Ross Hardison

List of Publications by Year in Descending Order

201 papers	38,047 citations	70 h-index	195 g-index
219 ext. papers	43,181 ext. citations	13.8 avg, IF	7.27 L-index

#	Paper	IF	Citations
201	Frequent somatic TET2 mutations in chronic NK-LGL leukemia with distinct patterns of cytopenias. *Blood*, **2021**, 138, 662-673	2.2	6
200	Effects of sheared chromatin length on ChIP-seq quality and sensitivity. *G3: Genes, Genomes, Genetics*, **2021**,	3.2	1
199	Single-nucleotide-level mapping of DNA regulatory elements that control fetal hemoglobin expression. *Nature Genetics*, **2021**, 53, 869-880	36.3	7
198	Clinically relevant updates of the HbVar database of human hemoglobin variants and thalassemia mutations. *Nucleic Acids Research*, **2021**, 49, D1192-D1196	20.1	25
197	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. *Molecular Cell*, **2021**, 81, 239-254.e8	17.6	20
196	Dynamic CTCF binding directly mediates interactions among cis-regulatory elements essential for hematopoiesis. *Blood*, **2021**, 137, 1327-1339	2.2	3
195	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. *Cell Reports*, **2021**, 34, 108783	10.6	10
194	HDAC1 is required for GATA-1 transcription activity, global chromatin occupancy and hematopoiesis. *Nucleic Acids Research*, **2021**, 49, 9783-9798	20.1	2
193	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. *Blood*, **2020**, 135, 1957-1968	2.2	14
192	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. *Blood*, **2020**, 135, 2121-2132	2.2	15
191	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. *Genome Research*, **2020**, 30, 472-484	9.7	11
190	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. *IUBMB Life*, **2020**, 72, 27-38	4.7	3
189	A map of cis-regulatory elements and 3D genome structures in zebrafish. *Nature*, **2020**, 588, 337-343	50.4	18
188	HRI depletion cooperates with pharmacologic inducers to elevate fetal hemoglobin and reduce sickle cell formation. *Blood Advances*, **2020**, 4, 4560-4572	7.8	8
187	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
186	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
185	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. *Nature*, **2020**, 583, 760-767	50.4	39

184	Alteration of genome folding via contact domain boundary insertion. *Nature Genetics*, **2020**, 52, 1076-1087	36.3	18
183	A Cambrian origin for globin gene regulation. *Blood*, **2020**, 136, 261-262	2.2	
182	The E3 ligase adaptor molecule SPOP regulates fetal hemoglobin levels in adult erythroid cells. *Blood Advances*, **2019**, 3, 1586-1597	7.8	17
181	Chromatin structure dynamics during the mitosis-to-G1 phase transition. *Nature*, **2019**, 576, 158-162	50.4	83
180	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. *Nature Communications*, **2018**, 9, 782	17.4	28
179	Selenoproteins regulate stress erythroid progenitors and spleen microenvironment during stress erythropoiesis. *Blood*, **2018**, 131, 2568-2580	2.2	24
178	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. *Science*, **2018**, 361, 285-290	33.3	82
177	Evolution of hemoglobin loci and their regulatory elements. *Blood Cells, Molecules, and Diseases*, **2018**, 70, 2-12	2.1	13
176	Integrative detection and analysis of structural variation in cancer genomes. *Nature Genetics*, **2018**, 50, 1388-1398	36.3	147
175	HiCRep: assessing the reproducibility of Hi-C data using a stratum-adjusted correlation coefficient. *Genome Research*, **2017**, 27, 1939-1949	9.7	171
174	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. *Genes and Development*, **2017**, 31, 1704-1713	12.6	70
173	Between form and function: the complexity of genome folding. *Human Molecular Genetics*, **2017**, 26, R208-R215	5.6	11
172	Accurate and reproducible functional maps in 127 human cell types via 2D genome segmentation. *Nucleic Acids Research*, **2017**, 45, 9823-9836	20.1	16
171	A genome-editing strategy to treat hemoglobinopathies that recapitulates a mutation associated with a benign genetic condition. *Nature Medicine*, **2016**, 22, 987-90	50.5	213
170	A hyperactive transcriptional state marks genome reactivation at the mitosis-G1 transition. *Genes and Development*, **2016**, 30, 1423-39	12.6	56
169	Jointly characterizing epigenetic dynamics across multiple human cell types. *Nucleic Acids Research*, **2016**, 44, 6721-31	20.1	54
168	Genome-Wide Organization of GATA1 and TAL1 Determined at High Resolution. *Molecular and Cellular Biology*, **2016**, 36, 157-72	4.8	20
167	SBR-Blood: systems biology repository for hematopoietic cells. *Nucleic Acids Research*, **2016**, 44, D925-31	20.1	2

166	A guide to translation of research results from model organisms to human. *Genome Biology*, **2016**, 17, 161	18.3	3
165	Unlinking an lncRNA from Its Associated cis Element. *Molecular Cell*, **2016**, 62, 104-10	17.6	164
164	Finding partners to play the music of regulation. *Blood*, **2016**, 127, 1624-6	2.2	
163	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. *BMC Genomics*, **2015**, 16, 87	4.5	46
162	The effects of chromatin organization on variation in mutation rates in the genome. *Nature Reviews Genetics*, **2015**, 16, 213-23	30.1	143
161	Genome accessibility is widely preserved and locally modulated during mitosis. *Genome Research*, **2015**, 25, 213-25	9.7	74
160	Functions of BET proteins in erythroid gene expression. *Blood*, **2015**, 125, 2825-34	2.2	70
159	Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. *Genomics Data*, **2015**, 4, 1-7		8
158	Pluripotent stem cells reveal erythroid-specific activities of the GATA1 N-terminus. *Journal of Clinical Investigation*, **2015**, 125, 993-1005	15.9	43
157	Principles of regulatory information conservation between mouse and human. *Nature*, **2014**, 515, 371-375	50.4	190
156	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
155	Topologically associating domains are stable units of replication-timing regulation. *Nature*, **2014**, 515, 402-5	50.4	563
154	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. *Blood*, **2014**, 123, 1927-37	2.2	114
153	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. *Nucleic Acids Research*, **2014**, 42, D1063-9	20.1	289
152	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	11.5	22
151	Defining functional DNA elements in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6131-8	11.5	490
150	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. *Genome Research*, **2014**, 24, 1932-44	9.7	67
149	Dynamic shifts in occupancy by TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis. *Genome Research*, **2014**, 24, 1945-62	9.7	51

148	A cluster to remember. *Cell*, **2013**, 154, 718-20	56.2	
147	Genetics. GWAS to therapy by genome edits?. *Science*, **2013**, 342, 206-7	33.3	11
146	Integrative annotation of chromatin elements from ENCODE data. *Nucleic Acids Research*, **2013**, 41, 827-41	20.1	383
145	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. *Genome Research*, **2013**, 23, 2136-48	9.7	39
144	Identification of biologically relevant enhancers in human erythroid cells. *Journal of Biological Chemistry*, **2013**, 288, 8433-8444	5.4	37
143	Function of GATA factors in the adult mouse liver. *PLoS ONE*, **2013**, 8, e83723	3.7	25
142	Genome-wide epigenetic data facilitate understanding of disease susceptibility association studies. *Journal of Biological Chemistry*, **2012**, 287, 30932-40	5.4	35
141	Tissue-specific mitotic bookmarking by hematopoietic transcription factor GATA1. *Cell*, **2012**, 150, 725-37	36.2	164
140	Evolution of hemoglobin and its genes. *Cold Spring Harbor Perspectives in Medicine*, **2012**, 2, a011627	5.4	85
139	Genomic approaches towards finding cis-regulatory modules in animals. *Nature Reviews Genetics*, **2012**, 13, 469-83	30.1	156
138	Revealing mammalian evolutionary relationships by comparative analysis of gene clusters. *Genome Biology and Evolution*, **2012**, 4, 586-601	3.9	8
137	Trisomy 21-associated defects in human primitive hematopoiesis revealed through induced pluripotent stem cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 17573-8	11.5	88
136	An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biology*, **2012**, 13, 418	18.3	340
135	A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biology*, **2011**, 9, e1001046	9.7	1060
134	Genome-wide ChIP-Seq reveals a dramatic shift in the binding of the transcription factor erythroid Kruppel-like factor during erythrocyte differentiation. *Blood*, **2011**, 118, e139-48	2.2	77
133	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. *Nature Genetics*, **2011**, 43, 295-301	36.3	125
132	What fraction of the human genome is functional?. *Genome Research*, **2011**, 21, 1769-76	9.7	104
131	Bromodomain protein Brd3 associates with acetylated GATA1 to promote its chromatin occupancy at erythroid target genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E159-68	11.5	162

130	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. *Genome Research*, **2011**, 21, 1659-71	9.7	100
129	Complete Khoisan and Bantu genomes from southern Africa. *Nature*, **2010**, 463, 943-7	50.4	342
128	An effective method for detecting gene conversion events in whole genomes. *Journal of Computational Biology*, **2010**, 17, 1281-97	1.7	11
127	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. *Genome Research*, **2009**, 19, 2172-84	9.7	163
126	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. *Nucleic Acids Research*, **2009**, 37, 7024-38	20.1	27
125	Sharing data between LSDBs and central repositories. *Human Mutation*, **2009**, 30, 493-5	4.7	17
124	Insights into GATA-1-mediated gene activation versus repression via genome-wide chromatin occupancy analysis. *Molecular Cell*, **2009**, 36, 682-95	17.6	232
123	SCL and associated proteins distinguish active from repressive GATA transcription factor complexes. *Blood*, **2009**, 113, 2191-201	2.2	142
122	It takes (LMO) 2 to tango. *Blood*, **2009**, 113, 5693	2.2	
121	Genome analysis of the platypus reveals unique signatures of evolution. *Nature*, **2008**, 453, 175-83	50.4	545
120	Human-macaque comparisons illuminate variation in neutral substitution rates. *Genome Biology*, **2008**, 9, R76	18.3	44
119	Exponential decay of GC content detected by strand-symmetric substitution rates influences the evolution of isochore structure. *Molecular Biology and Evolution*, **2008**, 25, 362-74	8.3	22
118	A GATA-1-regulated microRNA locus essential for erythropoiesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 3333-8	11.5	268
117	A T-to-G transversion at nucleotide -567 upstream of HBG2 in a GATA-1 binding motif is associated with elevated hemoglobin F. *Molecular and Cellular Biology*, **2008**, 28, 4386-93	4.8	33
116	An iron responsive element-like stem-loop regulates alpha-hemoglobin-stabilizing protein mRNA. *Journal of Biological Chemistry*, **2008**, 283, 26956-64	5.4	39
115	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. *Genome Research*, **2008**, 18, 1896-905	9.7	28
114	Evolutionary and biomedical insights from the rhesus macaque genome. *Science*, **2007**, 316, 222-34	33.3	1072
113	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Research*, **2007**, 17, 760-74	9.7	163

112	Finding cis-regulatory elements using comparative genomics: some lessons from ENCODE data. *Genome Research*, **2007**, 17, 775-86	9.7	61
111	PhenCode: connecting ENCODE data with mutations and phenotype. *Human Mutation*, **2007**, 28, 554-62	4.7	72
110	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
109	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. *Genome Research*, **2007**, 17, 1797-808	9.7	204
108	A framework for collaborative analysis of ENCODE data: making large-scale analyses biologist-friendly. *Genome Research*, **2007**, 17, 960-4	9.7	105
107	Experimental validation of predicted mammalian erythroid cis-regulatory modules. *Genome Research*, **2006**, 16, 1480-92	9.7	49
106	ESPERR: learning strong and weak signals in genomic sequence alignments to identify functional elements. *Genome Research*, **2006**, 16, 1596-604	9.7	97
105	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. *Genome Research*, **2005**, 15, 1051-60	9.7	164
104	Mulan: multiple-sequence local alignment and visualization for studying function and evolution. *Genome Research*, **2005**, 15, 184-94	9.7	199
103	Evolution and functional classification of vertebrate gene deserts. *Genome Research*, **2005**, 15, 137-45	9.7	179
102	Galaxy: a platform for interactive large-scale genome analysis. *Genome Research*, **2005**, 15, 1451-5	9.7	1509
101	Regulatory potential scores from genome-wide three-way alignments of human, mouse, and rat. *Genome Research*, **2004**, 14, 700-7	9.7	84
100	Patterns of insertions and their covariation with substitutions in the rat, mouse, and human genomes. *Genome Research*, **2004**, 14, 517-27	9.7	60
99	zPicture: dynamic alignment and visualization tool for analyzing conservation profiles. *Genome Research*, **2004**, 14, 472-7	9.7	119
98	Comparative analysis of the alpha-like globin clusters in mouse, rat, and human chromosomes indicates a mechanism underlying breaks in conserved synteny. *Genome Research*, **2004**, 14, 623-30	9.7	26
97	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004** , 428, 493-521	50.4	1689
96	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature*, **2004**, 432, 695-716	50.4	2143
95	Comparative genomics. *Annual Review of Genomics and Human Genetics*, **2004**, 5, 15-56	9.7	136

94	The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science*, **2004**, 306, 636-40	33.3	1692
93	Human-mouse alignments with BLASTZ. *Genome Research*, **2003**, 13, 103-7	9.7	920
92	Comparative genomics. *PLoS Biology*, **2003**, 1, E58	9.7	187
91	Global predictions and tests of erythroid regulatory regions. *Cold Spring Harbor Symposia on Quantitative Biology*, **2003**, 68, 335-44	3.9	6
90	Fishing for evolutionary clues to globin gene regulation. *Blood*, **2003**, 101, 2451-2451	2.2	
89	Covariation in frequencies of substitution, deletion, transposition, and recombination during eutherian evolution. *Genome Research*, **2003**, 13, 13-26	9.7	234
88	A complex chromatin landscape revealed by patterns of nuclease sensitivity and histone modification within the mouse beta-globin locus. *Molecular and Cellular Biology*, **2003**, 23, 5234-44	4.8	139
87	MultiPipMaker and supporting tools: Alignments and analysis of multiple genomic DNA sequences. *Nucleic Acids Research*, **2003**, 31, 3518-24	20.1	174
86	Cross-species sequence comparisons: a review of methods and available resources. *Genome Research*, **2003**, 13, 1-12	9.7	170
85	GALA, a database for genomic sequence alignments and annotations. *Genome Research*, **2003**, 13, 732-41	9.7	39
84	Distinguishing regulatory DNA from neutral sites. *Genome Research*, **2003**, 13, 64-72	9.7	103
83	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. *Human Mutation*, **2002**, 19, 225-33	4.7	354
82	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
81	PipTools: a computational toolkit to annotate and analyze pairwise comparisons of genomic sequences. *Genomics*, **2002**, 80, 681-90	4.3	28
80	Functional and binding studies of HS3.2 of the beta-globin locus control region. *Gene*, **2002**, 283, 185-97	3.8	9
79	Association between divergence and interspersed repeats in mammalian noncoding genomic DNA. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 14503-8	11.5	33
78	A negative cis-element regulates the level of enhancement by hypersensitive site 2 of the beta-globin locus control region. *Journal of Biological Chemistry*, **2001**, 276, 6289-98	5.4	16
77	Comparative genome analysis delimits a chromosomal domain and identifies key regulatory elements in the alpha globin cluster. *Human Molecular Genetics*, **2001**, 10, 371-82	5.6	125

76	New views of evolution and regulation of vertebrate beta-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, 1327-9	11.5	19
75	Databases of human hemoglobin variants and other resources at the globin gene server. *Hemoglobin*, **2001**, 25, 183-93	0.6	31
74	Sequences flanking hypersensitive sites of the beta-globin locus control region are required for synergistic enhancement. *Molecular and Cellular Biology*, **2001**, 21, 2969-80	4.8	47
73	Characterization of a widely expressed gene (LUC7-LIKE; LUC7L) defining the centromeric boundary of the human alpha-globin domain. *Genomics*, **2001**, 71, 307-14	4.3	25
72	Conserved noncoding sequences are reliable guides to regulatory elements. *Trends in Genetics*, **2000**, 16, 369-72	8.5	347
71	Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta-globin gene clusters. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 14560-5	11.5	68
70	PipMaker--a web server for aligning two genomic DNA sequences. *Genome Research*, **2000**, 10, 577-86	9.7	906
69	Levels of GATA-1/GATA-2 transcription factors modulate expression of embryonic and fetal hemoglobins. *Gene*, **2000**, 261, 277-87	3.8	53
68	Comparison of five methods for finding conserved sequences in multiple alignments of gene regulatory regions. *Nucleic Acids Research*, **1999**, 27, 3899-910	20.1	69
67	Efficient and reliable transfection of mouse erythroleukemia cells using cationic lipids. *Blood Cells, Molecules, and Diseases*, **1999**, 25, 299-304	2.1	11
66	The Evolution of Hemoglobin. *American Scientist*, **1999**, 87, 126	2.7	33
65	Access to a syllabus of human hemoglobin variants (1996) via the World Wide Web. *Hemoglobin*, **1998**, 22, 113-27	0.6	63
64	Electronic access to sequence alignments, experimental results, and human mutations as an aid to studying globin gene regulation. *Genomics*, **1998**, 47, 429-37	4.3	35
63	A database of experimental results on globin gene expression. *Genomics*, **1998**, 53, 325-37	4.3	12
62	Multiple regulatory elements in the 5Pflanking sequence of the human epsilon-globin gene. *Journal of Biological Chemistry*, **1998**, 273, 10202-9	5.4	19
61	Hemoglobins from bacteria to man: evolution of different patterns of gene expression. *Journal of Experimental Biology*, **1998**, 201, 1099-117	3	198
60	An electronic database of human hemoglobin variants on the World Wide Web. *Blood*, **1998**, 91, 2643-4	2.2	17
59	Description and targeted deletion of 5Phypersensitive site 5 and 6 of the mouse beta-globin locus control region. *Blood*, **1998**, 92, 4394-403	2.2	32

58	Conserved E boxes function as part of the enhancer in hypersensitive site 2 of the beta-globin locus control region. Role of basic helix-loop-helix proteins. *Journal of Biological Chemistry*, **1997**, 272, 369-78	5.4	70
57	Long human-mouse sequence alignments reveal novel regulatory elements: a reason to sequence the mouse genome. *Genome Research*, **1997**, 7, 959-66	9.7	268
56	CpG islands from the alpha-globin gene cluster increase gene expression in an integration-dependent manner. *Molecular and Cellular Biology*, **1997**, 17, 5856-66	4.8	15
55	The complete sequences of the galago and rabbit beta-globin locus control regions: extended sequence and functional conservation outside the cores of DNase hypersensitive sites. *Genomics*, **1997**, 39, 90-4	4.3	34
54	Locus control regions of mammalian beta-globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. *Gene*, **1997**, 205, 73-94	3.8	207
53	Phylogenetic footprinting of hypersensitive site 3 of the beta-globin locus control region. *Blood*, **1997**, 89, 3457-69	2.2	11
52	Restoration of the CCAAT box or insertion of the CACCC motif activates [corrected] delta-globin gene expression. *Blood*, **1997**, 90, 421-7	2.2	11
51	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, 5675-9	11.5	291
50	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, 4327-35	20.1	22
49	Role of DNA sequences outside the cores of DNase hypersensitive sites (HSs) in functions of the beta-globin locus control region. Domain opening and synergism between HS2 and HS3. *Journal of Biological Chemistry*, **1996**, 271, 11871-8	5.4	46
48	Flanking and intragenic sequences regulating the expression of the rabbit alpha-globin gene. *Journal of Biological Chemistry*, **1995**, 270, 3965-73	5.4	14
47	Constructing aligned sequence blocks. *Journal of Computational Biology*, **1994**, 1, 51-64	1.7	7
46	Expression of the large plastid gene, ORF2280, in tomato fruits and flowers. *Current Genetics*, **1994**, 26, 494-6	2.9	5
45	Globin gene server: a prototype E-mail database server featuring extensive multiple alignments and data compilation for electronic genetic analysis. *Genomics*, **1994**, 21, 344-53	4.3	31
44	Chaining multiple-alignment blocks. *Journal of Computational Biology*, **1994**, 1, 217-26	1.7	19
43	Recent developments in linear-space alignment methods: a survey. *Journal of Computational Biology*, **1994**, 1, 271-91	1.7	37
42	Comparative analysis of the locus control region of the rabbit beta-like gene cluster: HS3 increases transient expression of an embryonic epsilon-globin gene. *Nucleic Acids Research*, **1993**, 21, 1265-72	20.1	44
41	Use of long sequence alignments to study the evolution and regulation of mammalian globin gene clusters. *Molecular Biology and Evolution*, **1993**, 10, 73-102	8.3	58

40	Constrained sequence alignment. *Bulletin of Mathematical Biology*, **1993**, 55, 503-24	2.1	9
39	The 5Pends of LINE1 repeats in rabbit DNA define subfamilies and reveal a short sequence conserved between rabbits and humans. *Genomics*, **1992**, 14, 320-31	4.3	17
38	Analysis of conserved domains and sequence motifs in cellular regulatory proteins and locus control regions using new software tools for multiple alignment and visualization. *The New Biologist*, **1992**, 4, 247-60		12
37	Survey of plastid RNA abundance during tomato fruit ripening: the amounts of RNA from the ORF 2280 region increase in chromoplasts. *Plant Molecular Biology*, **1991**, 17, 1179-88	4.6	13
36	Software tools for analyzing pairwise alignments of long sequences. *Nucleic Acids Research*, **1991**, 19, 4663-7	20.1	30
35	Localization of the alpha-like globin gene cluster to region q12 of rabbit chromosome 6 by in situ hybridization. *Genomics*, **1991**, 9, 362-5	4.3	14
34	Sequence and comparative analysis of the rabbit alpha-like globin gene cluster reveals a rapid mode of evolution in a G + C-rich region of mammalian genomes. *Journal of Molecular Biology*, **1991**, 222, 233-49	6.5	38
33	An apparent pause site in the transcription unit of the rabbit alpha-globin gene. *Journal of Molecular Biology*, **1991**, 220, 255-70	6.5	14
32	Subfamily relationships and clustering of rabbit C repeats. *Molecular Biology and Evolution*, **1991**, 8, 1-30	8.3	26
31	Restriction site and genetic map of Cucurbita pepo chloroplast DNA. *Current Genetics*, **1990**, 18, 273-5	2.9	9
30	Short interspersed repeats in rabbit DNA can provide functional polyadenylation signals. *Molecular Biology and Evolution*, **1990**, 7, 1-8	8.3	18
29	Localization of the beta-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, 157-61	1.9	13
28	Unique sequence organization and erythroid cell-specific nuclear factor-binding of mammalian theta 1 globin promoters. *Nucleic Acids Research*, **1989**, 17, 5687-700	20.1	36
27	The L1 family of long interspersed repetitive DNA in rabbits: sequence, copy number, conserved open reading frames, and similarity to keratin. *Journal of Molecular Evolution*, **1989**, 29, 3-19	3.1	33
26	Complete nucleotide sequence of the rabbit beta-like globin gene cluster. Analysis of intergenic sequences and comparison with the human beta-like globin gene cluster. *Journal of Molecular Biology*, **1989**, 205, 15-40	6.5	75
25	The rabbit alpha-like globin gene cluster is polymorphic both in the sizes of BamHI fragments and in the numbers of duplicated sets of genes. *Molecular Biology and Evolution*, **1988**, 5, 486-98	8.3	4
24	Nucleotide sequence and expression of rabbit globin genes zeta 1, zeta 2, and zeta 3. Pseudogenes generated by block duplications are transcriptionally competent. *Journal of Biological Chemistry*, **1988**, 263, 9981-93	5.4	15
23	Block duplications of a zeta-zeta-alpha-theta gene set in the rabbit alpha-like globin gene cluster. *Journal of Biological Chemistry*, **1987**, 262, 5414-21	5.4	11

22	Rabbit alpha-like and beta-like globin gene clusters: comparisons among mammalian globin gene clusters. *Progress in Clinical and Biological Research*, **1987**, 251, 91-105		1
21	A previously undetected pseudogene in the human alpha globin gene cluster. *Nucleic Acids Research*, **1986**, 14, 1903-11	20.1	55
20	Restriction enzyme analysis of tomato chloroplast and chromoplast DNA. *Plant Physiology*, **1986**, 82, 1145-7	6.6	22
19	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	8.3	28
18	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	8.3	16
17	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	5.4	58
16	Variability within the rabbit C repeats and sequences shared with other SINES. *Nucleic Acids Research*, **1985**, 13, 1073-88	20.1	23
15	DNase I and nuclease S1 sensitivity of the rabbit beta 1 globin gene in nuclei and in supercoiled plasmids. *Journal of Molecular Biology*, **1985**, 184, 195-210	6.5	25
14	Rabbit globin pseudogene psi beta 2 is a hybrid of delta- and beta-globin gene sequences. *Molecular Biology and Evolution*, **1984**, 1, 302-16	8.3	22
13	The rabbit C family of short, interspersed repeats. Nucleotide sequence determination and transcriptional analysis. *Journal of Molecular Biology*, **1984**, 176, 1-20	6.5	52
12	Comparison of the beta-like globin gene families of rabbits and humans indicates that the gene cluster 5Pepsilon-gamma-delta-beta-3Ppredates the mammalian radiation. *Molecular Biology and Evolution*, **1984**, 1, 390-410	8.3	41
11	Analysis of rabbit beta-like globin gene transcripts during development. *Journal of Molecular Biology*, **1983**, 164, 395-417	6.5	25
10	The nucleotide sequence of the rabbit embryonic globin gene beta 4. *Journal of Biological Chemistry*, **1983**, 258, 8739-44	5.4	35
9	The nucleotide sequence of rabbit embryonic globin gene beta 3. *Journal of Biological Chemistry*, **1981**, 256, 11780-6	5.4	29
8	The linkage arrangement of four rabbit beta-like globin genes. *Cell*, **1979**, 18, 1273-83	56.2	131
7	The structure and transcription of four linked rabbit beta-like globin genes. *Cell*, **1979**, 18, 1285-97	56.2	159
6	The isolation of structural genes from libraries of eucaryotic DNA. *Cell*, **1978**, 15, 687-701	56.2	1870
5	Histone neighbors in nuclei and extended chromatin. *Cell*, **1977**, 12, 417-27	56.2	39

4	Synthesis of affinity labels for steroid-receptor proteins. *Methods in Enzymology*, **1975**, 36, 411-26	1.7	1
3	An approach to histone nearest neighbours in extended chromatin. *Nucleic Acids Research*, **1975**, 2, 1751-70	2.01	39
2	Genome-wide comparative analysis reveals human- mouse regulatory landscape and evolution		3
1	Domain adaptive neural networks improve cross-species prediction of transcription factor binding		2