

# Ross Hardison

## List of Publications by Year in descending order

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206  
papers

46,826  
citations

8732

75  
h-index

2116

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. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
3	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	13.7	2,421
4	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004, 306, 636-640.	6.0	2,121
5	The isolation of structural genes from libraries of eucaryotic DNA. <i>Cell</i> , 1978, 15, 687-701.	13.5	2,037
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
7	Galaxy: A platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005, 15, 1451-1455.	2.4	1,795
8	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
9	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
10	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
11	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
12	Human-Mouse Alignments with BLASTZ. <i>Genome Research</i> , 2003, 13, 103-107.	2.4	1,071
13	PipMaker--A Web Server for Aligning Two Genomic DNA Sequences. <i>Genome Research</i> , 2000, 10, 577-586.	2.4	1,070
14	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014, 515, 402-405.	13.7	779
15	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
16	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	3.3	635
17	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013, 41, 827-841.	6.5	490
18	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	13.9	410

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19	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. <i>Human Mutation</i> , 2002, 19, 225-233.	1.1	400
20	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010, 463, 943-947.	13.7	400
21	Conserved noncoding sequences are reliable guides to regulatory elements. <i>Trends in Genetics</i> , 2000, 16, 369-372.	2.9	385
22	HiCRep: assessing the reproducibility of Hi-C data using a stratum-adjusted correlation coefficient. <i>Genome Research</i> , 2017, 27, 1939-1949.	2.4	376
23	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. <i>Nucleic Acids Research</i> , 2014, 42, D1063-D1069.	6.5	361
24	A brief history of hemoglobins: plant, animal, protist, and bacteria.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 5675-5679.	3.3	332
25	A GATA-1-regulated microRNA locus essential for erythropoiesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3333-3338.	3.3	309
26	Long Human-Mouse Sequence Alignments Reveal Novel Regulatory Elements: A Reason to Sequence the Mouse Genome. <i>Genome Research</i> , 1997, 7, 959-966.	2.4	294
27	A genome-editing strategy to treat $\beta^2$ -hemoglobinopathies that recapitulates a mutation associated with a benign genetic condition. <i>Nature Medicine</i> , 2016, 22, 987-990.	15.2	279
28	Insights into GATA-1-Mediated Gene Activation versus Repression via Genome-wide Chromatin Occupancy Analysis. <i>Molecular Cell</i> , 2009, 36, 682-695.	4.5	278
29	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018, 50, 1388-1398.	9.4	268
30	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. <i>Genome Research</i> , 2003, 13, 13-26.	2.4	263
31	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	13.7	259
32	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	237
33	Locus control regions of mammalian $\beta^2$ -globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. <i>Gene</i> , 1997, 205, 73-94.	1.0	226
34	Comparative Genomics. <i>PLoS Biology</i> , 2003, 1, e58.	2.6	221
35	Hemoglobins from bacteria to man: evolution of different patterns of gene expression. <i>Journal of Experimental Biology</i> , 1998, 201, 1099-117.	0.8	219
36	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. <i>Genome Research</i> , 2005, 15, 184-194.	2.4	218

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37	Unlinking an lncRNA from Its Associated cis Element. <i>Molecular Cell</i> , 2016, 62, 104-110.	4.5	216
38	Tissue-Specific Mitotic Bookmarking by Hematopoietic Transcription Factor GATA1. <i>Cell</i> , 2012, 150, 725-737.	13.5	215
39	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. <i>Genome Research</i> , 2003, 13, 1-12.	2.4	210
40	Evolution and functional classification of vertebrate gene deserts. <i>Genome Research</i> , 2005, 15, 137-145.	2.4	203
41	Genomic approaches towards finding cis-regulatory modules in animals. <i>Nature Reviews Genetics</i> , 2012, 13, 469-483.	7.7	200
42	The effects of chromatin organization on variation in mutation rates in the genome. <i>Nature Reviews Genetics</i> , 2015, 16, 213-223.	7.7	199
43	MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3518-3524.	6.5	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.	3.3	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.	2.4	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.	2.4	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.	2.4	184
48	The structure and transcription of four linked rabbit $\beta$ -like globin genes. <i>Cell</i> , 1979, 18, 1285-1297.	13.5	178
49	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. <i>Blood</i> , 2014, 123, 1927-1937.	0.6	169
50	Chromatin structure dynamics during the mitosis-to-G1 phase transition. <i>Nature</i> , 2019, 576, 158-162.	13.7	167
51	SCL and associated proteins distinguish active from repressive GATA transcription factor complexes. <i>Blood</i> , 2009, 113, 2191-2201.	0.6	158
52	COMPARATIVE GENOMICS. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 15-56.	2.5	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.	1.4	151
54	A Complex Chromatin Landscape Revealed by Patterns of Nuclease Sensitivity and Histone Modification within the Mouse $\beta$ -Globin Locus. <i>Molecular and Cellular Biology</i> , 2003, 23, 5234-5244.	1.1	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.	9.4	142
56	The linkage arrangement of four rabbit $\beta^2$ -like globin genes. <i>Cell</i> , 1979, 18, 1273-1283.	13.5	140
57	What fraction of the human genome is functional?. <i>Genome Research</i> , 2011, 21, 1769-1776.	2.4	134
58	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	13.7	131
59	zPicture: Dynamic Alignment and Visualization Tool for Analyzing Conservation Profiles. <i>Genome Research</i> , 2004, 14, 472-477.	2.4	128
60	Evolution of Hemoglobin and Its Genes. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2012, 2, a011627-a011627.	2.9	124
61	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
62	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. <i>Genome Research</i> , 2007, 17, 960-964.	2.4	122
63	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. <i>Science</i> , 2018, 361, 285-290.	6.0	119
64	Distinguishing Regulatory DNA From Neutral Sites. <i>Genome Research</i> , 2003, 13, 64-72.	2.4	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.	2.7	113
66	ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements. <i>Genome Research</i> , 2006, 16, 1596-1604.	2.4	111
67	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	2.4	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.	3.3	108
69	Genome accessibility is widely preserved and locally modulated during mitosis. <i>Genome Research</i> , 2015, 25, 213-225.	2.4	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.	6.5	101
71	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. <i>Genome Research</i> , 2004, 14, 700-707.	2.4	93
72	Functions of BET proteins in erythroid gene expression. <i>Blood</i> , 2015, 125, 2825-2834.	0.6	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.	2.7	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.	0.6	91
75	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. <i>Genome Research</i> , 2014, 24, 1932-1944.	2.4	88
76	Jointly characterizing epigenetic dynamics across multiple human cell types. <i>Nucleic Acids Research</i> , 2016, 44, 6721-6731.	6.5	87
77	A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020, 588, 337-343.	13.7	80
78	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007, 28, 554-562.	1.1	79
79	Complete nucleotide sequence of the rabbit $\hat{\gamma}$ -like globin gene cluster. <i>Journal of Molecular Biology</i> , 1989, 205, 15-40.	2.0	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.	3.3	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.	3.5	74
82	Conserved E Boxes Function as Part of the Enhancer in Hypersensitive Site 2 of the $\hat{\gamma}$ -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 1997, 272, 369-378.	1.6	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.	2.4	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.	2.4	71
85	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. <i>Genome Research</i> , 2007, 17, 775-786.	2.4	69
86	Access to a Syllabus of Human Hemoglobin Variants (1996) Via the World Wide Web. <i>Hemoglobin</i> , 1998, 22, 113-127.	0.4	67
87	Pluripotent stem cells reveal erythroid-specific activities of the GATA1 N-terminus. <i>Journal of Clinical Investigation</i> , 2015, 125, 993-1005.	3.9	65
88	A previously undetected pseudogene in the human alpha globin gene cluster. <i>Nucleic Acids Research</i> , 1986, 14, 1903-1911.	6.5	62
89	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , 2015, 16, 87.	1.2	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.	6.5	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. <i>Journal of Biological Chemistry</i> , 1986, 261, 839-48.	1.6	59
92	Levels of GATA-1/GATA-2 transcription factors modulate expression of embryonic and fetal hemoglobins. <i>Gene</i> , 2000, 261, 277-287.	1.0	57
93	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006, 16, 1480-1492.	2.4	56
94	Human-macaque comparisons illuminate variation in neutral substitution rates. <i>Genome Biology</i> , 2008, 9, R76.	13.9	54
95	The rabbit C family of short, interspersed repeats. <i>Journal of Molecular Biology</i> , 1984, 176, 1-20.	2.0	53
96	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	2.9	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.. <i>Molecular Biology and Evolution</i> , 1984, 1, 390-410.	3.5	52
98	Role of DNA Sequences Outside the Cores of DNase Hypersensitive Sites (HSs) in Functions of the $\hat{\nu}$ -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 1996, 271, 11871-11878.	1.6	52
99	Recent Developments in Linear-Space Alignment Methods: A Survey. <i>Journal of Computational Biology</i> , 1994, 1, 271-291.	0.8	51
100	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , 2013, 23, 2136-2148.	2.4	51
101	Sequences Flanking Hypersensitive Sites of the $\hat{\nu}$ -Globin Locus Control Region Are Required for Synergistic Enhancement. <i>Molecular and Cellular Biology</i> , 2001, 21, 2969-2980.	1.1	49
102	Genome-wide Epigenetic Data Facilitate Understanding of Disease Susceptibility Association Studies. <i>Journal of Biological Chemistry</i> , 2012, 287, 30932-30940.	1.6	49
103	Identification of Biologically Relevant Enhancers in Human Erythroid Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 8433-8444.	1.6	49
104	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Molecular Cell</i> , 2021, 81, 239-254.e8.	4.5	48
105	Comparative analysis of the locus control region of the rabbit $\hat{\nu}$ -like globin gene cluster: HS3 increases transient expression of an embryonic $\hat{\mu}$ -globin gene. <i>Nucleic Acids Research</i> , 1993, 21, 1265-1272.	6.5	47
106	GALA, a Database for Genomic Sequence Alignments and Annotations. <i>Genome Research</i> , 2003, 13, 732-741.	2.4	45
107	An Iron Responsive Element-like Stem-Loop Regulates $\hat{\nu}$ -Hemoglobin-stabilizing Protein mRNA. <i>Journal of Biological Chemistry</i> , 2008, 283, 26956-26964.	1.6	45
108	Histone neighbors in nuclei and extended chromatin. <i>Cell</i> , 1977, 12, 417-427.	13.5	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.	6.5	42
110	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. <i>Blood</i> , 2020, 135, 2121-2132.	0.6	42
111	The Evolution of Hemoglobin. <i>American Scientist</i> , 1999, 87, 126.	0.1	41
112	Sequence and comparative analysis of the rabbit $\beta$ -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.	2.0	40
113	An approach to histone nearest neighbours in extended chromatin. <i>Nucleic Acids Research</i> , 1975, 2, 1751-1770.	6.5	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.	1.1	39
115	Selenoproteins regulate stress erythroid progenitors and spleen microenvironment during stress erythropoiesis. <i>Blood</i> , 2018, 131, 2568-2580.	0.6	39
116	Subfamily relationships and clustering of rabbit C repeats.. <i>Molecular Biology and Evolution</i> , 1991, 8, 1-30.	3.5	38
117	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	2.4	38
118	Evolution of hemoglobin loci and their regulatory elements. <i>Blood Cells, Molecules, and Diseases</i> , 2018, 70, 2-12.	0.6	37
119	Single-nucleotide-level mapping of DNA regulatory elements that control fetal hemoglobin expression. <i>Nature Genetics</i> , 2021, 53, 869-880.	9.4	37
120	Unique sequence organization and erythroid cell-specific nuclear factor-binding of mammalian $\beta$ I globin promoters. <i>Nucleic Acids Research</i> , 1989, 17, 5687-5700.	6.5	36
121	Software tools for analyzing pairwise alignments of long sequences. <i>Nucleic Acids Research</i> , 1991, 19, 4663-4667.	6.5	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.	3.3	36
123	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	5.8	36
124	The nucleotide sequence of the rabbit embryonic globin gene beta 4. <i>Journal of Biological Chemistry</i> , 1983, 258, 8739-44.	1.6	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.	0.8	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.	1.3	35



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127	PROGRAM DESCRIPTION. <i>Genomics</i> , 1998, 47, 429-437.	1.3	35
128	DATABASES OF HUMAN HEMOGLOBIN VARIANTS AND OTHER RESOURCES AT THE GLOBIN GENE SERVER. <i>Hemoglobin</i> , 2001, 25, 183-193.	0.4	35
129	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	9.4	35
130	Function of GATA Factors in the Adult Mouse Liver. <i>PLoS ONE</i> , 2013, 8, e83723.	1.1	35
131	The Complete Sequences of the Galago and Rabbit $\hat{\gamma}$ -Globin Locus Control Regions: Extended Sequence and Functional Conservation Outside the Cores of DNase Hypersensitive Sites. <i>Genomics</i> , 1997, 39, 90-94.	1.3	34
132	Description and targeted deletion of 5' hypersensitive site 5 and 6 of the mouse beta-globin locus control region. <i>Blood</i> , 1998, 92, 4394-403.	0.6	34
133	Assignment of orthologous relationships among mammalian alpha-globin genes by examining flanking regions reveals a rapid rate of evolution.. <i>Molecular Biology and Evolution</i> , 1986, 3, 243-61.	3.5	32
134	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. <i>Genomics</i> , 2002, 80, 681-690.	1.3	32
135	Genome-Wide Organization of GATA1 and TAL1 Determined at High Resolution. <i>Molecular and Cellular Biology</i> , 2016, 36, 157-172.	1.1	32
136	Short interspersed repeats in rabbit DNA can provide functional polyadenylation signals.. <i>Molecular Biology and Evolution</i> , 1990, 7, 1-8.	3.5	31
137	Characterization of a Widely Expressed Gene (LUC7-LIKE; LUC7L) Defining the Centromeric Boundary of the Human $\hat{\gamma}$ -Globin Domain. <i>Genomics</i> , 2001, 71, 307-314.	1.3	31
138	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. <i>Blood</i> , 2020, 135, 1957-1968.	0.6	30
139	Frequent somatic $\langle i \rangle$ TET2 $\langle /i \rangle$ mutations in chronic NK-LGL leukemia with distinct patterns of cytopenias. <i>Blood</i> , 2021, 138, 662-673.	0.6	30
140	Comparative Analysis of the $\hat{\gamma}$ -Like Globin Clusters in Mouse, Rat, and Human Chromosomes Indicates a Mechanism Underlying Breaks in Conserved Synteny. <i>Genome Research</i> , 2004, 14, 623-630.	2.4	29
141	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. <i>Genome Research</i> , 2008, 18, 1896-1905.	2.4	29
142	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. <i>Nucleic Acids Research</i> , 2009, 37, 7024-7038.	6.5	29
143	The nucleotide sequence of rabbit embryonic globin gene beta 3. <i>Journal of Biological Chemistry</i> , 1981, 256, 11780-6.	1.6	29
144	Analysis of rabbit $\hat{\gamma}$ -like globin gene transcripts during development. <i>Journal of Molecular Biology</i> , 1983, 164, 395-417.	2.0	27

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145	DNase I and nuclease S1 sensitivity of the rabbit $\beta^1$ globin gene in nuclei and in supercoiled plasmids. <i>Journal of Molecular Biology</i> , 1985, 184, 195-210.	2.0	27
146	Dynamic CTCF binding directly mediates interactions among <i>cis</i> -regulatory elements essential for hematopoiesis. <i>Blood</i> , 2021, 137, 1327-1339.	0.6	27
147	Rabbit globin pseudogene psi beta 2 is a hybrid of delta- and beta-globin gene sequences.. <i>Molecular Biology and Evolution</i> , 1984, 1, 302-16.	3.5	25
148	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3366.	3.3	25
149	The E3 ligase adaptor molecule SPOP regulates fetal hemoglobin levels in adult erythroid cells. <i>Blood Advances</i> , 2019, 3, 1586-1597.	2.5	25
150	Chaining Multiple-Alignment Blocks. <i>Journal of Computational Biology</i> , 1994, 1, 217-226.	0.8	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. <i>Nucleic Acids Research</i> , 1996, 24, 4327-4335.	6.5	24
152	Genomic landscape of TCR $\beta$ and TCR $\gamma$ T-large granular lymphocyte leukemia. <i>Blood</i> , 2022, 139, 3058-3072.	0.6	24
153	Variability within the rabbit C repeats and sequene shared with other SINES. <i>Nucleic Acids Research</i> , 1985, 13, 1073-1088.	6.5	23
154	Multiple Regulatory Elements in the 5' Flanking Sequence of the Human $\mu$ -Globin Gene. <i>Journal of Biological Chemistry</i> , 1998, 273, 10202-10209.	1.6	23
155	Exponential Decay of GC Content Detected by Strand-Symmetric Substitution Rates Influences the Evolution of Isochore Structure. <i>Molecular Biology and Evolution</i> , 2008, 25, 362-374.	3.5	23
156	Restriction Enzyme Analysis of Tomato Chloroplast and Chromoplast DNA. <i>Plant Physiology</i> , 1986, 82, 1145-1147.	2.3	22
157	An electronic database of human hemoglobin variants on the World Wide Web. <i>Blood</i> , 1998, 91, 2643-4.	0.6	22
158	Long interspersed L1 repeats in rabbit DNA are homologous to L1 repeats of rodents and primates in an open-reading-frame region.. <i>Molecular Biology and Evolution</i> , 1986, 3, 179-90.	3.5	20
159	New views of evolution and regulation of vertebrate $\lambda$ -like globin gene clusters from an orphaned gene in marsupials. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 1327-1329.	3.3	20
160	Between form and function: the complexity of genome folding. <i>Human Molecular Genetics</i> , 2017, 26, R208-R215.	1.4	20
161	Constrained sequence alignment. <i>Bulletin of Mathematical Biology</i> , 1993, 55, 503-524.	0.9	19
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