Sergey V Razin

List of Publications by Year
in descending order

226 papers	5,720 citations	94269 37 h-index	114278 63 g-index
236 all docs	236 docs citations	236 times ranked	5586 citing authors

#	Article	IF	Citations
1	Single-nucleus Hi-C reveals unique chromatin reorganization at oocyte-to-zygote transition. Nature, 2017, 544, 110-114.	13.7	604
2	Active chromatin and transcription play a key role in chromosome partitioning into topologically associating domains. Genome Research, 2016, 26, 70-84.	2.4	311
3	Replication origins are attached to the nuclear skeleton. Nucleic Acids Research, 1986, 14, 8189-8207.	6.5	172
4	Small molecule compounds that induce cellular senescence. Aging Cell, 2016, 15, 999-1017.	3.0	143
5	Cys2His2 zinc finger protein family: Classification, functions, and major members. Biochemistry (Moscow), 2012, 77, 217-226.	0.7	139
6	Large-scale Fragmentation of Mammalian DNA in the Course of Apoptosis Proceeds via Excision of Chromosomal DNA Loops and Their Oligomers. Journal of Biological Chemistry, 1995, 270, 20239-20241.	1.6	123
7	Nucleolus: A Central Hub for Nuclear Functions. Trends in Cell Biology, 2019, 29, 647-659.	3.6	119
8	Mechanisms of heat shock response in mammals. Cellular and Molecular Life Sciences, 2013, 70, 4229-4241.	2.4	109
9	Proteins tightly bound to DNA in the regions of DNA attachment to the skeletal structures of interphase nuclei and metaphase chromosomes. Cell, 1981, 27, 65-73.	13.5	90
10	Control of human cytomegalovirus gene expression by differential histone modifications during lytic and latent infection of a monocytic cell line. Gene, 2006, 384, 120-128.	1.0	83
11	Nuclear lamina integrity is required for proper spatial organization of chromatin in Drosophila. Nature Communications, 2019, 10, 1176.	5.8	83
12	Disclosure of a structural milieu for the proximity ligation reveals the elusive nature of an active chromatin hub. Nucleic Acids Research, 2013, 41, 3563-3575.	6.5	82
13	Specificity and Functional Significance of DNA Interaction with the Nuclear Matrix: New Approaches to Clarify the Old Questions. International Review of Cytology, 1996, 162B, 405-448.	6.2	81
14	Different topoisomerase II antitumor drugs direct similar specific long-range fragmentation of an amplified c-MYC gene locus in living cells and in high-salt-extracted nuclei.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 102-106.	3.3	79
15	The channels model of nuclear matrix structure. BioEssays, 1995, 17, 443-450.	1.2	78
16	Chromosome Conformation Capture (from 3C to 5C) and Its ChIP-Based Modification. Methods in Molecular Biology, 2009, 567, 171-188.	0.4	70
17	Chromatin Domains and Regulation of Transcription. Journal of Molecular Biology, 2007, 369, 597-607.	2.0	69
18	Characterization of DNA pattern in the site of permanent attachment to the nuclear matrix located in the vicinity of replication origin. Biochemical and Biophysical Research Communications, 1990, 168, 9-15.	1.0	68

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19	Dual effect of heat shock on DNA replication and genome integrity. Molecular Biology of the Cell, 2012, 23, 3450-3460.	0.9	68
20	Synthetically Lethal Interactions of ATM, ATR, and DNA-PKcs. Trends in Cancer, 2018, 4, 755-768.	3.8	68
21	Suppression of liquidâ€"liquid phase separation by 1,6-hexanediol partially compromises the 3D genome organization in living cells. Nucleic Acids Research, 2021, 49, 10524-10541.	6.5	68
22	In vivo formaldehyde cross-linking: it is time for black box analysis. Briefings in Functional Genomics, 2015, 14, 163-165.	1.3	64
23	Visualization of individual DNA loops and a map of loop domains in the human dystrophin gene. Nucleic Acids Research, 2004, 32, 2079-2086.	6.5	62
24	Mechanism of heat stress-induced cellular senescence elucidates the exclusive vulnerability of early S-phase cells to mild genotoxic stress. Nucleic Acids Research, 2015, 43, 6309-6320.	6.5	59
25	CTCF-dependent enhancer blockers at the upstream region of the chicken Â-globin gene domain. Nucleic Acids Research, 2004, 32, 1354-1362.	6.5	53
26	Transcription factories in the context of the nuclear and genome organization. Nucleic Acids Research, 2011, 39, 9085-9092.	6.5	53
27	Spatial configuration of the chicken Î±-globin gene domain: immature and active chromatin hubs. Nucleic Acids Research, 2008, 36, 4629-4640.	6.5	51
28	Nuclear matrix attachment regions and topoisomerase II binding and reaction sites in the vicinity of a chicken DNA replication origin. Biochemical and Biophysical Research Communications, 1991, 177, 265-270.	1.0	50
29	Long-range Fragmentation of the Eukaryotic Genome by Exogenous and Endogenous Nucleases Proceeds in a Specific Fashion via Preferential DNA Cleavage at Matrix Attachment Sites. Journal of Biological Chemistry, 1995, 270, 18685-18690.	1.6	50
30	Weak interactions in higher-order chromatin organization. Nucleic Acids Research, 2020, 48, 4614-4626.	6.5	50
31	Order and stochasticity in the folding of individual Drosophila genomes. Nature Communications, 2021, 12, 41.	5.8	49
32	Genomic Domains and Regulatory Elements Operating at the Domain Level. International Review of Cytology, 2003, 226, 63-125.	6.2	48
33	A requiem to the nuclear matrix: from a controversial concept to 3D organization of the nucleus. Chromosoma, 2014, 123, 217-224.	1.0	47
34	Low ionic strength extraction of nuclease-treated nuclei destroys the attachment of transcriptionally active DNA to the nuclear skeleton. Nucleic Acids Research, 1985, 13, 7427-7444.	6.5	46
35	Nuclear skeleton, DNA domains and control of replication and transcription. FEBS Journal, 1991, 200, 613-624.	0.2	45
36	The anti-cancer drugs curaxins target spatial genome organization. Nature Communications, 2019, 10, 1441.	5.8	44

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37	Organization of the 3â€²-boundary of the chicken Î± globin gene domain and characterization of a CR 1-specific protein binding site. Nucleic Acids Research, 1990, 18, 401-409.	6.5	43
38	Chromatin without the 30-nm fiber. Epigenetics, 2014, 9, 653-657.	1.3	43
39	Dynamics of double strand breaks and chromosomal translocations. Molecular Cancer, 2014, 13, 249.	7.9	42
40	Communication of genome regulatory elements in a folded chromosome. FEBS Letters, 2013, 587, 1840-1847.	1.3	37
41	Perinucleolar relocalization and nucleolin as crucial events in the transcriptional activation of key genes in mantle cell lymphoma. Blood, 2014, 123, 2044-2053.	0.6	37
42	Functional Architecture of Chromosomal DNA Domains. Critical Reviews in Eukaryotic Gene Expression, 1996, 6, 247-269.	0.4	36
43	Chromosomal DNA Loops May Constitute Basic Units of the Eukaryotic Genome Organization and Evolution. Critical Reviews in Eukaryotic Gene Expression, 1999, 9, 279-283.	0.4	35
44	DNA loop anchorage region colocalizes with the replication origin located downstream to the human gene encoding lamin B2. , 1998, 69, 13-18.		34
45	The 33 kb transcript of the chicken ?-globin gene domain is part of the nuclear matrix. Journal of Cellular Biochemistry, 2004, 92, 445-457.	1.2	34
46	Singleâ€cell Hiâ€C bridges microscopy and genomeâ€wide sequencing approaches to study 3D chromatin organization. BioEssays, 2017, 39, 1700104.	1.2	34
47	A CTCF-Dependent Silencer Located in the Differentially Methylated Area May Regulate Expression of a Housekeeping Gene Overlapping a Tissue-Specific Gene Domain. Molecular and Cellular Biology, 2006, 26, 1589-1597.	1.1	33
48	Identification of c-Myb Target Genes in K562 Cells Reveals a Role for c-Myb as a Master Regulator. Genes and Cancer, 2011, 2, 805-817.	0.6	33
49	Studying RNAâ€“DNA interactome by Red-C identifies noncoding RNAs associated with various chromatin types and reveals transcription dynamics. Nucleic Acids Research, 2020, 48, 6699-6714.	6.5	31
50	Non-clonability correlates with genomic instability: a case study of a unique DNA region11Edited by M. Yaniv. Journal of Molecular Biology, 2001, 307, 481-486.	2.0	30
51	Hypoosmotic stress induces R loop formation in nucleoli and ATR/ATM-dependent silencing of nucleolar transcription. Nucleic Acids Research, 2019, 47, 6811-6825.	6.5	30
52	The Role of Liquidâ€“Liquid Phase Separation in the Compartmentalization of Cell Nucleus and Spatial Genome Organization. Biochemistry (Moscow), 2020, 85, 643-650.	0.7	30
53	Induction of transcription within chromosomal DNA loops flanked by MAR elements causes an association of loop DNA with the nuclear matrix. Nucleic Acids Research, 2005, 33, 4157-4163.	6.5	29
54	Nuclear Compartments, Genome Folding, and Enhancer-Promoter Communication. International Review of Cell and Molecular Biology, 2015, 315, 183-244.	1.6	29

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55	Gene functioning and storage within a folded genome. Cellular and Molecular Biology Letters, 2017, 22, 18.	2.7	29
56	Breakpoint cluster regions of the AML-1 and ETO genes contain MAR elements and are preferentially associated with the nuclear matrix in proliferating HEL cells. Journal of Cell Science, 2004, 117, 4583-4590.	1.2	28
57	The 3D Genome as a Target for Anticancer Therapy. Trends in Molecular Medicine, 2020, 26, 141-149.	3.5	28
58	Transcriptional regulation and spatial organisation of the human AML1/RUNX1 gene. Journal of Cellular Biochemistry, 2011, 112, 1997-2005.	1.2	26
59	Functional analysis of DNA sequences located within a cluster of DNase U hypersensitive sites colocalizing with a MAR element at the upstream border of the chicken ?-globin gene domain. Journal of Cellular Biochemistry, 1999, 74, 38-49.	1.2	24
60	Quantitative analysis of genomic element interactions by molecular colony technique. Nucleic Acids Research, 2014, 42, e36-e36.	6.5	24
61	Early S-phase cell hypersensitivity to heat stress. Cell Cycle, 2016, 15, 337-344.	1.3	24
62	Mapping of Replication Origins and Termination Sites in the Duchenne Muscular Dystrophy Gene. Genomics, 1997, 45, 24-30.	1.3	23
63	Mapping long-range chromatin organization within the chicken Î±-globin gene domain using oligonucleotide DNA arrays. Genomics, 2005, 85, 143-151.	1.3	23
64	Breakpoint Clusters: Reason or Consequence?. Critical Reviews in Eukaryotic Gene Expression, 2004, 14, 65-78.	0.4	23
65	The distribution of tightly bound proteins along the DNA chain reflects the type of cell differentiation. Nucleic Acids Research, 1988, 16, 3617-3633.	6.5	22
66	Chromatin loops, illegitimate recombination, and genome evolution. BioEssays, 2009, 31, 278-286.	1.2	22
67	Extensive methylation of a part of the CpG island located 3.0â€“4.5 kbp upstream to the chicken alpha-globin gene cluster may contribute to silencing the globin genes in non-erythroid cells 1 1Edited by M. Yaniv. Journal of Molecular Biology, 2000, 299, 845-852.	2.0	21
68	Cellâ€cycleâ€dependent localization of human cytomegalovirus UL83 phosphoprotein in the nucleolus and modulation of viral gene expression in human embryo fibroblasts in vitro. Journal of Cellular Biochemistry, 2011, 112, 307-317.	1.2	21
69	Actual Ligation Frequencies in the Chromosome Conformation Capture Procedure. PLoS ONE, 2013, 8, e60403.	1.1	21
70	The Specificity of Human Lymphocyte Nucleolar DNA Long-Range Fragmentation by Endogenous Topoisomerase II and Exogenous Bal 31 Nuclease Depends on Cell Proliferation Status. Biochemistry, 1995, 34, 4133-4138.	1.2	20
71	Human cytomegalovirus proteins PP65 and IEP72 are targeted to distinct compartments in nuclei and nuclear matrices of infected human embryo fibroblasts. Journal of Cellular Biochemistry, 2003, 90, 1056-1067.	1.2	20
72	Distinct Distribution of Ectopically Expressed Histone Variants H2A.Bbd and MacroH2A in Open and Closed Chromatin Domains. PLoS ONE, 2012, 7, e47157.	1.1	20

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73	Assembly of nuclear matrixâ€“bound protein complexes involved in non-homologous end joining is induced by inhibition of DNA topoisomerase II. Journal of Cellular Physiology, 2006, 207, 660-667.	2.0	19
74	The clustering of CpG islands may constitute an important determinant of the 3D organization of interphase chromosomes. Epigenetics, 2014, 9, 951-963.	1.3	19
75	Topologically-associating domains: gene warehouses adapted to serve transcriptional regulation. Transcription, 2016, 7, 84-90.	1.7	19
76	Activation of the alpha-globin gene expression correlates with dramatic upregulation of nearby non-globin genes and changes in local and large-scale chromatin spatial structure. Epigenetics and Chromatin, 2017, 10, 35.	1.8	19
77	Manipulation of Cellular Processes via Nucleolus Hijaking in the Course of Viral Infection in Mammals. Cells, 2021, 10, 1597.	1.8	19
78	Chemotherapy-related secondary leukemias: A role for DNA repair by error-prone non-homologous end joining in topoisomerase II â€" Induced chromosomal rearrangements. Gene, 2007, 391, 76-79.	1.0	18
79	TMEM8 â€“ a non-globin gene entrapped in the globin web. Nucleic Acids Research, 2009, 37, 7394-7406.	6.5	18
80	Interaction in vivo between the Two Matrix Attachment Regions Flanking a Single Chromatin Loop. Journal of Molecular Biology, 2009, 386, 929-937.	2.0	18
81	SETDB1 fuels the lung cancer phenotype by modulating epigenome, 3D genome organization and chromatin mechanical properties. Nucleic Acids Research, 2022, 50, 4389-4413.	6.5	18
82	Initiated complexes of RNA polymerase II are concentrated in the nuclear skeleton associated DNA. Experimental Cell Research, 1985, 158, 273-275.	1.2	17
83	Transcriptional enhancer in the vicinity of a replication origin within the 5â€² region of the chicken Î±-globin gene domain. Journal of Molecular Biology, 1991, 217, 595-598.	2.0	17
84	Domain organization of eukaryotic genome. Cell Biology International Reports, 1992, 16, 697-708.	0.7	17
85	Characterization of the chromatin structure in the upstream region of the chicken alpha-globin gene domain. Molecular Genetics and Genomics, 1994, 242, 649-652.	2.4	17
86	In the Nucleus and Cytoplasm of Chicken Erythroleukemic Cells, Prosomes Containing the p23K Subunit Are Found in Centers of Globin (Pre-)mRNA Processing and Accumulation. Experimental Cell Research, 1999, 250, 569-575.	1.2	17
87	Mapping of the nuclear matrix-bound chromatin hubs by a new M3C experimental procedure. Nucleic Acids Research, 2010, 38, 8051-8060.	6.5	17
88	Quantitative differences in TAD border strength underly the TAD hierarchy in <i>Drosophila</i> chromosomes. Journal of Cellular Biochemistry, 2019, 120, 4494-4503.	1.2	17
89	Non-coding RNAs in chromatin folding and nuclear organization. Cellular and Molecular Life Sciences, 2021, 78, 5489-5504.	2.4	17
90	Organization of specific DNA sequence elements in the region of the replication origin and matrix attachment site in the chicken Î±-globin gene domain. Molecular Genetics and Genomics, 1992, 235, 381-388.	2.4	16

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91	The sequence-specific nuclear matrix binding factor F6 is a chicken GATA-like protein. Molecular Genetics and Genomics, 1993, 238, 309-314.	2.4	16
92	Analysis of the replication direction through the domain of Î±-globin-encoding chicken genes. Gene, 1995, 166, 255-259.	1.0	16
93	In Chicken Leukemia Cells Globin Genes Are Fully Transcribed but Their RNAs Are Retained in the Perinucleolar Area. Experimental Cell Research, 2001, 270, 159-165.	1.2	16
94	Spatial organization of the chicken beta-globin gene domain in erythroid cells of embryonic and adult lineages. Epigenetics and Chromatin, 2012, 5, 16.	1.8	16
95	Chromatin Domains and Territories: Flexibly Rigid. Critical Reviews in Eukaryotic Gene Expression, 2004, 14, 79-88.	0.4	16
96	Rearrangement of chromatin domains in cancer and development. Journal of Cellular Biochemistry, 2000, 79, 54-60.	1.2	15
97	Transgenic Goats in the World Pharmaceutical Industry of the 21st Century. Russian Journal of Genetics, 2002, 38, 1-14.	0.2	15
98	RNA-dependent nuclear matrix contains a 33 kb globin full domain transcript as well as prosomes but no 26S proteasomes. Journal of Cellular Biochemistry, 2005, 94, 529-539.	1.2	15
99	Repositioning of ETO gene in cells treated with VPâ€16, an inhibitor of DNAâ€Topoisomerase II. Journal of Cellular Biochemistry, 2008, 104, 692-699.	1.2	15
100	Unraveling the mechanisms of chromatin fibril packaging. Nucleus, 2016, 7, 319-324.	0.6	15
101	5-hydroxymethylcytosine in DNA repair: A new player or a red herring?. Cell Cycle, 2017, 16, 1499-1501.	1.3	15
102	Divide and Rule: Phase Separation in Eukaryotic Genome Functioning. Cells, 2020, 9, 2480.	1.8	15
103	The presence of sequence-specific protein binding sites correlate with replication activity and matrix binding in a 1.7 Kb-long DNA fragment of the chicken â^•globin gene domain. Biochemical and Biophysical Research Communications, 1991, 179, 512-519.	1.0	14
104	Specific radial positions of centromeres of human chromosomes X, 1, and 19 remain unchanged in chromatin-depleted nuclei of primary human fibroblasts: Evidence for the organizing role of the nuclear matrix. Journal of Cellular Biochemistry, 2005, 96, 850-857.	1.2	14
105	Compartmentalization of the cell nucleus and spatial organization of the genome. Molecular Biology, 2015, 49, 21-39.	0.4	14
106	3D genomics imposes evolution of the domain model of eukaryotic genome organization. Chromosoma, 2017, 126, 59-69.	1.0	14
107	Chromatin Domains and Regulation of Gene Expression: Familiar and Enigmatic Clusters of Chicken Globin Genes. Critical Reviews in Eukaryotic Gene Expression, 2001, 11, 16.	0.4	14
108	Association of the mammalian transcriptional regulator Kaiso with centrosomes and the midbody. Cell Cycle, 2009, 8, 2303-2304.	1.3	13

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109	Domains of Î±- and Î²-globin genes in the context of the structural-functional organization of the eukaryotic genome. Biochemistry (Moscow), 2012, 77, 1409-1423.	0.7	13
110	Nuclear matrix and structural and functional compartmentalization of the eucaryotic cell nucleus. Biochemistry (Moscow), 2014, 79, 608-618.	0.7	13
111	C-TALE, a new cost-effective method for targeted enrichment of Hi-C/3C-seq libraries. Methods, 2020, 170, 48-60.	1.9	13
112	RedChIP identifies noncoding RNAs associated with genomic sites occupied by Polycomb and CTCF proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	13
113	DNA fragments which specifically bind to isolated nuclear matrix in vitro interact with matrix-associated DNA topoisomerase II. Biochemical and Biophysical Research Communications, 1989, 159, 1263-1268.	1.0	12
114	DNA-protein interactions and spatial organization of DNA. Molecular Biology Reports, 1993, 18, 167-175.	1.0	12
115	Acetylation of Core Histones Causes the Unfolding of 30 nm Chromatin Fiber: Analysis by Agarose Gel Electrophoresis. Biochemical and Biophysical Research Communications, 1993, 196, 455-460.	1.0	12
116	Distribution of topoisomerase II-mediated cleavage sites and relation to structural and functional landmarks in 830 kb of Drosophila DNA. Nucleic Acids Research, 1997, 25, 2041-2046.	6.5	12
117	Changes in chromosome positioning may contribute to the development of diseases related to X-chromosome aneuploidy. Journal of Cellular Physiology, 2007, 213, 278-283.	2.0	12
118	In embryonic chicken erythrocytes actively transcribed alpha globin genes are not associated with the nuclear matrix. Journal of Cellular Biochemistry, 2009, 106, 170-178.	1.2	12
119	Heat stress-induced transcriptional repression. Biochemistry (Moscow), 2015, 80, 990-993.	0.7	12
120	Structuralâ€"Functional Domains of the Eukaryotic Genome. Biochemistry (Moscow), 2018, 83, 302-312.	0.7	12
121	Inducing cellular senescence in vitro by using genetically encoded photosensitizers. Aging, 2016, 8, 2449-2462.	1.4	12
122	Hi-C Metagenomics in the ICU: Exploring Clinically Relevant Features of Gut Microbiome in Chronically Critically Ill Patients. Frontiers in Microbiology, 2021, 12, 770323.	1.5	12
123	Early replication timing of the chicken Î±-globin gene domain correlates with its open chromatin state in cells of different lineages. Genomics, 2009, 93, 481-486.	1.3	11
124	Treacle and TOPBP1 control replication stress response in the nucleolus. Journal of Cell Biology, 2021, 220, .	2.3	11
125	Excision of chromosomal DNA loops by treatment of permeabilised cells with Bal 31 nuclease. Molecular Genetics and Genomics, 1995, 249, 253-256.	2.4	10
126	TGF-?1 is the factor secreted by proliferative chondrocytes to inhibit neo-angiogenesis. Journal of Cellular Biochemistry, 2001, 81, 79-88.	1.2	10

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127	Unusual compartmentalization of CTCF and other transcription factors in the course of terminal erythroid differentiation. Biochimica Et Biophysica Acta - Molecular Cell Research, 2007, 1773, 924-933.	1.9	10
128	Sensitivity of human embryonic and induced pluripotent stem cells to a topoisomerase II poison etoposide. Cell Cycle, 2011, 10, 2035-2037.	1.3	10
129	Distinct Patterns of Colocalization of the <i>CCND1</i> and <i>CMYC</i> Genes With Their Potential Translocation Partner <i>IGH</i> at Successive Stages of Bâ€Cell Differentiation. Journal of Cellular Biochemistry, 2016, 117, 1506-1510.	1.2	10
130	Evolution of the Genome 3D Organization: Comparison of Fused and Segregated Globin Gene Clusters. Molecular Biology and Evolution, 2017, 34, 1492-1504.	3.5	10
131	Histone chaperone FACT and curaxins: effects on genome structure and function. Journal of Cancer Metastasis and Treatment, 2019, 2019, .	0.5	10
132	Breakpoint clusters: reason or consequence?. Critical Reviews in Eukaryotic Gene Expression, 2004, 14, 65-77.	0.4	10
133	Analysis of the chicken DNA fragments that contain structural sites of attachment to the nuclear matrix: DNA-matrix interactions and replication. Journal of Cellular Biochemistry, 2000, 79, 1-14.	1.2	9
134	Spatial organization of the eukaryotic genome and the action of epigenetic mechanisms. Russian Journal of Genetics, 2006, 42, 1353-1361.	0.2	9
135	The Broken MLL Gene Is Frequently Located Outside the Inherent Chromosome Territory in Human Lymphoid Cells Treated with DNA Topoisomerase II Poison Etoposide. PLoS ONE, 2013, 8, e75871.	1.1	9
136	A modified protocol of Capture-C allows affordable and flexible high-resolution promoter interactome analysis. Scientific Reports, 2020, 10, 15491.	1.6	9
137	Specific cleavage of chicken ?A-globin and human c-Ha-ras genes by two molecular forms of calf thymus topoisomerase I. Molecular and Cellular Biochemistry, 1991, 101, 115-24.	1.4	8
138	A Simple and Reproducible Method for Analysis of Chromatin Condensation. Biochemical and Biophysical Research Communications, 1993, 193, 113-118.	1.0	8
139	Joint Cultivation of Human Erythroblastoid Cells and Mouse Fibroblasts Triggers Release of a Wide Spectrum of Cytotoxic Factors. Biochemical and Biophysical Research Communications, 1997, 234, 655-659.	1.0	8
140	Mechanisms controlling activation of the Î±-globin gene domain in chicken erythroid cells. Biochemistry (Moscow), 2007, 72, 467-470.	0.7	8
141	Modulatory effect of rRNA synthesis and ppUL83 nucleolar compartmentalization on human cytomegalovirus gene expression in vitro. Journal of Cellular Biochemistry, 2009, 108, 415-423.	1.2	8
142	The inactivation of the Ï€ gene in chicken erythroblasts of adult lineage is not mediated by packaging of the embryonic part of the Î±-globin gene domain into a repressive heterochromatin-like structure. Epigenetics, 2011, 6, 1481-1488.	1.3	8
143	Mammalian Diaphanous-related formin-1 restricts early phases of influenza A/NWS/33 virus (H1N1) infection in LLC-MK2 cells by affecting cytoskeleton dynamics. Molecular and Cellular Biochemistry, 2018, 437, 185-201.	1.4	8
144	The two waves in single-cell 3D genomics. Seminars in Cell and Developmental Biology, 2021, 121, 143-143.	2.3	8

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145	Co-Regulated Genes and Gene Clusters. Genes, 2021, 12, 907.	1.0	8
146	Studies on structure and function of chromatin. Molecular and Cellular Biochemistry, 1981, 40, 29-48.	1.4	7
147	Correlations of repetitive and AT-rich DNA segments within the chicken globin gene domains. Molecular Biology Reports, 1986, 11, 177-187.	1.0	7
148	DNA-protein complexes of the nuclear matrix: Visualization and partial characterization of the protein component. Biochemical and Biophysical Research Communications, 1989, 162, 175-183.	1.0	7
149	Formaldehyde fixation of cells does not greatly reduce the ability to amplify cellular DNA. Analytical Biochemistry, 2009, 390, 94-96.	1.1	7
150	The Role of Crowding Forces in Juxtaposing Î²-Globin Gene Domain Remote Regulatory Elements in Mouse Erythroid Cells. PLoS ONE, 2015, 10, e0139855.	1.1	7
151	Impact TMPRSS2â€“ERG Molecular Subtype on Prostate Cancer Recurrence. Life, 2021, 11, 588.	1.1	7
152	The<i>IGH</i>locus relocalizes to a â€œrecombination compartmentâ€•in the perinucleolar region of differentiating B-lymphocytes. Oncotarget, 2017, 8, 40079-40089.	0.8	7
153	The upstream area of the chicken Î±-globin gene domain is transcribed in both directions in the same cells. FEBS Letters, 2005, 579, 4746-4750.	1.3	6
154	Transcription Factories and Spatial Organization of Eukaryotic Genomes. Biochemistry (Moscow), 2010, 75, 1307-1315.	0.7	6
155	Heat shockâ€induced dissociation of TRF2 from telomeres does not initiate a telomereâ€dependent DNA damage response. Cell Biology International, 2014, 38, 675-681.	1.4	6
156	Transcription-controlling regulatory elements of the eukaryotic genome. Molecular Biology, 2015, 49, 185-194.	0.4	6
157	Single-cell genome-wide studies give new insight into nongenetic cell-to-cell variability in animals. Histochemistry and Cell Biology, 2016, 146, 239-254.	0.8	6
158	OUP accepted manuscript. Nucleic Acids Research, 2022, , .	6.5	6
159	Chromatin domains and territories: flexibly rigid. Critical Reviews in Eukaryotic Gene Expression, 2004, 14, 79-88.	0.4	6
160	The twisted path of the 3D genome: where does it lead?. Trends in Biochemical Sciences, 2022, 47, 736-744.	3.7	6
161	Inhibition of DNA topoisomerase II may trigger illegitimate recombination in living cells: Experiments with a model system. Journal of Cellular Biochemistry, 2006, 99, 598-608.	1.2	5
162	An unusual extended DNA loop attachment region is located in the human dystrophin gene. Journal of Cellular Physiology, 2006, 209, 515-521.	2.0	5

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163	Chromatin and transcription regulation. Molecular Biology, 2007, 41, 343-348.	0.4	5
164	Study of spatial organization of chicken Î±-globin gene domain by 3c technique. Biochemistry (Moscow), 2008, 73, 1192-1199.	0.7	5
165	Expression of full-length human pro-urokinase in mammary glands of transgenic mice. Transgenic Research, 2009, 18, 747-756.	1.3	5
166	Transcription factor RUNX1. Molecular Biology, 2012, 46, 755-767.	0.4	5
167	Fragment of intron 5.2 of the human RUNX1 gene important for transcription activation is neither enhancer nor MAR-element. Doklady Biochemistry and Biophysics, 2012, 442, 26-29.	0.3	5
168	Heat stress induces formation of cytoplasmic granules containing HSC70 protein. Doklady Biochemistry and Biophysics, 2015, 463, 213-215.	0.3	5
169	Automated Analysis of Cell Cycle Phaseâ€Specific DNA Damage Reveals Phaseâ€Specific Differences in Cell Sensitivity to Etoposide. Journal of Cellular Biochemistry, 2016, 117, 2209-2214.	1.2	5
170	Perspectives for the reconstruction of 3D chromatin conformation using single cell Hi-C data. PLoS Computational Biology, 2021, 17, e1009546.	1.5	5
171	HP1Î± is not necessary for the structural maintenance of centromeric heterochromatin. Epigenetics, 2011, 6, 380-387.	1.3	4
172	Characterization of the enhancer element of the Danio rerio minor globin gene locus. Histochemistry and Cell Biology, 2016, 145, 463-473.	0.8	4
173	3D Genomics. Molecular Biology, 2019, 53, 802-812.	0.4	4
174	LASCA: loop and significant contact annotation pipeline. Scientific Reports, 2021, 11, 6361.	1.6	4
175	Host-cell dependent role of phosphorylated keratin 8 during influenza A/NWS/33 virus (H1N1) infection in mammalian cells. Virus Research, 2021, 295, 198333.	1.1	4
176	Sensitivity of cohesinâ€"chromatin association to high-salt treatment corroborates non-topological mode of loop extrusion. Epigenetics and Chromatin, 2021, 14, 36.	1.8	4
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