <b>2014</b> , 158, 339-352	165
1209	Genome-wide mapping and characterization of Notch-regulated long noncoding RNAs in acute leukemia. <b>2014</b> , 158, 593-606	335
1208	The Alu-rich genomic architecture of SPAST predisposes to diverse and functionally distinct disease-associated CNV alleles. <b>2014</b> , 95, 143-61	66
1207	Integrated genomic characterization of adrenocortical carcinoma. <b>2014</b> , 46, 607-12	423
1206	Expanding the roles of chromatin insulators in nuclear architecture, chromatin organization and genome function. <b>2014</b> , 71, 4089-113	13
1205	The role of chromatin dynamics in immune cell development. <b>2014</b> , 261, 9-22	35
1204	Transcriptional and epigenetic networks of helper T and innate lymphoid cells. <b>2014</b> , 261, 23-49	65
1203	Yeast Genetics. <b>2014</b> ,	10
1202	Das methodische Potenzial der neuen Sequenziertechnologien jenseits der Mutationssuche. <b>2014</b> , 26, 264-272	
1201	PVT: an efficient computational procedure to speed up next-generation sequence analysis. <b>2014</b> , 15, 167	3
1200	Transcriptional regulation and spatial interactions of head-to-head genes. <b>2014</b> , 15, 519	9
1199	Distribution of segmental duplications in the context of higher order chromatin organisation of human chromosome 7. <b>2014</b> , 15, 537	4
1198	Targeted Chromatin Capture (T2C): a novel high resolution high throughput method to detect genomic interactions and regulatory elements. <b>2014</b> , 7, 10	66
1197	3D genome reconstruction from chromosomal contacts. <b>2014</b> , 11, 1141-3	173
1196	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. <b>2014</b> , 32, 1019-25	152

1195	Hi-C analysis in Arabidopsis identifies the KNOT, a structure with similarities to the flamenco locus of Drosophila. <b>2014</b> , 55, 678-93	190
1194	Chromatin as dynamic 10-nm fibers. <b>2014</b> , 123, 225-37	143
1193	Three-dimensional super-resolution microscopy of the inactive X chromosome territory reveals a collapse of its active nuclear compartment harboring distinct Xist RNA foci. <b>2014</b> , 7, 8	129
1192	Cohesin mutations in myeloid malignancies: underlying mechanisms. <b>2014</b> , 3, 13	34
1191	Genome-wide profiling of transcription factor binding and epigenetic marks in adipocytes by CHIP-seq. <b>2014</b> , 537, 261-79	20
1190	The establishment of B versus T cell identity. <b>2014</b> , 35, 205-10	30
1189	The Impact of Next-Generation Sequencing Technology on Bacterial Genomics. <b>2014</b> , 31-58	2
1188	A mechanistic link between gene regulation and genome architecture in mammalian development. <b>2014</b> , 27, 92-101	34
1187	A Systems Theoretic Approach to Systems and Synthetic Biology II: Analysis and Design of Cellular Systems. <b>2014</b> ,	
1186	Lange nichtkodierende RNA (lncRNA). <b>2014</b> , 26, 5-10	1
1185	Equal impact of diffusion and DNA binding rates on the potential spatial distribution of nuclear factor B transcription factor inside the nucleus. <b>2014</b> , 79, 577-80	
1184	Spatial organization of interphase chromosomes and the role of chromatin fibril dynamics in the positioning of genome elements. <b>2014</b> , 48, 332-339	
1183	Nucleosome positioning and histone modifications define relationships between regulatory elements and nearby gene expression in breast epithelial cells. <b>2014</b> , 15, 331	33
1182	Identification of alternative topological domains in chromatin. <b>2014</b> , 9, 14	142
1181	The intriguing complexities of mammalian gene regulation: how to link enhancers to regulated genes. Are we there yet?. <b>2014</b> , 588, 2379-91	14
1180	Multiscale representation of genomic signals. <b>2014</b> , 11, 689-94	21
1179	Cell-imprinted substrates act as an artificial niche for skin regeneration. <b>2014</b> , 6, 13280-92	55
1178	Quantitation of interactions between two DNA loops demonstrates loop domain insulation in E. coli cells. <b>2014</b> , 111, E4449-57	17

1177	Menzerath-Altmann law in mammalian exons reflects the dynamics of gene structure evolution. <b>2014</b> , 53 Pt A, 134-43	6
1176	Algorithms in Bioinformatics. <b>2014</b> ,	3
1175	Identifying and mitigating bias in next-generation sequencing methods for chromatin biology. <b>2014</b> , 15, 709-21	227
1174	Architectural proteins: regulators of 3D genome organization in cell fate. <b>2014</b> , 24, 703-11	76
1173	Statistical confidence estimation for Hi-C data reveals regulatory chromatin contacts. <b>2014</b> , 24, 999-1011	291
1172	Chromatin and epigenetic determinants of estrogen receptor alpha (ESR1) signaling. <b>2014</b> , 382, 633-641	41
1171	Chromatin hydrodynamics. <b>2014</b> , 106, 1871-81	71
1170	Nuclear architecture as an epigenetic regulator of neural development and function. <b>2014</b> , 264, 39-50	20
1169	Gene positioning and genome function. <b>2014</b> , 9, 255-268	
1168	Switching on sex: transcriptional regulation of the testis-determining gene Sry. <b>2014</b> , 141, 2195-205	86
1167	The impact of chromosomal rearrangements on regulation of gene expression. <b>2014</b> , 23, R76-82	54
1166	The 3D genome in transcriptional regulation and pluripotency. <b>2014</b> , 14, 762-75	259
1165	Reproducibility of 3D chromatin configuration reconstructions. <b>2014</b> , 15, 442-56	20
1164	Transcriptional consequences of 16p11.2 deletion and duplication in mouse cortex and multiplex autism families. <b>2014</b> , 94, 870-83	78
1163	Chromatin barcodes as biomarkers for melanoma. <b>2014</b> , 27, 788-800	17
1162	The 3DGD: a database of genome 3D structure. <b>2014</b> , 30, 1640-2	10
1161	Chromatin structure and replication origins: determinants of chromosome replication and nuclear organization. <b>2014</b> , 426, 3330-41	28
1160	Proximity within interphase chromosome contributes to the breakpoint distribution in radiation-induced intrachromosomal exchanges. <b>2014</b> , 2, 23-28	

1159	SMC complexes link gene expression and genome architecture. <b>2014</b> , 25, 131-7	13
1158	Unraveling architecture of the pluripotent genome. <b>2014</b> , 28, 96-104	22
1157	Imaging RNA Polymerase II transcription sites in living cells. <b>2014</b> , 25, 126-30	31
1156	Viscoelasticity of model interphase chromosomes. <b>2014</b> , 141, 245101	8
1155	Structures and functions in the crowded nucleus: new biophysical insights. <b>2014</b> , 2,	12
1154	Effect of chromosome tethering on nuclear organization in yeast. <b>2014</b> , 9, e102474	18
1153	The missing story behind Genome Wide Association Studies: single nucleotide polymorphisms in gene deserts have a story to tell. <b>2014</b> , 5, 39	33
1152	Binding the boundaries of chromatin domains. <b>2014</b> , 15, 121	1
1151	First-Passage Statistics for Random Walks in Bounded Domains. <b>2014</b> , 145-174	
1150	References. 301-333	
1149	Dynamics of enhancers in myeloid antigen presenting cells upon LPS stimulation. <b>2014</b> , 15 Suppl 10, S4	2
1148	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. <b>2014</b> , 15 Suppl 12, S11	55
1147	The epigenome, 4D nucleome and next-generation neuropsychiatric pharmacogenomics. <b>2015</b> , 16, 1649-69	14
1146	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. <b>2015</b> , 13, 1855-67	23
1145	Memory-Optimised Parallel Processing of Hi-C Data. <b>2015</b> ,	2
1144	Quantitative analysis of cellular traction forces using a micropillar substrate and estimation of the intracellular force applied to the nucleus. <b>2015</b> , 81, 14-00692-14-00692	1
1143	Effect of disorder on the contact probability of elongated conformations of biopolymers. <b>2015</b> , 92, 010702	1
1142	Facilitated diffusion of proteins through crumpled fractal DNA globules. <b>2015</b> , 92, 012702	6

1141	Coalescence Model for Crumpled Globules Formed in Polymer Collapse. <b>2015</b> , 115, 088303	13
1140	Confinement-Induced Glassy Dynamics in a Model for Chromosome Organization. <b>2015</b> , 115, 198102	50
1139	Functional analysis of the 11q23.3 glioma susceptibility locus implicates PHLDB1 and DDX6 in glioma susceptibility. <b>2015</b> , 5, 17367	21
1138	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <b>2015</b> , 11, 852	229
1137	DNA dynamics. 137-164	
1136	Analysis of a transgenic Oct4 enhancer reveals high fidelity long-range chromosomal interactions. <b>2015</b> , 5, 14558	4
1135	Epigenetic regulation in heart failure: part II DNA and chromatin. <b>2015</b> , 23, 269-81	7
1134	A novel method to identify topological domains using Hi-C data. <b>2015</b> , 3, 81-89	9
1133	Contribution of 3D Chromatin Architecture to the Maintenance of Pluripotency. <b>2015</b> , 1, 170-175	2
1132	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. <b>2015</b> , 16, 982	2
1131	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. <b>2015</b> , 16, 214	123
1130	HiCdat: a fast and easy-to-use Hi-C data analysis tool. <b>2015</b> , 16, 277	36
1129	Iterative reconstruction of three-dimensional models of human chromosomes from chromosomal contact data. <b>2015</b> , 16, 338	8
1128	Reconstruction of 3D genome architecture via a two-stage algorithm. <b>2015</b> , 16, 373	16
1127	Complete haplotype phasing of the MHC and KIR loci with targeted HaploSeq. <b>2015</b> , 16, 900	10
1126	Deciphering the association between gene function and spatial gene-gene interactions in 3D human genome conformation. <b>2015</b> , 16, 880	13
1125	GenomicInteractions: An R/Bioconductor package for manipulating and investigating chromatin interaction data. <b>2015</b> , 16, 963	29
1124	ChromContact: A web tool for analyzing spatial contact of chromosomes from Hi-C data. <b>2015</b> , 16, 1060	5

1123	Integrative modeling reveals the principles of multi-scale chromatin boundary formation in human nuclear organization. <b>2015</b> , 16, 110	26
1122	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. <b>2015</b> , 16, 156	89
1121	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. <b>2015</b> , 16, 180	132
1120	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. <b>2015</b> , 16, 237	52
1119	Local compartment changes and regulatory landscape alterations in histone H1-depleted cells. <b>2015</b> , 16, 289	37
1118	A possible role of Drosophila CTCF in mitotic bookmarking and maintaining chromatin domains during the cell cycle. <b>2015</b> , 48, 27	14
1117	Prioritization of cancer-related genomic variants by SNP association network. <b>2015</b> , 14, 57-70	4
1116	Forces, fluctuations, and self-organization in the nucleus. <b>2015</b> , 26, 3915-9	6
1115	Genome-Scale Analysis of Gene Expression and its Regulation in Bacteria. 89-190	
1114	Metagenomic Chromosome Conformation Capture (3C): techniques, applications, and challenges. <b>2015</b> , 4, 1377	11
1113	Contribution of Topological Domains and Loop Formation to 3D Chromatin Organization. <b>2015</b> , 6, 734-50	42
1112	Next-generation technologies for multiomics approaches including interactome sequencing. <b>2015</b> , 2015, 104209	22
1111	HiCUP: pipeline for mapping and processing Hi-C data. <b>2015</b> , 4, 1310	273
1110	Superresolution microscopy for bioimaging at the nanoscale: from concepts to applications in the nucleus. <b>2015</b> , 157	2
1109	Comparative analysis of T4 DNA ligases and DNA polymerases used in chromosome conformation capture assays. <b>2015</b> , 58, 195-9	5
1108	References for Haplotype Imputation in the Big Data Era. <b>2015</b> , 4,	2
1107	[The intimate genome in three dimensions]. <b>2015</b> , 31, 304-11	0
1106	One, Two, Three: Polycomb Proteins Hit All Dimensions of Gene Regulation. <b>2015</b> , 6, 520-42	17

1105	Chromatin Dynamics in the Regulation of CFTR Expression. <b>2015</b> , 6, 543-58	18
1104	Chromatin Dynamics in Lineage Commitment and Cellular Reprogramming. <b>2015</b> , 6, 641-61	11
1103	Connecting SNPs in Diabetes: A Spatial Analysis of Meta-GWAS Loci. <b>2015</b> , 6, 102	13
1102	Using linkage maps to correct and scaffold de novo genome assemblies: methods, challenges, and computational tools. <b>2015</b> , 6, 220	87
1101	Transcriptional Enhancers in the Regulation of T Cell Differentiation. <b>2015</b> , 6, 462	13
1100	Perturbed states of the bacterial chromosome: a thymineless death case study. <b>2015</b> , 6, 363	5
1099	Current theoretical models fail to predict the topological complexity of the human genome. <b>2015</b> , 2, 48	13
1098	Spatial positioning of all 24 chromosomes in the lymphocytes of six subjects: evidence of reproducible positioning and spatial repositioning following DNA damage with hydrogen peroxide and ultraviolet B. <b>2015</b> , 10, e0118886	10
1097	Inter-chromosomal contact networks provide insights into Mammalian chromatin organization. <b>2015</b> , 10, e0126125	23
1096	Chromosome Architecture and Genome Organization. <b>2015</b> , 10, e0143739	29
1095	Differential chromosome conformations as hallmarks of cellular identity revealed by mathematical polymer modeling. <b>2015</b> , 11, e1004306	20
1094	Manifold Based Optimization for Single-Cell 3D Genome Reconstruction. <b>2015</b> , 11, e1004396	22
1093	Emergent Self-Organized Criticality in Gene Expression Dynamics: Temporal Development of Global Phase Transition Revealed in a Cancer Cell Line. <b>2015</b> , 10, e0128565	32
1092	Identifying and Reducing Systematic Errors in Chromosome Conformation Capture Data. <b>2015</b> , 10, e0146007	1
1091	Can chromatin conformation technologies bring light into human molecular pathology?. <b>2015</b> , 62, 483-9	8
1090	Multiscale Modeling of Cellular Epigenetic States: Stochasticity in Molecular Networks, Chromatin Folding in Cell Nuclei, and Tissue Pattern Formation of Cells. <b>2015</b> , 43, 323-46	3
1089	Colloquium: Random first order transition theory concepts in biology and physics. <b>2015</b> , 87, 183-209	75
1088	Evolutionary comparison reveals that diverging CTCF sites are signatures of ancestral topological associating domains borders. <b>2015</b> , 112, 7542-7	117

1087	Condensin-driven remodelling of X chromosome topology during dosage compensation. <b>2015</b> , 523, 240-4	501
1086	Peaks cloaked in the mist: the landscape of mammalian replication origins. <b>2015</b> , 208, 147-60	66
1085	Long noncoding RNA in hematopoiesis and immunity. <b>2015</b> , 42, 792-804	135
1084	High-throughput sequencing technologies. <b>2015</b> , 58, 586-97	629
1083	Characterization and dynamics of pericentromere-associated domains in mice. <b>2015</b> , 25, 958-69	54
1082	A Genome-Wide Perspective on Metabolism. <b>2016</b> , 233, 1-28	3
1081	Dynamic changes in replication timing and gene expression during lineage specification of human pluripotent stem cells. <b>2015</b> , 25, 1091-103	96
1080	The chromatin fiber: multiscale problems and approaches. <b>2015</b> , 31, 124-39	55
1079	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. <b>2015</b> , 6, 7256	56
1078	Comparison of the three-dimensional organization of sperm and fibroblast genomes using the Hi-C approach. <b>2015</b> , 16, 77	78
1077	TADs as modular and dynamic units for gene regulation by hormones. <b>2015</b> , 589, 2885-92	14
1076	Topologically associating domains and their long-range contacts are established during early G1 coincident with the establishment of the replication-timing program. <b>2015</b> , 25, 1104-13	121
1075	Chromothripsis from DNA damage in micronuclei. <b>2015</b> , 522, 179-84	635
1074	Parallel Exploration of the Nuclear Chromosome Conformation with NuChart-II. <b>2015</b> ,	3
1073	The 4D nucleome: Evidence for a dynamic nuclear landscape based on co-aligned active and inactive nuclear compartments. <b>2015</b> , 589, 2931-43	160
1072	Anomalous diffusion in fractal globules. <b>2015</b> , 114, 178102	59
1071	On the demultiplexing of chromosome capture conformation data. <b>2015</b> , 589, 3005-13	18
1070	Protein-DNA binding in high-resolution. <b>2015</b> , 50, 269-83	31

1069	TRANSCRIPTOME ANALYSIS USING NEXT-GENERATION SEQUENCING. <b>2015</b> , 915-936	1
1068	Xist localization and function: new insights from multiple levels. <b>2015</b> , 16, 166	114
1067	From Mutational Mechanisms in Single Cells to Mutational Patterns in Cancer Genomes. <b>2015</b> , 80, 117-37	7
1066	diffHic: a Bioconductor package to detect differential genomic interactions in Hi-C data. <b>2015</b> , 16, 258	120
1065	Accessing the Inaccessible: The Organization, Transcription, Replication, and Repair of Heterochromatin in Plants. <b>2015</b> , 49, 439-59	31
1064	In the loop: promoter-enhancer interactions and bioinformatics. <b>2016</b> , 17, 980-995	67
1063	Predictive model of 3D domain formation via CTCF-mediated extrusion. <b>2015</b> , 112, 14404-5	2
1062	3D genome organization in health and disease: emerging opportunities in cancer translational medicine. <b>2015</b> , 6, 382-93	29
1061	The contribution of cohesin-SA1 to gene expression and chromatin architecture in two murine tissues. <b>2015</b> , 43, 3056-67	20
1060	A low-latency, big database system and browser for storage, querying and visualization of 3D genomic data. <b>2015</b> , 43, e103	6
1059	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <b>2015</b> , 163, 1611-27	585
1058	Fractal Characterization of Chromatin Decompaction in Live Cells. <b>2015</b> , 109, 2218-26	15
1057	Spatial Regulation of V-(D)J Recombination at Antigen Receptor Loci. <b>2015</b> , 128, 93-121	32
1056	Mechanisms of Recurrent Chromosomal Translocations. <b>2015</b> , 27-51	
1055	VizEpis : A visualization and mapping tool for interpreting epistasis. <b>2015</b> ,	2
1054	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. <b>2015</b> , 16, 259	811
1053	Remodeling of nuclear landscapes during human myelopoietic cell differentiation maintains co-aligned active and inactive nuclear compartments. <b>2015</b> , 8, 47	30
1052	Predicting chromatin organization using histone marks. <b>2015</b> , 16, 162	74

1051	Predicting the spatial organization of chromosomes using epigenetic data. <b>2015</b> , 16, 182	10
1050	Statistical Inference on Three-Dimensional Structure of Genome by Truncated Poisson Architecture Model. <b>2015</b> , 245-261	4
1049	Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. <b>2015</b> , 16, 149	73
1048	Remotely acting SMCHD1 gene regulatory elements: in silico prediction and identification of potential regulatory variants in patients with FSHD. <b>2015</b> , 9, 25	
1047	Unexpected Swelling of Stiff DNA in a Polydisperse Crowded Environment. <b>2015</b> , 137, 10970-8	29
1046	Genome Organization and Chromosome Architecture. <b>2015</b> , 80, 83-91	3
1045	The 3D organization of chromatin explains evolutionary fragile genomic regions. <b>2015</b> , 10, 1913-24	36
1044	A predictive modeling approach for cell line-specific long-range regulatory interactions. <b>2015</b> , 43, 8694-712	68
1043	Genomic perspectives of transcriptional regulation in forebrain development. <b>2015</b> , 85, 27-47	109
1042	Multiple dimensions of epigenetic gene regulation in the malaria parasite <i>Plasmodium falciparum</i> : gene regulation via histone modifications, nucleosome positioning and nuclear architecture in <i>P. falciparum</i> . <b>2015</b> , 37, 182-94	45
1041	Chromatin dynamics during differentiation of myeloid cells. <b>2015</b> , 427, 670-87	8
1040	Cohesin modulates transcription of estrogen-responsive genes. <b>2015</b> , 1849, 257-69	13
1039	Neuroepigenomics: Resources, Obstacles, and Opportunities. <b>2015</b> , 1, 2-13	14
1038	Understanding the dynamics of rings in the melt in terms of the annealed tree model. <b>2015</b> , 27, 064117	42
1037	Compartmentalization of the cell nucleus and spatial organization of the genome. <b>2015</b> , 49, 21-39	11
1036	Vision from next generation sequencing: multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. <b>2015</b> , 46, 1-30	43
1035	Epstein-Barr virus oncoprotein super-enhancers control B cell growth. <b>2015</b> , 17, 205-16	108
1034	Chromatin regulation at the frontier of synthetic biology. <b>2015</b> , 16, 159-71	76

1033	The linker histone in <i>Saccharomyces cerevisiae</i> interacts with actin-related protein 4 and both regulate chromatin structure and cellular morphology. <b>2015</b> , 59, 182-92	10
1032	Comprehensive characterization of the genomic alterations in human gastric cancer. <b>2015</b> , 137, 86-95	51
1031	Nuclear compartments, genome folding, and enhancer-promoter communication. <b>2015</b> , 315, 183-244	24
1030	Three-dimensional regulation of transcription. <b>2015</b> , 6, 241-53	15
1029	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. <b>2015</b> , 25, 504-13	106
1028	DNA binding by FOXP3 domain-swapped dimer suggests mechanisms of long-range chromosomal interactions. <b>2015</b> , 43, 1268-82	35
1027	The selection and function of cell type-specific enhancers. <b>2015</b> , 16, 144-54	573
1026	Thermodynamic model of heterochromatin formation through epigenetic regulation. <b>2015</b> , 27, 064109	16
1025	Expression of the DYRK1A gene correlates with its 3D positioning in the interphase nucleus of Down syndrome cells. <b>2015</b> , 23, 285-98	7
1024	Effects of macromolecular crowding on the collapse of biopolymers. <b>2015</b> , 114, 068303	91
1023	Integrative analysis of 111 reference human epigenomes. <b>2015</b> , 518, 317-30	3849
1022	Multi -omics and metabolic modelling pipelines: challenges and tools for systems microbiology. <b>2015</b> , 171, 52-64	90
1021	Long ncRNA expression associates with tissue-specific enhancers. <b>2015</b> , 14, 253-60	68
1020	The physical size of transcription factors is key to transcriptional regulation in chromatin domains. <b>2015</b> , 27, 064116	47
1019	Chromosome folding: driver or passenger of epigenetic state?. <b>2015</b> , 7, a018721	6
1018	Global reorganization of the nuclear landscape in senescent cells. <b>2015</b> , 10, 471-83	191
1017	Long-Range Order and Fractality in the Structure and Organization of Eukaryotic Genomes. <b>2015</b> , 221-252	
1016	Accounting for uncertainty in DNA sequencing data. <b>2015</b> , 31, 61-6	38

1015	The viscoelastic properties of chromatin and the nucleoplasm revealed by scale-dependent protein mobility. <b>2015</b> , 27, 064115	21
1014	A simple model for DNA bridging proteins and bacterial or human genomes: bridging-induced attraction and genome compaction. <b>2015</b> , 27, 064119	21
1013	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression. <b>2015</b> , 25, 544-57	50
1012	3D hotspots of recurrent retroviral insertions reveal long-range interactions with cancer genes. <b>2015</b> , 6, 6381	19
1011	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. <b>2015</b> , 16, 745-58	44
1010	Nicht-kodierende Mutationen. <b>2015</b> , 27, 19-30	
1009	Genome-wide epistatic expression quantitative trait loci discovery in four human tissues reveals the importance of local chromosomal interactions governing gene expression. <b>2015</b> , 16, 109	5
1008	Chromatin architecture reorganization during stem cell differentiation. <b>2015</b> , 518, 331-6	988
1007	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. <b>2015</b> , 6, 6178	131
1006	The role of regulatory variation in complex traits and disease. <b>2015</b> , 16, 197-212	577
1005	A variably occupied CTCF binding site in the ultrabithorax gene in the Drosophila bithorax complex. <b>2015</b> , 35, 318-30	13
1004	Nuclear Architecture and Transcriptional Regulation of MicroRNAs. <b>2015</b> , 1129-1158	
1003	Multi-layered global gene regulation in mouse embryonic stem cells. <b>2015</b> , 72, 199-216	5
1002	An Integrative Breakage Model of genome architecture, reshuffling and evolution: The Integrative Breakage Model of genome evolution, a novel multidisciplinary hypothesis for the study of genome plasticity. <b>2015</b> , 37, 479-88	38
1001	Chromosome togetherness at the onset of ESC differentiation. <b>2015</b> , 16, 213-4	
1000	Chromosome conformation of human fibroblasts grown in 3-dimensional spheroids. <b>2015</b> , 6, 55-65	8
999	Three-dimensional genome architecture: players and mechanisms. <b>2015</b> , 16, 245-57	338
998	Hi-C Chromatin Interaction Networks Predict Co-expression in the Mouse Cortex. <b>2015</b> , 11, e1004221	31

997	Architectural proteins, transcription, and the three-dimensional organization of the genome. <b>2015</b> , 589, 2923-30		46
996	Chromatin landscape and circadian dynamics: Spatial and temporal organization of clock transcription. <b>2015</b> , 112, 6863-70		50
995	Contact genomics: scaffolding and phasing (meta)genomes using chromosome 3D physical signatures. <b>2015</b> , 589, 2966-74		31
994	Clustering of mammalian Hox genes with other H3K27me3 targets within an active nuclear domain. <b>2015</b> , 112, 4672-7		105
993	Chromosomes. A comprehensive Xist interactome reveals cohesin repulsion and an RNA-directed chromosome conformation. <i>Science</i> , <b>2015</b> , 349,	33-3	316
992	Chromosome dynamics and folding in eukaryotes: Insights from live cell microscopy. <b>2015</b> , 589, 3014-22		27
991	Chromosome domain architecture and dynamic organization of the fission yeast genome. <b>2015</b> , 589, 2975-86		27
990	Phenome-Wide Association Studies: Embracing Complexity for Discovery. <b>2015</b> , 79, 111-23		13
989	Condensin promotes the juxtaposition of DNA flanking its loading site in <i>Bacillus subtilis</i> . <b>2015</b> , 29, 1661-75		150
988	High-throughput determination of RNA structure by proximity ligation. <b>2015</b> , 33, 980-4		78
987	Sedimentation Velocity Analysis of Large Oligomeric Chromatin Complexes Using Interference Detection. <b>2015</b> , 562, 349-62		3
986	A generalized Potts model for confocal microscopy images. <b>2015</b> , 29, 1550048		
985	The renaissance of developmental biology. <b>2015</b> , 13, e1002149		20
984	Long Noncoding RNAs. <b>2015</b> ,		2
983	Hi-C in Budding Yeast. <b>2015</b> , 2015, 649-61		14
982	Measuring Chromatin Structure in Budding Yeast. <b>2015</b> , 2015, 614-8		2
981	Breaking TADs: insights into hierarchical genome organization. <b>2015</b> , 7, 523-6		29
980	Accurate identification of centromere locations in yeast genomes using Hi-C. <b>2015</b> , 43, 5331-9		38

979	Integrated and comparative miRNA analysis of starvation-induced autophagy in mouse embryonic fibroblasts. <b>2015</b> , 571, 194-204	6
978	Mango: a bias-correcting ChIA-PET analysis pipeline. <b>2015</b> , 31, 3092-8	91
977	Comprehensive identification and analysis of human accelerated regulatory DNA. <b>2015</b> , 25, 1245-55	56
976	Chromatin at the nuclear periphery and the regulation of genome functions. <b>2015</b> , 144, 111-22	54
975	Condensin II Regulates Interphase Chromatin Organization Through the Mrg-Binding Motif of Cap-H2. <b>2015</b> , 5, 803-17	17
974	Lung cancer-a fractal viewpoint. <b>2015</b> , 12, 664-75	91
973	Third Report on Chicken Genes and Chromosomes 2015. <b>2015</b> , 145, 78-179	57
972	From structure to function of bacterial chromosomes: Evolutionary perspectives and ideas for new experiments. <b>2015</b> , 589, 2996-3004	20
971	Phase separation of a Lennard-Jones fluid interacting with a long, condensed polymer chain: implications for the nuclear body formation near chromosomes. <b>2015</b> , 11, 6450-9	4
970	Single-cell chromatin accessibility reveals principles of regulatory variation. <b>2015</b> , 523, 486-90	1110
969	Understanding the Complex Circuitry of lncRNAs at the X-inactivation Center and Its Implications in Disease Conditions. <b>2016</b> , 394, 1-27	7
968	Restraint-based three-dimensional modeling of genomes and genomic domains. <b>2015</b> , 589, 2987-95	70
967	Functional organization of the human 4D Nucleome. <b>2015</b> , 112, 8002-7	78
966	Polymer models of the organization of chromosomes in the nucleus of cells. <b>2015</b> , 29, 1530003	7
965	Topokaryotyping &ndash; a proposal for a novel approach to study nuclear organization. <b>2015</b> , 31, 72-79	
964	Puces &#x2212;ADN (microArrays) et s&#x2212;quenc&#x2212;age de nouvelle g&#x2212;n&#x2212;ration. <b>2015</b> , 2015, 63-70	
963	The Bromodomain protein BRD4 controls HOTAIR, a long noncoding RNA essential for glioblastoma proliferation. <b>2015</b> , 112, 8326-31	147
962	Improving 3D Genome Reconstructions Using Orthologous and Functional Constraints. <b>2015</b> , 11, e1004298	9

961	Mapping Nucleosome Resolution Chromosome Folding in Yeast by Micro-C. <b>2015</b> , 162, 108-19	341
960	A matter of scale: how emerging technologies are redefining our view of chromosome architecture. <b>2015</b> , 31, 454-64	17
959	Lessons from modENCODE. <b>2015</b> , 16, 31-53	31
958	Embryonic stem cell specific "master" replication origins at the heart of the loss of pluripotency. <b>2015</b> , 11, e1003969	14
957	Integrating multi-omic features exploiting Chromosome Conformation Capture data. <b>2015</b> , 6, 40	8
956	On enumeration of Hilbert-like curves. <b>2015</b> , 48, 195001	1
955	LRP8-Reelin-Regulated Neuronal Enhancer Signature Underlying Learning and Memory Formation. <b>2015</b> , 86, 696-710	87
954	Transcription outcome of promoters enriched in histone variant H3.3 defined by positioning of H3.3 and local chromatin marks. <b>2015</b> , 460, 348-53	
953	The pluripotent regulatory circuitry connecting promoters to their long-range interacting elements. <b>2015</b> , 25, 582-97	285
952	Topology, structures, and energy landscapes of human chromosomes. <b>2015</b> , 112, 6062-7	121
951	Effects of topological constraints on globular polymers. <b>2015</b> , 11, 665-71	41
950	Unraveling the 3D genome: genomics tools for multiscale exploration. <b>2015</b> , 31, 357-72	47
949	Identifying multi-locus chromatin contacts in human cells using tethered multiple 3C. <b>2015</b> , 16, 121	37
948	Structural organization of human replication timing domains. <b>2015</b> , 589, 2944-57	22
947	Ising-model description of long-range correlations in DNA sequences. <b>2015</b> , 91, 052703	11
946	Architectural hallmarks of the pluripotent genome. <b>2015</b> , 589, 2905-13	20
945	Drawing on millions of biomedical journal publications to do predictive biology. <b>2015</b> ,	
944	Principles of chromatin organization in yeast: relevance of polymer models to describe nuclear organization and dynamics. <b>2015</b> , 34, 54-60	25

943	The ensembl regulatory build. <b>2015</b> , 16, 56	255
942	Research in Computational Molecular Biology. <b>2015</b> ,	3
941	The role of chromosome domains in shaping the functional genome. <b>2015</b> , 160, 1049-59	281
940	Gene regulatory mechanisms orchestrated by p63 in epithelial development and related disorders. <b>2015</b> , 1849, 590-600	17
939	Inferential modeling of 3D chromatin structure. <b>2015</b> , 43, e54	55
938	Transient pairing of homologous Oct4 alleles accompanies the onset of embryonic stem cell differentiation. <b>2015</b> , 16, 275-88	37
937	Towards early detection of cervical cancer: Fractal dimension of AFM images of human cervical epithelial cells at different stages of progression to cancer. <b>2015</b> , 11, 1667-75	26
936	3D chromosome rendering from Hi-C data using virtual reality. <b>2015</b> ,	
935	Regulatory genomics: Combined experimental and computational approaches. <b>2015</b> , 51, 334-352	6
934	The role of loops on the order of eukaryotes and prokaryotes. <b>2015</b> , 589, 2958-65	22
933	Nuclear envelope and chromatin, lock and key of genome integrity. <b>2015</b> , 317, 267-330	16
932	Disruptions of topological chromatin domains cause pathogenic rewiring of gene-enhancer interactions. <b>2015</b> , 161, 1012-1025	1207
931	Mapping long-range promoter contacts in human cells with high-resolution capture Hi-C. <b>2015</b> , 47, 598-606	604
930	Haplotype-resolved genome sequencing: experimental methods and applications. <b>2015</b> , 16, 344-58	120
929	A statistical model of intra-chromosome contact maps. <b>2015</b> , 11, 1019-25	20
928	Widespread rearrangement of 3D chromatin organization underlies polycomb-mediated stress-induced silencing. <b>2015</b> , 58, 216-31	219
927	The effects of chromatin organization on variation in mutation rates in the genome. <b>2015</b> , 16, 213-23	143
926	Wash interacts with lamin and affects global nuclear organization. <b>2015</b> , 25, 804-810	40

925	Mean first-passage times in confined media: from Markovian to non-Markovian processes. <b>2015</b> , 48, 163001	27
924	Topologically Associating Domains: An invariant framework or a dynamic scaffold?. <b>2015</b> , 6, 430-4	16
923	Epigenomics and the structure of the living genome. <b>2015</b> , 25, 1482-90	37
922	Defining cell types and states with single-cell genomics. <b>2015</b> , 25, 1491-8	421
921	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in <i>Drosophila</i> . <b>2015</b> , 60, 146-62	58
920	Genetic Tailors: CTCF and Cohesin Shape the Genome During Evolution. <b>2015</b> , 31, 651-660	42
919	A high-resolution imaging approach to investigate chromatin architecture in complex tissues. <b>2015</b> , 163, 246-55	44
918	Genomic approaches to studying human-specific developmental traits. <b>2015</b> , 142, 3100-12	19
917	Computational Intelligence Methods for Bioinformatics and Biostatistics. <b>2015</b> ,	0
916	PRC1 proteins orchestrate three-dimensional genome architecture. <b>2015</b> , 47, 1105-6	2
915	Hot spots of DNA double-strand breaks and genomic contacts of human rDNA units are involved in epigenetic regulation. <b>2015</b> , 7, 366-82	43
914	Gene Positioning Effects on Expression in Eukaryotes. <b>2015</b> , 49, 627-46	30
913	Long-Range Chromatin Interactions. <b>2015</b> , 7, a019356	147
912	Getting the genome in shape: the formation of loops, domains and compartments. <b>2015</b> , 16, 154	78
911	Quantitative Analysis of Intra-chromosomal Contacts: The 3C-qPCR Method. <b>2017</b> , 1589, 75-88	9
910	Stable Chromosome Condensation Revealed by Chromosome Conformation Capture. <b>2015</b> , 163, 934-46	104
909	Single-cell Hi-C for genome-wide detection of chromatin interactions that occur simultaneously in a single cell. <b>2015</b> , 10, 1986-2003	105
908	Segregated structures of ring polymer melts near the surface: a molecular dynamics simulation study. <b>2015</b> , 11, 6018-28	12

907	Probing long-range interactions by extracting free energies from genome-wide chromosome conformation capture data. <b>2015</b> , 16, 171	3
906	Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes. <b>2015</b> , 112, E6456-65	1008
905	Distinct polymer physics principles govern chromatin dynamics in mouse and Drosophila topological domains. <b>2015</b> , 16, 607	8
904	Chromatin Interactions in the Control of Immunoglobulin Heavy Chain Gene Assembly. <b>2015</b> , 128, 41-92	25
903	Inferring 3D chromatin structure using a multiscale approach based on quaternions. <b>2015</b> , 16, 234	10
902	Progress in understanding epigenetic remodeling during induced pluripotency. <b>2015</b> , 60, 1713-1721	3
901	The yeast genome undergoes significant topological reorganization in quiescence. <b>2015</b> , 43, 8299-313	53
900	Somatic Rearrangement in B Cells: It's (Mostly) Nuclear Physics. <b>2015</b> , 162, 708-11	13
899	Identification of Gene Positioning Factors Using High-Throughput Imaging Mapping. <b>2015</b> , 162, 911-23	123
898	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. <b>2015</b> , 162, 900-10	612
897	Assessing the limits of restraint-based 3D modeling of genomes and genomic domains. <b>2015</b> , 43, 3465-77	40
896	An Overview of Genome Organization and How We Got There: from FISH to Hi-C. <b>2015</b> , 79, 347-72	145
895	Structural heterogeneity and functional diversity of topologically associating domains in mammalian genomes. <b>2015</b> , 43, 7237-46	12
894	Making the case for chromatin profiling: a new tool to investigate the immune-regulatory landscape. <b>2015</b> , 15, 585-94	24
893	Cohesin loss alters adult hematopoietic stem cell homeostasis, leading to myeloproliferative neoplasms. <b>2015</b> , 212, 1833-50	110
892	A glutamatergic network mediates lithium response in bipolar disorder as defined by epigenome pathway analysis. <b>2015</b> , 16, 1547-63	27
891	Effect of replication on epigenetic memory and consequences on gene transcription. <b>2015</b> , 12, 026007	11
890	Demystifying the secret mission of enhancers: linking distal regulatory elements to target genes. <b>2015</b> , 50, 550-73	62

889	Analysis methods for studying the 3D architecture of the genome. <b>2015</b> , 16, 183	109
888	Comparison of Hi-C results using in-solution versus in-nucleus ligation. <b>2015</b> , 16, 175	130
887	Single-cell epigenomics: techniques and emerging applications. <b>2015</b> , 16, 716-26	167
886	Chromothripsis: A New Mechanism for Rapid Karyotype Evolution. <b>2015</b> , 49, 183-211	122
885	A structural hierarchy mediated by multiple nuclear factors establishes IgH locus conformation. <b>2015</b> , 29, 1683-95	23
884	Scaling behavior of topologically constrained polymer rings in a melt. <b>2015</b> , 27, 354110	6
883	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <b>2015</b> , 162, 1051-65	240
882	Exploiting genomics and natural genetic variation to decode macrophage enhancers. <b>2015</b> , 36, 507-18	26
881	Chromatin in 3D: progress and prospects for plants. <b>2015</b> , 16, 170	45
880	Polycomb repressive complex PRC1 spatially constrains the mouse embryonic stem cell genome. <b>2015</b> , 47, 1179-1186	241
879	Molecular Biology Basics in the Omics Era: Genes to Proteins. <b>2015</b> , 3-65	1
878	Super-enhancers: Asset management in immune cell genomes. <b>2015</b> , 36, 519-26	31
877	DNA Brushing Shoulders: Targeted Looping and Scanning of Large DNA Strands. <b>2015</b> , 15, 5641-6	6
876	Transcriptional Regulation of the Pancreatic Islet: Implications for Islet Function. <b>2015</b> , 15, 66	10
875	Three-dimensional architecture of tandem repeats in chicken interphase nucleus. <b>2015</b> , 23, 625-39	11
874	Genome-wide maps of nuclear lamina interactions in single human cells. <b>2015</b> , 163, 134-47	291
873	Structural and functional diversity of Topologically Associating Domains. <b>2015</b> , 589, 2877-84	186
872	Mechanisms of Long Noncoding Xist RNA-Mediated Chromosome-Wide Gene Silencing in X-Chromosome Inactivation. <b>2015</b> , 151-171	2

871	Lung endoderm morphogenesis: gasping for form and function. <b>2015</b> , 31, 553-73	55
870	Algorithms in Bioinformatics. <b>2015</b> ,	1
869	Scrutinizing the FTO locus: compelling evidence for a complex, long-range regulatory context. <b>2015</b> , 134, 1183-93	17
868	Modeling chromosomes: Beyond pretty pictures. <b>2015</b> , 589, 3031-6	57
867	Hi-Corrector: a fast, scalable and memory-efficient package for normalizing large-scale Hi-C data. <b>2015</b> , 31, 960-2	56
866	Mathematical Models in Biology. <b>2015</b> ,	1
865	Chromatin dynamics and genome organization in development and disease. <b>2015</b> , 95-115	
864	Epigenetic gene regulation and stem cell function. <b>2015</b> , 149-181	
863	A Statistical Approach to Infer 3d Chromatin Structure. <b>2015</b> , 161-171	1
862	Uncovering drug-responsive regulatory elements. <b>2015</b> , 16, 1829-41	13
861	Metagenome Analysis Exploiting High-Throughput Chromosome Conformation Capture (3C) Data. <b>2015</b> , 31, 673-682	14
860	HiCPlotter integrates genomic data with interaction matrices. <b>2015</b> , 16, 198	105
859	Next generation limb development and evolution: old questions, new perspectives. <b>2015</b> , 142, 3810-20	87
858	Semi-nonparametric Modeling of Topological Domain Formation from Epigenetic Data. <b>2015</b> , 148-161	2
857	Paradigm shifts in genomics through the FANTOM projects. <b>2015</b> , 26, 391-402	73
856	Chromatin-driven behavior of topologically associating domains. <b>2015</b> , 427, 608-25	79
855	DNA methylation and its implications and accessibility for neuropsychiatric therapeutics. <b>2015</b> , 55, 591-611	57
854	HIPPIE: a high-throughput identification pipeline for promoter interacting enhancer elements. <b>2015</b> , 31, 1290-2	44

853	Genome-wide analysis of local chromatin packing in Arabidopsis thaliana. <b>2015</b> , 25, 246-56	181
852	The Hitchhiker's guide to Hi-C analysis: practical guidelines. <b>2015</b> , 72, 65-75	209
851	Fine-scale chromatin interaction maps reveal the cis-regulatory landscape of human lincRNA genes. <b>2015</b> , 12, 71-8	147
850	The genomic and functional characteristics of disease genes. <b>2015</b> , 16, 16-23	7
849	Assaying the epigenome in limited numbers of cells. <b>2015</b> , 72, 51-6	15
848	Computational schemes for the prediction and annotation of enhancers from epigenomic assays. <b>2015</b> , 72, 86-94	22
847	Prostate cancer risk locus at 8q24 as a regulatory hub by physical interactions with multiple genomic loci across the genome. <b>2015</b> , 24, 154-66	48
846	Enlight: web-based integration of GWAS results with biological annotations. <b>2015</b> , 31, 275-6	17
845	LOGIQA: a database dedicated to long-range genome interactions quality assessment. <b>2016</b> , 17, 355	3
844	Chromosome3D: reconstructing three-dimensional chromosomal structures from Hi-C interaction frequency data using distance geometry simulated annealing. <b>2016</b> , 17, 886	30
843	Orchestrating epigenetic roles targeting ocular tumors. <b>2016</b> , 9, 1001-9	3
842	Strategies for Sequence Assembly of Plant Genomes. <b>2016</b> ,	3
841	The evolution of genetics to genomics. <b>2016</b> , 26, 28	
840	RNA Polymerase II cluster dynamics predict mRNA output in living cells. <b>2016</b> , 5,	140
839	Genome Engineering with TALE and CRISPR Systems in Neuroscience. <b>2016</b> , 7, 47	21
838	Choreographing the Double Strand Break Response: Ubiquitin and SUMO Control of Nuclear Architecture. <b>2016</b> , 7, 103	11
837	Spatial Genome Organization and Its Emerging Role as a Potential Diagnosis Tool. <b>2016</b> , 7, 134	28
836	The Genome Conformation As an Integrator of Multi-Omic Data: The Example of Damage Spreading in Cancer. <b>2016</b> , 7, 194	15

835	Making Sense of the Tangle: Insights into Chromatin Folding and Gene Regulation. <b>2016</b> , 7,	10
834	Capture Hi-C identifies a novel causal gene, IL20RA, in the pan-autoimmune genetic susceptibility region 6q23. <b>2016</b> , 17, 212	62
833	Biophysically Motivated Regulatory Network Inference: Progress and Prospects. <b>2016</b> , 81, 62-77	19
832	4C-ker: A Method to Reproducibly Identify Genome-Wide Interactions Captured by 4C-Seq Experiments. <b>2016</b> , 12, e1004780	64
831	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. <b>2016</b> , 12, e1004892	15
830	Computational Identification of Genomic Features That Influence 3D Chromatin Domain Formation. <b>2016</b> , 12, e1004908	21
829	Effect of Interaction between Chromatin Loops on Cell-to-Cell Variability in Gene Expression. <b>2016</b> , 12, e1004917	10
828	Large Scale Chromosome Folding Is Stable against Local Changes in Chromatin Structure. <b>2016</b> , 12, e1004987	14
827	Dynamic Nucleosome Movement Provides Structural Information of Topological Chromatin Domains in Living Human Cells. <b>2016</b> , 12, e1005136	67
826	Long-Range Chromosome Interactions Mediated by Cohesin Shape Circadian Gene Expression. <b>2016</b> , 12, e1005992	40
825	Multiple Pairwise Analysis of Non-homologous Centromere Coupling Reveals Preferential Chromosome Size-Dependent Interactions and a Role for Bouquet Formation in Establishing the Interaction Pattern. <b>2016</b> , 12, e1006347	4
824	High-Resolution 4C Reveals Rapid p53-Dependent Chromatin Reorganization of the CDKN1A Locus in Response to Stress. <b>2016</b> , 11, e0163885	3
823	Self-Organizing Global Gene Expression Regulated through Criticality: Mechanism of the Cell-Fate Change. <b>2016</b> , 11, e0167912	30
822	Physiological and Pathological Aging Affects Chromatin Dynamics, Structure and Function at the Nuclear Edge. <b>2016</b> , 7, 153	22
821	Basic Principles of Noncoding RNAs in Epigenetics. <b>2016</b> , 47-63	
820	The Evolution of New Technologies and Methods in Clinical Epigenetics Research. <b>2016</b> , 67-89	1
819	Gene regulation during development in the light of topologically associating domains. <b>2016</b> , 5, 169-85	17
818	CRISPR/Cas9 genome editing throws descriptive 3-D genome folding studies for a loop. <b>2016</b> , 8, 286-99	3

817	Genetics and Genomics of Longitudinal Lung Function Patterns in Individuals with Asthma. <b>2016</b> , 194, 1465-1474	18
816	Nanoscale imaging of RNA with expansion microscopy. <b>2016</b> , 13, 679-84	220
815	UMI-4C for quantitative and targeted chromosomal contact profiling. <b>2016</b> , 13, 685-91	52
814	Transcription rate and transcript length drive formation of chromosomal interaction domain boundaries. <b>2016</b> , 35, 1582-95	69
813	CCSI: a database providing chromatin-chromatin spatial interaction information. <b>2016</b> , 2016,	11
812	Distribution of human single-nucleotide polymorphisms is approximated by the power law and represents a fractal structure. <b>2016</b> , 21, 396-407	4
811	Ensembl regulation resources. <b>2016</b> , 2016,	33
810	Genome Organisation and Chromosome Architecture from Interphase to Metaphase. <b>2016</b> , 1-8	
809	Predicting the Behaviour of Rings in Solution. <b>2016</b> , 11-27	
808	Computational strategies to address chromatin structure problems. <b>2016</b> , 13, 035006	9
807	First-Passage Processes in the Genome. <b>2016</b> , 45, 117-34	23
806	Peano modes at the $D = 2$ delocalisation transition. <b>2016</b> , 2016, 013302	
805	Applying CRISPR-Cas9 tools to identify and characterize transcriptional enhancers. <b>2016</b> , 17, 597-604	42
804	3CDB: a manually curated database of chromosome conformation capture data. <b>2016</b> , 2016,	6
803	Alterations in Three-Dimensional Organization of the Cancer Genome and Epigenome. <b>2016</b> , 81, 41-51	21
802	Deconvolution of Ensemble Chromatin Interaction Data Reveals the Latent Mixing Structures in Cell Subpopulations. <b>2016</b> , 23, 425-38	12
801	Constructing 3D interaction maps from 1D epigenomes. <b>2016</b> , 7, 10812	87
800	Mining 3D genome structure populations identifies major factors governing the stability of regulatory communities. <b>2016</b> , 7, 11549	27

799	PETModule: a motif module based approach for enhancer target gene prediction. <b>2016</b> , 6, 30043	17
798	The detailed 3D multi-loop aggregate/rosette chromatin architecture and functional dynamic organization of the human and mouse genomes. <b>2016</b> , 9, 58	18
797	Interactome-transcriptome analysis discovers signatures complementary to GWAS Loci of Type 2 Diabetes. <b>2016</b> , 6, 35228	16
796	Genome-wide epigenomic profiling for biomarker discovery. <b>2016</b> , 8, 122	49
795	Polymer physics of chromosome large-scale 3D organisation. <b>2016</b> , 6, 29775	99
794	Polymer model with Epigenetic Recoloring Reveals a Pathway for the de novo Establishment and 3D Organization of Chromatin Domains. <b>2016</b> , 6,	25
793	Polycomb "polypacks" the chromatin. <b>2016</b> , 113, 14878-14880	4
792	Scaling, crumpled wires, and genome packing in virions. <b>2016</b> , 94, 062406	3
791	- Protein-Protein Functional Linkage Predictions: Bringing Regulation to Context. <b>2016</b> , 172-191	
790	Capturing native interactions: intrinsic methods to study chromatin conformation. <b>2016</b> , 12, 897	3
789	A pathway-centric view of spatial proximity in the 3D nucleome across cell lines. <b>2016</b> , 6, 39279	5
788	Controlling gene expression by DNA mechanics: emerging insights and challenges. <b>2016</b> , 8, 23-32	6
787	Genome-wide analysis of histone modifications reveals dynamic associations between bivalent promoter and enhancer. <b>2016</b> ,	
786	Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods, and Challenges. <b>2016</b> , 81, 88-105	2
785	Genome-Wide Analysis of the Distinct Types of Chromatin Interactions in Arabidopsis thaliana. <b>2017</b> , 58, 57-70	7
784	The Functionality and Evolution of Eukaryotic Transcriptional Enhancers. <b>2016</b> , 96, 143-206	23
783	Deciphering DNA replication dynamics in eukaryotic cell populations in relation with their averaged chromatin conformations. <b>2016</b> , 6, 22469	7
782	GMOL: An Interactive Tool for 3D Genome Structure Visualization. <b>2016</b> , 6, 20802	17

781	A Cloud Solution for Multi-omics Data Integration. <b>2016,</b>	1
780	CRISPR Double Cutting through the Labyrinthine Architecture of 3D Genomes. <b>2016, 43, 273-88</b>	14
779	Chromosomes at Work: Organization of Chromosome Territories in the Interphase Nucleus. <b>2016, 117, 9-19</b>	28
778	Chromosome organisation during ageing and senescence. <b>2016, 40, 161-167</b>	35
777	Post-transcriptional and translational regulation modulates gene co-expression behavior in more synchronized pace to carry out molecular function in the cell. <b>2016, 587, 163-8</b>	1
776	Genome-wide analysis of chromatin packing in Arabidopsis thaliana at single-gene resolution. <b>2016, 26, 1057-68</b>	124
775	3D-GNOME: an integrated web service for structural modeling of the 3D genome. <b>2016, 44, W288-93</b>	28
774	Extruding Loops to Make Loopy Globules?. <b>2016, 110, 2133-5</b>	8
773	Formation of Chromosomal Domains by Loop Extrusion. <b>2016, 15, 2038-49</b>	973
772	A Key to Genome Maze in 3D. <b>2016, 14, 4-6</b>	
771	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. <b>2016, 26, 342-50</b>	415
770	The "lnc" between 3D chromatin structure and X chromosome inactivation. <b>2016, 56, 35-47</b>	13
769	Pairing and anti-pairing: a balancing act in the diploid genome. <b>2016, 37, 119-128</b>	47
768	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <b>2016, 26, 719-31</b>	186
767	Using ROADMAP Data to Identify Enhancers Associated with Disorders of Sex Development. <b>2016, 10, 59-65</b>	11
766	Human genome regulation. <b>2016, 7, 57-9</b>	1
765	The folding landscape of the epigenome. <b>2016, 13, 026001</b>	22
764	Structure and Functions of Linker Histones. <b>2016, 81, 213-23</b>	8

763	Extremely Long-Range Chromatin Loops Link Topological Domains to Facilitate a Diverse Antibody Repertoire. <b>2016</b> , 14, 896-906	41
762	CTCF and Cohesin in Genome Folding and Transcriptional Gene Regulation. <b>2016</b> , 17, 17-43	290
761	Genome maintenance in the context of 4D chromatin condensation. <b>2016</b> , 73, 3137-50	9
760	Simulated binding of transcription factors to active and inactive regions folds human chromosomes into loops, rosettes and topological domains. <b>2016</b> , 44, 3503-12	103
759	De novo deciphering three-dimensional chromatin interaction and topological domains by wavelet transformation of epigenetic profiles. <b>2016</b> , 44, e106	22
758	Spectral identification of topological domains. <b>2016</b> , 32, 2151-8	41
757	Imaging Specific Genomic DNA in Living Cells. <b>2016</b> , 45, 1-23	52
756	Put your 3D glasses on: plant chromatin is on show. <b>2016</b> , 67, 3205-21	45
755	Old cells, new tricks: chromatin structure in senescence. <b>2016</b> , 27, 320-31	30
754	FastHiC: a fast and accurate algorithm to detect long-range chromosomal interactions from Hi-C data. <b>2016</b> , 32, 2692-5	20
753	Local Genome Topology Can Exhibit an Incompletely Rewired 3D-Folding State during Somatic Cell Reprogramming. <b>2016</b> , 18, 611-24	92
752	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. <b>2016</b> , 44, e111	1
751	On the organization of human T-cell receptor loci: log-periodic distribution of T-cell receptor gene segments. <b>2016</b> , 13, 20150911	3
750	Topologically-associating domains: gene warehouses adapted to serve transcriptional regulation. <b>2016</b> , 7, 84-90	11
749	Replication timing and transcriptional control: beyond cause and effect-part III. <b>2016</b> , 40, 168-178	73
748	Enhancer, epigenetics, and human disease. <b>2016</b> , 36, 27-33	15
747	In Vivo Mapping of Eukaryotic RNA Interactomes Reveals Principles of Higher-Order Organization and Regulation. <b>2016</b> , 62, 603-17	193
746	RecA: Regulation and Mechanism of a Molecular Search Engine. <b>2016</b> , 41, 491-507	114

745	Architectural proteins Pita, Zw5, and ZIPIC contain homodimerization domain and support specific long-range interactions in <i>Drosophila</i> . <b>2016</b> , 44, 7228-41	38
744	Spectral imaging to visualize higher-order genomic organization. <b>2016</b> , 7, 325-38	6
743	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. <b>2016</b> , 127, e12-23	35
742	Epigenomic Consequences of Coding and Noncoding Driver Mutations. <b>2016</b> , 2, 585-605	7
741	Looping probability of random heteropolymers helps to understand the scaling properties of biopolymers. <b>2016</b> , 94, 032402	5
740	Extraordinary Cancer Epigenomics: Thinking Outside the Classical Coding and Promoter Box. <b>2016</b> , 2, 572-584	16
739	Three-dimensional Genomic Organization of Genes and Function in Eukaryotes. <b>2016</b> , 233-252	2
738	Polymer Physics of the Large-Scale Structure of Chromatin. <b>2016</b> , 1480, 201-6	4
737	Mapping 3D genome architecture through in situ DNase Hi-C. <b>2016</b> , 11, 2104-21	66
736	Transferable model for chromosome architecture. <b>2016</b> , 113, 12168-12173	179
735	High-resolution interrogation of functional elements in the noncoding genome. <i>Science</i> , <b>2016</b> , 353, 1545-1549	197
734	Systematic mapping of functional enhancer-promoter connections with CRISPR interference. <i>Science</i> , <b>2016</b> , 354, 769-773	333 314
733	The Chromatin Landscape of Cellular Senescence. <b>2016</b> , 32, 751-761	65
732	Three-dimensional chromosome structures from energy landscape. <b>2016</b> , 113, 11991-11993	5
731	Characterization of the replication timing program of 6 human model cell lines. <b>2016</b> , 9, 113-7	9
730	Spatial genome organization and cognition. <b>2016</b> , 17, 681-691	49
729	Minute-Made Data Analysis: Tools for Rapid Interrogation of Hi-C Contacts. <b>2016</b> , 64, 9-11	2
728	Label-free imaging of the native, living cellular nanoarchitecture using partial-wave spectroscopic microscopy. <b>2016</b> , 113, E6372-E6381	35

727	Polymer models of the hierarchical folding of the Hox-B chromosomal locus. <b>2016</b> , 94, 042402	20
726	A multi-task graph-clustering approach for chromosome conformation capture data sets identifies conserved modules of chromosomal interactions. <b>2016</b> , 17, 114	21
725	Micro-C XL: assaying chromosome conformation from the nucleosome to the entire genome. <b>2016</b> , 13, 1009-1011	88
724	Evolutionary Biology. <b>2016</b> ,	3
723	A Survey of the Computational Methods for Enhancers and Enhancer-target Predictions. <b>2016</b> , 3-27	1
722	Chromosome Conformation Capture on Chip (4C): Data Processing. <b>2016</b> , 1480, 243-61	
721	Emerging concepts of epigenetic dysregulation in hematological malignancies. <b>2016</b> , 17, 1016-24	63
720	A deep dive into genome assemblies of non-vertebrate animals. 2,	
719	Chromosome-level assembly, annotation and phylome of pelobates cultripes, the Western Spadefoot toad.. <b>2022</b> ,	
718	Expression regulation of genes is linked to their CpG density distributions around transcription start sites.. <b>2022</b> , 5,	0
717	3D chromatin structure changes during spermatogenesis and oogenesis. <b>2022</b> , 20, 2434-2441	1
716	Spatial chromatin accessibility sequencing resolves next-generation genome architecture.	
715	Multi-contact statistics distinguish models of chromosome organization.	0
714	Generation of dynamic three-dimensional genome structure through phase separation of chromatin. <b>2022</b> , 119,	1
713	Super-resolution visualization of chromatin loop folding in human lymphoblastoid cells using interferometric photoactivated localization microscopy. <b>2022</b> , 12,	0
712	Computational prediction and characterization of cell-type-specific and shared binding sites.	
711	Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex-predation.	0
710	Large-scale chromatin reorganization reactivates placenta-specific genes that drive cellular aging. <b>2022</b> ,	4

- 709 Context-dependent 3D genome regulation by cohesin and related factors. 0
- 708 Complexity of enhancer networks predicts cell identity and disease genes revealed by single-cell multi-omics analysis.
- 707 PHi-C2: interpreting Hi-C data as the dynamic 3D genome state.
- 706 Chromosome organization affects genome evolution in *Sulfolobus* archaea. 0
- 705 Multiplexed chromatin imaging reveals predominantly pairwise long-range coordination between *Drosophila* Polycomb genes. 0
- 704 Replication Labeling Methods for Super-Resolution Imaging of Chromosome Territories and Chromatin Domains. **2022**, 111-128
- 703 Studying the Dynamics of Chromatin-Binding Proteins in Mammalian Cells Using Single-Molecule Localization Microscopy. **2022**, 209-247
- 702 CTCF: A misguided jack-of-all-trades in cancer cells. **2022**, 20, 2685-2698 0
- 701 A New Perspective of Genome Regulation from the Physics of Life Standpoint. **2022**, 76, 163-167
- 700 HSV-1 exploits host heterochromatin for egress.
- 699 3D genome organization in the epithelial-mesenchymal transition spectrum. **2022**, 23, 0
- 698 Changes in Higher-Order Chromosomal Structure of *Klebsiella pneumoniae* Under Simulated Microgravity. **2022**, 13, 1
- 697 Retinoic acid induced meiosis initiation in female germline stem cells by remodelling three-dimensional chromatin structure. 0
- 696 Functional genomics in primary T cells and monocytes identifies mechanisms by which genetic susceptibility loci influence systemic sclerosis risk. 0
- 695 HiCUP-Plus: a fast open-source pipeline for accurately processing large scale Hi-C sequence data.
- 694 Deciphering Hierarchical Chromatin Structures and Preference of Genomic Positions in Single Mouse Embryonic Stem Cells.
- 693 Chromosome organization through the cell cycle at a glance. **2022**, 135,
- 692 Epigenetic regulation of T cell exhaustion. 3

- 691 Satellite DNAs and human sex chromosome variation. **2022**, 0
- 690 Nuclear position modulates long-range chromatin interactions.
- 689 How to tame your genes: mechanisms of inflammatory gene repression by glucocorticoids. 0
- 688 Phase Separation and Correlated Motions in Motorized Genome.
- 687 Hi-TrAC reveals fine-scale chromatin structures organized by transcription factors. 0
- 686 Complex chromosomal rearrangements induced by transposons in maize.
- 685 SAFA facilitates chromatin opening of immune genes through interacting with anti-viral host RNAs. **2022**, 18, e1010599 0
- 684 Machine learning methods for exploring sequence determinants of 3D genome organization. **2022**, 167666 0
- 683 Hi-C embedded polymer model of Escherichia coli reveals the origin of heterogeneous subdiffusion in chromosomal loci. **2022**, 105, 0
- 682 Chromosome-level genome of Entada phaseoloides provides insights into genome evolution and triterpenoid saponins biosynthesis.
- 681 The Visayan warty pig (*Sus cebifrons*) genome provides insight into chromosome evolution and sensory adaptation in pigs. 1
- 680 Chromatin behavior in living cells: Lessons from single-nucleosome imaging and tracking. 2200043 3
- 679 Position Effect Variegation: Role of the Local Chromatin Context in Gene Expression Regulation. **2022**, 56, 307-338
- 678 Kilobase-Level Nuclear Compartments Separate Active Regulatory Elements From Adjacent Regions.
- 677 Harnessing CRISPR-Cas9 for Epigenetic Engineering. **2022**, 237-251 0
- 676 Super-Enhancers, Phase-Separated Condensates, and 3D Genome Organization in Cancer. **2022**, 14, 2866 3
- 675 scHiCEmbed: Bin-Specific Embeddings of Single-Cell Hi-C Data Using Graph Auto-Encoders. **2022**, 13, 1048 0
- 674 MaxHiC: A robust background correction model to identify biologically relevant chromatin interactions in Hi-C and capture Hi-C experiments. **2022**, 18, e1010241 0

- 673 A proposed unified interphase nucleus chromosome structure: Preliminary preponderance of evidence. **2022**, 119, 1
- 672 Predicting 3D chromatin interactions from DNA sequence using Deep Learning. **2022**, 0
- 671 Heterogeneous interactions and polymer entropy decide organization and dynamics of chromatin domains. **2022**, 0
- 670 Embryonic heat conditioning in chicks induces transgenerational heat/immunological resilience via methylation on regulatory elements. **2022**, 36, 0
- 669 Condensin I folds the *C. elegans* genome. 1
- 668 Stable twin rDNA loci form a single nucleolus in brewer's yeast. 0
- 667 ZipHiC: a novel Bayesian framework to identify enriched interactions and experimental biases in Hi-C data. 0
- 666 Chromosome-level and haplotype-resolved genome provides insight into the tetraploid hybrid origin of patchouli. **2022**, 13, 0
- 665 Structural and Functional Insights into CP2c Transcription Factor Complexes. **2022**, 23, 6369 1
- 664 Regulatory Architecture of the RCA Gene Cluster Captures an Intragenic TAD Boundary, CTCF-Mediated Chromatin Looping and a Long-Range Intergenic Enhancer. 13, 1
- 663 YaHS: yet another Hi-C scaffolding tool. 0
- 662 EagleC: A deep-learning framework for detecting a full range of structural variations from bulk and single-cell contact maps. **2022**, 8, 1
- 661 The 3D architecture of the pepper genome and its relationship to function and evolution. **2022**, 13, 1
- 660 Cultivated hawthorn (*Crataegus pinnatifida* var. *major*) genome sheds light on the evolution of Maleae (apple tribe). 1
- 659 Gene structure heterogeneity drives transcription noise within human chromosomes. 0
- 658 Contribution of Immunoglobulin Enhancers to B Cell Nuclear Organization. 13, 0
- 657 POSTRE: a tool to predict the pathological effects of human structural variants. 0
- 656 Dissecting cell fate dynamics in pediatric glioblastoma through the lens of complex systems and cellular cybernetics. 0

- 655 Regulation of 3D Organization and Its Role in Cancer Biology. 10, 0
- 654 Sex-specific multi-level 3D genome dynamics in the mouse brain. **2022**, 13, 1
- 653 The relevance of chromatin architecture to genome rearrangements in *Drosophila*. **2022**, 377, 0
- 652 TADfit is a multivariate linear regression model for profiling hierarchical chromatin domains on replicate Hi-C data. **2022**, 5, 0
- 651 RNA polymerase II pausing contributes to maintain chromatin organization in erythrocytes. 0
- 650 Extracting physical characteristics of higher-order chromatin structures from 3D image data. **2022**, 0
- 649 GOnctact: using chromatin contacts to infer Gene Ontology enrichments for cis-regulatory elements. 0
- 648 Introduction to the principles and methods underlying the recovery of metagenome-assembled genomes from metagenomic data. **2022**, 11, 0
- 647 Chromosome-scale genomes reveal genomic consequences of inbreeding in the South China tiger: a comparative study with the Amur tiger. 0
- 646 Computed Three-Dimensional Atomic Force Microscopy Images of Biopolymers Using the Jarzynski Equality. 5365-5371 1
- 645 Characterizing collaborative transcription regulation with a graph-based deep learning approach. **2022**, 18, e1010162 0
- 644 Comparison of buckwheat genomes reveals the genetic basis of metabolomic divergence and ecotype differentiation. 0
- 643 Coming full circle: on the origin and evolution of the looping model for enhancer-promoter communication. **2022**, 102117 1
- 642 Three-dimensional genome structure shapes the recombination landscape of chromatin features during female germline stem cell development. **2022**, 12, 0
- 641 Multi-omics mapping of chromatin interaction resolves the fine hierarchy of 3D genome in allotetraploid cotton. 0
- 640 Integrated Analysis of Hi-C and RNA-Seq Reveals the Molecular Mechanism of Autopolyploid Growth Advantages in Pak Choi (*Brassica rapa* ssp. *chinensis*). 13, 0
- 639 Ribosomal RNA operons define a central functional compartment in the *Streptomyces* chromosome. 0
- 638 Chromosome-level genome assemblies of four wild peach species provide insights into genome evolution and genetic basis of stress resistance. **2022**, 20, 2

- 637 Genomic Profiling of HIV-1 Integration in Microglia Cells Links Viral Integration to TAD Organization.
- 636 Chromosome-level genome assembly and annotation of the native Chinese wild blueberry <i>Vaccinium bracteatum</i>. **2022**, 2, 1-14 ○
- 635 Lattice simulation-based diffusion modelling of 3D chromatin structure. **2022**, 20, 3351-3358
- 634 Plant In Situ Hi-C Experimental Protocol and Bioinformatic Analysis. **2022**, 217-247
- 633 Isolation of *Boechera stricta* Developing Embryos for Hi-C. **2022**, 249-257
- 632 Multi-scale phase separation by explosive percolation with single-chromatin loop resolution. **2022**, 20, 3591-3603
- 631 Chromatin Hubs: A biological and computational outlook. **2022**, 20, 3796-3813 ○
- 630 Contact Matrix Compressor. **2022**,
- 629 CTCF organizes inter-A compartment interactions through RYBP-dependent phase separation. 4
- 628 Structural variations in cancer and the 3D genome. ○
- 627 Hodge theory-based biomolecular data analysis. **2022**, 12, ○
- 626 A model-based analysis reveals three-dimensional genome organization heterogeneity and functional sub-compartments in cell populations.
- 625 Mapping the semi-nested community structure of 3D chromosome contact networks.
- 624 The slow evolving genome of the xenacoelomorph worm *Xenoturbella bocki*. ○
- 623 Dynamic DNA methylation contributes to carryover effects and beneficial acclimatization in geoduck clams. ○
- 622 The era of 3D and spatial genomics. **2022**, ○
- 621 3D spatial genome organization in the nervous system: From development and plasticity to disease. **2022**, 2
- 620 Chromosomal assembly of the flat oyster (*Ostrea edulis* L.) genome as a new genetic resource for aquaculture. ○

619	Structural changes in chromosomes driven by multiple condensin motors during mitosis.	
618	Context-dependent transcriptional remodeling of TADs during differentiation.	1
617	3D genome assisted protein-protein interaction prediction. <b>2022,</b>	
616	Higher-order Structure of Barley Chromosomes Observed by Electron Tomography. <b>2022, 103328</b>	
615	DeepLoop robustly maps chromatin interactions from sparse allele-resolved or single-cell Hi-C data at kilobase resolution. <b>2022, 54, 1013-1025</b>	1
614	In vivo dissection of a clustered-CTCF domain boundary reveals developmental principles of regulatory insulation. <b>2022, 54, 1026-1036</b>	2
613	Integrative genome modeling platform reveals essentiality of rare contact events in 3D genome organizations.	1
612	An atlas of endogenous DNA double-strand breaks arising during human neural cell fate determination. <b>2022, 9,</b>	0
611	Chromosome-level genome assembly and annotation of two lineages of the ant <i>Cataglyphis hispanica</i> : stepping stones towards genomic studies of hybridogenesis and thermal adaptation in desert ants. <b>2,</b>	0
610	Region Capture Micro-C reveals coalescence of enhancers and promoters into nested microcompartments.	0
609	Cell cycle arrest explains the observed bulk 3D genomic alterations in response to long-term heat shock in K562 cells.	
608	Chromatin dynamics controls epigenetic domain formation. <b>2022,</b>	0
607	Application of the 3C Method to Study the Developmental Genes in <i>Drosophila</i> Larvae. <b>13,</b>	
606	Beyond TADs: microscopy reveals 2 axes of chromosome organization by CTCF and cohesin.	0
605	Hi-TrAC reveals fractal nesting of super-enhancers.	
604	Senescence: An Identity Crisis Originating from Deep Within the Nucleus. <b>2022, 38,</b>	1
603	B cell receptor signaling drives APOBEC3 expression via direct enhancer regulation in chronic lymphocytic leukemia B cells. <b>2022, 12,</b>	0
602	Loop-extrusion and polymer phase-separation can co-exist at the single-molecule level to shape chromatin folding. <b>2022, 13,</b>	3

- 601 DNA damage reduces heterogeneity and coherence of chromatin motions. **2022**, 119,
- 600 Evaluating methylation of human ribosomal DNA at each CpG site reveals its utility for cancer detection using cell-free DNA. **2022**, 23,
- 599 Characterizing cis-regulatory elements using single-cell epigenomics. 2
- 598 Applications of single-cell multi-omics sequencing in deep understanding of brain diseases. **2022**, 2,
- 597 Whole-genome survey and phylogenetic analysis of *Gadus macrocephalus*. **2022**, 42, 1
- 596 Transcriptional enhancers at 40: evolution of a viral DNA element to nuclear architectural structures. **2022**, 1
- 595 Intrinsic linking of chromatin fiber in human cells.
- 594 Computational Enhanced Hi-C data reveals the function of structural geometry in genomic regulation. 0
- 593 Improving Bacterial Genome Assembly Using a Test of Strand Orientation.
- 592 StackEPI: identification of cell line-specific enhancer-promoter interactions based on stacking ensemble learning. **2022**, 23, 0
- 591 Nuclear speckles as driving force in gene expression. **2022**, 135, 0
- 590 DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. **2022**, 2, 100144 2
- 589 Dynamic reprogramming of H3K9me3 at hominoid-specific retrotransposons during human preimplantation development. **2022**, 29, 1031-1050.e12 1
- 588 Comparative genomic analysis of the human genome and six bat genomes using unsupervised machine learning: Mb-level CpG and TFBS islands. **2022**, 23,
- 587 KSHV Topologically Associating Domains in Latent and Reactivated Viral Chromatin. 0
- 586 Exploring the significance of PAK1 through chromosome conformation signatures in ibrutinib-resistant chronic lymphocytic leukemia. 1
- 585 The slow-evolving *Acorus tatarinowii* genome sheds light on ancestral monocot evolution. 1
- 584 Non-coding de novo mutations in chromatin interactions are implicated in autism spectrum disorder. 0

- 583 New mechanism of chromatin compartmentalization by BRD2. **2022**,
- 582 The ribonucleoprotein network of the nucleus: a historical perspective. **2022**, 75, 101940 ○
- 581 Uncovering the statistical physics of 3D chromosomal organization using data-driven modeling. **2022**, 75, 102418 ○
- 580 Genetic variation in correlated regulatory region of Immunity. ○
- 579 Polycomb-lamina antagonism partitions heterochromatin at the nuclear periphery. **2022**, 13, ○
- 578 A Review of Mathematical and Computational Methods in Cancer Dynamics. 12, ○
- 577 Topological screen identifies hundreds of Cp190 and CTCF dependent Drosophila chromatin insulator elements.
- 576 3D genome, on repeat: Higher-order folding principles of the heterochromatinized repetitive genome. **2022**, 185, 2690-2707 3
- 575 Regulatory roles of three-dimensional structures of topologically associating domains.
- 574 Translocation detection from Hi-C data via scan statistics.
- 573 A multi-omic dissection of super-enhancer driven oncogenic gene expression programs in ovarian cancer. **2022**, 13, 2
- 572 Phase Separation and Correlated Motions in Motorized Genome. 1
- 571 Are known bacterial strains really present?.
- 570 Chromatin structure in cancer. **2022**, 23, 2
- 569 Simultaneous Quantification of Spatial Genome Positioning and Transcriptomics in Single Cells with scDam&T-Seq. **2022**, 215-241 ○
- 568 Assessing Specific Networks of Chromatin Interactions with HiChIP. **2022**, 113-141 ○
- 567 Dissecting the Epigenome Driving Drug Resistance by ATAC-Seq. **2022**, 171-185
- 566 Quantitative Chromosome Conformation Capture (3C-qPCR). **2022**, 3-13

- 565 Influence of Active Loop Extrusion on the Statistics of Triple Contacts in the Model of Interphase Chromosomes. **2022**, 115, 763-769
- 564 Lineage-specific rearrangement of chromatin loops and epigenomic features during adipocytes and osteoblasts commitment. 2
- 563 Genome-wide association study identifies Sjögren's risk loci with functional implications in immune and glandular cells. **2022**, 13, 0
- 562 Chromosomal-level reference genome of the moth *Heortia vitessoides* (Lepidoptera: Crambidae), a major pest of agarwood-producing trees. **2022**, 114, 110440
- 561 Inner and Outer DNA Loops in Cell Nuclei: Evidence from Pulsed-Field Comet Assay. **2022**, 56, 313-318
- 560 Polymer dynamics relates chromosome mixing to temporal changes in biological contact maps. 1
- 559 Loss of Monoallelic Expression of IGF2 in the Adult Liver Via Alternative Promoter Usage and Chromatin Reorganization. 13, 1
- 558 Remodeling of IL4-IL13-IL5 locus underlies selective gene expression.
- 557 The anatomy of transcriptionally active chromatin loops in *Drosophila* primary spermatocytes using super-resolution microscopy.
- 556 A Genome for Edith's Checkerspot Butterfly: An Insect with Complex Host-Adaptive Suites and Rapid Evolutionary Responses to Environmental Changes. **2022**, 14, 1
- 555 Defining the separation landscape of topological domains for decoding consensus domain organization of 3D genome.
- 554 Chromosome-level Genome Assembly of the High-altitude Leopard (*Panthera pardus*) Sheds Light on Its Environmental Adaptation.
- 553 Characterizing the variation in chromosome structure ensembles in the context of the nuclear microenvironment. **2022**, 18, e1010392 0
- 552 DeDoc2 identifies and characterizes the hierarchy and dynamics of chromatin TAD-like domains in the single cells.
- 551 Plant Genome Sequencing: Modern Technologies and Novel Opportunities for Breeding. **2022**, 56, 495-507 1
- 550 Centuries of genome instability and evolution in soft-shell clam transmissible cancer. 0
- 549 Chromatin structure undergoes global and local reorganization during murine dendritic cell development and activation. **2022**, 119, 1
- 548 Predicting scale-dependent chromatin polymer properties from systematic coarse-graining.

- 547 Painters in chromatin: a unified quantitative framework to systematically characterize epigenome regulation and memory. 0
- 546 Single base-pair resolution analysis of DNA binding motif with MoMotif reveals an oncogenic function of CTCF zinc-finger 1 mutation. **2022**, 50, 8441-8458 0
- 545 Chromosomal assembly of the flat oyster (*Ostrea edulis* L.) genome as a new genetic resource for aquaculture. 0
- 544 The 3D genome landscape: Diverse chromosomal interactions and their functional implications. 10, 0
- 543 Two-step regulation of centromere distribution by condensin II and the nuclear envelope proteins. **2022**, 8, 940-953 2
- 542 CTCF shapes chromatin structure and gene expression in health and disease. 0
- 541 The evolution and diversification of oakleaf butterflies. **2022**, 185, 3138-3152.e20 1
- 540 Reorganization of 3D chromatin architecture in doxorubicin-resistant breast cancer cells. 10, 0
- 539 A chromosome-level genome assembly of the Walking goby (*Scartelaos histophorus*). 9, 0
- 538 DNA methylation in transposable elements buffers the connection between three-dimensional chromatin organization and gene transcription upon rice genome duplication. **2022**, 0
- 537 When 3D genome technology meets viral infection, including SARS-CoV-2. 0
- 536 A chromosome-level genome resource for studying virulence mechanisms and evolution of the coffee rust pathogen *Hemileia vastatrix*. 0
- 535 Quantitative multiplexed imaging of chromatin ultrastructure with Decode-PAINT. 0
- 534 Long-distance association of topological boundaries through nuclear condensates. **2022**, 119, 0
- 533 BinSPreader: Refine binning results for fuller MAG reconstruction. **2022**, 25, 104770 0
- 532 KLF4 recruits SWI/SNF to increase chromatin accessibility and reprogram the endothelial enhancer landscape under laminar shear stress. **2022**, 13, 0
- 531 Phase separation in epigenetics and cancer stem cells. 12, 0
- 530 Sample-multiplexing approaches for single-cell sequencing. **2022**, 79, 1

- 529 DNA capture and loop extrusion dynamics by cohesin-NIPBL. 0
- 528 Characterization of network hierarchy reflects cell-state specificity in genome organization.
- 527 SnapHiC-D: a computational pipeline to identify differential chromatin contacts from single cell Hi-C data.
- 526 Scalable approaches for functional analyses of whole-genome sequencing non-coding variants.
- 525 Quantifying Chromosome Structural Reorganizations during Differentiation, Reprogramming, and Transdifferentiation. **2022**, 129, 1
- 524 Recombination of repeat elements generates somatic complexity in human genomes. **2022**, 185, 3025-3040.e61
- 523 Chromosome dynamics: Rearranging the choreography of a multipartite bacterial genome. **2022**, 32, R889-R891
- 522 CLNN-loop: A deep learning model to predict CTCF-mediated chromatin loops in the different cell lines and CTCF-binding sites (CBS) pair types. 0
- 521 Causality in transcription and genome folding: Insights from X inactivation. 2200105
- 520 Dissecting the co-segregation probability from genome architecture mapping.
- 519 Capturing the Hierarchically Assorted Modules of Protein Interaction in the Organized Nucleome.
- 518 Understanding the function of regulatory DNA interactions in the interpretation of non-coding GWAS variants. 10, 0
- 517 Single-chromosome fission yeast models reveal the configuration robustness of a functional genome. **2022**, 40, 111237 0
- 516 Prolonged FOS activity disrupts a global myogenic transcriptional program by altering 3D chromatin architecture in primary muscle progenitor cells. **2022**, 12, 1
- 515 Inferring Single-Molecule Chromatin Interactions via Online Convex Network Dictionary Learning.
- 514 Hmga2 protein loss alters nuclear envelope and 3D chromatin structure. **2022**, 20, 1
- 513 Single-cell diploid Hi-C reveals the role of spatial aggregations in complex rearrangements and KMT2A fusions in leukemia. **2022**, 23, 1
- 512 Genomic investigation of the Chinese alligator reveals wild-extinct genetic diversity and genomic consequences of their continuous decline. 0

511	Rearrangement of T Cell genome architecture regulates GVHD. <b>2022</b> , 25, 104846	
510	Integrative epigenomics in chronic lymphocytic leukaemia: Biological insights and clinical applications.	0
509	Decrypting the complexity of the human malaria parasite biology through systems biology approaches. 2,	0
508	Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. <b>2022</b> , 119,	1
507	A chromosome-level genome assembly of the highly heterozygous sea urchin <i>Echinometra</i> sp. EZ reveals adaptation in the regulatory regions of stress response genes.	0
506	The transcriptome of acute dehydration in Myeloid Leukemia cells.	0
505	Balanced SET levels favor the correct enhancer repertoire during cell fate acquisition.	0
504	MCIBox: a toolkit for single-molecule multi-way chromatin interaction visualization and micro-domains identification.	0
503	The native mussel <i>Mytilus chilensis</i> genome reveals adaptative molecular signatures facing the marine environment.	2
502	The role of spatiotemporal organization and dynamics of clock complexes in circadian regulation. <b>2022</b> , 78, 102129	0
501	Long-range interaction within the chromatin domain determines regulatory patterns in porcine skeletal muscle. <b>2022</b> , 114, 110482	0
500	DARIC, a Computational Framework for Identifying Quantitatively Differential Compartments from Hi-C Data.	0
499	CEBPA Phase Separation Links Transcriptional Activity and 3D Chromatin Hubs.	0
498	A Unified-Field Theory of Genome Organization and Gene Regulation.	0
497	High-Throughput Preparation of Improved Single-Cell Hi-C Libraries Using an Automated Liquid Handling System. <b>2022</b> , 201-214	0
496	Mapping Mammalian 3D Genomes by Micro-C. <b>2022</b> , 51-71	0
495	True-to-Scale DNA-Density Maps Correlate With Major Accessibility Differences Between Active and Inactive Chromatin.	0
494	Mapping nucleosome and chromatin architectures: A survey of computational methods. <b>2022</b> , 20, 3955-3962	0

- 493 Chromatin organization and DNA damage. **2022**, ○
- 492 Detection of Allele-Specific 3D Chromatin Interactions Using High-Resolution In-Nucleus 4C-seq. **2022**, 15-33 ○
- 491 Tough Tissue Hi-C. **2022**, 35-50 ○
- 490 Targeted Chromosome Conformation Capture (HiCap). **2022**, 75-94 ○
- 489 CASPIAN: A method to identify chromatin topological associated domains based on spatial density cluster. **2022**, 20, 4816-4824 ○
- 488 A possible strategy for generating polymer chains with an entanglement-free structure. **2022**, 18, 6888-6898 ○
- 487 Assessment of Multiway Interactions with Tri-C. **2022**, 95-112 ○
- 486 Structural Changes in Chromosomes Driven by Multiple Condensin Motors During Mitosis. ○
- 485 Acute Protein Depletion Strategies to Functionally Dissect the 3D Genome. **2022**, 311-331 ○
- 484 Chromosome Conformation Capture in Bacteria and Archaea. **2022**, 1-28 ○
- 483 Higher-order Chromatin Organization in Diseases, from Chromosomal Position Effect to Phenotype Variegation. **2023**, 89-110 ○
- 482 Chromosome-Level Genome Assembly of a Fragrant Japonica Rice Cultivar [Changxianggeng 1813] Provides Insights into Genomic Variations between Fragrant and Non-Fragrant Japonica Rice. **2022**, 23, 9705 ○
- 481 3D chromatin remodeling potentiates transcriptional programs driving cell invasion. **2022**, 119, ○
- 480 Recurrent Translocations in Topoisomerase Inhibitor-Related Leukemia Are Determined by the Features of DNA Breaks Rather Than by the Proximity of the Translocating Genes. **2022**, 23, 9824 ○
- 479 Diffusion controls local versus dispersed inheritance of histones during replication and shapes epigenomic architecture. ○
- 478 Karyotype engineering reveals spatio-temporal control of replication firing and gene contacts. **2022**, 2, 100163 ○
- 477 A chromosome-scale genome assembly of *Quercus gilva*: Insights into the evolution of *Quercus* section *Cyclobalanopsis* (Fagaceae). 13, ○
- 476 Chromosome-level assembly of *Culex pipiens molestus* and improved reference genome of *Culex pipiens pallens* (Culicidae, Diptera). ○

475	ParticleChromo3D: a Particle Swarm Optimization algorithm for chromosome 3D structure prediction from Hi-C data. <b>2022</b> , 15,	1
474	Clinical application of advanced multi-omics tumor profiling: Shaping precision oncology of the future. <b>2022</b> , 40, 920-938	2
473	Organization and regulation of nuclear condensates by gene activity.	0
472	Bioinformatics Pipelines for Identification of Super-Enhancers and 3D Chromatin Contacts. <b>2023</b> , 123-146	0
471	Global mapping of RNA-chromatin contacts reveals a proximity-dominated connectivity model for ncRNA-gene interactions.	0
470	A survey of current methods to detect and genotype inversions.	0
469	Deficiency of Heterogeneous Nuclear Ribonucleoprotein U leads to delayed neurogenesis.	0
468	Three-dimensional chromatin re-organization during muscle stem cell aging.	0
467	A review and performance evaluation of clustering frameworks for single-cell Hi-C data.	0
466	Nonparametric single-cell multiomic characterization of trio relationships between transcription factors, target genes, and cis-regulatory regions. <b>2022</b> , 13, 737-751.e4	0
465	Applying genetic technologies to combat infectious diseases in aquaculture.	0
464	Multiscale 3D genome organization underlies ILC2 ontogenesis and allergic airway inflammation.	0
463	Regulation associated modules reflect 3D genome modularity associated with chromatin activity. <b>2022</b> , 13,	0
462	PHI-C2: interpreting Hi-C data as the dynamic 3D genome state.	0
461	Structural Reorganization and Relaxation Dynamics of Axially Stressed Chromosomes.	0
460	Pluripotency factors are repurposed to shape the epigenomic landscape of neural crest cells. <b>2022</b> ,	0
459	Random Knotting in Fractal Ring Polymers. <b>2022</b> , 55, 8409-8417	0
458	The Epstein-Barr Virus Enhancer Interaction Landscapes in Virus-Associated Cancer Cell Lines. <b>2022</b> , 96,	1

457	Deciphering multi-way interactions in the human genome. <b>2022</b> , 13,	0
456	3D genome alterations in T cells associated with disease activity of systemic lupus erythematosus. <i>annrheumdis-2022-2</i>	0
455	Genome architecture plasticity underlies DNA replication timing dynamics in cell differentiation. 13,	0
454	Genomic analyses of the <i>Linum distyly</i> supergene reveal convergent evolution at the molecular level. <b>2022</b> ,	1
453	Novel strategies to improve chicken performance and welfare by unveiling host-microbiota interactions through hologenomics. 13,	0
452	False gene and chromosome losses in genome assemblies caused by GC content variation and repeats. <b>2022</b> , 23,	1
451	Mobilome-driven segregation of the resistome in biological wastewater treatment. 11,	1
450	A high-quality chromosome-level genome assembly of the bivalve mollusk <i>Macrta veneriformis</i> .	1
449	Promoting validation and cross-phylogenetic integration in model organism research. <b>2022</b> , 15,	2
448	HiC4D: Forecasting spatiotemporal Hi-C data with residual ConvLSTM.	0
447	Predicting 3D genome architecture directly from the nucleotide sequence with DNA-DDA.	0
446	MATR3-antisense LINE1 RNA meshwork scaffolds higher-order chromatin organization.	0
445	Complex chromosomal rearrangements induced by transposons in maize.	2
444	Regulation of chromatin microphase separation by adsorbed protein complexes.	1
443	Hi-C Analysis to Identify Genome-Wide Chromatin Structural Aberration in Cancer. <b>2023</b> , 127-140	0
442	Chromatin transitions triggered by LH density as epigenetic regulators of the genome.	0
441	Polymer Models of Chromatin Imaging Data in Single Cells. <b>2022</b> , 15, 330	1
440	Dissecting the cosegregation probability from genome architecture mapping. <b>2022</b> ,	0

439	The three-dimensional landscape of cortical chromatin accessibility in Alzheimer's disease. <b>2022</b> , 25, 1366-1378	0
438	Epigenomic dynamics of early <i>Xenopus</i> embryos.	1
437	Interpretation of the role of germline and somatic non-coding mutations in cancer: expression and chromatin conformation informed analysis. <b>2022</b> , 14,	0
436	The reference genome of the Vernal Pool Tadpole Shrimp, <i>Lepidurus packardii</i> .	0
435	scHiMe: Predicting single-cell DNA methylation levels based on single-cell Hi-C data.	0
434	Nucleus size and its effect on nucleosome stability in living cells.. <b>2022</b> ,	0
433	Catch me if you can: Capturing extracellular DNA transformation in mixed cultures via Hi-C sequencing.	0
432	Improving bacterial genome assembly using a test of strand orientation. <b>2022</b> , 38, ii34-ii41	0
431	Prenatal diagnosis of 21 fetuses with balanced chromosomal abnormalities (BCAs) using whole-genome sequencing. 13,	0
430	Testing for association with rare variants in the coding and non-coding genome: RAVA-FIRST, a new approach based on CADD deleteriousness score. <b>2022</b> , 18, e1009923	0
429	Chromatin epigenetics and nuclear lamina keep the nucleus in shape: examples from natural and accelerated ageing.	0
428	The spatial organization of transcriptional control.	3
427	New insights into genome folding by loop extrusion from inducible degron technologies.	1
426	EWS/FLI mediated reprogramming of 3D chromatin promotes an altered transcriptional state in Ewing sarcoma. <b>2022</b> , 50, 9814-9837	1
425	Differential contributions of nuclear lamina association and genome compartmentalization to gene regulation.	0
424	High quality mapping of chromatin at or near the nuclear lamina from small numbers of cells reveals cell cycle and developmental changes of chromatin at the nuclear periphery.	0
423	Every gene everywhere all at once: High-precision measurement of 3D chromosome architecture with single-cell Hi-C. 9,	0
422	Modulation of the high-order chromatin structure by Polycomb complexes. 10,	1

421	Hypothesis-driven probabilistic modelling enables a principled perspective of genomic compartments.	0
420	scHiCPTR: unsupervised pseudotime inference through dual graph refinement for single-cell Hi-C data.	0
419	Design, Construction, and Functional Characterization of a tRNA Neochromosome in Yeast.	0
418	High-resolution genome topology of human retina uncovers super enhancer-promoter interactions at tissue-specific and multifactorial disease loci. <b>2022</b> , 13,	1
417	Single-cell epigenome analysis reveals age-associated decay of heterochromatin domains in excitatory neurons in the mouse brain.	0
416	Chromosome-Level Genome Assembly of <i>Trichoderma cornu-damae</i> Using Hi-C Data.	0
415	Chromatin architectural alterations due to null mutation of a major CG methylase in rice.	0
414	Chromatin architecture and cis-regulatory landscape of the DACT2-SMOC2 locus in the developing synovial joint..	0
413	DLoopCaller: A deep learning approach for predicting genome-wide chromatin loops by integrating accessible chromatin landscapes. <b>2022</b> , 18, e1010572	0
412	CTCF-TCF loops and intra-TAD interactions show differential dependence on cohesin ring integrity.	2
411	Can abnormal chromatin folding cause high-penetrance cancer predisposition?. <b>2022</b> , 54, 380-388	0
410	Nuclear position modulates long-range chromatin interactions. <b>2022</b> , 18, e1010451	0
409	Genome organization in cardiomyocytes expressing mutated A-type lamins. 10,	0
408	Human microglia phenotypes in the brain associated with HIV infection. <b>2022</b> , 77, 102637	0
407	Epigenomic Measurements in Brain Tissues. <b>2022</b> , 3221-3261	0
406	Best genome sequencing strategies for annotation of complex immune gene families in wildlife. <b>2022</b> , 11,	0
405	Symmetry-based classification of forces driving chromatin dynamics. <b>2022</b> , 18, 8134-8146	0
404	Architecture of Condensed DNA in the Nucleoid of <i>Escherichia coli</i> Bacterium. <b>2022</b> , 67, 506-517	0

- 403 ChromLoops: a comprehensive database for specific protein-mediated chromatin loops in diverse organisms. ○
- 402 High-resolution promoter interaction analysis in Type 3 Innate Lymphoid Cells implicates Batten Disease gene *CLN3* in Crohn's Disease aetiology. ○
- 401 Functional genomics in primary T cells and monocytes identifies mechanisms by which genetic susceptibility loci influence systemic sclerosis risk. ○
- 400 A draft reference genome of the Vernal Pool Fairy Shrimp, *Branchinecta lynchi*. ○
- 399 MiOS, an integrated imaging and computational strategy to model gene folding with nucleosome resolution. **2022**, 29, 1011-1023 ○
- 398 Statistical and functional convergence of common and rare genetic influences on autism at chromosome 16p. ○
- 397 DeepChIA-PET: Accurately predicting ChIA-PET from Hi-C and ChIP-seq with deep dilated networks. ○
- 396 MED1 Regulates BMP/TGF- $\beta$  in Endothelium: Implication for Pulmonary Hypertension. **2022**, 131, 828-841 ○
- 395 Folding Features and Dynamics of 3D Genome Architecture in Plant Fungal Pathogens. ○
- 394 Episomes and Transposases Utilities to Maintain Transgene Expression from Nonviral Vectors. **2022**, 13, 1872 ○
- 393 Sequencing and chromosome-scale assembly of the giant *Pleurodeles waltl* genome. 1
- 392 Rapid intuitive interpretation of heterochromatin and euchromatin through Hi-C analysis. ○
- 391 An Associative Memory Hamiltonian Model for DNA and Nucleosomes. ○
- 390 3D genome organization links non-coding disease-associated variants to genes. 10, ○
- 389 Tangentially Driven Active Polar Linear Polymers - An Analytical Study. ○
- 388 Establishment of 3D chromatin structure after fertilization and the metabolic switch at the morula-to-blastocyst transition require CTCF. **2022**, 41, 111501 ○
- 387 Subtype-specific 3D genome alteration in acute myeloid leukaemia. 1
- 386 A Tremendous Reorganization Journey for the 3D Chromatin Structure from Gametes to Embryos. **2022**, 13, 1864 1

- 385 Chromosome territory reorganization through artificial chromosome fusion is negligible to cell fate determination and mouse development. ○
- 384 3D genome topologies distinguish pluripotent epiblast and primitive endoderm cells in the mouse blastocyst. ○
- 383 A chromosome-level reference genome for the Versatile Fairy Shrimp, *Branchinecta lindahli*. ○
- 382 A multi-enhancer hub at the *Ets1* locus controls T cell differentiation and allergic inflammation through 3D genome topology. ○
- 381 Chromosome decompaction and cohesin direct Topoisomerase II activity to establish and maintain an unentangled interphase genome. ○
- 380 Spatial organization of the 3D genome encodes gene co-expression programs in single cells. ○
- 379 On the origin of the integrity of a subset of Topologically Associating Domains upon Cohesin loss in Interphase Chromosomes. ○
- 378 Remodeling and compaction of the inactive X is regulated by *Xist* during female B cell activation. ○
- 377 Chromosome-level genome assembly of the *Verasper variegatus* provides insights into left eye migration. 9, ○
- 376 EUGENE: A Python toolkit for predictive analyses of regulatory sequences. ○
- 375 Rare and common autism risk variants converge across 16p. ○
- 374 Advanced genomics and clinical phenotypes in psoriatic arthritis. **2022**, 101665 ○
- 373 The Transcriptional Regulator *Prdm1* Is Essential for the Early Development of the Sensory Whisker Follicle and Is Linked to the Beta-Catenin First Dermal Signal. **2022**, 10, 2647 ○
- 372 Navigation and Use of Custom Tracks within the Axolotl Genome Browser. **2023**, 273-289 ○
- 371 Ultrafast and interpretable single-cell 3D genome analysis with Fast-Higashi. **2022**, 13, 798-807.e6 ○
- 370 Integration of Hi-C with short and long-read genome sequencing reveals the structure of germline rearranged genomes. **2022**, 13, ○
- 369 Phase separation as higher-order catalyst. ○
- 368 Chromosome-scale genome assembly of the brown anole (*Anolis sagrei*), an emerging model species. **2022**, 5, 2

367	Can changes in 3D genome architecture create new regulatory landscapes that contribute to phenotypic evolution?.	1
366	HiChIPdb: a comprehensive database of HiChIP regulatory interactions.	1
365	Using single-cell multi-omics screening of human fetal pancreas to identify novel players in human beta cell development.	1
364	Untangling the roles of TOP2A and TOP2B in transcription and cancer. <b>2022</b> , 8,	1
363	Eight principal chromatin states functionally segregate the fly genome into developmental and housekeeping roles.	0
362	Temporal analysis suggests a reciprocal relationship between 3D chromatin structure and transcription. <b>2022</b> , 41, 111567	1
361	Falign: An effective alignment tool for long noisy 3C data.	0
360	Transcriptional and functional consequences of alterations to MEF2C and its topological organization in neuronal models. <b>2022</b> , 109, 2049-2067	2
359	Acute depletion of human core nucleoporin reveals direct roles in transcription control but dispensability for 3D genome organization. <b>2022</b> , 41, 111576	0
358	Genomic insights into local adaptation and future climate-induced vulnerability of a keystone forest tree in East Asia. <b>2022</b> , 13,	1
357	Multi-scale gene regulation mechanism: Spatiotemporal transmission of genetic information. <b>2022</b> , 77, 102487	0
356	Integrative studies of 3D genome organization and chromatin structure. <b>2022</b> , 77, 102493	0
355	Networks and Islands of Genome Nano-architecture and Their Potential Relevance for Radiation Biology. <b>2022</b> , 3-34	2
354	Simulation of Different Three-Dimensional Models of Whole Interphase Nuclei Compared to Experiments - A Consistent Scale-Bridging Simulation Framework for Genome Organization. <b>2022</b> , 495-549	0
353	How Genomes Emerge, Function, and Evolve: Living Systems Emergence Genotype-Phenotype-Multilism Genome/Systems Ecology. <b>2022</b> , 103-156	0
352	Epigenetic-Mediated Regulation of Gene Expression for Biological Control and Cancer: Cell and Tissue Structure, Function, and Phenotype. <b>2022</b> , 339-373	0
351	The Role of Nuclear Actin in Genome Organization and Gene Expression Regulation During Differentiation. <b>2022</b> , 607-624	0
350	Neural Space-Filling Curves. <b>2022</b> , 418-434	0

- 349 Scaling Relationship in Chromatin as a Polymer. **2022**, 263-277 0
- 348 Phase separation in chromatin-based intranuclear processes. **2023**, 461-483 0
- 347 Biomolecular Topology: Modelling and Analysis. **2022**, 38, 1901-1938 0
- 346 Hi-TrAC reveals division of labor of transcription factors in organizing chromatin loops. **2022**, 13, 1
- 345 Epigenetic regulation of aging: implications for interventions of aging and diseases. **2022**, 7, 8
- 344 dcHiC detects differential compartments across multiple Hi-C datasets. **2022**, 13, 0
- 343 ACTIVATION OF HIV-1 PROVIRUSES INCREASES DOWNSTREAM CHROMATIN ACCESSIBILITY. **2022**, 105490 0
- 342 Spatial and Temporal Organization of Chromatin at Small and Large Scales. **2023**, 14, 0
- 341 Algorithmic considerations when analysing capture Hi-C data. 5, 289 0
- 340 Cell division drives DNA methylation loss in late-replicating domains in primary human cells. **2022**, 13, 0
- 339 Learning the histone codes with large genomic windows and three-dimensional chromatin interactions using transformer. **2022**, 13, 1
- 338 De novo whole-genome assembly in an interspecific hybrid table grape, *Bhine Muscat* 1
- 337 Destin2: integrative and cross-modality analysis of single-cell chromatin accessibility data. 0
- 336 Chromosome-scale scaffolding of the fungus gnat genome (Diptera:Bradysia coprophila). 0
- 335 Combined promoter-capture Hi-C and Hi-C analysis reveals a fine-tuned regulation of 3D chromatin architecture in colorectal cancer. 0
- 334 Low input capture Hi-C (liChi-C) identifies promoter-enhancer interactions at high-resolution. 0
- 333 Lamin A/C-dependent chromatin architecture safeguards naïve pluripotency to prevent aberrant cardiovascular cell fate and function. **2022**, 13, 1
- 332 A chromosomal-scale reference genome of the New World Screwworm, *Cochliomyia hominivorax*. 0

331	The 3D enhancer network of the developing T cell genome is shaped by SATB1. <b>2022</b> , 13,	0
330	FORGEdb: systematic analysis of candidate causal variants to uncover target genes and mechanisms in complex traits..	0
329	GILoop: robust chromatin loop calling across multiple sequencing depths on Hi-C data. <b>2022</b> , 105535	0
328	A global high-density chromatin interaction network reveals functional long-range and trans-chromosomal relationships. <b>2022</b> , 23,	0
327	TADMaster: a comprehensive web-based tool for the analysis of topologically associated domains. <b>2022</b> , 23,	0
326	Phased Genome Assemblies. <b>2023</b> , 273-286	0
325	Cancer Epigenetics: An Overview. <b>2022</b> ,	0
324	Sex-determining 3D regulatory hubs revealed by genome spatial auto-correlation analysis.	1
323	Double-strand break repair and mis-repair in 3D. <b>2022</b> , 103430	0
322	Genomic, transcriptomic, and epigenomic analysis of a medicinal snake, <i>Bungarus multicinctus</i> , to provides insights into the origin of Elapidae neurotoxins. <b>2022</b> ,	1
321	Recovery of high-quality genomes from the fecal microbiome of the domestic cat ( <i>Felis catus</i> ) using Hi-C proximity ligation.	0
320	Histone exchange sensors reveal variant specific dynamics in mouse embryonic stem cells.	0
319	Sequencing of <i>Camelina neglecta</i> , a diploid progenitor of the hexaploid oilseed <i>Camelina sativa</i> .	0
318	ChromFormer: A transformer-based model for 3D genome structure prediction.	0
317	Multilevel view on chromatin architecture alterations in cancer. 13,	2
316	Universality and Identity Ordering in Heteropolymer Coil-Globule Transition.	1
315	Widespread Increase in Enhancer-Promoter Interactions during Developmental Enhancer Activation in Mammals.	0
314	Runx factors launch T-cell and innate lymphoid programs via direct and gene network-based mechanisms.	0

- 313 Novel biological insights revealed from the investigation of multiscale genome architecture. **2023**, 21, 312-325 ○
- 312 Multivalent binding proteins can drive collapse and reswelling of chromatin in confinement. **2022**, 19, 153-163 ○
- 311 Chromosomal-level genome and multi-omics dataset provides new insights into leaf pigmentation in *Acer palmatum*. **2023**, 227, 93-104 ○
- 310 Complete chromosome-level genome assembly data from the tawny crazy ant, *Nylanderia fulva* (Mayr) (Hymenoptera: Formicidae). **2023**, 46, 108833 ○
- 309 Six Fractal Codes of Biological Life Unifying ATOMS, WAVES and INFORMATION: Perspectives in Exobiology, Cancers Basic Research and Artificial Intelligence Biomimetism Decisions Making. **2021**, 1, 22-79 ○
- 308 A Multigraph-Based Representation of Hi-C Data. **2022**, 13, 2189 ○
- 307 Accurate prediction of cohesin-mediated 3D genome organization from 2D chromatin features. ○
- 306 Entanglement Length Scale Separates Threading from Branching of Unknotted and Non-concatenated Ring Polymers in Melts. **2022**, 55, 10723-10736 1
- 305 Hi-C analysis of genomic contacts revealed karyotype abnormalities in chicken HD3 cell line. ○
- 304 Poly ADP-ribosylation of SET8 leads to aberrant H4K20 methylation in mammalian nuclear genome. **2022**, 5, ○
- 303 MoDLE: high-performance stochastic modeling of DNA loop extrusion interactions. **2022**, 23, ○
- 302 Quiescence in *Saccharomyces cerevisiae*. **2022**, 56, 253-278 ○
- 301 The Nodewalk assay to quantitate chromatin fiber interactomes in very small cell populations. ○
- 300 Ultra-long-range interactions between active regulatory elements. ○
- 299 Easy Hi-C: A Low-Input Method for Capturing Genome Organization. **2023**, 113-125 1
- 298 Integration of 3D genome topology and local chromatin features uncovers enhancers underlying craniofacial-specific cartilage defects. **2022**, 8, ○
- 297 MCI-frcnn: A deep learning method for topological micro-domain boundary detection. 10, ○
- 296 Essential role of MESP1-RING1A complex in cardiac differentiation. **2022**, 57, 2533-2549.e7 ○

- 295 Ribosomal RNA operons define a central functional compartment in the *Streptomyces* chromosome. **2022**, 50, 11654-11669 ○
- 294 Chromatin activity identifies differential gene regulation across human ancestries. ○
- 293 Development and Evolution of *Drosophila* Chromatin Landscape in a 3D genome context. ○
- 292 Chromatin accessibility: methods, mechanisms, and biological insights. **2022**, 13, 238-278 1
- 291 Interpretation of organizational role of proteins on *E. coli* nucleoid via Hi-C integrated model. **2022**, ○
- 290 A 3D genome atlas of genetic variants and their pathological effects. ○
- 289 Integrative chromatin domain annotation through graph embedding of Hi-C data. ○
- 288 Simultaneous mapping of 3D structure and nascent RNAs argues against nuclear compartments that preclude transcription. **2022**, 41, 111730 1
- 287 Complexity of enhancer networks predicts cell identity and disease genes revealed by single-cell multi-omics analysis. ○
- 286 Genome and Genetic Engineering of the House Cricket (*Acheta domesticus*): Applications for Sustainable Agriculture. ○
- 285 Detection and genomic analysis of BRAF fusions in Juvenile Pilocytic Astrocytoma through the combination and integration of multi-omic data. **2022**, 22, ○
- 284 Epigenetic Regulation of Fungal Genes Involved in Plant Colonization. **2023**, 255-281 ○
- 283 The Role of Chromatin and Transcriptional Control in the Formation of Sexual Fruiting Bodies in Fungi. **2022**, 86, ○
- 282 SnapFISH: a computational pipeline to identify chromatin loops from multiplexed DNA FISH data. ○
- 281 HNF1B-driven three-dimensional chromatin structure for molecular classification in pancreatic cancers. ○
- 280 Reorganization of the DNA replication landscape during adipogenesis is closely linked with adipogenic gene expression. ○
- 279 Multiscale reorganization of the genome following DNA damage facilitates chromosome translocations via nuclear actin polymerization. ○
- 278 Visualizing the Genome: Experimental Approaches for Live-Cell Chromatin Imaging. **2022**, 11, 4086 ○

- 277 Plant Genomics. **2022**, 1-9 ○
- 276 Epigenomic complexity of the human brain revealed by single-cell DNA methylomes and 3D genome structures. ○
- 275 Euchromatin Activity Enhances Segregation and Compaction of Heterochromatin in the Cell Nucleus. **2022**, 12, ○
- 274 Polymer folding through active processes recreates features of genome organization. ○
- 273 The 3D chromatin landscape of rhabdomyosarcoma. ○
- 272 Dynamic chromatin organization and regulatory interactions in human endothelial cell differentiation. **2022**, ○
- 271 Histone variants and modifications during abiotic stress response. 13, ○
- 270 Chromatin modules and their implication in genomic organization and gene regulation. **2022**, ○
- 269 Deciphering the mechanical code of the genome and epigenome. **2022**, 29, 1178-1187 ○
- 268 Structural variant analysis of a cancer reference cell line sample using multiple sequencing technologies. **2022**, 23, ○
- 267 Spatial chromatin accessibility sequencing resolves next-generation genome architecture. ○
- 266 Insights into the cell fate decision-making processes from chromosome structural reorganizations. **2022**, 3, 041402 ○
- 265 Aberrant chromatin organization at the nexus of laminopathy disease pathways. **2022**, 13, 302-314 ○
- 264 YaHS: yet another Hi-C scaffolding tool. 1
- 263 Histology-associated transcriptomic heterogeneity in ovarian folliculogenesis revealed by quantitative single-cell RNA-sequencing for tissue sections with DRAqL. ○
- 262 How enzymatic activity is involved in chromatin organization. 11, ○
- 261 Structural insights into p300 regulation and acetylation-dependent genome organisation. **2022**, 13, ○
- 260 StripeDiff: Model-based algorithm for differential analysis of chromatin stripe. **2022**, 8, ○

- 259 EndHiC: assemble large contigs into chromosome-level scaffolds using the Hi-C links from contig ends. **2022**, 23, ○
- 258 DiffDomain enables identification of structurally reorganized topologically associating domains. ○
- 257 Interferon opens up: HIV-induced inflammation reconfigures 3D chromatin conformation and affects where HIV integrates. **2022**, 82, 4585-4587 ○
- 256 Reference panel guided topological structure annotation of Hi-C data. **2022**, 13, ○
- 255 A chromosome level genome assembly of longnose gar, *Lepisosteus osseus*. ○
- 254 GWAS of Chronic Dizziness in the Elderly Identifies Significant Loci Implicating *MLLT10*, *BPTF*, *LINC01225*, and *ROS1*. ○
- 253 Falign: An effective alignment tool for long noisy 3C data. ○
- 252 CanMethdb: a database for genome-wide DNA methylation annotation in cancers. ○
- 251 Integrating extrusion complex-associated pattern to predict cell type-specific long-range chromatin loops. **2022**, 25, 105687 ○
- 250 Three-Dimensional Organization of Chicken Genome Provides Insights into Genetic Adaptation to Extreme Environments. **2022**, 13, 2317 ○
- 249 Pattern recognition of topologically associating domains using deep learning. **2021**, 22, ○
- 248 Roles of Polycomb Complexes in the Reconstruction of 3D Genome Architecture during Preimplantation Embryonic Development. **2022**, 13, 2382 ○
- 247 Enhancer-promoter interactions and transcription are largely maintained upon acute loss of CTCF, cohesin, WAPL or YY1. **2022**, 54, 1919-1932 4
- 246 Development and implementation of a metaphase DNA model for ionizing radiation induced DNA damage calculation. **2023**, 68, 014001 ○
- 245 Form and function of archaeal genomes. **2022**, 50, 1931-1939 ○
- 244 *Syringa oblata* genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. 13, ○
- 243 Proximity-dependent recruitment of Polycomb Repressive Complexes by the lncRNA *Airn*. ○
- 242 The influence of high-order chromatin state in the regulation of stem cell fate. **2022**, 50, 1809-1822 1

241	Characterizing chromatin interactions of regulatory elements and nucleosome positions, using Hi-C, Micro-C, and promoter capture Micro-C. <b>2022</b> , 15,	0
240	Exogenous chromosomes reveal how sequence composition drives chromatin assembly, activity, folding and compartmentalization.	0
239	Diverse silent chromatin states modulate genome compartmentalization and loop extrusion barriers.	0
238	Multimodal learning of noncoding variant effects using genome sequence and chromatin structure.	0
237	The dynamics of three-dimensional chromatin organization and phase separation in cell fate transitions and diseases. <b>2022</b> , 11,	1
236	3D genome organization. <b>2022</b> , 12,	0
235	Genomes of endangered great hammerhead and shortfin mako sharks reveal historic population declines and high levels of inbreeding in great hammerhead. <b>2022</b> , 105815	0
234	Structural variants drive context-dependent oncogene activation in cancer. <b>2022</b> , 612, 564-572	2
233	Emerging regulatory mechanisms of noncoding RNAs in topologically associating domains. <b>2023</b> ,	0
232	Chromosome-level genome assembly and sex-specific differential transcriptome of the white-backed planthopper, <i>Sogatella furcifera</i> . <b>2023</b> , 24,	0
231	CHIATAC is an efficient strategy for multi-omics mapping of 3D epigenomes from low-cell inputs. <b>2023</b> , 14,	0
230	Artificial intelligence-based multi-omics analysis fuels cancer precision medicine. <b>2023</b> , 88, 187-200	1
229	HPTAD: a computational method to identify topologically associating domains from HiChIP and PLAC-seq datasets. <b>2023</b> ,	0
228	TRPM8 promotes hepatocellular carcinoma progression by inducing SNORA55 mediated nuclear-mitochondrial communication.	0
227	Application of massive parallel reporter analysis in biotechnology and medicine.	0
226	A chromosome-level genome assembly of the <i>Henosepilachna vigintioctomaculata</i> provides insights into the evolution of ladybird beetles.	0
225	Elucidating the structure and function of the nucleus—the NIH Common Fund 4D Nucleome program. <b>2023</b> ,	0
224	Development of digital Hi-C assay.	0

223	Loss of epigenetic information as a cause of mammalian aging. <b>2023</b> ,	2
222	Genetic conversion of a split-drive into a full-drive element. <b>2023</b> , 14,	0
221	HiC-GNN: A generalizable model for 3D chromosome reconstruction using graph convolutional neural networks. <b>2023</b> , 21, 812-836	1
220	Plasmid-Encoded Traits Vary across Environments.	0
219	Hypothesis-driven probabilistic modelling enables a principled perspective of genomic compartments.	0
218	Advances in sequencing technologies for amyotrophic lateral sclerosis research. <b>2023</b> , 18,	0
217	Chromatin Structure from Development to Ageing. <b>2023</b> , 7-51	0
216	Characterizing crosstalk in epigenetic signaling to understand disease physiology. <b>2023</b> , 480, 57-85	0
215	A multicolour polymer model for the prediction of 3D structure and transcription in human chromatin.	0
214	Cell-type-specific prediction of 3D chromatin organization enables high-throughput in silico genetic screening.	0
213	DNA supercoiling-induced shapes alter minicircle hydrodynamic properties.	0
212	PFSET2 Is Involved in Genome Organization of Var Gene Family in Plasmodium falciparum.	0
211	Applications of deep learning in understanding gene regulation. <b>2023</b> , 100384	0
210	Long-read metagenomics paves the way toward a complete microbial tree of life. <b>2023</b> , 20, 30-31	0
209	Low input capture Hi-C (liChi-C) identifies promoter-enhancer interactions at high-resolution. <b>2023</b> , 14,	0
208	A spatial genome aligner for resolving chromatin architectures from multiplexed DNA FISH.	0
207	Influence of ionic conditions on knotting in a coarse-grained model for DNA. 10,	0
206	Random allelic expression in the adult human body. <b>2023</b> , 42, 111945	0

205	Hooked Up from a Distance: Charting Genome-Wide Long-Range Interaction Maps in Neural Cells Chromatin to Identify Novel Candidate Genes for Neurodevelopmental Disorders. <b>2023</b> , 24, 1164	1
204	Inference of genome 3D architecture by modeling overdispersion of Hi-C data.	0
203	A universal sequencing read interpreter. <b>2023</b> , 9,	0
202	Genome modeling: From chromatin fibers to genes. <b>2023</b> , 78, 102506	1
201	Era of gapless plant genomes: innovations in sequencing and mapping technologies revolutionize genomics and breeding. <b>2023</b> , 79, 102886	1
200	Topological implications of DNA tumor viral episomes. <b>2022</b> , 55, 587-594	0
199	ST-ChIP: Accurate prediction of spatiotemporal ChIP-seq data with recurrent neural networks. <b>2022</b> , ,	0
198	The Interplay of Transcription and Genome Topology Programs T Cell Development and Differentiation. <b>2022</b> , 209, 2269-2278	1
197	Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. <b>2022</b> , 12,	0
196	DNA methylation in human gastric epithelial cells defines regional identity without restricting lineage plasticity. <b>2022</b> , 14,	0
195	Exploring the contribution of ARMS2 and HTRA1 genetic risk factors in age-related macular degeneration. <b>2022</b> , 101159	1
194	TADBay: A Bayesian Construction of Topologically Associated Domains. <b>2022</b> ,	0
193	Epimutations and Their Effect on Chromatin Organization: Exciting Avenues for Cancer Treatment. <b>2023</b> , 15, 215	0
192	Epigenetic regulation of cis-regulatory elements and transcription factors during development. <b>2023</b> , 71-113	0
191	Maintenance and dynamic reprogramming of chromatin organization during development.	0
190	Development of a Data-driven Integrative Model of Bacterial Chromosome.	0
189	Enhancer-instructed epigenetic landscape and chromatin compartmentalization dictate a primary antibody repertoire protective against specific bacterial pathogens. <b>2023</b> , 24, 320-336	0
188	Computational approaches to understand transcription regulation in development.	1

- 187 Chromosome conformation capture approaches to investigate 3D genome architecture in Ankylosing Spondylitis. 14, 0
- 186 The Emerging field of epigenetic editing: implication for translational purposes for diseases with developmental origin. **2023**, 355-375 0
- 185 A high-quality Ixodes scapularis genome advances tick science. 0
- 184 Genome wide clustering on integrated chromatin states and Micro-C contacts reveals chromatin interaction signatures. 0
- 183 An atlas of lamina-associated chromatin across twelve human cell types reveals an intermediate chromatin subtype. **2023**, 24, 2
- 182 Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons. 0
- 181 Joint tensor modeling of single cell 3D genome and epigenetic data with Muscle. 0
- 180 HSFA1a modulates plant heat stress responses and alters the 3D chromatin organization of enhancer-promoter interactions. **2023**, 14, 1
- 179 Multi-modular structure of the gene regulatory network for specification and commitment of murine T cells. 14, 0
- 178 3D Chromatin Dynamics during Innate and Adaptive Immune Memory Acquisition. 0
- 177 Mapping nucleolus-associated chromatin interactions using nucleolus Hi-C reveals pattern of heterochromatin interactions. **2023**, 14, 0
- 176 Sex chromosome evolution in beetles. 0
- 175 Predicting Chromatin Interactions from DNA Sequence Using DeepC. **2023**, 19-42 0
- 174 The adapted Activity-By-Contact model for enhancer-gene assignment and its application to single-cell data. 0
- 173 Sequencing and Assembly of Polyploid Genomes. **2023**, 429-458 0
- 172 Deciphering Hierarchical Chromatin Domains and Preference of Genomic Position Forming Boundaries in Single Mouse Embryonic Stem Cells. 2205162 0
- 171 HiCLift: A fast and efficient tool for converting chromatin interaction data between genome assemblies. 0
- 170 An intellectual disability-related MED23 mutation dysregulates gene expression by altering chromatin conformation and enhancer activities. 0

- 169 Pan-3D genome analysis reveals structural and functional differentiation of soybean genomes. **2023**, 24, ○
- 168 Deciphering the chromatin spatial organization landscapes during BMMSC differentiation. **2023**, ○
- 167 Combinatorial single-cell profiling of all major chromatin types with MAbID. ○
- 166 Epigenetics of T cell-mediated immunological responses. **2023**, 149-179 ○
- 165 Chromosome territory reorganization through artificial chromosome fusion is compatible with cell fate determination and mouse development. **2023**, 9, ○
- 164 Consistencies and contradictions in different polymer models of chromatin architecture. **2023**, 21, 1084-1091 ○
- 163 Different Tumor Types Share a Common Nuclear Map of Chromosome Territories. **2023**, 22, 117693512211485○
- 162 The role of structural variations in Alzheimer's disease and other neurodegenerative diseases. 14, ○
- 161 An Integrated Approach of Learning Genetic Networks From Genome-Wide Gene Expression Data Using Gaussian Graphical Model and Monte Carlo Method. **2023**, 17, 117793222311529 ○
- 160 Analysis of Chromatin Interaction and Accessibility by Trac-Looping. **2023**, 85-97 ○
- 159 Visualizing the Nucleome Using the CRISPR-Cas9 System: From in vitro to in vivo. **2023**, 88, S123-S149 ○
- 158 Horizontal Gene Transfer of Antibiotic Resistance Genes in Biofilms. **2023**, 12, 328 2
- 157 Chromosome Three-Dimensional Structure Reconstruction: An Iterative ShRec3D Algorithm. ○
- 156 Short structural variation fuelled CAM evolution within an explosive bromeliad radiation. ○
- 155 Nuclear architecture and the structural basis of mitotic memory. **2023**, 31, ○
- 154 3D genome-selected microRNAs to improve Alzheimer's disease prediction. 14, ○
- 153 Defining the separation landscape of topological domains for decoding consensus domain organization of the 3D genome. **2023**, 33, 386-400 ○
- 152 ParticleChromo3D+: A Web Server for ParticleChromo3D Algorithm for 3D Chromosome Structure Reconstruction. **2023**, 45, 2549-2560 ○

- 151 Ipsilateral restriction of chromosome movement along a centrosome, and apical-basal axis during the cell cycle. ○
- 150 Translating non-coding genetic associations into a better understanding of immune-mediated disease. **2023**, 16, ○
- 149 Chromosome-scale genome assembly of marigold (*Tagetes erecta* L.): an ornamental plant and feedstock for industrial lutein production. **2023**, ○
- 148 Systematic fine-mapping and functional studies of prostate cancer risk variants. **2023**, 26, 106497 ○
- 147 Characterization of altered molecular mechanisms in Parkinson’s disease through cell type-resolved multiomics analyses. **2023**, 9, ○
- 146 Rewiring of the 3D genome during acquisition of carboplatin resistance in a triple-negative breast cancer patient-derived xenograft. **2023**, 13, ○
- 145 *Drosophila* Models Reveal Properties of Mutant Lamins That Give Rise to Distinct Diseases. **2023**, 12, 1142 ○
- 144 3D genome organization and its study in livestock breeding. **2023**, ○
- 143 Prediction of CTCF loop anchor based on machine learning. 14, ○
- 142 Considerations and caveats for analyzing chromatin compartments. 10, ○
- 141 Comparative genomics analyses reveal sequence determinants underlying interspecies variations in injury-responsive enhancers. **2023**, 24, ○
- 140 SATB1 regulates 3D genome architecture in T cells by constraining chromatin interactions surrounding CTCF-binding sites. **2023**, 42, 112323 ○
- 139 The chromosome-level genome of double-petal phenotype jasmine (*Jasminum sambac* Aiton) provides insights into the biosynthesis of floral scent. **2023**, ○
- 138 The non-coding genome in Autism Spectrum Disorders. **2023**, 66, 104752 ○
- 137 Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of *Poncirus polyandra*. **2023**, 115, 110617 ○
- 136 The *Populus koreana* genome provides insights into the biosynthesis of plant aroma. **2023**, 197, 116453 ○
- 135 Loss of the crumbs cell polarity complex disrupts epigenetic transcriptional control and cell cycle progression in the developing retina. **2023**, 259, 441-454 ○
- 134 Interphase chromosomes of the *Aedes aegypti* mosquito are liquid crystalline and can sense mechanical cues. **2023**, 14, ○

- 133 Examining the biological mechanisms of human mental disorders resulting from gene-environment interdependence using novel functional genomic approaches. **2023**, 178, 106008 ○
- 132 A reference genome for Bluegill (Centrarchidae:Lepomis macrochirus). **2023**, 13, ○
- 131 Actin mediated H3K27ac changes demonstrate the link between compartment switching and enhancer-dependent transcriptional regulation. **2023**, 24, ○
- 130 Chromosomal-level genome assembly of *Melastoma candidum* provides insights into trichome evolution. 14, ○
- 129 Three-dimensional chromatin re-organization during muscle stem cell aging. **2023**, 22, ○
- 128 High-content image-based CRISPR screening reveals regulators of 3D genome architectures. ○
- 127 How Hi-C ignited the era of 3D genome biology. ○
- 126 Topological screen identifies hundreds of Cp190- and CTCF-dependent *Drosophila* chromatin insulator elements. **2023**, 9, ○
- 125 Fluidification of Entanglements by a DNA Bending Protein. **2023**, 130, ○
- 124 The Foundational Data Initiative for Parkinson Disease: Enabling efficient translation from genetic maps to mechanism. **2023**, 3, 100261 ○
- 123 Hi-C analysis of genomic contacts revealed karyotype abnormalities in chicken HD3 cell line. **2023**, 24, ○
- 122 Multi-omics analysis reveals spatiotemporal regulation and function of heteromorphic leaves in *Populus*. ○
- 121 3D genome alterations and editing in pathology. **2023**, 31, 924-933 ○
- 120 Direct observation of a crescent-shape chromosome in *Bacillus subtilis*. ○
- 119 HiConfidence: a novel approach uncovering the biological signal in Hi-C data affected by technical biases. **2023**, 24, ○
- 118 Conserved noncoding sequences correlate with distant gene contacts in *Arabidopsis* and *Brassica*. ○
- 117 A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. ○
- 116 An improved reference genome for *Trifolium subterraneum* L. provides insight into molecular diversity and intra-specific phylogeny. 14, ○

115	Chromosome-Level Genome Assembly of the Rough-Toothed Dolphin ( <i>Steno bredanensis</i> ). <b>2023</b> , 11, 418	0
114	Pairtools: from sequencing data to chromosome contacts.	0
113	Genomic profiling of HIV-1 integration in microglia cells links viral integration to the topologically associated domains. <b>2023</b> , 42, 112110	0
112	polishCLR: A Nextflow Workflow for Polishing PacBio CLR Genome Assemblies. <b>2023</b> , 15,	1
111	Phase Separation: Direct and Indirect Driving Force for High-Order Chromatin Organization. <b>2023</b> , 14, 499	0
110	Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons.	0
109	Mini-review: Gene regulatory network benefits from three-dimensional chromatin conformation and structural biology. <b>2023</b> , 21, 1728-1737	0
108	Destin2: Integrative and cross-modality analysis of single-cell chromatin accessibility data. 14,	0
107	The effect of configurational complexity in hetero-polymers on the coil-globule phase transition. <b>2023</b> , 138,	0
106	Polymeric nature of tandemly repeated genes enhances assembly of constitutive heterochromatin in fission yeast.	0
105	Extruding transcription elongation loops observed in high-resolution single-cell 3D genomes.	0
104	Kinetic networks identify TWIST2 as a key regulatory node in adipogenesis. <b>2023</b> , 33, 314-331	0
103	Tracing cancer evolution and heterogeneity using Hi-C.	0
102	Phased nanopore assembly with Shasta and modular graph phasing with GFase.	0
101	Plant chromatin on the move: an overview of chromatin mobility during transcription and DNA repair.	0
100	Evolutionarily distinct and sperm-specific supersized chromatin loops are marked by Helitron transposons in <i>Xenopus tropicalis</i> . <b>2023</b> , 42, 112151	0
99	Delta.EPI: a probabilistic voting-based enhancer-promoter interaction prediction platform. <b>2023</b> ,	0
98	Through the lens of phase separation: intrinsically unstructured protein and chromatin looping. <b>2023</b> , 14,	0

- 97 Structural Variations and Adaptations of Synthetic Chromosome Ends Driven by SCRaMBLE in Haploid and Diploid Yeasts. **2023**, 12, 689-699 ○
- 96 Foxp3 Orchestrates Reorganization of Chromatin Architecture to Establish Regulatory T Cell Identity. ○
- 95 Does multi-way, long-range chromatin contact data advance 3D genome reconstruction?. **2023**, 24, ○
- 94 A genome and single-nucleus cerebral cortex transcriptome atlas of the short-finned pilot whale *Globicephala macrorhynchus*. ○
- 93 Characterization of network hierarchy reflects cell state specificity in genome organization. **2023**, 33, 247-260 ○
- 92 Understanding the OMICS techniques: an introduction to genomics and proteomics. **2023**, 1-28 ○
- 91 Active maintenance of CD8+T cell naivety through regulation of global genome architecture. ○
- 90 A layer cake model for plant and metazoan chromatin. ○
- 89 High-Resolution 3D Genome Map of Brucella Chromosomes in Exponential and Stationary Phases. **2023**, 11, ○
- 88 In vitro reconstitution of chromatin domains. ○
- 87 Genome assembly of the deep-sea coral *Lophelia pertusa*. ○
- 86 A maximum-entropy model to predict 3D structural ensembles of chromatin from pairwise distances with applications to interphase chromosomes and structural variants. **2023**, 14, ○
- 85 Using QTL to Identify Genes and Pathways Underlying the Regulation and Production of Milk Components in Cattle. **2023**, 13, 911 ○
- 84 Epigenetics in LMNA-Related Cardiomyopathy. **2023**, 12, 783 ○
- 83 Epigenetic Regulations in Mammalian Cells: Roles and Profiling Techniques. **2023**, 46, 86-98 ○
- 82 MukBEF-dependent chromosomal organization in widened *Escherichia coli*. 14, ○
- 81 The anatomy of transcriptionally active chromatin loops in *Drosophila* primary spermatocytes using super-resolution microscopy. **2023**, 19, e1010654 ○
- 80 Modelling chromosome-wide target search. **2023**, 25, 033024 ○

- 79 3D genomics and its applications in precision medicine. **2023**, 28, ○
- 78 High-throughput Pore-C reveals the single-allele topology and cell type-specificity of 3D genome folding. **2023**, 14, ○
- 77 Contributions of 3D chromatin structure to cell-type-specific gene regulation. **2023**, 79, 102032 ○
- 76 A comprehensive review of bioinformatics tools for chromatin loop calling. **2023**, 24, ○
- 75 Morphine Re-arranges Chromatin Spatial Architecture of Primate Cortical Neurons. ○
- 74 CTCF controls three-dimensional enhancer network underlying the inflammatory response of bone marrow-derived dendritic cells. **2023**, 14, ○
- 73 Influence of human peripheral blood samples preprocessing on the quality of Hi-C libraries. **2023**, 27, 83-87 ○
- 72 The diverging epigenomic landscapes of honeybee queens and workers revealed by multiomic sequencing. **2023**, 155, 103929 1
- 71 Phenotypic dimorphism between honeybee queen and worker is regulated by complicated epigenetic modifications. **2023**, 26, 106308 ○
- 70 A chromosome-scale genome sequence of sudangrass (*Sorghum sudanense*) highlights the genome evolution and regulation of dhurrin biosynthesis. **2023**, 136, ○
- 69 Heterochromatin rewiring and domain disruption-mediated chromatin compaction during erythropoiesis. **2023**, 30, 463-474 ○
- 68 Imaging large cell populations with fast, automated super-resolution. ○
- 67 A Kaleidoscope of Keratin Gene Expression and the Mosaic of Its Regulatory Mechanisms. **2023**, 24, 5603 ○
- 66 Whole-genome doubling drives oncogenic loss of chromatin segregation. **2023**, 615, 925-933 ○
- 65 Assignment of the somatic A/B compartments to chromatin domains in giant transcriptionally active lampbrush chromosomes. ○
- 64 Regulation of loop extrusion on the interphase genome. 1-18 ○
- 63 Modulation of chromatin architecture influences the neuronal nucleus through activity-regulated gene expression. ○
- 62 Senescence-associated transcriptional derepression in subtelomeres is determined in a chromosome-end-specific manner. ○

- 61 Genome assembly of the deep-sea coral *Lophelia pertusa*. 2023, 1-12 ○
- 60 Evolution of chemosensory and detoxification gene families across herbivorous *Drosophilidae*. ○
- 59 Draft Genome Assembly of the Ancient Tetraploid Orphan Legume Marama Bean (*Tylosema esculentum*) with PacBio HiFi data. ○
- 58 Structural reorganization and relaxation dynamics of axially stressed chromosomes. 2023, ○
- 57 Efficient Hi-C inversion facilitates chromatin folding mechanism discovery and structure prediction. ○
- 56 A DNA tumor virus globally reprograms host 3D genome architecture to achieve immortal growth. 2023, 14, ○
- 55 Langevin analogy between particle trajectories and polymer configurations. 2023, 107, ○
- 54 Single Molecule Dynamics of Sister Chromatid Cohesin. 2023, 63, 21-23 ○
- 53 Genomic rearrangements and evolutionary changes in 3D chromatin topologies in the cotton tribe (*Gossypieae*). 2023, 21, ○
- 52 Genome doubling perturbs DNA packing and promotes cancer development. ○
- 51 Genome and Genetic Engineering of the House Cricket (*Acheta domesticus*): A Resource for Sustainable Agriculture. 2023, 13, 589 ○
- 50 Dynamics of nuclear architecture during early embryonic development and lessons from liveimaging. 2023, 58, 435-449 ○
- 49 Chromosome-scale de novo genome assembly and annotation of three representative *Casuarina* species: *C. equisetifolia* , *C. glauca* , and *C. cunninghamiana*. ○
- 48 Toward a comprehensive catalog of regulatory elements. ○
- 47 Functional characterization of human genomic variation linked to polygenic diseases. 2023, ○
- 46 Genetic variation in cis-regulatory domains suggests cell type-specific regulatory mechanisms in immunity. 2023, 6, ○
- 45 BIND&MODIFY: a long-range method for single-molecule mapping of chromatin modifications in eukaryotes. 2023, 24, ○
- 44 Determining chromatin architecture with Micro Capture-C. ○

- 43 Oncogenic epidermal growth factor receptor signal-induced histone deacetylation suppresses chemokine gene expression in human lung adenocarcinoma. **2023**, 13,
- 42 A reference assembly for the legume cover crop, hairy vetch (*Vicia villosa*).
- 41 The EN-TE<sub>x</sub> resource of multi-tissue personal epigenomes & variant-impact models. **2023**, 186, 1493-1511.
- 40 Somatic chromosome pairing has a determinant impact on 3D chromatin organization.
- 39 Highly connected 3D chromatin networks established by an oncogenic fusion protein shape tumor cell identity. **2023**, 9,
- 38 Nuclei on the Rise: When Nuclei-Based Methods Meet Next-Generation Sequencing. **2023**, 12, 1051
- 37 Three-dimensional and single-cell sequencing of liver cancer reveals comprehensive host-virus interactions in HBV infection. 14,
- 36 A method for extracting effective interactions from Hi-C data with applications to interphase chromosomes and inverted nuclei.
- 35 Matrin3 mediates differentiation through stabilizing chromatin accessibility and chromatin loop-domain interactions, and YY1 mediated enhancer-promoter interactions.
- 34 Genetic impacts on DNA methylation help elucidate regulatory genomic processes.
- 33 NSD2 E1099K drives relapse in pediatric acute lymphoblastic leukemia by disrupting 3D chromatin organization. **2023**, 24,
- 32 High changing curvature regions detect chromatin enrichment in single cell data.
- 31 The interplay of 3D genome organization with UV-induced DNA damage and repair. **2023**, 104679
- 30 Comparing chromatin contact maps at scale: methods and insights.
- 29 Three-dimensional chromatin organization promotes genome evolution in a fungal plant pathogen.
- 28 Condensed but liquid-like domain organization of active chromatin regions in living human cells. **2023**, 9,
- 27 Differential contributions of nuclear lamina association and genome compartmentalization to gene regulation. **2023**, 14,
- 26 Structural changes in chromosomes driven by multiple condensin motors during mitosis. **2023**, 42, 112348

- 25 Chromatin conformation dynamics during CD4+ T cell activation implicates autoimmune disease-associated genes and regulatory elements. ○
- 24 Noncoding RNA-chromatin association: Functions and mechanisms. **2023**, ○
- 23 Chromosome-Level Genome Assembly of the Blue Mussel *Mytilus chilensis* Reveals Molecular Signatures Facing the Marine Environment. **2023**, 14, 876 ○
- 22 Toward cis-regulation in soybean: a 3D genome scope. **2023**, 43, ○
- 21 Chromosome-length genome assemblies and cytogenomic analyses of pangolins reveal remarkable chromosome counts and plasticity. **2023**, 31, ○
- 20 Dynamic chromatin conformation and accessibility changes mediate the spatial-specific gene regulatory network in *Bombyx mori*. **2023**, 124415 ○
- 19 The magic of unraveling genome architecture and function. **2023**, 112361 ○
- 18 The role of heterochromatin in 3D genome organization during preimplantation development. **2023**, 112248 ○
- 17 Dynamic chromatin architectures provide insights into the genetics of cattle myogenesis. **2023**, 14, ○
- 16 A chromosome-scale genome assembly of *Malus domestica*, a multi-stress resistant apple variety. **2023**, 115, 110627 ○
- 15 Dynamic changes in P300 enhancers and enhancer-promoter contacts control mouse cardiomyocyte maturation. **2023**, ○
- 14 Omics Views of Mechanisms for Cell Fate Determination in Early Mammalian Development. **2023**, ○
- 13 Scale-free models of chromosome structure, dynamics, and mechanics. ○
- 12 Predicting enhancer-promoter interaction based on epigenomic signals. 14, ○
- 11 Population genomic analysis provides evidence of the past success and future potential of South China tiger captive conservation. **2023**, 21, ○
- 10 Single-cell DNA Methylome and 3D Multi-omic Atlas of the Adult Mouse Brain. ○
- 9 Cell Type-Specific Regulation by a Heptad of Transcription Factors in Human Hematopoietic Stem and Progenitor Cells. ○
- 8 Role of Next Generation Sequencing in Trait Identification, Genetic Mapping, and Crop Improvement. **2023**, 425-440 ○

- 7 Putting hornets on the genomic map. **2023**, 13,
- 6 Single-cell technologies for multimodal omics measurements. 3,
- 5 Development of a Data-Driven Integrative Model of a Bacterial Chromosome.
- 4 Igh and Igk loci use different folding principles for V gene recombination due to distinct chromosomal architectures of pro-B and pre-B cells. **2023**, 14,
- 3 The Principles and Applications of High-Throughput Sequencing Technologies. **2023**, 27, 9-24
- 2 The local density of H3K9me3 dictates the stability of HP1 $\alpha$ -condensates-mediated genomic interactions. **2023**,
- 1 PIBF1 regulates multiple gene expression via impeding long-range chromatin interaction to drive the malignant transformation of HPV16 integration epithelial cells. **2023**,