

Ross Hardison

List of Publications by Year in descending order

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206
papers

46,826
citations

8755

75
h-index

2127

203
g-index

219
all docs

219
docs citations

219
times ranked

52362
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
3	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
4	The ENCODE (ENCyclopedia Of DNA Elements) Project. Science, 2004, 306, 636-640.	12.6	2,121
5	The isolation of structural genes from libraries of eucaryotic DNA. Cell, 1978, 15, 687-701.	28.9	2,037
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
7	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5.5	1,795
8	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
9	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
10	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
11	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
12	Human-Mouse Alignments with BLASTZ. Genome Research, 2003, 13, 103-107.	5.5	1,071
13	PipMaker-A Web Server for Aligning Two Genomic DNA Sequences. Genome Research, 2000, 10, 577-586.	5.5	1,070
14	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	27.8	779
15	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
16	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	7.1	635
17	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	14.5	490
18	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410

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19	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. Human Mutation, 2002, 19, 225-233.	2.5	400
20	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	27.8	400
21	Conserved noncoding sequences are reliable guides to regulatory elements. Trends in Genetics, 2000, 16, 369-372.	6.7	385
22	HiCRep: assessing the reproducibility of Hi-C data using a stratum-adjusted correlation coefficient. Genome Research, 2017, 27, 1939-1949.	5.5	376
23	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. Nucleic Acids Research, 2014, 42, D1063-D1069.	14.5	361
24	A brief history of hemoglobins: plant, animal, protist, and bacteria.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 5675-5679.	7.1	332
25	A GATA-1-regulated microRNA locus essential for erythropoiesis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3333-3338.	7.1	309
26	Long Human-Mouse Sequence Alignments Reveal Novel Regulatory Elements: A Reason to Sequence the Mouse Genome. Genome Research, 1997, 7, 959-966.	5.5	294
27	A genome-editing strategy to treat β^2 -hemoglobinopathies that recapitulates a mutation associated with a benign genetic condition. Nature Medicine, 2016, 22, 987-990.	30.7	279
28	Insights into GATA-1-Mediated Gene Activation versus Repression via Genome-wide Chromatin Occupancy Analysis. Molecular Cell, 2009, 36, 682-695.	9.7	278
29	Integrative detection and analysis of structural variation in cancer genomes. Nature Genetics, 2018, 50, 1388-1398.	21.4	268
30	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	5.5	263
31	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259
32	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
33	Locus control regions of mammalian β^2 -globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. Gene, 1997, 205, 73-94.	2.2	226
34	Comparative Genomics. PLoS Biology, 2003, 1, e58.	5.6	221
35	Hemoglobins from bacteria to man: evolution of different patterns of gene expression. Journal of Experimental Biology, 1998, 201, 1099-117.	1.7	219
36	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. Genome Research, 2005, 15, 184-194.	5.5	218

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37	Unlinking an lncRNA from Its Associated cis Element. <i>Molecular Cell</i> , 2016, 62, 104-110.	9.7	216
38	Tissue-Specific Mitotic Bookmarking by Hematopoietic Transcription Factor GATA1. <i>Cell</i> , 2012, 150, 725-737.	28.9	215
39	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. <i>Genome Research</i> , 2003, 13, 1-12.	5.5	210
40	Evolution and functional classification of vertebrate gene deserts. <i>Genome Research</i> , 2005, 15, 137-145.	5.5	203
41	Genomic approaches towards finding cis-regulatory modules in animals. <i>Nature Reviews Genetics</i> , 2012, 13, 469-483.	16.3	200
42	The effects of chromatin organization on variation in mutation rates in the genome. <i>Nature Reviews Genetics</i> , 2015, 16, 213-223.	16.3	199
43	MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3518-3524.	14.5	196
44	Bromodomain protein Brd3 associates with acetylated GATA1 to promote its chromatin occupancy at erythroid target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E159-68.	7.1	190
45	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. <i>Genome Research</i> , 2005, 15, 1051-1060.	5.5	185
46	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	5.5	184
47	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. <i>Genome Research</i> , 2009, 19, 2172-2184.	5.5	184
48	The structure and transcription of four linked rabbit β^2 -like globin genes. <i>Cell</i> , 1979, 18, 1285-1297.	28.9	178
49	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. <i>Blood</i> , 2014, 123, 1927-1937.	1.4	169
50	Chromatin structure dynamics during the mitosis-to-G1 phase transition. <i>Nature</i> , 2019, 576, 158-162.	27.8	167
51	SCL and associated proteins distinguish active from repressive GATA transcription factor complexes. <i>Blood</i> , 2009, 113, 2191-2201.	1.4	158
52	COMPARATIVE GENOMICS. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 15-56.	6.2	156
53	Comparative genome analysis delimits a chromosomal domain and identifies key regulatory elements in the alpha globin cluster. <i>Human Molecular Genetics</i> , 2001, 10, 371-382.	2.9	151
54	A Complex Chromatin Landscape Revealed by Patterns of Nuclease Sensitivity and Histone Modification within the Mouse β^2 -Globin Locus. <i>Molecular and Cellular Biology</i> , 2003, 23, 5234-5244.	2.3	143

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55	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. <i>Nature Genetics</i> , 2011, 43, 295-301.	21.4	142
56	The linkage arrangement of four rabbit β^2 -like globin genes. <i>Cell</i> , 1979, 18, 1273-1283.	28.9	140
57	What fraction of the human genome is functional?. <i>Genome Research</i> , 2011, 21, 1769-1776.	5.5	134
58	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	27.8	131
59	zPicture: Dynamic Alignment and Visualization Tool for Analyzing Conservation Profiles. <i>Genome Research</i> , 2004, 14, 472-477.	5.5	128
60	Evolution of Hemoglobin and Its Genes. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2012, 2, a011627-a011627.	6.2	124
61	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
62	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. <i>Genome Research</i> , 2007, 17, 960-964.	5.5	122
63	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. <i>Science</i> , 2018, 361, 285-290.	12.6	119
64	Distinguishing Regulatory DNA From Neutral Sites. <i>Genome Research</i> , 2003, 13, 64-72.	5.5	118
65	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. <i>Genes and Development</i> , 2017, 31, 1704-1713.	5.9	113
66	ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements. <i>Genome Research</i> , 2006, 16, 1596-1604.	5.5	111
67	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	5.5	110
68	Trisomy 21-associated defects in human primitive hematopoiesis revealed through induced pluripotent stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17573-17578.	7.1	108
69	Genome accessibility is widely preserved and locally modulated during mitosis. <i>Genome Research</i> , 2015, 25, 213-225.	5.5	103
70	Comparison of five methods for finding conserved sequences in multiple alignments of gene regulatory regions. <i>Nucleic Acids Research</i> , 1999, 27, 3899-3910.	14.5	101
71	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. <i>Genome Research</i> , 2004, 14, 700-707.	5.5	93
72	Functions of BET proteins in erythroid gene expression. <i>Blood</i> , 2015, 125, 2825-2834.	1.4	93

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73	A hyperactive transcriptional state marks genome reactivation at the mitosis→G1 transition. <i>Genes and Development</i> , 2016, 30, 1423-1439.	5.9	92
74	Genome-wide ChIP-Seq reveals a dramatic shift in the binding of the transcription factor erythroid Kruppel-like factor during erythrocyte differentiation. <i>Blood</i> , 2011, 118, e139-e148.	1.4	91
75	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. <i>Genome Research</i> , 2014, 24, 1932-1944.	5.5	88
76	Jointly characterizing epigenetic dynamics across multiple human cell types. <i>Nucleic Acids Research</i> , 2016, 44, 6721-6731.	14.5	87
77	A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020, 588, 337-343.	27.8	80
78	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007, 28, 554-562.	2.5	79
79	Complete nucleotide sequence of the rabbit β -like globin gene cluster. <i>Journal of Molecular Biology</i> , 1989, 205, 15-40.	4.2	78
80	Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta -globin gene clusters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 14560-14565.	7.1	77
81	Use of long sequence alignments to study the evolution and regulation of mammalian globin gene clusters.. <i>Molecular Biology and Evolution</i> , 1993, 10, 73-102.	8.9	74
82	Conserved E Boxes Function as Part of the Enhancer in Hypersensitive Site 2 of the β -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 1997, 272, 369-378.	3.4	74
83	Patterns of Insertions and Their Covariation With Substitutions in the Rat, Mouse, and Human Genomes. <i>Genome Research</i> , 2004, 14, 517-527.	5.5	73
84	Dynamic shifts in occupancy by TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis. <i>Genome Research</i> , 2014, 24, 1945-1962.	5.5	71
85	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. <i>Genome Research</i> , 2007, 17, 775-786.	5.5	69
86	Access to a Syllabus of Human Hemoglobin Variants (1996) Via the World Wide Web. <i>Hemoglobin</i> , 1998, 22, 113-127.	0.8	67
87	Pluripotent stem cells reveal erythroid-specific activities of the GATA1 N-terminus. <i>Journal of Clinical Investigation</i> , 2015, 125, 993-1005.	8.2	65
88	A previously undetected pseudogene in the human alpha globin gene cluster. <i>Nucleic Acids Research</i> , 1986, 14, 1903-1911.	14.5	62
89	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , 2015, 16, 87.	2.8	62
90	Clinically relevant updates of the HbVar database of human hemoglobin variants and thalassemia mutations. <i>Nucleic Acids Research</i> , 2021, 49, D1192-D1196.	14.5	62

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91	Isolation and nucleotide sequence of the rabbit globin gene cluster psi zeta-alpha 1-psi alpha. Absence of a pair of alpha-globin genes evolving in concert. Journal of Biological Chemistry, 1986, 261, 839-48.	3.4	59
92	Levels of GATA-1/GATA-2 transcription factors modulate expression of embryonic and fetal hemoglobins. Gene, 2000, 261, 277-287.	2.2	57
93	Experimental validation of predicted mammalian erythroid cis-regulatory modules. Genome Research, 2006, 16, 1480-1492.	5.5	56
94	Human-macaque comparisons illuminate variation in neutral substitution rates. Genome Biology, 2008, 9, R76.	9.6	54
95	The rabbit C family of short, interspersed repeats. Journal of Molecular Biology, 1984, 176, 1-20.	4.2	53
96	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. Cell Reports, 2021, 34, 108783.	6.4	53
97	Comparison of the beta-like globin gene families of rabbits and humans indicates that the gene cluster 5'-epsilon-gamma-delta-beta-3' predates the mammalian radiation.. Molecular Biology and Evolution, 1984, 1, 390-410.	8.9	52
98	Role of DNA Sequences Outside the Cores of DNase Hypersensitive Sites (HSs) in Functions of the Î²-Globin Locus Control Region. Journal of Biological Chemistry, 1996, 271, 11871-11878.	3.4	52
99	Recent Developments in Linear-Space Alignment Methods: A Survey. Journal of Computational Biology, 1994, 1, 271-291.	1.6	51
100	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. Genome Research, 2013, 23, 2136-2148.	5.5	51
101	Sequences Flanking Hypersensitive Sites of the Î²-Globin Locus Control Region Are Required for Synergistic Enhancement. Molecular and Cellular Biology, 2001, 21, 2969-2980.	2.3	49
102	Genome-wide Epigenetic Data Facilitate Understanding of Disease Susceptibility Association Studies. Journal of Biological Chemistry, 2012, 287, 30932-30940.	3.4	49
103	Identification of Biologically Relevant Enhancers in Human Erythroid Cells. Journal of Biological Chemistry, 2013, 288, 8433-8444.	3.4	49
104	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. Molecular Cell, 2021, 81, 239-254.e8.	9.7	48
105	Comparative analysis of the locus control region of the rabbit Î²-like globin gene cluster: HS3 increases transient expression of an embryonic Îµ-globin gene. Nucleic Acids Research, 1993, 21, 1265-1272.	14.5	47
106	GALA, a Database for Genomic Sequence Alignments and Annotations. Genome Research, 2003, 13, 732-741.	5.5	45
107	An Iron Responsive Element-like Stem-Loop Regulates Î±-Hemoglobin-stabilizing Protein mRNA. Journal of Biological Chemistry, 2008, 283, 26956-26964.	3.4	45
108	Histone neighbors in nuclei and extended chromatin. Cell, 1977, 12, 417-427.	28.9	42

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109	Accurate and reproducible functional maps in 127 human cell types via 2D genome segmentation. <i>Nucleic Acids Research</i> , 2017, 45, 9823-9836.	14.5	42
110	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. <i>Blood</i> , 2020, 135, 2121-2132.	1.4	42
111	The Evolution of Hemoglobin. <i>American Scientist</i> , 1999, 87, 126.	0.1	41
112	Sequence and comparative analysis of the rabbit ϵ -like globin gene cluster reveals a rapid mode of evolution in a G + C-rich region of mammalian genomes. <i>Journal of Molecular Biology</i> , 1991, 222, 233-249.	4.2	40
113	An approach to histone nearest neighbours in extended chromatin. <i>Nucleic Acids Research</i> , 1975, 2, 1751-1770.	14.5	39
114	A T-to-G Transversion at Nucleotide \sim 567 Upstream of $\langle i \rangle$ HBG2 $\langle /i \rangle$ in a GATA-1 Binding Motif Is Associated with Elevated Hemoglobin F. <i>Molecular and Cellular Biology</i> , 2008, 28, 4386-4393.	2.3	39
115	Selenoproteins regulate stress erythroid progenitors and spleen microenvironment during stress erythropoiesis. <i>Blood</i> , 2018, 131, 2568-2580.	1.4	39
116	Subfamily relationships and clustering of rabbit C repeats.. <i>Molecular Biology and Evolution</i> , 1991, 8, 1-30.	8.9	38
117	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	5.5	38
118	Evolution of hemoglobin loci and their regulatory elements. <i>Blood Cells, Molecules, and Diseases</i> , 2018, 70, 2-12.	1.4	37
119	Single-nucleotide-level mapping of DNA regulatory elements that control fetal hemoglobin expression. <i>Nature Genetics</i> , 2021, 53, 869-880.	21.4	37
120	Unique sequence organization and erythroid cell-specific nuclear factor-binding of mammalian ϵ I globin promoters. <i>Nucleic Acids Research</i> , 1989, 17, 5687-5700.	14.5	36
121	Software tools for analyzing pairwise alignments of long sequences. <i>Nucleic Acids Research</i> , 1991, 19, 4663-4667.	14.5	36
122	Association between divergence and interspersed repeats in mammalian noncoding genomic DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 14503-14508.	7.1	36
123	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	12.8	36
124	The nucleotide sequence of the rabbit embryonic globin gene beta 4. <i>Journal of Biological Chemistry</i> , 1983, 258, 8739-44.	3.4	36
125	The L1 family of long interspersed repetitive DNA in rabbits: Sequence, copy number, conserved open reading frames, and similarity to keratin. <i>Journal of Molecular Evolution</i> , 1989, 29, 3-19.	1.8	35
126	Globin Gene Server: A Prototype E-Mail Database Server Featuring Extensive Multiple Alignments and Data Compilation for Electronic Genetic Analysis. <i>Genomics</i> , 1994, 21, 344-353.	2.9	35

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127	PROGRAM DESCRIPTION. Genomics, 1998, 47, 429-437.	2.9	35
128	DATABASES OF HUMAN HEMOGLOBIN VARIANTS AND OTHER RESOURCES AT THE GLOBIN GENE SERVER. Hemoglobin, 2001, 25, 183-193.	0.8	35
129	Alteration of genome folding via contact domain boundary insertion. Nature Genetics, 2020, 52, 1076-1087.	21.4	35
130	Function of GATA Factors in the Adult Mouse Liver. PLoS ONE, 2013, 8, e83723.	2.5	35
131	The Complete Sequences of the Galago and Rabbit β^2 -Globin Locus Control Regions: Extended Sequence and Functional Conservation Outside the Cores of DNase Hypersensitive Sites. Genomics, 1997, 39, 90-94.	2.9	34
132	Description and targeted deletion of 5' hypersensitive site 5 and 6 of the mouse beta-globin locus control region. Blood, 1998, 92, 4394-403.	1.4	34
133	Assignment of orthologous relationships among mammalian alpha-globin genes by examining flanking regions reveals a rapid rate of evolution.. Molecular Biology and Evolution, 1986, 3, 243-61.	8.9	32
134	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. Genomics, 2002, 80, 681-690.	2.9	32
135	Genome-Wide Organization of GATA1 and TAL1 Determined at High Resolution. Molecular and Cellular Biology, 2016, 36, 157-172.	2.3	32
136	Short interspersed repeats in rabbit DNA can provide functional polyadenylation signals.. Molecular Biology and Evolution, 1990, 7, 1-8.	8.9	31
137	Characterization of a Widely Expressed Gene (LUC7-LIKE; LUC7L) Defining the Centromeric Boundary of the Human β^2 -Globin Domain. Genomics, 2001, 71, 307-314.	2.9	31
138	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. Blood, 2020, 135, 1957-1968.	1.4	30
139	Frequent somatic $\langle i \rangle$ TET2 $\langle /i \rangle$ mutations in chronic NK-LGL leukemia with distinct patterns of cytopenias. Blood, 2021, 138, 662-673.	1.4	30
140	Comparative Analysis of the \hat{A} -Like Globin Clusters in Mouse, Rat, and Human Chromosomes Indicates a Mechanism Underlying Breaks in Conserved Synteny. Genome Research, 2004, 14, 623-630.	5.5	29
141	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. Genome Research, 2008, 18, 1896-1905.	5.5	29
142	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. Nucleic Acids Research, 2009, 37, 7024-7038.	14.5	29
143	The nucleotide sequence of rabbit embryonic globin gene beta 3. Journal of Biological Chemistry, 1981, 256, 11780-6.	3.4	29
144	Analysis of rabbit \hat{A} -like globin gene transcripts during development. Journal of Molecular Biology, 1983, 164, 395-417.	4.2	27

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145	DNase I and nuclease S1 sensitivity of the rabbit γ 1 globin gene in nuclei and in supercoiled plasmids. Journal of Molecular Biology, 1985, 184, 195-210.	4.2	27
146	Dynamic CTCF binding directly mediates interactions among <i>cis</i> -regulatory elements essential for hematopoiesis. Blood, 2021, 137, 1327-1339.	1.4	27
147	Rabbit globin pseudogene psi beta 2 is a hybrid of delta- and beta-globin gene sequences.. Molecular Biology and Evolution, 1984, 1, 302-16.	8.9	25
148	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3366.	7.1	25
149	The E3 ligase adaptor molecule SPOP regulates fetal hemoglobin levels in adult erythroid cells. Blood Advances, 2019, 3, 1586-1597.	5.2	25
150	Chaining Multiple-Alignment Blocks. Journal of Computational Biology, 1994, 1, 217-226.	1.6	24
151	Sequences within and flanking hypersensitive sites 3 and 2 of the beta- globin locus control region required for synergistic versus additive interaction with the epsilon-globin gene promoter. Nucleic Acids Research, 1996, 24, 4327-4335.	14.5	24
152	Genomic landscape of TCR α and TCR β T-large granular lymphocyte leukemia. Blood, 2022, 139, 3058-3072.	1.4	24
153	Variability within the rabbit C repeats and sequene shared with other SINES. Nucleic Acids Research, 1985, 13, 1073-1088.	14.5	23
154	Multiple Regulatory Elements in the 5' Flanking Sequence of the Human μ -Globin Gene. Journal of Biological Chemistry, 1998, 273, 10202-10209.	3.4	23
155	Exponential Decay of GC Content Detected by Strand-Symmetric Substitution Rates Influences the Evolution of Isochore Structure. Molecular Biology and Evolution, 2008, 25, 362-374.	8.9	23
156	Restriction Enzyme Analysis of Tomato Chloroplast and Chromoplast DNA. Plant Physiology, 1986, 82, 1145-1147.	4.8	22
157	An electronic database of human hemoglobin variants on the World Wide Web. Blood, 1998, 91, 2643-4.	1.4	22
158	Long interspersed L1 repeats in rabbit DNA are homologous to L1 repeats of rodents and primates in an open-reading-frame region.. Molecular Biology and Evolution, 1986, 3, 179-90.	8.9	20
159	New views of evolution and regulation of vertebrate γ -like globin gene clusters from an orphaned gene in marsupials. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 1327-1329.	7.1	20
160	Between form and function: the complexity of genome folding. Human Molecular Genetics, 2017, 26, R208-R215.	2.9	20
161	Constrained sequence alignment. Bulletin of Mathematical Biology, 1993, 55, 503-524.	1.9	19
162	Localization of the β -like globin gene cluster and the genes for parathyroid hormone and c-Harvey-ras 1 to region q14;q21 of rabbit chromosome 1 by in situ hybridization. Cytogenetic and Genome Research, 1989, 52, 157-161.	1.1	18

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163	The 5' ends of LINE1 repeats in rabbit DNA define subfamilies and reveal a short sequence conserved between rabbits and humans. <i>Genomics</i> , 1992, 14, 320-331.	2.9	18
164	Sharing data between LSDBs and central repositories. <i>Human Mutation</i> , 2009, 30, 493-495.	2.5	18
165	A Negative Cis-element Regulates the Level of Enhancement by Hypersensitive Site 2 of the γ -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 2001, 276, 6289-6298.	3.4	17
166	Localization of the γ -like globin gene cluster to region q12 of rabbit chromosome 6 by in situ hybridization. <i>Genomics</i> , 1991, 9, 362-365.	2.9	16
167	Flanking and Intragenic Sequences Regulating the Expression of the Rabbit γ -Globin Gene. <i>Journal of Biological Chemistry</i> , 1995, 270, 3965-3973.	3.4	16
168	CpG Islands from the γ -Globin Gene Cluster Increase Gene Expression in an Integration-Dependent Manner. <i>Molecular and Cellular Biology</i> , 1997, 17, 5856-5866.	2.3	16
169	Domain-adaptive neural networks improve cross-species prediction of transcription factor binding. <i>Genome Research</i> , 2022, 32, 512-523.	5.5	16
170	Survey of plastid RNA abundance during tomato fruit ripening: the amounts of RNA from the ORF 2280 region increase in chromoplasts. <i>Plant Molecular Biology</i> , 1991, 17, 1179-1188.	3.9	15
171	HRI depletion cooperates with pharmacologic inducers to elevate fetal hemoglobin and reduce sickle cell formation. <i>Blood Advances</i> , 2020, 4, 4560-4572.	5.2	15
172	Nucleotide sequence and expression of rabbit globin genes zeta 1, zeta 2, and zeta 3. Pseudogenes generated by block duplications are transcriptionally competent. <i>Journal of Biological Chemistry</i> , 1988, 263, 9981-93.	3.4	15
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