Sergey V Razin

List of Publications by Year in Descending Order

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

56 4,349 220 34 h-index g-index citations papers 5,061 6.4 236 5.74 avg, IF L-index ext. citations ext. papers

#	Paper	IF	Citations
220	Pentad: a tool for distance-dependent analysis of Hi-C interactions within and between chromatin compartments <i>BMC Bioinformatics</i> , 2022 , 23, 116	3.6	O
219	RedChIP identifies noncoding RNAs associated with genomic sites occupied by Polycomb and CTCF proteins <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	3
218	SETDB1 fuels the lung cancer phenotype by modulating epigenome, 3D genome organization and chromatin mechanical properties <i>Nucleic Acids Research</i> , 2022 ,	20.1	1
217	The twisted path of the 3D genome: where does it lead?. Trends in Biochemical Sciences, 2022,	10.3	1
216	Hi-C Metagenomics in the ICU: Exploring Clinically Relevant Features of Gut Microbiome in Chronically Critically Ill Patients <i>Frontiers in Microbiology</i> , 2021 , 12, 770323	5.7	O
215	Perspectives for the reconstruction of 3D chromatin conformation using single cell Hi-C data. <i>PLoS Computational Biology</i> , 2021 , 17, e1009546	5	0
214	LASCA: loop and significant contact annotation pipeline. Scientific Reports, 2021, 11, 6361	4.9	1
213	Suppression of liquid-liquid phase separation by 1,6-hexanediol partially compromises the 3D genome organization in living cells. <i>Nucleic Acids Research</i> , 2021 , 49, 10524-10541	20.1	14
212	Host-cell dependent role of phosphorylated keratin 8 during influenza A/NWS/33 virus (H1N1) infection in mammalian cells. <i>Virus Research</i> , 2021 , 295, 198333	6.4	1
211	The two waves in single-cell 3D genomics. Seminars in Cell and Developmental Biology, 2021, 121, 143-16	4 3 .5	3
210	Treacle and TOPBP1 control replication stress response in the nucleolus. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	3
209	Manipulation of Cellular Processes via Nucleolus Hijaking in the Course of Viral Infection in Mammals. <i>Cells</i> , 2021 , 10,	7.9	3
208	Non-coding RNAs in chromatin folding and nuclear organization. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 5489-5504	10.3	5
207	Mechanisms mediating suppression of globin gene transcription in Danio rerio nonerythroid cells. <i>Biochimie</i> , 2021 , 181, 96-99	4.6	О
206	Sensitivity of cohesin-chromatin association to high-salt treatment corroborates non-topological mode of loop extrusion. <i>Epigenetics and Chromatin</i> , 2021 , 14, 36	5.8	O
205	Order and stochasticity in the folding of individual Drosophila genomes. <i>Nature Communications</i> , 2021 , 12, 41	17.4	11
204	Studying RNA-DNA interactome by Red-C identifies noncoding RNAs associated with various chromatin types and reveals transcription dynamics. <i>Nucleic Acids Research</i> , 2020 , 48, 6699-6714	20.1	14

(2018-2020)

203	Benchmark of software tools for prokaryotic chromosomal interaction domain identification. <i>Bioinformatics</i> , 2020 , 36, 4560-4567	7.2	2
202	The Role of Liquid-Liquid Phase Separation in the Compartmentalization of Cell Nucleus and Spatial Genome Organization. <i>Biochemistry (Moscow)</i> , 2020 , 85, 643-650	2.9	21
201	Chromatin Trapping of Factors Involved in DNA Replication and Repair Underlies Heat-Induced Radio- and Chemosensitization. <i>Cells</i> , 2020 , 9,	7.9	2
200	Eukaryotic Genome in Three Dimensions 2020 , 11-34		
199	The 3D Genome as a Target for Anticancer Therapy. <i>Trends in Molecular Medicine</i> , 2020 , 26, 141-149	11.5	17
198	Divide and Rule: Phase Separation in Eukaryotic Genome Functioning. <i>Cells</i> , 2020 , 9,	7.9	11
197	A modified protocol of Capture-C allows affordable and flexible high-resolution promoter interactome analysis. <i>Scientific Reports</i> , 2020 , 10, 15491	4.9	4
196	C-TALE, a new cost-effective method for targeted enrichment of Hi-C/3C-seq libraries. <i>Methods</i> , 2020 , 170, 48-60	4.6	8
195	Weak interactions in higher-order chromatin organization. <i>Nucleic Acids Research</i> , 2020 , 48, 4614-4626	20.1	30
194	Nucleolus: A Central Hub for Nuclear Functions. <i>Trends in Cell Biology</i> , 2019 , 29, 647-659	18.3	61
193	Hypoosmotic stress induces R loop formation in nucleoli and ATR/ATM-dependent silencing of nucleolar transcription. <i>Nucleic Acids Research</i> , 2019 , 47, 6811-6825	20.1	15
192	Nuclear lamina integrity is required for proper spatial organization of chromatin in Drosophila. <i>Nature Communications</i> , 2019 , 10, 1176	17.4	52
191	The anti-cancer drugs curaxins target spatial genome organization. <i>Nature Communications</i> , 2019 , 10, 1441	17.4	22
190	Histone Chaperone FACT and Curaxins: Effects on Genome Structure and Function. <i>Journal of Cancer Metastasis and Treatment</i> , 2019 , 5,	3.8	5
189	3D Genomics. <i>Molecular Biology</i> , 2019 , 53, 802-812	1.2	3
188	Quantitative differences in TAD border strength underly the TAD hierarchy in Drosophila chromosomes. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 4494-4503	4.7	12
187	Structural-Functional Organization of the Eukaryotic Cell Nucleus and Transcription Regulation: Introduction to This Special Issue of Biochemistry (Moscow). <i>Biochemistry (Moscow)</i> , 2018 , 83, 299-301	2.9	2
186	Structural-Functional Domains of the Eukaryotic Genome. <i>Biochemistry (Moscow)</i> , 2018 , 83, 302-312	2.9	6

185	Mammalian Diaphanous-related formin-1 restricts early phases of influenza A/NWS/33 virus (H1N1) infection in LLC-MK2 cells by affecting cytoskeleton dynamics. <i>Molecular and Cellular Biochemistry</i> , 2018 , 437, 185-201	4.2	5
184	Synthetically Lethal Interactions of ATM, ATR, and DNA-PKcs. <i>Trends in Cancer</i> , 2018 , 4, 755-768	12.5	40
183	3D genomics imposes evolution of the domain model of eukaryotic genome organization. <i>Chromosoma</i> , 2017 , 126, 59-69	2.8	14
182	Self-organization of a chromatin fibril into topologically-associated domains. <i>Russian Journal of Bioorganic Chemistry</i> , 2017 , 43, 99-106	1	
181	Comparative analysis of the synchronization methods of normal and transformed human cells. <i>Molecular Biology</i> , 2017 , 51, 130-135	1.2	1
180	Evolution of the Genome 3D Organization: Comparison of Fused and Segregated Globin Gene Clusters. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1492-1504	8.3	7
179	Single-nucleus Hi-C reveals unique chromatin reorganization at oocyte-to-zygote transition. <i>Nature</i> , 2017 , 544, 110-114	50.4	418
178	Gene functioning and storage within a folded genome. <i>Cellular and Molecular Biology Letters</i> , 2017 , 22, 18	8.1	14
177	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. <i>Epigenetics and Chromatin</i> , 2017 , 10, 35	5.8	11
176	Single-cell Hi-C bridges microscopy and genome-wide sequencing approaches to study 3D chromatin organization. <i>BioEssays</i> , 2017 , 39, 1700104	4.1	32
175	5-hydroxymethylcytosine in DNA repair: A new player or a red herring?. <i>Cell Cycle</i> , 2017 , 16, 1499-1501	4.7	15
174	The IGH locus relocalizes to a "recombination compartment" in the perinucleolar region of differentiating B-lymphocytes. <i>Oncotarget</i> , 2017 , 8, 40079-40089	3.3	6
173	Small molecule compounds that induce cellular senescence. <i>Aging Cell</i> , 2016 , 15, 999-1017	9.9	82
172	Single-cell genome-wide studies give new insight into nongenetic cell-to-cell variability in animals. <i>Histochemistry and Cell Biology</i> , 2016 , 146, 239-54	2.4	4
171	Distinct Patterns of Colocalization of the CCND1 and CMYC Genes With Their Potential Translocation Partner IGH at Successive Stages of B-Cell Differentiation. <i>Journal of Cellular Biochemistry</i> , 2016 , 117, 1506-10	4.7	8
170	Unraveling the mechanisms of chromatin fibril packaging. <i>Nucleus</i> , 2016 , 7, 319-24	3.9	11
169	Characterization of the enhancer element of the Danio rerio minor globin gene locus. <i>Histochemistry and Cell Biology</i> , 2016 , 145, 463-73	2.4	1
168	Early S-phase cell hypersensitivity to heat stress. <i>Cell Cycle</i> , 2016 , 15, 337-44	4.7	16

(2014-2016)

167	Active chromatin and transcription play a key role in chromosome partitioning into topologically associating domains. <i>Genome Research</i> , 2016 , 26, 70-84	9.7	225
166	Inducing cellular senescence by using genetically encoded photosensitizers. <i>Aging</i> , 2016 , 8, 2449-2462	5.6	8
165	Automated Analysis of Cell Cycle Phase-Specific DNA Damage Reveals Phase-Specific Differences in Cell Sensitivity to Etoposide. <i>Journal of Cellular Biochemistry</i> , 2016 , 117, 2209-14	4.7	2
164	Main regulatory element (MRE) of the Danio rerio Æglobin gene domain exerts enhancer activity toward the promoters of the embryonic-larval and adult globin genes. <i>Molecular Biology</i> , 2016 , 50, 900-	908	2
163	Topologically-associating domains: gene warehouses adapted to serve transcriptional regulation. <i>Transcription</i> , 2016 , 7, 84-90	4.8	11
162	Mechanism of heat stress-induced cellular senescence elucidates the exclusive vulnerability of early S-phase cells to mild genotoxic stress. <i>Nucleic Acids Research</i> , 2015 , 43, 6309-20	20.1	43
161	Transcription-controlling regulatory elements of the eukaryotic genome. <i>Molecular Biology</i> , 2015 , 49, 185-194	1.2	4
160	Joint locus of a/b-globin genes in Danio rerio is segregated into structural subdomains active at different stages of development. <i>Molecular Biology</i> , 2015 , 49, 442-449	1.2	
159	Heat Stress-Induced Transcriptional Repression. <i>Biochemistry (Moscow)</i> , 2015 , 80, 990-3	2.9	7
158	Heat stress induces formation of cytoplasmic granules containing HSC70 protein. <i>Doklady Biochemistry and Biophysics</i> , 2015 , 463, 213-5	0.8	5
157	Detection of complementary transcripts for the intergenic region of the chicken Eglobin gene domain. <i>Molecular Biology</i> , 2015 , 49, 899-903	1.2	
156	The Role of Crowding Forces in Juxtaposing EGlobin Gene Domain Remote Regulatory Elements in Mouse Erythroid Cells. <i>PLoS ONE</i> , 2015 , 10, e0139855	3.7	7
155	In vivo formaldehyde cross-linking: it is time for black box analysis. <i>Briefings in Functional Genomics</i> , 2015 , 14, 163-5	4.9	48
154	Proteasomes raise the microtubule dynamics in influenza A (H1N1) virus-infected LLC-MK2 cells. <i>Cellular and Molecular Biology Letters</i> , 2015 , 20, 840-66	8.1	2
153	Organization of functional processes in the cell nucleus: The order emerging out of the disorder. <i>Moscow University Biological Sciences Bulletin</i> , 2015 , 70, 115-121	0.5	
152	Compartmentalization of the cell nucleus and spatial organization of the genome. <i>Molecular Biology</i> , 2015 , 49, 21-39	1.2	11
151	Nuclear compartments, genome folding, and enhancer-promoter communication. <i>International Review of Cell and Molecular Biology</i> , 2015 , 315, 183-244	6	24
150	A requiem to the nuclear matrix: from a controversial concept to 3D organization of the nucleus. <i>Chromosoma</i> , 2014 , 123, 217-24	2.8	33

149	Nuclear matrix and structural and functional compartmentalization of the eucaryotic cell nucleus. <i>Biochemistry (Moscow)</i> , 2014 , 79, 608-18	2.9	8
148	Heat shock-induced dissociation of TRF2 from telomeres does not initiate a telomere-dependent DNA damage response. <i>Cell Biology International</i> , 2014 , 38, 675-81	4.5	4
147	Spatial organization of interphase chromosomes and the role of chromatin fibril dynamics in the positioning of genome elements. <i>Molecular Biology</i> , 2014 , 48, 332-339	1.2	
146	Dynamics of double strand breaks and chromosomal translocations. <i>Molecular Cancer</i> , 2014 , 13, 249	42.1	33
145	Evolution of Eland Eglobin genes and their regulatory systems in light of the hypothesis of domain organization of the genome. <i>Biochemistry (Moscow)</i> , 2014 , 79, 1141-50	2.9	1
144	Spatial organization of housekeeping genes in interphase nuclei. <i>Molecular Biology</i> , 2014 , 48, 886-895	1.2	2
143	The clustering of CpG islands may constitute an important determinant of the 3D organization of interphase chromosomes. <i>Epigenetics</i> , 2014 , 9, 951-63	5.7	13
142	Quantitative analysis of genomic element interactions by molecular colony technique. <i>Nucleic Acids Research</i> , 2014 , 42, e36	20.1	21
141	Chromatin without the 30-nm fiber: constrained disorder instead of hierarchical folding. <i>Epigenetics</i> , 2014 , 9, 653-7	5.7	35
140	Folded genome as a platform for the functional compartmentalization of the eukaryotic cell nucleus. <i>Biopolymers and Cell</i> , 2014 , 30, 83-89	0.3	3
139	Nucleosomal packaging of eukaryotic DNA and regulation of transcription. <i>Biopolymers and Cell</i> , 2014 , 30, 413-425	0.3	1
138	Perinucleolar relocalization and nucleolin as crucial events in the transcriptional activation of key genes in mantle cell lymphoma. <i>Blood</i> , 2014 , 123, 2044-53	2.2	30
137	Russian science: academy reform needs a reality check. <i>Nature</i> , 2013 , 499, 284	50.4	1
136	Heat-shock induced H2AX foci are associated with the nuclear matrix only in S-phase cells. <i>Doklady Biochemistry and Biophysics</i> , 2013 , 450, 130-3	0.8	
135	Mechanisms of heat shock response in mammals. Cellular and Molecular Life Sciences, 2013, 70, 4229-41	10.3	86
134	Actual ligation frequencies in the chromosome conformation capture procedure. <i>PLoS ONE</i> , 2013 , 8, e60403	3.7	18
133	Chromatin structure of the joint Æglobin gene locus of Danio rerio. <i>Doklady Biochemistry and Biophysics</i> , 2013 , 448, 59-61	0.8	1
132	Communication of genome regulatory elements in a folded chromosome. FEBS Letters, 2013, 587, 1840)- 3 .8	34

(2011-2013)

131	Disclosure of a structural milieu for the proximity ligation reveals the elusive nature of an active chromatin hub. <i>Nucleic Acids Research</i> , 2013 , 41, 3563-75	20.1	72
130	The broken MLL gene is frequently located outside the inherent chromosome territory in human lymphoid cells treated with DNA topoisomerase II poison etoposide. <i>PLoS ONE</i> , 2013 , 8, e75871	3.7	6
129	Fragment of intron 5.2 of the human RUNX1 gene important for transcription activation is neither enhancer nor MAR-element. <i>Doklady Biochemistry and Biophysics</i> , 2012 , 442, 26-9	0.8	5
128	Transcription factor RUNX1. <i>Molecular Biology</i> , 2012 , 46, 755-767	1.2	4
127	Unmethylated CpG islands are clustered inside the interphase human cell nuclei. <i>Doklady Biochemistry and Biophysics</i> , 2012 , 443, 123-6	0.8	
126	Dual effect of heat shock on DNA replication and genome integrity. <i>Molecular Biology of the Cell</i> , 2012 , 23, 3450-60	3.5	50
125	Transcription of the AML1/ETO chimera is guided by the P2 promoter of the AML1 gene in the Kasumi-1 cell line. <i>Gene</i> , 2012 , 510, 142-6	3.8	1
124	Domains of Eland Eglobin genes in the context of the structural-functional organization of the eukaryotic genome. <i>Biochemistry (Moscow)</i> , 2012 , 77, 1409-23	2.9	10
123	Spatial organization of the chicken beta-globin gene domain in erythroid cells of embryonic and adult lineages. <i>Epigenetics and Chromatin</i> , 2012 , 5, 16	5.8	13
122	Distinct distribution of ectopically expressed histone variants H2A.Bbd and MacroH2A in open and closed chromatin domains. <i>PLoS ONE</i> , 2012 , 7, e47157	3.7	15
121	Cys2His2 zinc finger protein family: classification, functions, and major members. <i>Biochemistry</i> (Moscow), 2012 , 77, 217-26	2.9	107
120	The inactivation of the Igene in chicken erythroblasts of adult lineage is not mediated by packaging of the embryonic part of the Iglobin gene domain into a repressive heterochromatin-like structure. <i>Epigenetics</i> , 2011 , 6, 1481-8	5.7	6
119	Identification of c-Myb Target Genes in K562 Cells Reveals a Role for c-Myb as a Master Regulator. <i>Genes and Cancer</i> , 2011 , 2, 805-17	2.9	27
118	Patterns of histone modifications across the chicken alfa-globin genesIdomain. <i>Molecular Biology</i> , 2011 , 45, 608-613	1.2	
117	Cell-cycle-dependent localization of human cytomegalovirus UL83 phosphoprotein in the nucleolus and modulation of viral gene expression in human embryo fibroblasts in vitro. <i>Journal of Cellular Biochemistry</i> , 2011 , 112, 307-17	4.7	16
116	Transcriptional regulation and spatial organisation of the human AML1/RUNX1 gene. <i>Journal of Cellular Biochemistry</i> , 2011 , 112, 1997-2005	4.7	25
115	Sensitivity of human embryonic and induced pluripotent stem cells to a topoisomerase II poison etoposide. <i>Cell Cycle</i> , 2011 , 10, 2035-7	4.7	10
114	HP1IIs not necessary for the structural maintenance of centromeric heterochromatin. <i>Epigenetics</i> , 2011 , 6, 380-7	5.7	4

113	Transcription factories in the context of the nuclear and genome organization. <i>Nucleic Acids Research</i> , 2011 , 39, 9085-92	20.1	46
112	Transcription factories and spatial organization of eukaryotic genomes. <i>Biochemistry (Moscow)</i> , 2010 , 75, 1307-15	2.9	5
111	Expansion of the functional domain of chicken alpha-globin genes. <i>Russian Journal of Genetics</i> , 2010 , 46, 1033-1035	0.6	2
110	Mapping of the nuclear matrix-bound chromatin hubs by a new M3C experimental procedure. <i>Nucleic Acids Research</i> , 2010 , 38, 8051-60	20.1	15
109	TMEM8 - a non-globin gene entrapped in the globin web. <i>Nucleic Acids Research</i> , 2009 , 37, 7394-406	20.1	14
108	Association of the mammalian transcriptional regulator kaiso with centrosomes and the midbody. <i>Cell Cycle</i> , 2009 , 8, 2303-4	4.7	11
107	In embryonic chicken erythrocytes actively transcribed alpha globin genes are not associated with the nuclear matrix. <i>Journal of Cellular Biochemistry</i> , 2009 , 106, 170-8	4.7	10
106	Modulatory effect of rRNA synthesis and ppUL83 nucleolar compartmentalization on human cytomegalovirus gene expression in vitro. <i>Journal of Cellular Biochemistry</i> , 2009 , 108, 415-23	4.7	8
105	Chromatin loops, illegitimate recombination, and genome evolution. <i>BioEssays</i> , 2009 , 31, 278-86	4.1	18
104	Expression of full-length human pro-urokinase in mammary glands of transgenic mice. <i>Transgenic Research</i> , 2009 , 18, 747-56	3.3	5
103	Formaldehyde fixation of cells does not greatly reduce the ability to amplify cellular DNA. <i>Analytical Biochemistry</i> , 2009 , 390, 94-6	3.1	7
102	Early replication timing of the chicken alpha-globin gene domain correlates with its open chromatin state in cells of different lineages. <i>Genomics</i> , 2009 , 93, 481-6	4.3	11
101	Interaction in vivo between the two matrix attachment regions flanking a single chromatin loop. Journal of Molecular Biology, 2009 , 386, 929-37	6.5	17
100	Chromosome conformation capture (from 3C to 5C) and its ChIP-based modification. <i>Methods in Molecular Biology</i> , 2009 , 567, 171-88	1.4	63
99	Study of spatial organization of chicken alpha-globin gene domain by 3C technique. <i>Biochemistry</i> (Moscow), 2008 , 73, 1192-9	2.9	5
98	Spatial configuration of the chicken alpha-globin gene domain: immature and active chromatin hubs. <i>Nucleic Acids Research</i> , 2008 , 36, 4629-40	20.1	46
97	Repositioning of ETO gene in cells treated with VP-16, an inhibitor of DNA-topoisomerase II. Journal of Cellular Biochemistry, 2008 , 104, 692-9	4.7	14
96	Genes surrounding the cluster of tissue-specific alpha-globin genes in chicken genome are expressed in both erythroid and lymphoid cells. <i>Doklady Biochemistry and Biophysics</i> , 2008 , 421, 224-6	0.8	1

(2005-2008)

95	Inhibition of DNA topoisomerase II with etoposide induces association of DNA topoisomerase II alpha, DNA topoisomerase II beta, and nucleolin with BCR 2 of the ETO gene. <i>Doklady Biochemistry and Biophysics</i> , 2008 , 423, 334-6	0.8	
94	Changes in chromosome positioning may contribute to the development of diseases related to X-chromosome aneuploidy. <i>Journal of Cellular Physiology</i> , 2007 , 213, 278-83	7	10
93	Mechanisms controlling activation of the alpha-globin gene domain in chicken erythroid cells. <i>Biochemistry (Moscow)</i> , 2007 , 72, 467-70	2.9	8
92	Chromatin and transcription regulation. <i>Molecular Biology</i> , 2007 , 41, 343-348	1.2	4
91	Unusual compartmentalization of CTCF and other transcription factors in the course of terminal erythroid differentiation. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2007 , 1773, 924-33	4.9	7
90	Chemotherapy-related secondary leukemias: A role for DNA repair by error-prone non-homologous end joining in topoisomerase II - Induced chromosomal rearrangements. <i>Gene</i> , 2007 , 391, 76-9	3.8	16
89	Chromatin domains and regulation of transcription. <i>Journal of Molecular Biology</i> , 2007 , 369, 597-607	6.5	61
88	Inhibition of DNA topoisomerase II may trigger illegitimate recombination in living cells: experiments with a model system. <i>Journal of Cellular Biochemistry</i> , 2006 , 99, 598-608	4.7	5
87	Assembly of nuclear matrix-bound protein complexes involved in non-homologous end joining is induced by inhibition of DNA topoisomerase II. <i>Journal of Cellular Physiology</i> , 2006 , 207, 660-7	7	18
86	An unusual extended DNA loop attachment region is located in the human dystrophin gene. <i>Journal of Cellular Physiology</i> , 2006 , 209, 515-21	7	4
85	A CTCF-dependent silencer located in the differentially methylated area may regulate expression of a housekeeping gene overlapping a tissue-specific gene domain. <i>Molecular and Cellular Biology</i> , 2006 , 26, 1589-97	4.8	30
84	Control of human cytomegalovirus gene expression by differential histone modifications during lytic and latent infection of a monocytic cell line. <i>Gene</i> , 2006 , 384, 120-8	3.8	78
83	Illegitimate recombination as a possible mechanism of topoisomerase-II-induced chromosomal rearrangements. <i>Molecular Biology</i> , 2006 , 40, 790-796	1.2	1
82	Spatial organization of the eukaryotic genome and the action of epigenetic mechanisms. <i>Russian Journal of Genetics</i> , 2006 , 42, 1353-1361	0.6	6
81	The upstream area of the chicken alpha-globin gene domain is transcribed in both directions in the same cells. <i>FEBS Letters</i> , 2005 , 579, 4746-50	3.8	6
80	Mapping long-range chromatin organization within the chicken alpha-globin gene domain using oligonucleotide DNA arrays. <i>Genomics</i> , 2005 , 85, 143-51	4.3	22
79	RNA-dependent nuclear matrix contains a 33 kb globin full domain transcript as well as prosomes but no 26S proteasomes. <i>Journal of Cellular Biochemistry</i> , 2005 , 94, 529-39	4.7	14
78	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. <i>Journal of Cellular Biochemistry</i> , 2005 , 96, 850-7	4.7	14

77	Inhibition of DNA topoisomerase II in living cells stimulates illegitimate recombination. <i>Doklady Biochemistry and Biophysics</i> , 2005 , 405, 423-5	0.8	
76	Chromosome Rearrangement Breakpoint Clustering: The Role of Clonal Selection. <i>Molecular Biology</i> , 2005 , 39, 313-320	1.2	1
75	Spatial Organization of DNA in the Nucleus May Determine Positions of Recombination Hot Spots. <i>Molecular Biology</i> , 2005 , 39, 543-548	1.2	1
74	Spatial Organization of the Chicken EGlobin Gene Domain in Cells of Different Origins. <i>Molecular Biology</i> , 2005 , 39, 851-856	1.2	
73	Induction of transcription within chromosomal DNA loops flanked by MAR elements causes an association of loop DNA with the nuclear matrix. <i>Nucleic Acids Research</i> , 2005 , 33, 4157-63	20.1	28
72	Visualization of individual DNA loops and a map of loop domains in the human dystrophin gene. <i>Nucleic Acids Research</i> , 2004 , 32, 2079-86	20.1	60
71	CTCF-dependent enhancer blockers at the upstream region of the chicken alpha-globin gene domain. <i>Nucleic Acids Research</i> , 2004 , 32, 1354-62	20.1	49
70	The CpG island of chicken alpha-globin genes contains no signals sufficient for the maintenance of its nonmethylated state in transgenic mouse genome. <i>Doklady Biochemistry and Biophysics</i> , 2004 , 396, 143-5	0.8	
69	Characteristic of the silencer located in the CpG-rich region upstream of the cluster of chicken alpha-globin genes. <i>Doklady Biochemistry and Biophysics</i> , 2004 , 398, 307-9	0.8	
68	Visualization of DNA Loops and Nuclear Matrix Anchorage Regions in the Human Dystrophin Gene. <i>Molecular Biology</i> , 2004 , 38, 871-874	1.2	
67	Heterologous CpG island becomes extensively methylated in the genome of transgenic mice. <i>Journal of Cellular Biochemistry</i> , 2004 , 92, 99-103	4.7	
66	The 33 kb transcript of the chicken alpha-globin gene domain is part of the nuclear matrix. <i>Journal of Cellular Biochemistry</i> , 2004 , 92, 445-57	4.7	30
65	Effect of DNA loop anchorage regions (LARs) and microinjection timing on expression of beta-galactosidase gene injected into one-cell rabbit embryos. <i>Journal of Cellular Biochemistry</i> , 2004 , 92, 1171-9	4.7	1
64	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. <i>Journal of Cell Science</i> , 2004 , 117, 4583-90	5.3	27
63	Breakpoint Clusters: Reason or Consequence?. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2004 , 14, 65-78	1.3	21
62	Chromatin Domains and Territories: Flexibly Rigid. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2004 , 14, 79-88	1.3	13
61	Breakpoint clusters: reason or consequence?. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2004 , 14, 65-77	1.3	9
60	Chromatin domains and territories: flexibly rigid. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2004 , 14, 79-88	1.3	5

59	Genomic domains and regulatory elements operating at the domain level. <i>International Review of Cytology</i> , 2003 , 226, 63-125		41	
58	Initiation of DNA Replication in Cells of Higher Eukaryotes. <i>Russian Journal of Genetics</i> , 2003 , 39, 120-	1275.6		
57	Regulatory Systems of Genome Domains with Vague Boundaries. <i>Russian Journal of Genetics</i> , 2003 , 39, 128-132	0.6	1	
56	Human cytomegalovirus proteins PP65 and IEP72 are targeted to distinct compartments in nuclei and nuclear matrices of infected human embryo fibroblasts. <i>Journal of Cellular Biochemistry</i> , 2003 , 90, 1056-67	4.7	20	
55	Transgenic Goats in the World Pharmaceutical Industry of the 21st Century. <i>Russian Journal of Genetics</i> , 2002 , 38, 1-14	0.6	8	
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1	SETDB1 Fuels the Lung Cancer Phenotype by Modulating Epigenome, 3D Genome Organization and Chromatin Mechanical Properties		1