Evolutionarily conserved elements in vertebrate, insect

Genome Research

15, 1034-1050

DOI: 10.1101/gr.3715005

Citation Report

#	Article	IF	Citations
3	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	13.7	2,215
4	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. Genome Research, 2005, 15, 1051-1060.	2.4	185
5	A retrocopy of a gene can functionally displace the source gene in evolution. Nucleic Acids Research, 2005, 33, 6654-6661.	6.5	41
6	Transposon-free regions in mammalian genomes. Genome Research, 2005, 16, 164-172.	2.4	102
7	Evaluation of the RET regulatory landscape reveals the biological relevance of a HSCR-implicated enhancer. Human Molecular Genetics, 2005, 14, 3837-3845.	1.4	75
8	Histone hyperacetylated domains across the Ifng gene region in natural killer cells and T cells. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17095-17100.	3.3	79
9	Gene regulatory networks. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4935-4935.	3.3	225
10	Structure and function of the human genome. Genome Research, 2005, 15, 1759-1766.	2.4	38
11	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	2.4	1,795
12	Sequence features in regions of weak and strong linkage disequilibrium. Genome Research, 2005, 15, 1519-1534.	2.4	89
13	Gene function and expression level influence the insertion/fixation dynamics of distinct transposon families in mammalian introns. Genome Biology, 2006, 7, R120.	13.9	28
14	Patterns of sequence conservation in presynaptic neural genes. Genome Biology, 2006, 7, R105.	13.9	21
15	Primate-specific evolution of an LDLR enhancer. Genome Biology, 2006, 7, R68.	13.9	16
16	Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage. Genome Biology, 2006, 7, R56.	13.9	41
17	Genome-wide computational prediction of transcriptional regulatory modules reveals new insights into human gene expression. Genome Research, 2006, 16, 656-668.	2.4	229
18	A Chromosomal Rearrangement Hotspot Can Be Identified from Population Genetic Variation and Is Coincident with a Hotspot for Allelic Recombination. American Journal of Human Genetics, 2006, 79, 890-902.	2.6	92
19	Evaluating the biological relevance of putative enhancers using Tol2 transposon-mediated transgenesis in zebrafish. Nature Protocols, 2006, 1, 1297-1305.	5.5	235
20	Transposable element derived DNaseI-hypersensitive sites in the human genome. Biology Direct, 2006, 1, 20.	1.9	33

#	Article	IF	Citations
21	Transcriptional Regulatory Elements in the Human Genome. Annual Review of Genomics and Human Genetics, 2006, 7, 29-59.	2.5	724
22	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. Science, 2006, 311, 392-394.	6.0	519
23	Identifying transcription factor functions and targets by phenotypic activation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12045-12050.	3.3	156
24	Control of Developmental Regulators by Polycomb in Human Embryonic Stem Cells. Cell, 2006, 125, 301-313.	13.5	2,059
25	Functional variation and evolution of non-coding DNA. Current Opinion in Genetics and Development, 2006, 16, 559-564.	1.5	48
26	Identification and analysis of putative regulatory sequences for the MYF5/MYF6 locus in different vertebrate species. Gene, 2006, 379, 141-147.	1.0	33
27	Non-coding RNA. Human Molecular Genetics, 2006, 15, R17-R29.	1.4	2,052
28	Graemlin: General and robust alignment of multiple large interaction networks. Genome Research, 2006, 16, 1169-1181.	2.4	274
29	The first radiation hybrid map of a perch-like fish: The gilthead seabream (Sparus aurata L). Genomics, 2006, 87, 793-800.	1.3	59
30	Genomics of the evolutionary process. Trends in Ecology and Evolution, 2006, 21, 316-321.	4.2	26
31	Functional single nucleotide polymorphism-based association studies. Human Genomics, 2006, 2, 391.	1.4	25
32	Signatures of adaptive evolution within human non-coding sequence. Human Molecular Genetics, 2006, 15, R170-R175.	1.4	45
34	Genomic organization, alternative splicing, and multiple regulatory regions of the zebrafish fgf8 gene. Development Growth and Differentiation, 2006, 48, 447-462.	0.6	27
35	Conserved noncoding sequences are selectively constrained and not mutation cold spots. Nature Genetics, 2006, 38, 223-227.	9.4	214
36	A common genetic variant in the NOS1 regulator NOS1AP modulates cardiac repolarization. Nature Genetics, 2006, 38, 644-651.	9.4	500
37	Mammalian ultraconserved elements are strongly depleted among segmental duplications and copy number variants. Nature Genetics, 2006, 38, 1216-1220.	9.4	105
38	Genome-wide analysis of estrogen receptor binding sites. Nature Genetics, 2006, 38, 1289-1297.	9.4	1,227
39	A distal enhancer and an ultraconserved exon are derived from a novel retroposon. Nature, 2006, 441, 87-90.	13.7	452

#	Article	IF	Citations
40	A novel class of small RNAs bind to MILI protein in mouse testes. Nature, 2006, 442, 203-207.	13.7	1,303
41	An RNA gene expressed during cortical development evolved rapidly in humans. Nature, 2006, 443, 167-172.	13.7	884
42	The value of gene-based selection of tag SNPs in genome-wide association studies. European Journal of Human Genetics, 2006, 14, 1209-1214.	1.4	18
43	The expanding transcriptome: the genome as the â€˜Book of Sandâ€™. EMBO Journal, 2006, 25, 923-931.	3.5	78
44	Evolution of cis-regulatory sequence and function in Diptera. Heredity, 2006, 97, 139-147.	1.2	69
45	A novel trinucleotide repeat expansion at chromosome 3q26.2 identified by a CAG/CTG repeat expansion detection array. Human Genetics, 2006, 120, 193-200.	1.8	1
46	K-SPMM: a database of murine spermatogenic promoters modules & motifs. BMC Bioinformatics, 2006, 7, 238.	1.2	6
47	A hidden Markov model approach for determining expression from genomic tiling micro arrays. BMC Bioinformatics, 2006, 7, 239.	1.2	24
48	XRate: a fast prototyping, training and annotation tool for phylo-grammars. BMC Bioinformatics, 2006, 7, 428.	1.2	49
49	CpGcluster: a distance-based algorithm for CpG-island detection. BMC Bioinformatics, 2006, 7, 446.	1.2	155
50	GONOME: measuring correlations between GO terms and genomic positions. BMC Bioinformatics, 2006, 7, 94.	1.2	14
51	Conservation of alternative polyadenylation patterns in mammalian genes. BMC Genomics, 2006, 7, 189.	1.2	47
52	Evolution and comparative analysis of the MHC Class III inflammatory region. BMC Genomics, 2006, 7, 281.	1.2	54
53	Genome-wide sequence and functional analysis of early replicating DNA in normal human fibroblasts. BMC Genomics, 2006, 7, 301.	1.2	15
54	Further understanding human disease genes by comparing with housekeeping genes and other genes. BMC Genomics, 2006, 7, 31.	1.2	126
55	A comparative analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors. Nucleic Acids Research, 2006, 34, e146-e146.	6.5	59
56	Identification of the REST regulon reveals extensive transposable element-mediated binding site duplication. Nucleic Acids Research, 2006, 34, 3862-3877.	6.5	121
57	Genome-wide identification of peroxisome proliferator response elements using integrated computational genomics. Journal of Lipid Research, 2006, 47, 1583-1587.	2.0	123

#	Article	IF	Citations
58	CisView: A Browser and Database of cis-regulatory Modules Predicted in the Mouse Genome. DNA Research, 2006, 13, 123-134.	1.5	28
59	The UCSC Genome Browser Database: update 2006. Nucleic Acids Research, 2006, 34, D590-D598.	6.5	1,156
60	FootPrinter3: phylogenetic footprinting in partially alignable sequences. Nucleic Acids Research, 2006, 34, W617-W620.	6.5	23
61	MicroRNA enrichment among short 'ultraconserved' sequences in insects. Nucleic Acids Research, 2006, 34, e65-e65.	6.5	15
62	ProMiR II: a web server for the probabilistic prediction of clustered, nonclustered, conserved and nonconserved microRNAs. Nucleic Acids Research, 2006, 34, W455-W458.	6.5	68
63	CEAS: cis-regulatory element annotation system. Nucleic Acids Research, 2006, 34, W551-W554.	6.5	170
64	Zfp206 regulates ES cell gene expression and differentiation. Nucleic Acids Research, 2006, 34, 4780-4790.	6.5	45
65	snoSeeker: an advanced computational package for screening of guide and orphan snoRNA genes in the human genome. Nucleic Acids Research, 2006, 34, 5112-5123.	6.5	112
66	Functional noncoding sequences derived from SINEs in the mammalian genome. Genome Research, 2006, 16, 864-874.	2.4	207
67	Experimental validation of predicted mammalian erythroid cis-regulatory modules. Genome Research, 2006, 16, 1480-1492.	2.4	56
68	Advances in the Discovery of cis-Regulatory Elements. Current Bioinformatics, 2006, 1, 321-336.	0.7	10
69	Computational analysis of tissue-specific combinatorial gene regulation: predicting interaction between transcription factors in human tissues. Nucleic Acids Research, 2006, 34, 4925-4936.	6.5	134
70	ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements. Genome Research, 2006, 16, 1596-1604.	2.4	111
71	Genome-Wide Identification of Human Functional DNA Using a Neutral Indel Model. PLoS Computational Biology, 2006, 2, e5.	1.5	157
72	Genomic Selective Constraints in Murid Noncoding DNA. PLoS Genetics, 2006, 2, e204.	1.5	60
73	Evolution at the nucleotide level: the problem of multiple whole-genome alignment. Human Molecular Genetics, 2006, 15, R51-R56.	1.4	51
74	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33.	1.5	439
75	Forces Shaping the Fastest Evolving Regions in the Human Genome. PLoS Genetics, 2006, 2, e168.	1.5	399

#	Article	IF	Citations
76	A Genomics Approach to the Study of Ancient Polyploidy and Floral Developmental Genetics. Advances in Botanical Research, 2006, 44, 527-549.	0.5	5
77	SPA: A Probabilistic Algorithm for Spliced Alignment. PLoS Genetics, 2006, 2, e24.	1.5	21
78	Upf1/Upf2 Regulation of 3â€² Untranslated Region Splice Variants of AUF1 Links Nonsense-Mediated and A+U-Rich Element-Mediated mRNA Decay. Molecular and Cellular Biology, 2006, 26, 8743-8754.	1.1	27
79	Conserved distances between vertebrate highly conserved elements. Human Molecular Genetics, 2006, 15, 2911-2922.	1.4	28
80	Identifying cis-regulatory modules by combining comparative and compositional analysis of DNA. Bioinformatics, 2006, 22, 2858-2864.	1.8	33
81	Polymorphisms in the Glucokinase-Associated, Dual-Specificity Phosphatase 12 (DUSP12) Gene Under Chromosome 1q21 Linkage Peak Are Associated With Type 2 Diabetes. Diabetes, 2006, 55, 2631-2639.	0.3	27
82	Hairpins in a Haystack: recognizing microRNA precursors in comparative genomics data. Bioinformatics, 2006, 22, e197-e202.	1.8	180
83	Candidate Single Nucleotide Polymorphism Selection using Publicly Available Tools: A Guide for Epidemiologists. American Journal of Epidemiology, 2006, 164, 794-804.	1.6	49
84	Scale-invariant structure of strongly conserved sequence in genomic intersections and alignments. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13121-13125.	3.3	21
85	A family of conserved noncoding elements derived from an ancient transposable element. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11659-11664.	3.3	64
86	Identifying gene regulatory elements by genomic microarray mapping of DNaseI hypersensitive sites. Genome Research, 2006, 16, 1310-1319.	2.4	34
87	Scan of Human Genome Reveals No New Loci Under Ancient Balancing Selection. Genetics, 2006, 173, 2165-2177.	1.2	117
88	Ubiquitous selective constraints in the Drosophila genome revealed by a genome-wide interspecies comparison. Genome Research, 2006, 16, 875-884.	2.4	217
89	Locating mammalian transcription factor binding sites: A survey of computational and experimental techniques. Genome Research, 2006, 16, 1455-1464.	2.4	188
90	Lateral Transfer: A Survey and New Developments. Israel Journal of Ecology and Evolution, 2006, 52, 443-459.	0.2	1
91	Unraveling transcription regulatory networks by protein-DNA and protein-protein interaction mapping. Genome Research, 2006, 16, 1445-1454.	2.4	136
92	Transgenic analysis of Dlx regulation in fish tooth development reveals evolutionary retention of enhancer function despite organ loss. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19390-19395.	3.3	57
93	Klf4 and corticosteroids activate an overlapping set of transcriptional targets to accelerate in utero epidermal barrier acquisition. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18668-18673.	3.3	66

#	Article	IF	Citations
94	Challenges of SNP genotyping and genetic variation: its future role in diagnosis and treatment of cancer. Expert Review of Molecular Diagnostics, 2006, 6, 319-331.	1.5	73
95	The colorectal microRNAome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3687-3692.	3.3	890
96	A high-resolution map of transcription in the yeast genome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5320-5325.	3.3	613
97	The landscape of histone modifications across 1% of the human genome in five human cell lines. Genome Research, 2007, 17, 691-707.	2.4	353
98	Computation and Analysis of Genomic Multi-Sequence Alignments. Annual Review of Genomics and Human Genetics, 2007, 8, 193-213.	2.5	30
99	Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7145-7150.	3.3	272
100	miRRim: A novel system to find conserved miRNAs with high sensitivity and specificity. Rna, 2007, 13, 2081-2090.	1.6	51
101	A gene regulatory network in mouse embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16438-16443.	3.3	246
102	VISTA Enhancer Browser--a database of tissue-specific human enhancers. Nucleic Acids Research, 2007, 35, D88-D92.	6.5	950
103	Non-EST-based prediction of novel alternatively spliced cassette exons with cell signaling function in Caenorhabditis elegans and human. Nucleic Acids Research, 2007, 35, 3192-3202.	6.5	11
104	Thousands of human mobile element fragments undergo strong purifying selection near developmental genes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8005-8010.	3.3	219
105	Analysis of Sequence Conservation at Nucleotide Resolution. PLoS Computational Biology, 2007, 3, e254.	1.5	65
106	Identification and Characterization of Cell Typeâ€“Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. PLoS Genetics, 2007, 3, e136.	1.5	196
107	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	2.4	237
108	RankMotif++: a motif-search algorithm that accounts for relative ranks of K-mers in binding transcription factors. Bioinformatics, 2007, 23, i72-i79.	1.8	52
109	Divergent Evolution of Human p53 Binding Sites: Cell Cycle Versus Apoptosis. PLoS Genetics, 2007, 3, e127.	1.5	88
110	Integration of Genome and Chromatin Structure with Gene Expression Profiles To Predict c-MYC Recognition Site Binding and Function. PLoS Computational Biology, 2007, 3, e63.	1.5	27
111	A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms. PLoS Computational Biology, 2007, 3, e106.	1.5	24

#	Article	IF	Citations
112	Ancient Exaptation of a CORE-SINE Retroposon into a Highly Conserved Mammalian Neuronal Enhancer of the Proopiomelanocortin Gene. PLoS Genetics, 2007, 3, e166.	1.5	114
113	A Macaque's-Eye View of Human Insertions and Deletions: Differences in Mechanisms. PLoS Computational Biology, 2007, 3, e176.	1.5	55
114	Adaptive Evolution of Conserved Noncoding Elements in Mammals. PLoS Genetics, 2007, 3, e147.	1.5	79
115	Genome Organization and Gene Expression Shape the Transposable Element Distribution in the Drosophila melanogaster Euchromatin. PLoS Genetics, 2007, 3, e210.	1.5	55
116	Genetic Screening of Leber Congenital Amaurosis in a Large Consanguineous Iranian Family. Ophthalmic Genetics, 2007, 28, 224-228.	0.5	7
117	Whole-Genome Cartography of Estrogen Receptor Î± Binding Sites. PLoS Genetics, 2007, 3, e87.	1.5	400
118	The ENCODE Project at UC Santa Cruz. Nucleic Acids Research, 2007, 35, D663-D667.	6.5	92
119	NATsDB: Natural Antisense Transcripts DataBase. Nucleic Acids Research, 2007, 35, D156-D161.	6.5	54
120	The UCSC genome browser database: update 2007. Nucleic Acids Research, 2007, 35, D668-D673.	6.5	260
121	DroSpeGe: rapid access database for new Drosophila species genomes. Nucleic Acids Research, 2007, 35, D480-D485.	6.5	43
122	Biased clustered substitutions in the human genome: The footprints of male-driven biased gene conversion. Genome Research, 2007, 17, 1420-1430.	2.4	93
123	Raising the estimate of functional human sequences: Figure 1.. Genome Research, 2007, 17, 1245-1253.	2.4	217
124	Revisiting the protein-coding gene catalog of Drosophila melanogaster using 12 fly genomes. Genome Research, 2007, 17, 1823-1836.	2.4	135
125	G-Boxes, Bigfoot Genes, and Environmental Response: Characterization of Intragenomic Conserved Noncoding Sequences in Arabidopsis. Plant Cell, 2007, 19, 1441-1457.	3.1	42
126	miRNAs. Organogenesis, 2007, 3, 25-33.	0.4	4
127	Systematic variation in mRNA 3â€²-processing signals during mouse spermatogenesis. Nucleic Acids Research, 2007, 35, 234-246.	6.5	114
128	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	2.4	150
129	Characterization and predictive discovery of evolutionarily conserved mammalian alternative promoters. Genome Research, 2007, 17, 145-155.	2.4	81

#	Article	IF	Citations
130	A novel syndrome of cerebral cavernous malformation and Greig cephalopolysyndactyly. Journal of Neurosurgery: Pediatrics, 2007, 107, 495-499.	0.8	7
131	Diploid genome reconstruction of Ciona intestinalis and comparative analysis with Ciona savignyi. Genome Research, 2007, 17, 1101-1110.	2.4	65
132	Genomic regulatory blocks underlie extensive microsynteny conservation in insects. Genome Research, 2007, 17, 1898-1908.	2.4	181
133	The Mathematics of Phylogenomics. SIAM Review, 2007, 49, 3-31.	4.2	34
134	Global analysis of exon creation versus loss and the role of alternative splicing in 17 vertebrate genomes. Rna, 2007, 13, 661-670.	1.6	114
135	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. Genome Research, 2007, 17, 839-851.	2.4	191
136	Mining and Predicting CpG islands. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	2
137	Efficient Enumeration of Phylogenetically Informative Substrings. Journal of Computational Biology, 2007, 14, 701-723.	0.8	2
138	The microRNA.org resource: targets and expression. Nucleic Acids Research, 2007, 36, D149-D153.	6.5	2,280
139	Scan Statistics With Weighted Observations. Journal of the American Statistical Association, 2007, 102, 595-602.	1.8	27
140	Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs. Genome Research, 2007, 17, 556-565.	2.4	632
141	Heterogeneous Rate of Protein Evolution in Serotonin Genes. Molecular Biology and Evolution, 2007, 24, 2707-2715.	3.5	19
142	Arabidopsis intragenomic conserved noncoding sequence. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3348-3353.	3.3	55
143	Comparison of Pax1/9 Locus Reveals 500-Myr-Old Syntenic Block and Evolutionary Conserved Noncoding Regions. Molecular Biology and Evolution, 2007, 24, 784-791.	3.5	23
144	Bmp2 Transcription in Osteoblast Progenitors Is Regulated by a Distant 3â€² Enhancer Located 156.3 Kilobases from the Promoter. Molecular and Cellular Biology, 2007, 27, 2934-2951.	1.1	70
145	Structural RNAs of known and unknown function identified in malaria parasites by comparative genomics and RNA analysis. Rna, 2007, 13, 1923-1939.	1.6	89
146	Identification of novel peptide hormones in the human proteome by hidden Markov model screening. Genome Research, 2007, 17, 320-327.	2.4	231
147	Mechanisms of primary and secondary estrogen target gene regulation in breast cancer cells. Nucleic Acids Research, 2007, 36, 76-93.	6.5	102

#	Article	IF	Citations
148	A 3â€² Enhancer Controls Snail Expression in Melanoma Cells. Cancer Research, 2007, 67, 6113-6120.	0.4	30
149	The UCSC Genome Browser Database: 2008 update. Nucleic Acids Research, 2007, 36, D773-D779.	6.5	459
150	Significant gene content variation characterizes the genomes of inbred mouse strains. Genome Research, 2007, 17, 1743-1754.	2.4	89
151	Genetic Influences on Preterm Birth. Seminars in Reproductive Medicine, 2007, 25, 040-051.	0.5	53
152	Ultraconserved elements are associated with homeostatic control of splicing regulators by alternative splicing and nonsense-mediated decay. Genes and Development, 2007, 21, 708-718.	2.7	470
153	Reliable prediction of regulator targets using 12 Drosophila genomes. Genome Research, 2007, 17, 1919-1931.	2.4	141
154	New Approaches to Phylogenetic Tree Search and Their Application to Large Numbers of Protein Alignments. Systematic Biology, 2007, 56, 727-740.	2.7	30
155	Haplotype Analysis of CYP11A1 Identifies Promoter Variants Associated with Breast Cancer Risk. Cancer Research, 2007, 67, 5673-5682.	0.4	15
156	Universal patterns of purifying selection at noncoding positions in bacteria. Genome Research, 2008, 18, 148-160.	2.4	55
157	Breed relationships facilitate fine-mapping studies: A 7.8-kb deletion cosegregates with Collie eye anomaly across multiple dog breeds. Genome Research, 2007, 17, 1562-1571.	2.4	133
158	Life-history traits drive the evolutionary rates of mammalian coding and noncoding genomic elements. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20443-20448.	3.3	97
159	Purifying Selection Maintains Highly Conserved Noncoding Sequences in Drosophila. Molecular Biology and Evolution, 2007, 24, 2222-2234.	3.5	63
160	PDE4B5, a Novel, Super-Short, Brain-Specific cAMP Phosphodiesterase-4 Variant Whose Isoform-Specifying N-Terminal Region Is Identical to That of cAMP Phosphodiesterase-4D6 (PDE4D6). Journal of Pharmacology and Experimental Therapeutics, 2007, 322, 600-609.	1.3	65
161	Multiple sequence alignment: In pursuit of homologous DNA positions. Genome Research, 2007, 17, 127-135.	2.4	115
162	Evolutionary dynamics of transposable elements in the short-tailed opossum Monodelphis domestica. Genome Research, 2007, 17, 992-1004.	2.4	137
163	COMPARING SEQUENCE AND EXPRESSION FOR PREDICTING microRNA TARGETS USING GenMiR3. , 2007, , 52-63.		27
164	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2007, 17, Unit 1.4.	25.8	41
165	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	2.4	122

#	Article	IF	Citations
166	Enhancer identification through comparative genomics. Seminars in Cell and Developmental Biology, 2007, 18, 140-152.	2.3	97
167	Conserved interactions of a compact highly active enhancer/promoter upstream of the rhodopsin kinase (GRK1) gene. Genomics, 2007, 90, 236-248.	1.3	7
168	Characterization of 5â€² untranslated regions of the voltage-gated sodium channels SCN1A, SCN2A, and SCN3A and identification of cis-conserved noncoding sequences. Genomics, 2007, 90, 225-235.	1.3	29
169	Differential regulation of splicing, localization and stability of mammalian ARD1235 and ARD1225 isoforms. Biochemical and Biophysical Research Communications, 2007, 353, 18-25.	1.0	20
170	Analysis of the Vertebrate Insulator Protein CTCF-Binding Sites in the Human Genome. Cell, 2007, 128, 1231-1245.	13.5	910
171	SMAUG Is a Major Regulator of Maternal mRNA Destabilization in Drosophila and Its Translation Is Activated by the PAN GU Kinase. Developmental Cell, 2007, 12, 143-155.	3.1	280
172	Widely distributed noncoding purifying selection in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12410-12415.	3.3	84
173	Analysis of invariant sequences in 266 complete genomes. Gene, 2007, 401, 172-180.	1.0	10
174	Enriching the Analysis of Genomewide Association Studies with Hierarchical Modeling. American Journal of Human Genetics, 2007, 81, 397-404.	2.6	82
175	Arts Syndrome Is Caused by Loss-of-Function Mutations in PRPS1. American Journal of Human Genetics, 2007, 81, 507-518.	2.6	80
176	Origin and Evolution of Human microRNAs From Transposable Elements. Genetics, 2007, 176, 1323-1337.	1.2	311
177	Functional coordination of alternative splicing in the mammalian central nervous system. Genome Biology, 2007, 8, R108.	13.9	97
178	Fast-evolving noncoding sequences in the human genome. Genome Biology, 2007, 8, R118.	13.9	163
179	Measuring the accuracy of genome-size multiple alignments. Genome Biology, 2007, 8, R124.	13.9	34
180	Large-scale analysis of transcriptional cis-regulatory modules reveals both common features and distinct subclasses. Genome Biology, 2007, 8, R101.	13.9	64
181	Regulatory conservation of protein coding and microRNA genes in vertebrates: lessons from the opossum genome. Genome Biology, 2007, 8, R84.	13.9	26
182	Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. Genome Biology, 2007, 8, R15.	13.9	117
183	Retroviral enhancer detection insertions in zebrafish combined with comparative genomics reveal genomic regulatory blocks - a fundamental feature of vertebrate genomes. Genome Biology, 2007, 8, S4.	13.9	43

#	Article	IF	Citations
184	Detection of weakly conserved ancestral mammalian regulatory sequences by primate comparisons. Genome Biology, 2007, 8, R1.	13.9	59
185	SwissRegulon: a database of genome-wide annotations of regulatory sites. Nucleic Acids Research, 2007, 35, D127-D131.	6.5	123
186	Regulation of SHOOT MERISTEMLESS genes via an upstream-conserved noncoding sequence coordinates leaf development. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15953-15958.	3.3	67
187	Finding cis-regulatory modules in Drosophila using phylogenetic hidden Markov models. Bioinformatics, 2007, 23, 2031-2037.	1.8	9
188	Noncoding RNAs and RNA Editing in Brain Development, Functional Diversification, and Neurological Disease. Physiological Reviews, 2007, 87, 799-823.	13.1	275
189	Initial sequence and comparative analysis of the cat genome. Genome Research, 2007, 17, 1675-1689.	2.4	311
190	Accurate gene-tree reconstruction by learning gene- and species-specific substitution rates across multiple complete genomes. Genome Research, 2007, 17, 1932-1942.	2.4	73
191	Principles and Limitations of Computational MicroRNA Gene and Target Finding. DNA and Cell Biology, 2007, 26, 339-351.	0.9	84
192	Exact and Heuristic Algorithms for the Indel Maximum Likelihood Problem. Journal of Computational Biology, 2007, 14, 446-461.	0.8	33
193	Information Theoretic Distance Measures in Phylogenomics. , 2007, , .		1
194	A Haplotyping Algorithm for Non-recombinant Pedigree Data Containing Missing Members. , 2007, , .		0
195	Computational Identification of Protein-Coding Sequences by Comparative Analysis. , 2007, , .		1
196	Ribosomal frameshifting in decoding antizyme mRNAs from yeast and protists to humans: close to 300 cases reveal remarkable diversity despite underlying conservation. Nucleic Acids Research, 2007, 35, 1842-1858.	6.5	114
197	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
198	Novel expressed sequences identified in a model of androgen independent prostate cancer. BMC Genomics, 2007, 8, 32.	1.2	3
199	Repetitive Sequences in Complex Genomes: Structure and Evolution. Annual Review of Genomics and Human Genetics, 2007, 8, 241-259.	2.5	299
200	Functionalin Silico Analysis of Gene Regulatory Polymorphism. , 0, , 281-309.		1
201	Novel Crohn Disease Locus Identified by Genome-Wide Association Maps to a Gene Desert on 5p13.1 and Modulates Expression of PTGER4. PLoS Genetics, 2007, 3, e58.	1.5	506

#	Article	IF	Citations
202	A Family of Human MicroRNA Genes from Miniature Inverted-Repeat Transposable Elements. PLoS ONE, 2007, 2, e203.	1.1	264
203	Mammalian MicroRNA Prediction through a Support Vector Machine Model of Sequence and Structure. PLoS ONE, 2007, 2, e946.	1.1	51
204	Orthologous MicroRNA Genes Are Located in Cancer-Associated Genomic Regions in Human and Mouse. PLoS ONE, 2007, 2, e1133.	1.1	34
205	Gene-Centric Characteristics of Genome-Wide Association Studies. PLoS ONE, 2007, 2, e1262.	1.1	7
206	Identification of Novel Drosophila melanogaster MicroRNAs. PLoS ONE, 2007, 2, e1265.	1.1	22
207	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. Genome Research, 2007, 17, 775-786.	2.4	69
209	The relationship between non-protein-coding DNA and eukaryotic complexity. BioEssays, 2007, 29, 288-299.	1.2	578
210	Sequence variation in ultraconserved and highly conserved elements does not cause X-linked mental retardation. American Journal of Medical Genetics, Part A, 2007, 143A, 888-890.	0.7	5
211	Molecular genetic studies of DMT1 on 12q in Frenchâ€Canadian restless legs syndrome patients and families. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 911-917.	1.1	29
212	PhenCode: connecting ENCODE data with mutations and phenotype. Human Mutation, 2007, 28, 554-562.	1.1	79
213	On genomic coding theory. European Transactions on Telecommunications, 2007, 18, 873-879.	1.2	10
214	CONDOR: a database resource of developmentally associated conserved non-coding elements. BMC Developmental Biology, 2007, 7, 100.	2.1	60
215	Dynamic changes in histone-methylation 'marks' across the locus encoding interferon-Î³ during the differentiation of T helper type 2 cells. Nature Immunology, 2007, 8, 723-731.	7.0	155
216	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. Nature Methods, 2007, 4, 651-657.	9.0	1,254
217	Genome-wide transcription and the implications for genomic organization. Nature Reviews Genetics, 2007, 8, 413-423.	7.7	652
218	Recent and ongoing selection in the human genome. Nature Reviews Genetics, 2007, 8, 857-868.	7.7	446
219	Enrichment of HapMap recombination hotspot predictions around human nervous system genes: evidence for positive selection ?. European Journal of Human Genetics, 2007, 15, 1071-1078.	1.4	14
220	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	13.7	661

#	Article	IF	Citations
221	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
222	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	13.7	573
223	Comparative and physical mapping of 111 previously reported and 105 new porcine microsatellites. Animal Genetics, 2007, 38, 584-594.	0.6	0
224	A search engine to identify pathway genes from expression data on multiple organisms. BMC Systems Biology, 2007, 1, 20.	3.0	6
225	Considerations in the identification of functional RNA structural elements in genomic alignments. BMC Bioinformatics, 2007, 8, 33.	1.2	56
226	Statistical power of phylo-HMM for evolutionarily conserved element detection. BMC Bioinformatics, 2007, 8, 374.	1.2	10
227	How accurately is ncRNA aligned within whole-genome multiple alignments?. BMC Bioinformatics, 2007, 8, 417.	1.2	20
228	Identifications of conserved 7-mers in 3'-UTRs and microRNAs in Drosophila. BMC Bioinformatics, 2007, 8, 432.	1.2	12
229	Identification of tissue-specific cis-regulatory modules based on interactions between transcription factors. BMC Bioinformatics, 2007, 8, 437.	1.2	27
230	WeederH: an algorithm for finding conserved regulatory motifs and regions in homologous sequences. BMC Bioinformatics, 2007, 8, 46.	1.2	37
231	The nuclear OXPHOS genes in insecta: a common evolutionary origin, a common cis-regulatory motif, a common destiny for gene duplicates. BMC Evolutionary Biology, 2007, 7, 215.	3.2	39
233	Identifying dramatic selection shifts in phylogenetic trees. BMC Evolutionary Biology, 2007, 7, S10.	3.2	13
234	Detecting non-coding selective pressure in coding regions. BMC Evolutionary Biology, 2007, 7, S9.	3.2	26
235	Use of tiling array data and RNA secondary structure predictions to identify noncoding RNA genes. BMC Genomics, 2007, 8, 244.	1.2	12
236	Sequences conserved by selection across mouse and human malaria species. BMC Genomics, 2007, 8, 372.	1.2	9
237	Vertebrate conserved non coding DNA regions have a high persistence length and a short persistence time. BMC Genomics, 2007, 8, 398.	1.2	13
238	Computational RNomics of Drosophilids. BMC Genomics, 2007, 8, 406.	1.2	38
239	Maintenance of transposon-free regions throughout vertebrate evolution. BMC Genomics, 2007, 8, 470.	1.2	28

#	Article	IF	Citations
240	Protein Polymorphism Is Negatively Correlated with Conservation of Intronic Sequences and Complexity of Expression Patterns in Drosophila melanogaster. Journal of Molecular Evolution, 2007, 64, 511-518.	0.8	5
241	An Ancient Repeat Sequence in the ATP Synthase Î²-Subunit Gene of Forcipulate Sea Stars. Journal of Molecular Evolution, 2007, 65, 564-573.	0.8	7
242	Information and communication theory in molecular biology. Electrical Engineering, 2007, 90, 161-173.	1.2	10
243	A stochastic model for the evolution of transcription factor binding site abundance. Journal of Theoretical Biology, 2007, 247, 544-553.	0.8	8
244	Cancer-associated genomic regions (CAGRs) and noncoding RNAs: bioinformatics and therapeutic implications. Mammalian Genome, 2008, 19, 526-40.	1.0	65
245	Identification and characterization of new long conserved noncoding sequences in vertebrates. Mammalian Genome, 2008, 19, 703-712.	1.0	29
246	Folliculin mutations are not associated with severe COPD. BMC Medical Genetics, 2008, 9, 120.	2.1	15
247	Sequence variation in the human transcription factor gene POU5F1. BMC Genetics, 2008, 9, 15.	2.7	8
248	Genotype-phenotype correlations in MYCN-related Feingold syndrome. Human Mutation, 2008, 29, 1125-1132.	1.1	72
249	Familyâ€based SNP association study on 8q24 in bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 612-618.	1.1	22
250	Mouse ES cells express endogenous shRNAs, siRNAs, and other Microprocessor-independent, Dicer-dependent small RNAs. Genes and Development, 2008, 22, 2773-2785.	2.7	739
251	Mapping of Small RNAs in the Human ENCODE Regions. American Journal of Human Genetics, 2008, 82, 971-981.	2.6	25
252	WW-Domain-Containing Oxidoreductase Is Associated with Low Plasma HDL-C Levels. American Journal of Human Genetics, 2008, 83, 180-192.	2.6	54
253	Understanding the development of human bladder cancer by using a whole-organ genomic mapping strategy. Laboratory Investigation, 2008, 88, 694-721.	1.7	71
254	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	9.4	662
255	Ultraconservation identifies a small subset of extremely constrained developmental enhancers. Nature Genetics, 2008, 40, 158-160.	9.4	299
256	Approaches to comparative sequence analysis: towards a functional view of vertebrate genomes. Nature Reviews Genetics, 2008, 9, 303-313.	7.7	55
257	Transposable elements and the evolution of regulatory networks. Nature Reviews Genetics, 2008, 9, 397-405.	7.7	1,108

#	Article	IF	Citations
258	The functional repertoires of metazoan genomes. Nature Reviews Genetics, 2008, 9, 689-698.	7.7	100
259	SEARCHING FOR FUNCTIONAL GENETIC VARIANTS IN NONâ€CODING DNA. Clinical and Experimental Pharmacology and Physiology, 2008, 35, 372-375.	0.9	17
260	Fetal haemoglobin response to hydroxycarbamide treatment and sar1a promoter polymorphisms in sickle cell anaemia. British Journal of Haematology, 2008, 141, 254-259.	1.2	49
261	Comparative genomics and the study of evolution by natural selection. Molecular Ecology, 2008, 17, 4586-4596.	2.0	133
262	How to usefully compare homologous plant genes and chromosomes as DNA sequences. Plant Journal, 2008, 53, 661-673.	2.8	469
263	Multiple organism algorithm for finding ultraconserved elements. BMC Bioinformatics, 2008, 9, 15.	1.2	10
264	BioSAVE: Display of scored annotation within a sequence context. BMC Bioinformatics, 2008, 9, 157.	1.2	2
265	Local conservation scores without a priori assumptions on neutral substitution rates. BMC Bioinformatics, 2008, 9, 190.	1.2	6
266	TiGER: A database for tissue-specific gene expression and regulation. BMC Bioinformatics, 2008, 9, 271.	1.2	336
267	SNP@Promoter: a database of human SNPs (Single Nucleotide Polymorphisms) within the putative promoter regions. BMC Bioinformatics, 2008, 9, S2.	1.2	48
268	A genome-wide screen for noncoding elements important in primate evolution. BMC Evolutionary Biology, 2008, 8, 17.	3.2	90
269	Two different classes of co-occurring motif pairs found by a novel visualization method in human promoter regions. BMC Genomics, 2008, 9, 112.	1.2	6
270	Hidden layers of human small RNAs. BMC Genomics, 2008, 9, 157.	1.2	255
271	Comparative analysis of sequence features involved in the recognition of tandem splice sites. BMC Genomics, 2008, 9, 202.	1.2	9
272	Evolutionary rates and patterns for human transcription factor binding sites derived from repetitive DNA. BMC Genomics, 2008, 9, 226.	1.2	62
273	MicroRNA-encoding long non-coding RNAs. BMC Genomics, 2008, 9, 236.	1.2	60
274	Identification of direct regulatory targets of the transcription factor Sox10 based on function and conservation. BMC Genomics, 2008, 9, 408.	1.2	30
275	Evolution of conserved secondary structures and their function in transcriptional regulation networks. BMC Genomics, 2008, 9, 520.	1.2	2

#	Article	IF	Citations
276	Identifying Positioned Nucleosomes with Epigenetic Marks in Human from ChIP-Seq. BMC Genomics, 2008, 9, 537.	1.2	122
277	Alternative splicing resulting in nonsense-mediated mRNA decay: what is the meaning of nonsense?. Trends in Biochemical Sciences, 2008, 33, 385-393.	3.7	327
278	Tuning in to the signals: noncoding sequence conservation in vertebrate genomes. Trends in Genetics, 2008, 24, 344-352.	2.9	168
279	Evolutionary footprints of nucleosome positions in yeast. Trends in Genetics, 2008, 24, 583-587.	2.9	70
280	Human-macaque comparisons illuminate variation in neutral substitution rates. Genome Biology, 2008, 9, R76.	13.9	54
281	Classifying transcription factor targets and discovering relevant biological features. Biology Direct, 2008, 3, 22.	1.9	9
282	In silico regulatory analysis for exploring human disease progression. Biology Direct, 2008, 3, 24.	1.9	6
283	Pitfalls of the most commonly used models of context dependent substitution. Biology Direct, 2008, 3, 52.	1.9	18
284	Inferring Trees. Methods in Molecular Biology, 2008, 452, 287-309.	0.4	13
285	Human-Mouse Quantitative Trait Locus Concordance and the Dissection of a Human Neuroticism Locus. Biological Psychiatry, 2008, 63, 874-883.	0.7	17
286	Linkage Disequilibrium Mapping of a Chromosome 15q25-26 Major Depression Linkage Region and Sequencing of NTRK3. Biological Psychiatry, 2008, 63, 1185-1189.	0.7	35
287	ModuleMiner - improved computational detection of cis-regulatory modules: are there different modes of gene regulation in embryonic development and adult tissues?. Genome Biology, 2008, 9, R66.	13.9	31
288	Human-Specific Gain of Function in a Developmental Enhancer. Science, 2008, 321, 1346-1350.	6.0	330
289	The Impact of Natural Selection on the Genome: Emerging Patterns in Drosophila and Arabidopsis. Annual Review of Ecology, Evolution, and Systematics, 2008, 39, 193-213.	3.8	97
290	Posttranscriptional Regulation of miRNAs Harboring Conserved Terminal Loops. Molecular Cell, 2008, 32, 383-393.	4.5	316
291	Genetic association studies of neurotensin gene and restless legs syndrome in French Canadians. Sleep Medicine, 2008, 9, 273-282.	0.8	5
292	NcDNAlign: Plausible multiple alignments of non-protein-coding genomic sequences. Genomics, 2008, 92, 65-74.	1.3	18
293	Screening reveals conserved and nonconserved transcriptional regulatory elements including an E3/E4 allele-dependent APOE coding region enhancer. Genomics, 2008, 92, 292-300.	1.3	17

#	Article	IF	Citations
294	Identification of Conserved Regulatory Elements in Mammalian Promoter Regions: A Case Study Using the PCK1 Promoter. Genomics, Proteomics and Bioinformatics, 2008, 6, 129-143.	3.0	8
295	Long-range chromosomal interactions and gene regulation. Molecular BioSystems, 2008, 4, 1046.	2.9	179
296	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. Genome Research, 2008, 18, 1433-1445.	2.4	698
297	Confirming the Phylogeny of Mammals by Use of Large Comparative Sequence Data Sets. Molecular Biology and Evolution, 2008, 25, 1795-1808.	3.5	220
298	Chromatin structure analyses identify miRNA promoters. Genes and Development, 2008, 22, 3172-3183.	2.7	541
299	Mapping DNA structural variation in dogs. Genome Research, 2009, 19, 500-509.	2.4	119
300	A systematic characterization of factors that regulate Drosophila segmentation via a bacterial one-hybrid system. Nucleic Acids Research, 2008, 36, 2547-2560.	6.5	152
301	Species-specific Differences among KCNMB3 BK Î²3 Auxiliary Subunits: Some Î²3 N-terminal Variants May Be Primate-specific Subunits. Journal of General Physiology, 2008, 132, 115-129.	0.9	20
302	Combining statistical alignment and phylogenetic footprinting to detect regulatory elements. Bioinformatics, 2008, 24, 1236-1242.	1.8	27
303	Annotation-Modules: a tool for finding significant combinations of multisource annotations for gene lists. Bioinformatics, 2008, 24, 1386-1393.	1.8	32
304	Long, abundantly expressed non-coding transcripts are altered in cancer. Human Molecular Genetics, 2008, 17, 642-655.	1.4	193
305	Novel Single Nucleotide Polymorphisms in the Promoter and Intron 1 of Human Pregnane X Receptor/NR1I2 and Their Association with CYP3A4 Expression. Drug Metabolism and Disposition, 2008, 36, 169-181.	1.7	130
306	Predicting functional regulatory polymorphisms. Bioinformatics, 2008, 24, 1787-1792.	1.8	21
307	Genomewide Association Analysis Followed by a Replication Study Implicates a Novel Candidate Gene for Neuroticism. Archives of General Psychiatry, 2008, 65, 1062.	13.8	120
308	Screening of human SNP database identifies recoding sites of A-to-I RNA editing. Rna, 2008, 14, 2074-2085.	1.6	42
309	Induction of PPM1D following DNA-damaging treatments through a conserved p53 response element coincides with a shift in the use of transcription initiation sites. Nucleic Acids Research, 2008, 36, 7168-7180.	6.5	52
310	Confidence in comparative genomics. Genome Research, 2008, 18, 199-200.	2.4	5
311	Evolution of the mammalian transcription factor binding repertoire via transposable elements. Genome Research, 2008, 18, 1752-1762.	2.4	501

#	Article	IF	Citations
312	Sequencing and Comparative Analysis of a Conserved Syntenic Segment in the Solanaceae. Genetics, 2008, 180, 391-408.	1.2	105
313	Human and mouse introns are linked to the same processes and functions through each genome's most frequent non-conserved motifs. Nucleic Acids Research, 2008, 36, 3484-3493.	6.5	30
315	PPARÎ³ and C/EBP factors orchestrate adipocyte biology via adjacent binding on a genome-wide scale. Genes and Development, 2008, 22, 2941-2952.	2.7	690
316	xREI: a phylo-grammar visualization webserver. Nucleic Acids Research, 2008, 36, W65-W69.	6.5	3
317	T-Bet Dependent Removal of Sin3A-Histone Deacetylase Complexes at the Ifng Locus Drives Th1 Differentiation. Journal of Immunology, 2008, 181, 8372-8381.	0.4	44
318	Navigating the genome. Journal of Cell Science, 2008, 121, 921-923.	1.2	0
319	Nkx3-1 and LEF-1 Function as Transcriptional Inhibitors of Estrogen Receptor Activity. Cancer Research, 2008, 68, 7380-7385.	0.4	39
320	A Catalog of Neutral and Deleterious Polymorphism in Yeast. PLoS Genetics, 2008, 4, e1000183.	1.5	212
321	Cervical and Vulvar Cancer Risk in Relation to the Joint Effects of Cigarette Smoking and Genetic Variation in Interleukin 2. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1790-1799.	1.1	37
322	Novel Low Abundance and Transient RNAs in Yeast Revealed by Tiling Microarrays and Ultra Highâ€“Throughput Sequencing Are Not Conserved Across Closely Related Yeast Species. PLoS Genetics, 2008, 4, e1000299.	1.5	31
323	Comprehensive Analysis of DNA Repair Gene Variants and Risk of Meningioma. Journal of the National Cancer Institute, 2008, 100, 270-276.	3.0	56
324	Probabilistic Phylogenetic Inference with Insertions and Deletions. PLoS Computational Biology, 2008, 4, e1000172.	1.5	51
325	Extracting sequence features to predict proteinâ€“DNA interactions: a comparative study. Nucleic Acids Research, 2008, 36, 4137-4148.	6.5	40
326	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. PLoS Biology, 2008, 6, e256.	2.6	172
327	Epigenetic inheritance of DNA methylation limits activation-induced expression of FOXP3 in conventional human CD25-CD4+ T cells. International Immunology, 2008, 20, 1041-1055.	1.8	72
328	Transcription Factors Bind Thousands of Active and Inactive Regions in the Drosophila Blastoderm. PLoS Biology, 2008, 6, e27.	2.6	428
329	Using native and syntenically mapped cDNA alignments to improve de novo gene finding. Bioinformatics, 2008, 24, 637-644.	1.8	1,618
330	A Novel Bayesian DNA Motif Comparison Method for Clustering and Retrieval. PLoS Computational Biology, 2008, 4, e1000010.	1.5	40

#	Article	IF	Citations
331	Linking Fold, Function and Phylogeny: A Comparative Genomics View on Protein (Domain) Evolution. Current Genomics, 2008, 9, 88-96.	0.7	6
332	Up-Regulation of Peroxiredoxin 1 in Lung Cancer and Its Implication as a Prognostic and Therapeutic Target. Clinical Cancer Research, 2008, 14, 2326-2333.	3.2	82
333	In Silico Detection of Sequence Variations Modifying Transcriptional Regulation. PLoS Computational Biology, 2008, 4, e5.	1.5	94
334	Modeling an Evolutionary Conserved Circadian Cis-Element. PLoS Computational Biology, 2008, 4, e38.	1.5	31
335	Genome-Wide Occupancy of SREBP1 and Its Partners NFY and SP1 Reveals Novel Functional Roles and Combinatorial Regulation of Distinct Classes of Genes. PLoS Genetics, 2008, 4, e1000133.	1.5	191
336	Assessing the fraction of short-distance tandem splice sites under purifying selection. Rna, 2008, 14, 616-629.	1.6	17
337	High-resolution human core-promoter prediction with CoreBoost_HM. Genome Research, 2009, 19, 266-275.	2.4	96
338	Splicing factor SFRS1 recognizes a functionally diverse landscape of RNA transcripts. Genome Research, 2009, 19, 381-394.	2.4	284
339	Genome evolution in Caenorhabditis. Briefings in Functional Genomics & Proteomics, 2008, 7, 211-216.	3.8	14
340	Metrics of sequence constraint overlook regulatory sequences in an exhaustive analysis at phox2b. Genome Research, 2008, 18, 252-260.	2.4	101
341	Large-Scale Appearance of Ultraconserved Elements in Tetrapod Genomes and Slowdown of the Molecular Clock. Molecular Biology and Evolution, 2008, 25, 402-408.	3.5	103
342	Comprehensive analysis of the role of DNA repair gene polymorphisms on risk of glioma. Human Molecular Genetics, 2008, 17, 800-805.	1.4	67
343	Evaluation of cis-regulatory function in zebrafish. Briefings in Functional Genomics & Proteomics, 2008, 7, 465-473.	3.8	7
344	Regulation of Multiple Core Spliceosomal Proteins by Alternative Splicing-Coupled Nonsense-Mediated mRNA Decay. Molecular and Cellular Biology, 2008, 28, 4320-4330.	1.1	183
345	Cross-species de novo identification of cis-regulatory modules with GibbsModule: Application to gene regulation in embryonic stem cells. Genome Research, 2008, 18, 1325-1335.	2.4	29
346	Chromatin profiling across the human tumour necrosis factor gene locus reveals a complex, cell type-specific landscape with novel regulatory elements. Nucleic Acids Research, 2008, 36, 4845-4862.	6.5	23
347	Identification of Arx transcriptional targets in the developing basal forebrain. Human Molecular Genetics, 2008, 17, 3740-3760.	1.4	121
348	Retroviral promoters in the human genome. Bioinformatics, 2008, 24, 1563-1567.	1.8	112

#	Article	IF	Citations
349	The opossum genome: Insights and opportunities from an alternative mammal. Genome Research, 2008, 18, 1199-1215.	2.4	40
350	Comparative genomics beyond sequence-based alignments: RNA structures in the ENCODE regions. Genome Research, 2008, 18, 242-251.	2.4	82
351	A Core Paired-Type and POU Homeodomain-Containing Transcription Factor Program Drives Retinal Bipolar Cell Gene Expression. Journal of Neuroscience, 2008, 28, 7748-7764.	1.7	105
352	Spatial and Temporal Heterogeneity in Nucleotide Sequence Evolution. Molecular Biology and Evolution, 2008, 25, 1683-1694.	3.5	36
353	Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843.	2.4	164
354	Accelerated sequence divergence of conserved genomic elements in Drosophila melanogaster. Genome Research, 2008, 18, 1592-1601.	2.4	23
355	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. Genome Research, 2008, 18, 1896-1905.	2.4	29
356	Ultraconserved Elements: Analyses of Dosage Sensitivity, Motifs and Boundaries. Genetics, 2008, 180, 2277-2293.	1.2	37
357	Delineating Slowly and Rapidly Evolving Fractions of the Drosophila Genome. Journal of Computational Biology, 2008, 15, 407-430.	0.8	19
358	Strategies for Reliable Exploitation of Evolutionary Concepts in High Throughput Biology. Evolutionary Bioinformatics, 2008, 4, EBO.S597.	0.6	15
359	ChromaSig: A Probabilistic Approach to Finding Common Chromatin Signatures in the Human Genome. PLoS Computational Biology, 2008, 4, e1000201.	1.5	135
360	Structural Relationships between Highly Conserved Elements and Genes in Vertebrate Genomes. PLoS ONE, 2008, 3, e3727.	1.1	10
361	THE MOLECULAR, CELLULAR, AND GENETIC BASIS OF HEMOGLOBIN DISORDERS. , 2009, , 1-2.		0
362	Big Genomes Facilitate the Comparative Identification of Regulatory Elements. PLoS ONE, 2009, 4, e4688.	1.1	41
363	Evolutionary Modeling and Prediction of Non-Coding RNAs in Drosophila. PLoS ONE, 2009, 4, e6478.	1.1	13
364	Prediction and Experimental Validation of Novel STAT3 Target Genes in Human Cancer Cells. PLoS ONE, 2009, 4, e6911.	1.1	27
365	Screening for Microsatellite Instability Identifies Frequent 3â€²-Untranslated Region Mutation of the RB1-Inducible Coiled-Coil 1 Gene in Colon Tumors. PLoS ONE, 2009, 4, e7715.	1.1	12
366	Regulation of p110Î´ PI 3-Kinase Gene Expression. PLoS ONE, 2009, 4, e5145.	1.1	45

#	Article	IF	Citations
367	Accurate Prediction of Alternatively Spliced Cassette Exons Using Evolutionary Conservation Information and Logitlinear Model. , 2009, , .		3
368	Adaptive evolution of young gene duplicates in mammals. Genome Research, 2009, 19, 859-867.	2.4	176
369	The tedious task of finding homologous noncoding RNA genes. Rna, 2009, 15, 2075-2082.	1.6	55
370	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3264-3269.	3.3	201
371	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. Journal of Immunology, 2009, 182, 7738-7748.	0.4	221
372	TargetMiner: microRNA target prediction with systematic identification of tissue-specific negative examples. Bioinformatics, 2009, 25, 2625-2631.	1.8	207
373	SNPLogic: an interactive single nucleotide polymorphism selection, annotation, and prioritization system. Nucleic Acids Research, 2009, 37, D803-D809.	6.5	25
374	Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10â€‰000 Vertebrate Species. Journal of Heredity, 2009, 100, 659-674.	1.0	504
375	Detection of intergenic non-coding RNAs expressed in the main developmental stages in Drosophila melanogaster. Nucleic Acids Research, 2009, 37, 4308-4314.	6.5	21
376	Caenorhabditis elegans cisRED: a catalogue of conserved genomic elements. Nucleic Acids Research, 2009, 37, 1323-1334.	6.5	16
377	NRED: a database of long noncoding RNA expression. Nucleic Acids Research, 2009, 37, D122-D126.	6.5	252
378	Estimating the Rate of Adaptive Molecular Evolution in the Presence of Slightly Deleterious Mutations and Population Size Change. Molecular Biology and Evolution, 2009, 26, 2097-2108.	3.5	413
379	The PAZAR database of gene regulatory information coupled to the ORCA toolkit for the study of regulatory sequences. Nucleic Acids Research, 2009, 37, D54-D60.	6.5	97
380	Web-based tools and approaches to study long-range gene regulation in Metazoa. Briefings in Functional Genomics & Proteomics, 2009, 8, 231-242.	3.8	6
381	MotifMap: a human genome-wide map of candidate regulatory motif sites. Bioinformatics, 2009, 25, 167-174.	1.8	118
382	Identifying novel constrained elements by exploiting biased substitution patterns. Bioinformatics, 2009, 25, i54-i62.	1.8	296
383	Whole-genome association study identifies STK39 as a hypertension susceptibility gene. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 226-231.	3.3	280
384	A gene regulatory network directed by zebrafish No tail accounts for its roles in mesoderm formation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3829-3834.	3.3	109

#	Article	IF	Citations
385	The UCSC Genome Browser Database: update 2009. Nucleic Acids Research, 2009, 37, D755-D761.	6.5	329
386	A predictive model for identifying mini-regulatory modules in the mouse genome. Bioinformatics, 2009, 25, 353-357.	1.8	3
387	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2009, 28, Unit1.4.	25.8	149
388	FOXC2 controls formation and maturation of lymphatic collecting vessels through cooperation with NFATc1. Journal of Cell Biology, 2009, 185, 439-457.	2.3	295
389	High-throughput chromatin information enables accurate tissue-specific prediction of transcription factor binding sites. Nucleic Acids Research, 2009, 37, 14-25.	6.5	57
390	Population Genetics and Comparative Genetics of <i>CLDN1</i>, a Gene Involved in Hepatitis C Virus Entry. Human Heredity, 2009, 67, 206-216.	0.4	2
391	Accurate Estimation of Gene Evolutionary Rates Using XRATE, with an Application to Transmembrane Proteins. Molecular Biology and Evolution, 2009, 26, 1715-1721.	3.5	9
392	Analysis of Exonic Elastin Variants in Severe, Early-Onset Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2009, 40, 751-755.	1.4	17
393	Disease-Causing 7.4 kb Cis-Regulatory Deletion Disrupting Conserved Non-Coding Sequences and Their Interaction with the FOXL2 Promotor: Implications for Mutation Screening. PLoS Genetics, 2009, 5, e1000522.	1.5	83
394	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. PLoS Computational Biology, 2009, 5, e1000566.	1.5	143
395	Pervasive Natural Selection in the Drosophila Genome?. PLoS Genetics, 2009, 5, e1000495.	1.5	329
396	Predicting Functional Alternative Splicing by Measuring RNA Selection Pressure from Multigenome Alignments. PLoS Computational Biology, 2009, 5, e1000608.	1.5	22
397	The Relationship between DNA Replication and Human Genome Organization. Molecular Biology and Evolution, 2009, 26, 729-741.	3.5	43
398	Alu and B1 Repeats Have Been Selectively Retained in the Upstream and Intronic Regions of Genes of Specific Functional Classes. PLoS Computational Biology, 2009, 5, e1000610.	1.5	74
399	Pervasive Hitchhiking at Coding and Regulatory Sites in Humans. PLoS Genetics, 2009, 5, e1000336.	1.5	134
400	Human miRNA Precursors with Box H/ACA snoRNA Features. PLoS Computational Biology, 2009, 5, e1000507.	1.5	167
401	Hotspots of Biased Nucleotide Substitutions in Human Genes. PLoS Biology, 2009, 7, e1000026.	2.6	134
402	Genomic and Transcriptional Co-Localization of Protein-Coding and Long Non-Coding RNA Pairs in the Developing Brain. PLoS Genetics, 2009, 5, e1000617.	1.5	354

#	Article	IF	Citations
403	Genetic Variation in Immune Regulation and DNA Repair Pathways and Stomach Cancer in China. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2304-2309.	1.1	43
404	Transcriptional and post-transcriptional profile of human chromosome 21. Genome Research, 2009, 19, 1471-1479.	2.4	2
405	Conserved introns reveal novel transcripts in Drosophila melanogaster. Genome Research, 2009, 19, 1289-1300.	2.4	38
406	Visualization of genomic data with the Hilbert curve. Bioinformatics, 2009, 25, 1231-1235.	1.8	61
407	A Common Copy Number Variation on Chromosome 6 Association With the Gene Expression Level of Endothelin 1 in Transformed B Lymphocytes From Three Racial Groups. Circulation: Cardiovascular Genetics, 2009, 2, 483-488.	5.1	8
408	Evolutionary Genetics of Coronary Heart Disease. Circulation, 2009, 119, 459-467.	1.6	35
409	Transcripts of unknown function in multiple-signaling pathways involved in human stem cell differentiation. Nucleic Acids Research, 2009, 37, 4987-5000.	6.5	51
410	Phylogenomics of primates and their ancestral populations. Genome Research, 2009, 19, 1929-1941.	2.4	53
411	MicroRNA-like off-target transcript regulation by siRNAs is species specific. Rna, 2009, 15, 308-315.	1.6	71
412	Stochastic models of sequence evolution including insertionâ€"deletion events. Statistical Methods in Medical Research, 2009, 18, 453-485.	0.7	22
413	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. Human Molecular Genetics, 2009, 18, 1692-1703.	1.4	110
414	Deeply conserved chordate noncoding sequences preserve genome synteny but do not drive gene duplicate retention. Genome Research, 2009, 19, 2036-2051.	2.4	43
415	Genome-wide colonization of gene regulatory elements by G4 DNA motifs. Nucleic Acids Research, 2009, 37, 6784-6798.	6.5	76
416	Profile analysis and prediction of tissue-specific CpG island methylation classes. BMC Bioinformatics, 2009, 10, 116.	1.2	28
417	GenomeGraphs: integrated genomic data visualization with R. BMC Bioinformatics, 2009, 10, 2.	1.2	68
418	OHMM: a Hidden Markov Model accurately predicting the occupancy of a transcription factor with a self-overlapping binding motif. BMC Bioinformatics, 2009, 10, 208.	1.2	11
419	Algorithms for locating extremely conserved elements in multiple sequence alignments. BMC Bioinformatics, 2009, 10, 432.	1.2	4
420	ContDist: a tool for the analysis of quantitative gene and promoter properties. BMC Bioinformatics, 2009, 10, 7.	1.2	8

#	Article	IF	Citations
421	Statistical assessment of discriminative features for protein-coding and non coding cross-species conserved sequence elements. BMC Bioinformatics, 2009, 10, S2.	1.2	2
422	Long-range regulation is a major driving force in maintaining genome integrity. BMC Evolutionary Biology, 2009, 9, 203.	3.2	21
423	BigFoot: Bayesian alignment and phylogenetic footprinting with MCMC. BMC Evolutionary Biology, 2009, 9, 217.	3.2	24
424	Weak preservation of local neutral substitution rates across mammalian genomes. BMC Evolutionary Biology, 2009, 9, 89.	3.2	8
425	Genomic regions with distinct genomic distance conservation in vertebrate genomes. BMC Genomics, 2009, 10, 133.	1.2	4
426	Primate phylogenomics: developing numerous nuclear non-coding, non-repetitive markers for ecological and phylogenetic applications and analysis of evolutionary rate variation. BMC Genomics, 2009, 10, 247.	1.2	27
427	A new measurement of sequence conservation. BMC Genomics, 2009, 10, 623.	1.2	4
428	Upstream sequence elements direct post-transcriptional regulation of gene expression under stress conditions in yeast. BMC Genomics, 2009, 10, 7.	1.2	87
429	Asymmetrical distribution of non-conserved regulatory sequences at PHOX2B is reflected at the ENCODE loci and illuminates a possible genome-wide trend. BMC Genomics, 2009, 10, 8.	1.2	22
430	Somatic, germline and sex hierarchy regulated gene expression during Drosophila metamorphosis. BMC Genomics, 2009, 10, 80.	1.2	49
431	Word-based characterization of promoters involved in human DNA repair pathways. BMC Genomics, 2009, 10, S18.	1.2	12
432	COMUS: Clinician-Oriented locus-specific MUtation detection and deposition System. BMC Genomics, 2009, 10, S35.	1.2	2
433	Atypical Xâ€¢chromosome inactivation in an X;1 translocation patient demonstrating Xq28 functional disomy. American Journal of Medical Genetics, Part A, 2009, 149A, 408-414.	0.7	9
434	Deletion of a conserved noncoding sequence in Plzf intron leads to Plzf downâ€•regulation in limb bud and polydactyly in the rat. Developmental Dynamics, 2009, 238, 673-684.	0.8	26
435	Conserved noncoding elements and the evolution of animal body plans. BioEssays, 2009, 31, 727-735.	1.2	30
436	Evolutionary characteristics of exons expressed at different abundance levels in mammals. Science Bulletin, 2009, 54, 3546-3554.	4.3	0
437	Genome Desertification in Eutherians: Can Gene Deserts Explain the Uneven Distribution of Genes in Placental Mammalian Genomes?. Journal of Molecular Evolution, 2009, 69, 207-216.	0.8	8
438	Unravelling cis-Regulatory Elements in the Genome of the Smallest Photosynthetic Eukaryote: Phylogenetic Footprinting in Ostreococcus. Journal of Molecular Evolution, 2009, 69, 249-259.	0.8	10

#	Article	IF	Citations
439	Identification and analysis of miRNAs in human breast cancer and teratoma samples using deep sequencing. BMC Medical Genomics, 2009, 2, 35.	0.7	40
440	Conservation of core gene expression in vertebrate tissues. Journal of Biology, 2009, 8, 33.	2.7	165
441	Epigenetics and T helper 1 differentiation. Immunology, 2009, 126, 299-305.	2.0	68
442	Family-based association of FKBP5 in bipolar disorder. Molecular Psychiatry, 2009, 14, 261-268.	4.1	140
443	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature, 2009, 458, 223-227.	13.7	3,801
444	ChIP-seq accurately predicts tissue-specific activity of enhancers. Nature, 2009, 457, 854-858.	13.7	1,526
445	Common genetic variants on 5p14.1 associate with autism spectrum disorders. Nature, 2009, 459, 528-533.	13.7	912
446	Genomic views of distant-acting enhancers. Nature, 2009, 461, 199-205.	13.7	549
447	Implications of chimaeric non-co-linear transcripts. Nature, 2009, 461, 206-211.	13.7	195
448	Combinatorial binding predicts spatio-temporal cis-regulatory activity. Nature, 2009, 462, 65-70.	13.7	361
449	Understanding genome browsing. Nature Biotechnology, 2009, 27, 153-155.	9.4	22
450	The non-coding RNA of the multidrug resistance-linked vault particle encodes multiple regulatory small RNAs. Nature Cell Biology, 2009, 11, 1268-1271.	4.6	147
451	Tiny RNAs associated with transcription start sites in animals. Nature Genetics, 2009, 41, 572-578.	9.4	327
452	Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. Nature Methods, 2009, 6, 283-289.	9.0	533
453	An RNA code for the FOX2 splicing regulator revealed by mapping RNA-protein interactions in stem cells. Nature Structural and Molecular Biology, 2009, 16, 130-137.	3.6	536
454	Splice site strengthâ€“dependent activity and genetic buffering by poly-G runs. Nature Structural and Molecular Biology, 2009, 16, 1094-1100.	3.6	112
455	Transforming growth factorâ€alfa gene (TGFA), human tooth agenesis, and evidence of segmental uniparental isodisomy. European Journal of Oral Sciences, 2009, 117, 20-26.	0.7	14
456	Deconstructing the Dogma. Annals of the New York Academy of Sciences, 2009, 1178, 29-46.	1.8	75

#	Article	IF	Citations
457	The Fragmented Gene. Annals of the New York Academy of Sciences, 2009, 1178, 186-193.	1.8	22
458	IFRD1 Is a Candidate Gene for SMNA on Chromosome 7q22-q23. American Journal of Human Genetics, 2009, 84, 692-697.	2.6	45
459	X Chromosomal Variation Is Associated with Slow Progression to AIDS in HIV-1-Infected Women. American Journal of Human Genetics, 2009, 85, 228-239.	2.6	41
460	MEIS1 intronic risk haplotype associated with restless legs syndrome affects its mRNA and protein expression levels. Human Molecular Genetics, 2009, 18, 1065-1074.	1.4	85
461	Regulatory DNAs and the evolution of human development. Current Opinion in Genetics and Development, 2009, 19, 557-564.	1.5	11
462	Embryonic nervous system genes predominate in searches for dinucleotide simple sequence repeats flanked by conserved sequences. Gene, 2009, 429, 74-79.	1.0	26
463	UTR dinucleotide simple sequence repeat evolution exhibits recurring patterns including regulatory sequence motif replacements. Gene, 2009, 429, 80-86.	1.0	28
464	The transcription factor PITX3 is associated with sporadic Parkinson's disease. Neurobiology of Aging, 2009, 30, 731-738.	1.5	108
465	Identification of an ancient Bmp4 mesoderm enhancer located 46Âkb from the promoter. Developmental Biology, 2009, 327, 590-602.	0.9	30
466	Flexibility of transcription factor target site position in conserved cis-regulatory modules. Developmental Biology, 2009, 336, 122-135.	0.9	20
467	Genomics made easier: An introductory tutorial to genome datamining. Genomics, 2009, 93, 187-195.	1.3	12
468	Discovering sequences with potential regulatory characteristics. Genomics, 2009, 93, 314-322.	1.3	13
469	Functional autonomy of distant-acting human enhancers. Genomics, 2009, 93, 509-513.	1.3	56
470	Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. Genomics, 2009, 94, 308-316.	1.3	11
471	Chromatin Immunoprecipitation on Microarray Analysis of Smad2/3 Binding Sites Reveals Roles of ETS1 and TFAP2A in Transforming Growth Factor Î² Signaling. Molecular and Cellular Biology, 2009, 29, 172-186.	1.1	179
472	Chapter 3 Genotypeâ€“Phenotype Mapping. International Review of Cell and Molecular Biology, 2009, 278, 119-148.	1.6	7
473	Small RNAs derived from snoRNAs. Rna, 2009, 15, 1233-1240.	1.6	384
474	Importin-13 genetic variation is associated with improved airway responsiveness in childhood asthma. Respiratory Research, 2009, 10, 67.	1.4	32

#	Article	IF	Citations
475	Local DNA Topography Correlates with Functional Noncoding Regions of the Human Genome. Science, 2009, 324, 389-392.	6.0	188
476	Searching for microRNA prostate cancer target genes. , 2009, , .		0
478	Catalogues of mammalian long noncoding RNAs: modest conservation and incompleteness. Genome Biology, 2009, 10, R124.	13.9	232
479	COMIT: identification of noncoding motifs under selection in coding sequences. Genome Biology, 2009, 10, R133.	13.9	7
480	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. Genome Biology, 2009, 10, R79.	13.9	131
481	Motifs and cis-regulatory modules mediating the expression of genes co-expressed in presynaptic neurons. Genome Biology, 2009, 10, R72.	13.9	15
482	Statistical Alignment with a Sequence Evolution Model Allowing Rate Heterogeneity along the Sequence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 281-295.	1.9	7
483	Assessing the Discordance of Multiple Sequence Alignments. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 542-551.	1.9	4
484	Genome-wide evolutionary analysis of the noncoding RNA genes and noncoding DNA of Paramecium tetraurelia. Rna, 2009, 15, 503-514.	1.6	11
485	Mining “junk” DNA to find hidden transcriptional gems. , 2009, , .		2
486	An integrative genomics approach identifies Hypoxia Inducible Factor-1 (HIF-1)-target genes that form the core response to hypoxia. Nucleic Acids Research, 2009, 37, 4587-4602.	6.5	400
487	Cancer-Specific High-Throughput Annotation of Somatic Mutations: Computational Prediction of Driver Missense Mutations. Cancer Research, 2009, 69, 6660-6667.	0.4	416
488	Chromatin Architecture and Transcription Factor Binding Regulate Expression of Erythrocyte Membrane Protein Genes. Molecular and Cellular Biology, 2009, 29, 5399-5412.	1.1	32
489	The Eukaryotic Chromosome. , 0, , 638-695.		0
490	Expression of the leukemia oncogene Lmo2 is controlled by an array of tissue-specific elements dispersed over 100 kb and bound by Tal1/Lmo2, Ets, and Gata factors. Blood, 2009, 113, 5783-5792.	0.6	69
491	Computational identification of protein-coding sequences by comparative analysis. International Journal of Data Mining and Bioinformatics, 2009, 3, 160.	0.1	6
492	The Normal Structure and Regulation of Human Globin Gene Clusters. , 0, , 46-61.		8
493	Orientation, distance, regulation and function of neighbouring genes. Human Genomics, 2009, 3, 143-56.	1.4	22

#	Article	IF	Citations
494	A general integrative genomic feature transcription factor binding site prediction method applied to analysis of USF1 binding in cardiovascular disease. Human Genomics, 2009, 3, 221.	1.4	7
495	CGDSNPdb: a database resource for error-checked and imputed mouse SNPs. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq008.	1.4	8
496	The Nature of Protein Domain Evolution: Shaping the Interaction Network. Current Genomics, 2010, 11, 368-376.	0.7	46
497	Is Transcription Factor Binding Site Turnover a Sufficient Explanation for Cis-Regulatory Sequence Divergence?. Genome Biology and Evolution, 2010, 2, 851-858.	1.1	24
498	Novel Data Fusion Method and Exploration of Multiple Information Sources for Transcription Factor Target Gene Prediction. Eurasip Journal on Advances in Signal Processing, 2010, 2010, .	1.0	2
499	Conservation of Human Microsatellites across 450 Million Years of Evolution. Genome Biology and Evolution, 2010, 2, 153-165.	1.1	41
500	The EM Algorithm and the Rise of Computational Biology. Statistical Science, 2010, 25, .	1.6	7
501	Dynamic CRM occupancy reflects a temporal map of developmental progression. Molecular Systems Biology, 2010, 6, 383.	3.2	44
502	Complete characterization of the microRNAome in a patient with acute myeloid leukemia. Blood, 2010, 116, 5316-5326.	0.6	63
503	Exon-intron structure of the Xist gene in elephant, armadillo, and the ancestor of placental mammals. Russian Journal of Genetics, 2010, 46, 1217-1222.	0.2	0
504	Next-Generation Sequencing of a 40 Mb Linkage Interval Reveals TSPAN12 Mutations in Patients with Familial Exudative Vitreoretinopathy. American Journal of Human Genetics, 2010, 86, 240-247.	2.6	202
505	Targeted Next-Generation Sequencing of a 12.5 Mb Homozygous Region Reveals ANO10 Mutations in Patients with Autosomal-Recessive Cerebellar Ataxia. American Journal of Human Genetics, 2010, 87, 813-819.	2.6	125
506	In junk we trust: repetitive DNA, epigenetics and facioscapulohumeral muscular dystrophy. Epigenomics, 2010, 2, 271-287.	1.0	26
507	Coordination of leaf development via regulation of KNOX1 genes. Journal of Plant Research, 2010, 123, 7-14.	1.2	44
508	De novo prediction of structured RNAs from genomic sequences. Trends in Biotechnology, 2010, 28, 9-19.	4.9	58
509	Conserved expression without conserved regulatory sequence: the more things change, the more they stay the same. Trends in Genetics, 2010, 26, 66-74.	2.9	139
510	Gene regulation and the origins of human biological uniqueness. Trends in Genetics, 2010, 26, 110-118.	2.9	41
511	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. BMC Bioinformatics, 2010, 11, 369.	1.2	94

#	Article	IF	Citations
512	SeqAnt: A web service to rapidly identify and annotate DNA sequence variations. BMC Bioinformatics, 2010, 11, 471.	1.2	38
513	Towards realistic benchmarks for multiple alignments of non-coding sequences. BMC Bioinformatics, 2010, 11, 54.	1.2	21
514	Functional conservation of a forebrain enhancer from the elephant shark (Callorhinchus milii) in zebrafish and mice. BMC Evolutionary Biology, 2010, 10, 157.	3.2	11
515	Correlation between sequence conservation and structural thermodynamics of microRNA precursors from human, mouse, and chicken genomes. BMC Evolutionary Biology, 2010, 10, 329.	3.2	11
516	Origin and evolution of a placental-specific microRNA family in the human genome. BMC Evolutionary Biology, 2010, 10, 346.	3.2	53
517	Two Frequenins in Drosophila: unveiling the evolutionary history of an unusual Neuronal Calcium Sensor (NCS) duplication. BMC Evolutionary Biology, 2010, 10, 54.	3.2	14
518	Detection of novel 3' untranslated region extensions with 3' expression microarrays. BMC Genomics, 2010, 11, 205.	1.2	12
519	Small RNA expression and strain specificity in the rat. BMC Genomics, 2010, 11, 249.	1.2	71
520	Paucity and preferential suppression of transgenes in late replication domains of the D. melanogaster genome. BMC Genomics, 2010, 11, 318.	1.2	16
521	Prediction of CpG-island function: CpG clustering vs. sliding-window methods. BMC Genomics, 2010, 11, 327.	1.2	40
522	Comprehensive survey of human brain microRNA by deep sequencing. BMC Genomics, 2010, 11, 409.	1.2	142
523	Expression proteomics of UPF1 knockdown in HeLa cells reveals autoregulation of hnRNP A2/B1 mediated by alternative splicing resulting in nonsense-mediated mRNA decay. BMC Genomics, 2010, 11, 565.	1.2	67
524	Imprinted genes show unique patterns of sequence conservation. BMC Genomics, 2010, 11, 649.	1.2	30
525	Comparison of transcriptomic landscapes of bovine embryos using RNA-Seq. BMC Genomics, 2010, 11, 711.	1.2	75
526	Identification of novel non-coding RNAs using profiles of short sequence reads from next generation sequencing data. BMC Genomics, 2010, 11, 77.	1.2	46
527	Massively parallel sequencing of ataxia genes after array-based enrichment. Human Mutation, 2010, 31, 494-499.	1.1	86
528	Impact of DNA physical properties on local sequence bias of human mutation. Human Mutation, 2010, 31, 1316-1325.	1.1	9
529	Identification of a distantcisâ€regulatory element controlling pharyngeal archâ€specific expression of zebrafishgdf6a/radar. Developmental Dynamics, 2010, 239, 1047-1060.	0.8	15

#	Article	IF	Citations
530	Identification of novel FMR1 variants by massively parallel sequencing in developmentally delayed males. American Journal of Medical Genetics, Part A, 2010, 152A, 2512-2520.	0.7	108
531	Identification and Characterization of Enhancers Controlling the Inflammatory Gene Expression Program in Macrophages. Immunity, 2010, 32, 317-328.	6.6	567
532	The long noncoding RNA RNCR2 directs mouse retinal cell specification. BMC Developmental Biology, 2010, 10, 49.	2.1	156
533	AlignMiner: a Web-based tool for detection of divergent regions in multiple sequence alignments of conserved sequences. Algorithms for Molecular Biology, 2010, 5, 24.	0.3	5
534	Structural constraints revealed in consistent nucleosome positions in the genome of S. cerevisiae. Epigenetics and Chromatin, 2010, 3, 20.	1.8	19
535	Evolutionary analysis of regulatory sequences (EARS) in plants. Plant Journal, 2010, 64, no-no.	2.8	28
536	Proteome analysis and genomeâ€wide regulatory motif prediction identify novel potentially sexâ€hormone regulated proteins in rat efferent ducts. Journal of Developmental and Physical Disabilities, 2010, 33, 661-674.	3.6	15
537	Comprehensive discovery of endogenous Argonaute binding sites in Caenorhabditis elegans. Nature Structural and Molecular Biology, 2010, 17, 173-179.	3.6	279
538	FoxO1 regulates Tlr4 inflammatory pathway signalling in macrophages. EMBO Journal, 2010, 29, 4223-4236.	3.5	203
539	Quantitative fine-tuning of photoreceptor cis-regulatory elements through affinity modulation of transcription factor binding sites. Gene Therapy, 2010, 17, 1390-1399.	2.3	35
540	High-density SNP association study and copy number variation analysis of the AUTS1 and AUTS5 loci implicate the IMMP2Lâ€“DOCK4 gene region in autism susceptibility. Molecular Psychiatry, 2010, 15, 954-968.	4.1	126
541	Comparative assessment of methods for aligning multiple genome sequences. Nature Biotechnology, 2010, 28, 567-572.	9.4	42
542	Discovery and characterization of chromatin states for systematic annotation of the human genome. Nature Biotechnology, 2010, 28, 817-825.	9.4	947
543	Enhancer element potentially involved in human survivin gene promoter regulation in lung cancer cell lines. Biochemistry (Moscow), 2010, 75, 182-191.	0.7	9
544	Transposable elements have rewired the core regulatory network of human embryonic stem cells. Nature Genetics, 2010, 42, 631-634.	9.4	698
545	ChIP-Seq identification of weakly conserved heart enhancers. Nature Genetics, 2010, 42, 806-810.	9.4	395
546	Whole-genome sequencing and comprehensive variant analysis of a Japanese individual using massively parallel sequencing. Nature Genetics, 2010, 42, 931-936.	9.4	106
547	Visualizing genomes: techniques and challenges. Nature Methods, 2010, 7, S5-S15.	9.0	146

#	Article	IF	Citations
548	Annotating non-coding regions of the genome. Nature Reviews Genetics, 2010, 11, 559-571.	7.7	398
549	An Examination of KCNE1 Mutations and Common Variants in Chronic Tinnitus. Genes, 2010, 1, 23-37.	1.0	20
550	A Large Fraction of Extragenic RNA Pol II Transcription Sites Overlap Enhancers. PLoS Biology, 2010, 8, e1000384.	2.6	762
551	Cytosine Methylation Dysregulation in Neonates Following Intrauterine Growth Restriction. PLoS ONE, 2010, 5, e8887.	1.1	120
552	Array-Based FMR1 Sequencing and Deletion Analysis in Patients with a Fragile X Syndromeâ€“Like Phenotype. PLoS ONE, 2010, 5, e9476.	1.1	26
553	Hypoxia Promotes Glycogen Accumulation through Hypoxia Inducible Factor (HIF)-Mediated Induction of Glycogen Synthase 1. PLoS ONE, 2010, 5, e9644.	1.1	209
554	A Systems Biology Approach to Transcription Factor Binding Site Prediction. PLoS ONE, 2010, 5, e9878.	1.1	11
555	MER41 Repeat Sequences Contain Inducible STAT1 Binding Sites. PLoS ONE, 2010, 5, e11425.	1.1	47
556	Weakly Positioned Nucleosomes Enhance the Transcriptional Competency of Chromatin. PLoS ONE, 2010, 5, e12984.	1.1	7
557	RNAi Screen Indicates Widespread Biological Function for Human Natural Antisense Transcripts. PLoS ONE, 2010, 5, e13177.	1.1	35
558	Scaffolding a Caenorhabditis nematode genome with RNA-seq. Genome Research, 2010, 20, 1740-1747.	2.4	83
559	Analysis of Human Small Nucleolar RNAs (snoRNA) and the Development of snoRNA Modulator of Gene Expression Vectors. Molecular Biology of the Cell, 2010, 21, 1569-1584.	0.9	40
560	Genome-wide identification of hypoxia-inducible factor binding sites and target genes by a probabilistic model integrating transcription-profiling data and in silico binding site prediction. Nucleic Acids Research, 2010, 38, 2332-2345.	6.5	179
561	Tight Junctionâ€“associated MARVEL Proteins MarvelD3, Tricellulin, and Occludin Have Distinct but Overlapping Functions. Molecular Biology of the Cell, 2010, 21, 1200-1213.	0.9	264
562	deepBase: a database for deeply annotating and mining deep sequencing data. Nucleic Acids Research, 2010, 38, D123-D130.	6.5	141
563	Genome-wide functional element detection using pairwise statistical alignment outperforms multiple genome footprinting techniques. Bioinformatics, 2010, 26, 2116-2120.	1.8	7
564	Association of Î±-, Î²-, and Î³-Synuclein With Diffuse Lewy Body Disease. Archives of Neurology, 2010, 67, 970-5.	4.9	63
565	CRX ChIP-seq reveals the cis-regulatory architecture of mouse photoreceptors. Genome Research, 2010, 20, 1512-1525.	2.4	183

#	Article	IF	Citations
566	Polymorphisms in the hepatic lipase gene affect plasma HDL-cholesterol levels in a Turkish population. Journal of Lipid Research, 2010, 51, 422-430.	2.0	34
567	Distributions of Selectively Constrained Sites and Deleterious Mutation Rates in the Hominid and Murid Genomes. Molecular Biology and Evolution, 2010, 27, 177-192.	3.5	88
568	Large-scale discovery of insertion hotspots and preferential integration sites of human transposed elements. Nucleic Acids Research, 2010, 38, 1515-1530.	6.5	31
569	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. Nucleic Acids Research, 2010, 38, D75-D80.	6.5	285
570	The UCSC Genome Browser database: update 2010. Nucleic Acids Research, 2010, 38, D613-D619.	6.5	537
571	An integrated expression phenotype mapping approach defines common variants in LEP, ALOX15 and CAPNS1 associated with induction of IL-6. Human Molecular Genetics, 2010, 19, 720-730.	1.4	23
572	Integrating multiple evidence sources to predict transcription factor binding in the human genome. Genome Research, 2010, 20, 526-536.	2.4	85
573	Evolutionary constraint facilitates interpretation of genetic variation in resequenced human genomes. Genome Research, 2010, 20, 301-310.	2.4	77
574	CPEB2, CPEB3 and CPEB4 are coordinately regulated by miRNAs recognizing conserved binding sites in paralog positions of their 3â€²-UTRs. Nucleic Acids Research, 2010, 38, 7698-7710.	6.5	25
575	Epigenetic Changes in the Hypothalamic Proopiomelanocortin and Glucocorticoid Receptor Genes in the Ovine Fetus after Periconceptional Undernutrition. Endocrinology, 2010, 151, 3652-3664.	1.4	146
576	A Novel Technique for Detecting Putative Horizontal Gene Transfer in the Sequence Space. Journal of Computational Biology, 2010, 17, 1535-1548.	0.8	2
577	Detection of nonneutral substitution rates on mammalian phylogenies. Genome Research, 2010, 20, 110-121.	2.4	1,878
578	MicroRNA, mRNA, and protein expression link development and aging in human and macaque brain. Genome Research, 2010, 20, 1207-1218.	2.4	283
579	Genome-Wide Identification of Orthologs of miR-1302 Genes in Placental Mammals. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0
580	A regulatory toolbox of MiniPromoters to drive selective expression in the brain. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16589-16594.	3.3	74
581	Finding regulatory DNA motifs using alignment-free evolutionary conservation information. Nucleic Acids Research, 2010, 38, e90-e90.	6.5	38
582	Shifts in the intensity of purifying selection: An analysis of genome-wide polymorphism data from two closely related yeast species. Genome Research, 2010, 20, 1558-1573.	2.4	74
583	Binding site number variation and high-affinity binding consensus of Myb-SANT-like transcription factor Adf-1 in Drosophilidae. Nucleic Acids Research, 2010, 38, 6404-6417.	6.5	9

#	Article	IF	Citations
584	The (r)evolution of SINE versus LINE distributions in primate genomes: Sex chromosomes are important. Genome Research, 2010, 20, 600-613.	2.4	48
585	Analysis of Multiple Ethyl Methanesulfonate-MutagenizedCaenorhabditis elegansStrains by Whole-Genome Sequencing. Genetics, 2010, 185, 417-430.	1.2	88
586	A two-step site and mRNA-level model for predicting microRNA targets. BMC Bioinformatics, 2010, 11, 612.	1.2	15
587	Intergenic and Repeat Transcription in Human, Chimpanzee and Macaque Brains Measured by RNA-Seq. PLoS Computational Biology, 2010, 6, e1000843.	1.5	62
588	A Population Genetic Hidden Markov Model for Detecting Genomic Regions Under Selection. Molecular Biology and Evolution, 2010, 27, 1673-1685.	3.5	19
589	On the Utility of Short Intron Sequences as a Reference for the Detection of Positive and Negative Selection in Drosophila. Molecular Biology and Evolution, 2010, 27, 1226-1234.	3.5	105
590	Identifying a High Fraction of the Human Genome to be under Selective Constraint Using GERP++. PLoS Computational Biology, 2010, 6, e1001025.	1.5	1,443
591	Modeling the Evolution of Regulatory Elements by Simultaneous Detection and Alignment with Phylogenetic Pair HMMs. PLoS Computational Biology, 2010, 6, e1001037.	1.5	11
592	Nomadic Enhancers: Tissue-Specific cis-Regulatory Elements of yellow Have Divergent Genomic Positions among Drosophila Species. PLoS Genetics, 2010, 6, e1001222.	1.5	60
593	Genome-Wide Profiling of p63 DNAâ€“Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. PLoS Genetics, 2010, 6, e1001065.	1.5	169
594	G-Quadruplex DNA Sequences Are Evolutionarily Conserved and Associated with Distinct Genomic Features in Saccharomyces cerevisiae. PLoS Computational Biology, 2010, 6, e1000861.	1.5	221
595	A Comprehensive Genetic Analysis of Candidate Genes Regulating Response to Trypanosoma congolense Infection in Mice. PLoS Neglected Tropical Diseases, 2010, 4, e880.	1.3	14
596	Evolution of an X-Linked Primate-Specific Micro RNA Cluster. Molecular Biology and Evolution, 2010, 27, 671-683.	3.5	64
597	Multiple Evolutionary Rate Classes in Animal Genome Evolution. Molecular Biology and Evolution, 2010, 27, 942-953.	3.5	15
598	Regulatory network nodes ofcheck point factorsin DNA repair pathways. , 2010, , .		1
599	Long nuclear-retained non-coding RNAs and allele-specific higher-order chromatin organization at imprinted snoRNA gene arrays. Journal of Cell Science, 2010, 123, 70-83.	1.2	71
600	Human Variation in Short Regions Predisposed to Deep Evolutionary Conservation. Molecular Biology and Evolution, 2010, 27, 1279-1288.	3.5	7
601	Both Noncoding and Protein-Coding RNAs Contribute to Gene Expression Evolution in the Primate Brain. Genome Biology and Evolution, 2010, 2, 67-79.	1.1	103

#	Article	IF	Citations
602	Illuminating transcription pathways using fluorescent reporter genes and yeast functional genomics. Transcription, 2010, 1, 76-80.	1.7	4
603	Massive turnover of functional sequence in human and other mammalian genomes. Genome Research, 2010, 20, 1335-1343.	2.4	86
604	Estimates of the Effect of Natural Selection on Protein-Coding Content. Molecular Biology and Evolution, 2010, 27, 726-734.	3.5	40
605	Evidence that Localized Variation in Primate Sequence Divergence Arises from an Influence of Nucleosome Placement on DNA Repair. Molecular Biology and Evolution, 2010, 27, 637-649.	3.5	31
606	Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
607	Profiling spermatogenic failure in adult testes bearing Sox9-deficient Sertoli cells identifies genes involved in feminization, inflammation and stress. Reproductive Biology and Endocrinology, 2010, 8, 154.	1.4	11
608	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
609	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. Nucleic Acids Research, 2010, 38, e164-e164.	6.5	10,960
610	Regulatory Regions in DNA: Promoters, Enhancers, Silencers, and Insulators. Methods in Molecular Biology, 2010, 674, 33-42.	0.4	88
611	Population Genetic Principles and Human Populations. , 2010, , 487-506.		0
612	Comparative Genomics. , 2010, , 557-587.		0
613	Temperature and length-dependent modulation of the MH class IÎ² gene expression in brook charr (Salvelinus fontinalis) by a cis-acting minisatellite. Molecular Immunology, 2010, 47, 1817-1829.	1.0	22
614	Genetics and phenomics of hypothyroidism and goiter due to TPO mutations. Molecular and Cellular Endocrinology, 2010, 322, 38-43.	1.6	106
615	Identification of a FOXA-dependent enhancer of human alcohol dehydrogenase 4 (ADH4). Gene, 2010, 460, 1-7.	1.0	10
616	Epidermal Wound Repair Is Regulated by the Planar Cell Polarity Signaling Pathway. Developmental Cell, 2010, 19, 138-147.	3.1	180
617	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. Cell Metabolism, 2010, 12, 443-455.	7.2	190
618	Conservation and regulatory associations of a wide affinity range of mouse transcription factor binding sites. Genomics, 2010, 95, 185-195.	1.3	44
619	Efficient discovery of ASCL1 regulatory sequences through transgene pooling. Genomics, 2010, 95, 363-369.	1.3	3

#	Article	IF	Citations
620	Prediction of Polycomb target genes in mouse embryonic stem cells. Genomics, 2010, 96, 17-26.	1.3	33
621	Identification of conserved Drosophila-specific euchromatin-restricted non-coding sequence motifs. Genomics, 2010, 96, 154-166.	1.3	4
622	Databases and Genome Browsers. , 2010, , 905-921.		0
623	Comprehensive modeling of microRNA targets predicts functional non-conserved and non-canonical sites. Genome Biology, 2010, 11, R90.	13.9	1,478
624	Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes. Genome Biology, 2010, 11, R72.	13.9	215
625	Genome-wide prediction of transcription factor binding sites using an integrated model. Genome Biology, 2010, 11, R7.	13.9	100
626	Enhancers of GnRH Transcription Embedded in an Upstream Gene Use Homeodomain Proteins to Specify Hypothalamic Expression. Molecular Endocrinology, 2010, 24, 1949-1964.	3.7	29
627	Genomics of Long-Range Regulatory Elements. Annual Review of Genomics and Human Genetics, 2010, 11, 1-23.	2.5	139
628	Improved prediction of transcription binding sites from chromatin modification data. , 2010, , .		0
629	Transcriptional regulation by miRNA mimics that target sequences downstream of gene termini. Molecular BioSystems, 2011, 7, 2383.	2.9	28
630	Three Periods of Regulatory Innovation During Vertebrate Evolution. Science, 2011, 333, 1019-1024.	6.0	127
631	GWAS-identified colorectal cancer susceptibility locus associates with disease prognosis. European Journal of Cancer, 2011, 47, 1699-1707.	1.3	38
632	The Analysis of ChIP-Seq Data. Methods in Enzymology, 2011, 497, 51-73.	0.4	19
633	Using CisGenome to Analyze ChIPâ€chip and ChIPâ€seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
634	A CommonMUC5BPromoter Polymorphism and Pulmonary Fibrosis. New England Journal of Medicine, 2011, 364, 1503-1512.	13.9	986
635	Snat: a SNP annotation tool for bovine by integrating various sources of genomic information. BMC Genetics, 2011, 12, 85.	2.7	8
636	Rapid Turnover of Functional Sequence in Human and Other Genomes. Annual Review of Genomics and Human Genetics, 2011, 12, 275-299.	2.5	21
637	Cistrome: an integrative platform for transcriptional regulation studies. Genome Biology, 2011, 12, R83.	13.9	598

#	Article	IF	Citations
638	Dynamic reprogramming of chromatin accessibility during Drosophila embryo development. Genome Biology, 2011, 12, R43.	13.9	174
639	Delay in Feedback Repression by Cryptochrome 1 Is Required for Circadian Clock Function. Cell, 2011, 144, 268-281.	13.5	288
640	Evolution of Gene Regulatory Networks Controlling Body Plan Development. Cell, 2011, 144, 970-985.	13.5	351
641	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. Cell, 2011, 147, 358-369.	13.5	2,390
642	An Extensive MicroRNA-Mediated Network of RNA-RNA Interactions Regulates Established Oncogenic Pathways in Glioblastoma. Cell, 2011, 147, 370-381.	13.5	671
643	Conserved Function of lincRNAs in Vertebrate Embryonic Development despite Rapid Sequence Evolution. Cell, 2011, 147, 1537-1550.	13.5	1,072
644	ATXN1 Protein Family and CIC Regulate Extracellular Matrix Remodeling and Lung Alveolarization. Developmental Cell, 2011, 21, 746-757.	3.1	89
645	Claudin-18 gene structure, regulation, and expression is evolutionary conserved in mammals. Gene, 2011, 481, 83-92.	1.0	63
646	When needles look like hay: How to find tissue-specific enhancers in model organism genomes. Developmental Biology, 2011, 350, 239-254.	0.9	28
647	Identification of a dopaminergic enhancer indicates complexity in vertebrate dopamine neuron phenotype specification. Developmental Biology, 2011, 352, 393-404.	0.9	40
649	Developing a series of conservative anchor markers and their application to phylogenomics of Laurasiatherian mammals. Molecular Ecology Resources, 2011, 11, 134-140.	2.2	9
650	Targeted enrichment beyond the consensus coding DNA sequence exome reveals exons with higher variant densities. Genome Biology, 2011, 12, R68.	13.9	192
651	Computational and statistical approaches to analyzing variants identified by exome sequencing. Genome Biology, 2011, 12, 227.	13.9	116
652	Expression of distinct RNAs from 3â€² untranslated regions. Nucleic Acids Research, 2011, 39, 2393-2403.	6.5	185
653	Tbx20 regulates a genetic program essential to adult mouse cardiomyocyte function. Journal of Clinical Investigation, 2011, 121, 4640-4654.	3.9	136
655	Molecular Evolution of the Non-Coding Eosinophil Granule Ontogeny Transcript. Frontiers in Genetics, 2011, 2, 69.	1.1	12
656	Genome-Wide and Phase-Specific DNA-Binding Rhythms of BMAL1 Control Circadian Output Functions in Mouse Liver. PLoS Biology, 2011, 9, e1000595.	2.6	395
657	MicroRNA Genes Derived from Repetitive Elements and Expanded by Segmental Duplication Events in Mammalian Genomes. PLoS ONE, 2011, 6, e17666.	1.1	77

#	Article	IF	Citations
658	Genes Expressed in Specific Areas of the Human Fetal Cerebral Cortex Display Distinct Patterns of Evolution. PLoS ONE, 2011, 6, e17753.	1.1	66
659	Long Range Regulation of Human FXN Gene Expression. PLoS ONE, 2011, 6, e22001.	1.1	9
660	CpG Islands Undermethylation in Human Genomic Regions under Selective Pressure. PLoS ONE, 2011, 6, e23156.	1.1	16
661	Systematic Clustering of Transcription Start Site Landscapes. PLoS ONE, 2011, 6, e23409.	1.1	59
663	Comparative Genomic Analysis of the Streptococcus dysgalactiae Species Group: Gene Content, Molecular Adaptation, and Promoter Evolution. Genome Biology and Evolution, 2011, 3, 168-185.	1.1	52
664	Substitution Patterns Are GC-Biased in Divergent Sequences across the Metazoans. Genome Biology and Evolution, 2011, 3, 516-527.	1.1	35
665	Significant Selective Constraint at 4-Fold Degenerate Sites in the Avian Genome and Its Consequence for Detection of Positive Selection. Genome Biology and Evolution, 2011, 3, 1381-1389.	1.1	31
666	Long Conserved Fragments Upstream of Mammalian Polyadenylation Sites. Genome Biology and Evolution, 2011, 3, 654-666.	1.1	4
667	The Accumulation of Gene Regulation Through Time. Genome Biology and Evolution, 2011, 3, 667-673.	1.1	31
668	Faster than Neutral Evolution of Constrained Sequences: The Complex Interplay of Mutational Biases and Weak Selection. Genome Biology and Evolution, 2011, 3, 383-395.	1.1	30
669	RNA-seq analysis of 2 closely related leukemia clones that differ in their self-renewal capacity. Blood, 2011, 117, e27-e38.	0.6	57
670	A liver enhancer in the fibrinogen gene cluster. Blood, 2011, 117, 276-282.	0.6	17
671	Familial hemophagocytic lymphohistiocytosis type 3 (FHL3) caused by deep intronic mutation and inversion in UNC13D. Blood, 2011, 118, 5783-5793.	0.6	115
672	The UCSC Genome Browser. Current Protocols in Human Genetics, 2011, 71, Unit18.6.	3.5	38
673	Reptiles and Mammals Have Differentially Retained Long Conserved Noncoding Sequences from the Amniote Ancestor. Genome Biology and Evolution, 2011, 3, 102-113.	1.1	28
674	Association of a functional variant downstream of TNFAIP3 with systemic lupus erythematosus. Nature Genetics, 2011, 43, 253-258.	9.4	242
675	Needles in stacks of needles: finding disease-causal variants in a wealth of genomic data. Nature Reviews Genetics, 2011, 12, 628-640.	7.7	531
676	Transcriptome-wide sequencing reveals numerous APOBEC1 mRNA-editing targets in transcript 3â€² UTRs. Nature Structural and Molecular Biology, 2011, 18, 230-236.	3.6	217

#	Article	IF	Citations
677	Genome-wide identification of Ago2 binding sites from mouse embryonic stem cells with and without mature microRNAs. Nature Structural and Molecular Biology, 2011, 18, 237-244.	3.6	229
678	Transcriptional repression and DNA looping associated with a novel regulatory element in the final exon of the lymphotoxin-Î² gene. Genes and Immunity, 2011, 12, 126-135.	2.2	13
679	Chromosome-wide linkage disequilibrium caused by an inversion polymorphism in the white-throated sparrow (Zonotrichia albicollis). Heredity, 2011, 106, 537-546.	1.2	68
680	A double hit implicates DIAPH3 as an autism risk gene. Molecular Psychiatry, 2011, 16, 442-451.	4.1	68
681	Initial impact of the sequencing of the human genome. Nature, 2011, 470, 187-197.	13.7	919
682	Mapping and analysis of chromatin state dynamics in nine human cell types. Nature, 2011, 473, 43-49.	13.7	2,630
683	HypertrophyâCAssociated Polymorphisms Ascertained in a Founder Cohort Applied to Heart Failure Risk and Mortality. Clinical and Translational Science, 2011, 4, 17-23.	1.5	35
684	MotifMap: integrative genome-wide maps of regulatory motif sites for model species. BMC Bioinformatics, 2011, 12, 495.	1.2	154
685	microRNA regulation of expression of the cystic fibrosis transmembrane conductance regulator gene. Biochemical Journal, 2011, 438, 25-32.	1.7	132
686	Identification and molecular genetic characterization of the polytene chromosome interbands in Drosophila melanogaster. Russian Journal of Genetics, 2011, 47, 521-532.	0.2	13
687	A genome-wide view of mutation rate co-variation using multivariate analyses. Genome Biology, 2011, 12, R27.	13.9	37
688	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
689	A Genome-wide Comparison of the Functional Properties of Rare and Common Genetic Variants in Humans. American Journal of Human Genetics, 2011, 88, 458-468.	2.6	89
690	Vertebrate endothelial lipase: comparative studies of an ancient gene and protein in vertebrate evolution. Genetica, 2011, 139, 291-304.	0.5	10
691	Genetic factors and diet affect long-bone length in the F34 LG,SM advanced intercross. Mammalian Genome, 2011, 22, 178-196.	1.0	25
692	Deep resequencing of the voltage-gated potassium channel subunit KCNE3 gene in chronic tinnitus. Behavioral and Brain Functions, 2011, 7, 39.	1.4	19
693	WordCluster: detecting clusters of DNA words and genomic elements. Algorithms for Molecular Biology, 2011, 6, 2.	0.3	21
694	The long noncoding RNA Six3OS acts in trans to regulate retinal development by modulating Six3 activity. Neural Development, 2011, 6, 32.	1.1	128

#	Article	IF	Citations
695	Meta-Alignment with Crumble and Prune: Partitioning very large alignment problems for performance and parallelization. BMC Bioinformatics, 2011, 12, 144.	1.2	6
696	A mutation degree model for the identification of transcriptional regulatory elements. BMC Bioinformatics, 2011, 12, 262.	1.2	3
697	Detection of lineage-specific evolutionary changes among primate species. BMC Bioinformatics, 2011, 12, 274.	1.2	19
698	An integrated ChIP-seq analysis platform with customizable workflows. BMC Bioinformatics, 2011, 12, 277.	1.2	80
699	miRTar: an integrated system for identifying miRNA-target interactions in human. BMC Bioinformatics, 2011, 12, 300.	1.2	128
700	Evaluation of methods for detecting conversion events in gene clusters. BMC Bioinformatics, 2011, 12, S45.	1.2	7
701	Detecting genomic regions associated with a disease using variability functions and Adjusted Rand Index. BMC Bioinformatics, 2011, 12, S9.	1.2	6
702	SOX10 directly modulates ERBB3 transcription via an intronic neural crest enhancer. BMC Developmental Biology, 2011, 11, 40.	2.1	51
703	Analysis of the dynamics of limb transcriptomes during mouse development. BMC Developmental Biology, 2011, 11, 47.	2.1	9
704	Conversion events in gene clusters. BMC Evolutionary Biology, 2011, 11, 226.	3.2	12
705	Lineage-specific evolution of the vertebrate Otopetringene family revealed by comparative genomic analyses. BMC Evolutionary Biology, 2011, 11, 23.	3.2	16
706	Visualization and Exploration of Conserved Regulatory Modules Using ReXSpecies 2. BMC Evolutionary Biology, 2011, 11, 267.	3.2	3
707	Rice-Map: a new-generation rice genome browser. BMC Genomics, 2011, 12, 165.	1.2	10
708	Chromosome-wide mapping of DNA methylation patterns in normal and malignant prostate cells reveals pervasive methylation of gene-associated and conserved intergenic sequences. BMC Genomics, 2011, 12, 313.	1.2	62
709	MicroRNA genes preferentially expressed in dendritic cells contain sites for conserved transcription factor binding motifs in their promoters. BMC Genomics, 2011, 12, 330.	1.2	26
710	A genome-wide survey for SNPs altering microRNA seed sites identifies functional candidates in GWAS. BMC Genomics, 2011, 12, 504.	1.2	78
711	Rigorous and thorough bioinformatic analyses of olfactory receptor promoters confirm enrichment of O/E and homeodomain binding sites but reveal no new common motifs. BMC Genomics, 2011, 12, 561.	1.2	11
712	Erroneous attribution of relevant transcription factor binding sites despite successful prediction of cis-regulatory modules. BMC Genomics, 2011, 12, 578.	1.2	13

#	Article	IF	Citations
713	Ancient Pbx-Hox signatures define hundreds of vertebrate developmental enhancers. BMC Genomics, 2011, 12, 637.	1.2	27
714	Genetic variants of Î±â€synuclein are not associated with essential tremor. Movement Disorders, 2011, 26, 2552-2556.	2.2	14
715	C/EBPÎ² regulates dexamethasoneâ€induced muscle cell atrophy and expression of atroginâ€1 and MuRF1. Journal of Cellular Biochemistry, 2011, 112, 1737-1748.	1.2	29
716	Identifying functional single nucleotide polymorphisms in the human CArGome. Physiological Genomics, 2011, 43, 1038-1048.	1.0	44
717	Genome-wide identification of conserved regulatory function in diverged sequences. Genome Research, 2011, 21, 1139-1149.	2.4	72
718	Identification and experimental validation of splicing regulatory elements in Drosophila melanogaster reveals functionally conserved splicing enhancers in metazoans. Rna, 2011, 17, 1884-1894.	1.6	14
719	Intraspecific phenotypic variation in deer: the role of genetic and epigenetic processes. Animal Production Science, 2011, 51, 365.	0.6	10
720	Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes. Genome Research, 2011, 21, 1916-1928.	2.4	83
721	Conservation of an RNA regulatory map between Drosophila and mammals. Genome Research, 2011, 21, 193-202.	2.4	208
722	What fraction of the human genome is functional?. Genome Research, 2011, 21, 1769-1776.	2.4	134
723	Species-Specific Strategies Underlying Conserved Functions of Metabolic Transcription Factors. Molecular Endocrinology, 2011, 25, 694-706.	3.7	53
724	Toward a Systematic Understanding of mRNA 3' Untranslated Regions. Proceedings of the American Thoracic Society, 2011, 8, 163-166.	3.5	21
725	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. Genome Research, 2011, 21, 456-464.	2.4	286
726	RNAcode: Robust discrimination of coding and noncoding regions in comparative sequence data. Rna, 2011, 17, 578-594.	1.6	188
727	Neutral Evolution of Robustness in Drosophila microRNA Precursors. Molecular Biology and Evolution, 2011, 28, 2115-2123.	3.5	23
728	Negative Correlation between Expression Level and Evolutionary Rate of Long Intergenic Noncoding RNAs. Genome Biology and Evolution, 2011, 3, 1390-1404.	1.1	86
729	Current Concepts of Follicle-Stimulating Hormone Receptor Gene Regulation1. Biology of Reproduction, 2011, 84, 7-17.	1.2	102
730	Predicting site-specific human selective pressure using evolutionary signatures. Bioinformatics, 2011, 27, i266-i274.	1.8	7

#	Article	IF	Citations
731	A Slit/miR-218/Robo regulatory loop is required during heart tube formation in zebrafish. Development (Cambridge), 2011, 138, 1409-1419.	1.2	142
732	Enhancers in embryonic stem cells are enriched for transposable elements and genetic variations associated with cancers. Nucleic Acids Research, 2011, 39, 7371-7379.	6.5	21
733	GAMES identifies and annotates mutations in next-generation sequencing projects. Bioinformatics, 2011, 27, 9-13.	1.8	28
734	The sufficient minimal set of miRNA seed types. Bioinformatics, 2011, 27, 1346-1350.	1.8	110
735	PHAST and RPHAST: phylogenetic analysis with space/time models. Briefings in Bioinformatics, 2011, 12, 41-51.	3.2	396
736	Deep congenic analysis identifies many strong, context-dependent QTLs, one of which, Slc35b4, regulates obesity and glucose homeostasis. Genome Research, 2011, 21, 1065-1073.	2.4	51
737	High resolution mapping of Twist to DNA in Drosophila embryos: Efficient functional analysis and evolutionary conservation. Genome Research, 2011, 21, 566-577.	2.4	48
738	The Origins, Evolution, and Functional Potential of Alternative Splicing in Vertebrates. Molecular Biology and Evolution, 2011, 28, 2949-2959.	3.5	74
739	Ultraconserved cDNA segments in the human transcriptome exhibit resistance to folding and implicate function in translation and alternative splicing. Nucleic Acids Research, 2011, 39, 1967-1979.	6.5	21
740	Genome-wide screening in human growth plates during puberty in one patient suggests a role for RUNX2 in epiphyseal maturation. Journal of Endocrinology, 2011, 209, 245-254.	1.2	6
741	Selective Genomic Targeting by FRA-2/FOSL2 Transcription Factor. Journal of Biological Chemistry, 2011, 286, 15227-15239.	1.6	22
742	Loss of exon identity is a common mechanism of human inherited disease. Genome Research, 2011, 21, 1563-1571.	2.4	156
743	Quantifying the Variation in the Effective Population Size Within a Genome. Genetics, 2011, 189, 1389-1402.	1.2	91
744	Genomic Selection Identifies Vertebrate Transcription Factor Fezf2 Binding Sites and Target Genes. Journal of Biological Chemistry, 2011, 286, 18641-18649.	1.6	18
745	Discriminative prediction of mammalian enhancers from DNA sequence. Genome Research, 2011, 21, 2167-2180.	2.4	222
746	Mapping Association between Long-Range cis-Regulatory Regions and Their Target Genes Using Synteny. Journal of Computational Biology, 2011, 18, 1115-1130.	0.8	5
747	PSAR: measuring multiple sequence alignment reliability by probabilistic sampling. Nucleic Acids Research, 2011, 39, 6359-6368.	6.5	35
748	Identification of human miRNA precursors that resemble box C/D snoRNAs. Nucleic Acids Research, 2011, 39, 3879-3891.	6.5	123

#	Article	IF	Citations
749	MicroRNA-Driven Developmental Remodeling in the Brain Distinguishes Humans from Other Primates. PLoS Biology, 2011, 9, e1001214.	2.6	198
750	Study of FoxA Pioneer Factor at Silent Genes Reveals Rfx-Repressed Enhancer at Cdx2 and a Potential Indicator of Esophageal Adenocarcinoma Development. PLoS Genetics, 2011, 7, e1002277.	1.5	60
751	Identification of Widespread Ultra-Edited Human RNAs. PLoS Genetics, 2011, 7, e1002317.	1.5	79
752	Cactus: Algorithms for genome multiple sequence alignment. Genome Research, 2011, 21, 1512-1528.	2.4	245
753	Sufficient statistics and expectation maximization algorithms in phylogenetic tree models. Bioinformatics, 2011, 27, 2346-2353.	1.8	8
754	Topological entropy of DNA sequences. Bioinformatics, 2011, 27, 1061-1067.	1.8	54
755	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326.	1.5	146
756	Computational discovery of human coding and non-coding transcripts with conserved splice sites. Bioinformatics, 2011, 27, 1894-1900.	1.8	24
757	The Cardiac Transcription Network Modulated by Gata4, Mef2a, Nkx2.5, Srf, Histone Modifications, and MicroRNAs. PLoS Genetics, 2011, 7, e1001313.	1.5	180
758	Temporal Coordination of Gene Networks by Zelda in the Early Drosophila Embryo. PLoS Genetics, 2011, 7, e1002339.	1.5	222
759	A Complex Genomic Rearrangement Involving the Endothelin 3 Locus Causes Dermal Hyperpigmentation in the Chicken. PLoS Genetics, 2011, 7, e1002412.	1.5	139
760	Activation of Src and transformation by an RPTPÎ± splice mutant found in human tumours. EMBO Journal, 2011, 30, 3200-3211.	3.5	26
761	Depression and anxiety in children with CFS/ME: cause or effect?. Archives of Disease in Childhood, 2011, 96, 211-214.	1.0	30
762	Variation of BMP3 Contributes to Dog Breed Skull Diversity. PLoS Genetics, 2012, 8, e1002849.	1.5	159
763	Antagonistic Regulation of Apoptosis and Differentiation by the Cut Transcription Factor Represents a Tumor-Suppressing Mechanism in Drosophila. PLoS Genetics, 2012, 8, e1002582.	1.5	45
764	A complex immunodeficiency is based on U1 snRNP-mediated poly(A) site suppression. EMBO Journal, 2012, 31, 4035-4044.	3.5	24
765	Tissue-Restricted Transcription from a Conserved Intragenic CpG Island in the Klf1 Gene in Mice1. Biology of Reproduction, 2012, 87, 108.	1.2	9
766	Evidence for Positive Selection on a Number of MicroRNA Regulatory Interactions during Recent Human Evolution. PLoS Genetics, 2012, 8, e1002578.	1.5	63

#	Article	IF	Citations
767	Rescuing Alu: Recovery of New Inserts Shows LINE-1 Preserves Alu Activity through A-Tail Expansion. PLoS Genetics, 2012, 8, e1002842.	1.5	33
768	Hundreds of conserved non-coding genomic regions are independently lost in mammals. Nucleic Acids Research, 2012, 40, 11463-11476.	6.5	48
769	Meiosis-induced alterations in transcript architecture and noncoding RNA expression in S. cerevisiae. Rna, 2012, 18, 1142-1153.	1.6	20
770	Extensive Evolutionary Changes in Regulatory Element Activity during Human Origins Are Associated with Altered Gene Expression and Positive Selection. PLoS Genetics, 2012, 8, e1002789.	1.5	135
771	Proteome-Wide Discovery of Evolutionary Conserved Sequences in Disordered Regions. Science Signaling, 2012, 5, rs1.	1.6	109
772	Chromatin signature discovery via histone modification profile alignments. Nucleic Acids Research, 2012, 40, 10642-10656.	6.5	19
773	Genome-wide polycomb target gene prediction in Drosophila melanogaster. Nucleic Acids Research, 2012, 40, 5848-5863.	6.5	28
774	Heterozygous Mutations Causing Partial Prohormone Convertase 1 Deficiency Contribute to Human Obesity. Diabetes, 2012, 61, 383-390.	0.3	94
775	i-cisTarget: an integrative genomics method for the prediction of regulatory features and cis-regulatory modules. Nucleic Acids Research, 2012, 40, e114-e114.	6.5	176
776	Integrated analysis identifies a class of androgen-responsive genes regulated by short combinatorial long-range mechanism facilitated by CTCF. Nucleic Acids Research, 2012, 40, 4754-4764.	6.5	39
777	The chromatin insulator CTCF and the emergence of metazoan diversity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17507-17512.	3.3	161
778	Inferring Divergence of Context-Dependent Substitution Rates in Drosophila Genomes with Applications to Comparative Genomics. Molecular Biology and Evolution, 2012, 29, 1769-1780.	3.5	7
779	A 4.1-Mb Congenic Region of Rf-4 Contributes to Glomerular Permeability. Journal of the American Society of Nephrology: JASN, 2012, 23, 825-833.	3.0	6
780	The CHR promoter element controls cell cycle-dependent gene transcription and binds the DREAM and MMB complexes. Nucleic Acids Research, 2012, 40, 1561-1578.	6.5	90
781	A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells. Genome Research, 2012, 22, 1668-1679.	2.4	75
782	Systematic elucidation and in vivo validation of sequences enriched in hindbrain transcriptional control. Genome Research, 2012, 22, 2278-2289.	2.4	17
783	Autosomal Dominant Familial Dyskinesia and Facial Myokymia. Archives of Neurology, 2012, 69, 630.	4.9	109
784	Involvement of long noncoding RNAs in diseases affecting the central nervous system. RNA Biology, 2012, 9, 860-870.	1.5	93

#	Article	IF	Citations
785	Long noncoding RNAs in C. elegans. Genome Research, 2012, 22, 2529-2540.	2.4	191
786	Personal and population genomics of human regulatory variation. Genome Research, 2012, 22, 1689-1697.	2.4	98
787	Splicing of internal large exons is defined by novel cis -acting sequence elements. Nucleic Acids Research, 2012, 40, 9244-9254.	6.5	25
788	Genome-wide identification of enhancers in skeletal muscle: the role of MyoD1. Genes and Development, 2012, 26, 2763-2779.	2.7	164
789	Cold-Inducible RNA-Binding Protein Modulates Circadian Gene Expression Posttranscriptionally. Science, 2012, 338, 379-383.	6.0	229
790	The UCSC Genome Browser database: extensions and updates 2011. Nucleic Acids Research, 2012, 40, D918-D923.	6.5	294
791	Global mapping of translation initiation sites in mammalian cells at single-nucleotide resolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2424-32.	3.3	534
792	Identification and Characterization of Lineage-Specific Highly Conserved Noncoding Sequences in Mammalian Genomes. Genome Biology and Evolution, 2012, 4, 641-657.	1.1	27
793	Identification and Properties of 1,119 Candidate LincRNA Loci in the Drosophila melanogaster Genome. Genome Biology and Evolution, 2012, 4, 427-442.	1.1	217
794	Dual transcriptional activator and repressor roles of TBX20 regulate adult cardiac structure and function. Human Molecular Genetics, 2012, 21, 2194-2204.	1.4	75
795	Transcription Factors Are Targeted by Differentially Expressed miRNAs in Primates. Genome Biology and Evolution, 2012, 4, 552-564.	1.1	30
796	SNPnexus: a web server for functional annotation of novel and publicly known genetic variants (2012) Tj ETQq1 1 0.784314 rgBT /Ov	6.5	161
797	Cardiac Structural and Sarcomere Genes Associated With Cardiomyopathy Exhibit Marked Intolerance of Genetic Variation. Circulation: Cardiovascular Genetics, 2012, 5, 602-610.	5.1	59
798	Evaluating Pathogenicity of Rare Variants From Dilated Cardiomyopathy in the Exome Era. Circulation: Cardiovascular Genetics, 2012, 5, 167-174.	5.1	112
799	Regulated Expression of Chromobox Homolog 5 Revealed in Tumors of ApcMin/+ ROSA11 Gene Trap Mice. G3: Genes, Genomes, Genetics, 2012, 2, 569-578.	0.8	4
800	Genome-wide enhancer prediction from epigenetic signatures using genetic algorithm-optimized support vector machines. Nucleic Acids Research, 2012, 40, e77-e77.	6.5	109
801	An ancient genomic regulatory block conserved across bilaterians and its dismantling in tetrapods by retrogene replacement. Genome Research, 2012, 22, 642-655.	2.4	35
802	Nrf2â€“MafG heterodimers contribute globally to antioxidant and metabolic networks. Nucleic Acids Research, 2012, 40, 10228-10239.	6.5	317

#	Article	IF	Citations
803	MotEvo: integrated Bayesian probabilistic methods for inferring regulatory sites and motifs on multiple alignments of DNA sequences. Bioinformatics, 2012, 28, 487-494.	1.8	114
804	Measuring Microsatellite Conservation in Mammalian Evolution with a Phylogenetic Birthâ€“Death Model. Genome Biology and Evolution, 2012, 4, 636-647.	1.1	30
805	Nucleosome occupancy reveals regulatory elements of the CFTR promoter. Nucleic Acids Research, 2012, 40, 625-637.	6.5	8
806	RNA-binding protein HuR autoregulates its expression by promoting alternative polyadenylation site usage. Nucleic Acids Research, 2012, 40, 787-800.	6.5	123
807	Sequence and expression analysis of gaps in human chromosome 20. Nucleic Acids Research, 2012, 40, 6660-6672.	6.5	5
808	Considerations for creating and annotating the budding yeast Genome Map at SGD: a progress report. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar057-bar057.	1.4	10
809	Natural Selection in Gene-Dense Regions Shapes the Genomic Pattern of Polymorphism in Wild and Domesticated Rice. Molecular Biology and Evolution, 2012, 29, 675-687.	3.5	63
810	Evaluating the Evidence for Transmission Distortion in Human Pedigrees. Genetics, 2012, 191, 215-232.	1.2	43
811	Mitochondrial DNA Sequence Variation Associated with Dementia and Cognitive Function in the Elderly. Journal of Alzheimer's Disease, 2012, 32, 357-372.	1.2	37
812	Genome-wide analysis of STAT3 binding in vivo predicts effectors of the anti-inflammatory response in macrophages. Blood, 2012, 119, e110-e119.	0.6	103
813	STATs Shape the Active Enhancer Landscape of T Cell Populations. Cell, 2012, 151, 981-993.	13.5	325
814	NMNAT1 mutations cause Leber congenital amaurosis. Nature Genetics, 2012, 44, 1040-1045.	9.4	171
815	Novel Foxo1-dependent transcriptional programs control Treg cell function. Nature, 2012, 491, 554-559.	13.7	348
816	A Machine Learning Approach for Identifying Novel Cell Typeâ€“Specific Transcriptional Regulators of Myogenesis. PLoS Genetics, 2012, 8, e1002531.	1.5	35
817	Role of CCCTC binding factor (CTCF) and cohesin in the generation of single-cell diversity of Protocadherin-Î± gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9125-9130.	3.3	131
818	The impact of intronic single nucleotide polymorphisms and ethnic diversity for studies on the obesity gene FTO. Obesity Reviews, 2012, 13, 1096-1109.	3.1	37
819	A Two-Stage Evaluation of Genetic Variation in Immune and Inflammation Genes with Risk of Non-Hodgkin Lymphoma Identifies New Susceptibility Locus in 6p21.3 Region. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1799-1806.	1.1	22
820	The Effects of Alignment Error and Alignment Filtering on the Sitewise Detection of Positive Selection. Molecular Biology and Evolution, 2012, 29, 1125-1139.	3.5	164

#	Article	IF	Citations
821	Mitochondrial DNA Sequence Variation and Risk of Pancreatic Cancer. Cancer Research, 2012, 72, 686-695.	0.4	55
822	KLHL3 mutations cause familial hyperkalemic hypertension by impairing ion transport in the distal nephron. Nature Genetics, 2012, 44, 456-460.	9.4	281
823	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, R7.	13.9	188
824	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. Genome Biology, 2012, 13, R84.	13.9	140
825	EpiExplorer: live exploration and global analysis of large epigenomic datasets. Genome Biology, 2012, 13, R96.	13.9	72
826	Predicting the effects of frameshifting indels. Genome Biology, 2012, 13, R9.	13.9	99
827	Regulation of alternative splicing by the circadian clock and food related cues. Genome Biology, 2012, 13, R54.	13.9	89
828	Analysis of variation at transcription factor binding sites in Drosophila and humans. Genome Biology, 2012, 13, R49.	13.9	83
829	The Expanding Role of <scp>MBD</scp> Genes in Autism: Identification of a <scp>MECP2</scp> Duplication and Novel Alterations in <scp>MBD5</scp>, <scp>MBD6</scp>, and <scp>SETDB1</scp>. Autism Research, 2012, 5, 385-397.	2.1	81
830	A â€œForward Genomicsâ€•Approach Links Genotype to Phenotype using Independent Phenotypic Losses among Related Species. Cell Reports, 2012, 2, 817-823.	2.9	133
831	Discovery and characterization of new transcripts from RNA-seq data in mouse CD4+ T cells. Genomics, 2012, 100, 303-313.	1.3	12
832	Multilevel regulation of HIF-1 signaling by TTP. Molecular Biology of the Cell, 2012, 23, 4129-4141.	0.9	15
833	Deep Resequencing Unveils Genetic Architecture of ADIPOQ and Identifies a Novel Low-Frequency Variant Strongly Associated With Adiponectin Variation. Diabetes, 2012, 61, 1297-1301.	0.3	29
834	Large-scale discovery of enhancers from human heart tissue. Nature Genetics, 2012, 44, 89-93.	9.4	257
835	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	2.4	4,428
836	Identification of long non-protein coding RNAs in chicken skeletal muscle using next generation sequencing. Genomics, 2012, 99, 292-298.	1.3	173
837	Population genetics of cisâ€•regulatory sequences that operate during embryonic development in the sea urchin <scp>S</scp>trongylocentrotus purpuratus. Evolution & Development, 2012, 14, 152-167.	1.1	21
838	Regulation of eukaryotic gene expression by the untranslated gene regions and other non-coding elements. Cellular and Molecular Life Sciences, 2012, 69, 3613-3634.	2.4	481

#	Article	IF	Citations
839	A differential sequencing-based analysis of the C. elegans noncoding transcriptome. Rna, 2012, 18, 626-639.	1.6	11
840	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. Nature Methods, 2012, 9, 473-476.	9.0	562
841	Coordinated regulation of neuronal mRNA steady-state levels through developmentally controlled intron retention. Genes and Development, 2012, 26, 1209-1223.	2.7	247
842	Dynamics of enhancer chromatin signatures mark the transition from pluripotency to cell specification during embryogenesis. Genome Research, 2012, 22, 2043-2053.	2.4	219
843	Understanding MicroRNA Regulation: A computational perspective. IEEE Signal Processing Magazine, 2012, 29, 77-88.	4.6	7
844	Human box C/D snoRNA processing conservation across multiple cell types. Nucleic Acids Research, 2012, 40, 3676-3688.	6.5	79
845	Anchored Hybrid Enrichment for Massively High-Throughput Phylogenomics. Systematic Biology, 2012, 61, 727-744.	2.7	704
846	Mutations in the mechanotransduction protein PIEZO1 are associated with hereditary xerocytosis. Blood, 2012, 120, 1908-1915.	0.6	357
847	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. Cell, 2012, 149, 1368-1380.	13.5	912
848	Comparative Epigenomic Annotation of Regulatory DNA. Cell, 2012, 149, 1381-1392.	13.5	188
849	Global Analysis of RNA Secondary Structure in Two Metazoans. Cell Reports, 2012, 1, 69-82.	2.9	126
850	Prioritizing Genetic Variants for Causality on the Basis of Preferential Linkage Disequilibrium. American Journal of Human Genetics, 2012, 91, 422-434.	2.6	19
851	A common polymorphism near PER1 and the timing of human behavioral rhythms. Annals of Neurology, 2012, 72, 324-334.	2.8	48
852	NRE: a tool for exploring neutral loci in the human genome. BMC Bioinformatics, 2012, 13, 301.	1.2	29
853	Enhancer identification in mouse embryonic stem cells using integrative modeling of chromatin and genomic features. BMC Genomics, 2012, 13, 152.	1.2	60
854	Composition and organization of active centromere sequences in complex genomes. BMC Genomics, 2012, 13, 324.	1.2	20
855	Dose-dependent effects of small-molecule antagonists on the genomic landscape of androgen receptor binding. BMC Genomics, 2012, 13, 355.	1.2	7
856	Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. BMC Genomics, 2012, 13, 713.	1.2	16

#	Article	IF	Citations
857	A missense founder mutation in VLDLR is associated with Dysequilibrium Syndrome without quadrupedal locomotion. BMC Medical Genetics, 2012, 13, 80.	2.1	31
858	Distinct groups of repetitive families preserved in mammals correspond to different periods of regulatory innovations in vertebrates. Biology Direct, 2012, 7, 36.	1.9	20
859	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	6.0	1,695
860	Methods to Detect Selection on Noncoding DNA. Methods in Molecular Biology, 2012, 856, 141-159.	0.4	29
861	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2012, 40, Unit1.4.	25.8	86
862	A computational pipeline for comparative ChIP-seq analyses. Nature Protocols, 2012, 7, 45-61.	5.5	110
863	Global changes in the nuclear positioning of genes and intra- and interdomain genomic interactions that orchestrate B cell fate. Nature Immunology, 2012, 13, 1196-1204.	7.0	249
864	Dysfunction of lipid sensor GPR120 leads to obesity in both mouse and human. Nature, 2012, 483, 350-354.	13.7	572
865	The Long Non-Coding RNAs: A New (P)layer in the â€œDark Matterâ€• Frontiers in Genetics, 2011, 2, 107.	1.1	113
866	Lossâ€ofâ€Function Mutations in MC4R Are Very Rare in the Greek Severely Obese Adult Population. Obesity, 2012, 20, 2278-2282.	1.5	13
867	A Hypermorphic Missense Mutation in PLCG2 , Encoding Phospholipase Cî²2, Causes a Dominantly Inherited Autoinflammatory Disease with Immunodeficiency. American Journal of Human Genetics, 2012, 91, 713-720.	2.6	327
868	Multiple enhancers associated with ACAN suggest highly redundant transcriptional regulation in cartilage. Matrix Biology, 2012, 31, 328-337.	1.5	34
869	Selection on the Protein-Coding Genome. Methods in Molecular Biology, 2012, 856, 113-140.	0.4	26
870	Mutation in angiotensin II type 1 receptor disrupts its binding to angiotensin II leading to hypotension: An insight into hydrogen bonding patterns. Frontiers in Biology, 2012, 7, 477-484.	0.7	2
871	Mitochondrial DNA sequence variation is associated with free-living activity energy expenditure in the elderly. Biochimica Et Biophysica Acta - Bioenergetics, 2012, 1817, 1691-1700.	0.5	13
872	Extensive conservation of ancient microsynteny across metazoans due to cis-regulatory constraints. Genome Research, 2012, 22, 2356-2367.	2.4	126
873	Cis-regulation and conserved non-coding elements in amphioxus. Briefings in Functional Genomics, 2012, 11, 118-130.	1.3	8
874	Exploiting ancestral mammalian genomes for the prediction of human transcription factor binding sites. BMC Bioinformatics, 2012, 13, S2.	1.2	1

#	Article	IF	Citations
875	Identification of 3â€² gene ends using transcriptional and genomic conservation across vertebrates. BMC Genomics, 2012, 13, 708.	1.2	5
876	CBS: an open platform that integrates predictive methods and epigenetics information to characterize conserved regulatory features in multiple Drosophila genomes. BMC Genomics, 2012, 13, 688.	1.2	1
877	Design of a tobacco exon array with application to investigate the differential cadmium accumulation property in two tobacco varieties. BMC Genomics, 2012, 13, 674.	1.2	18
878	MirSNP, a database of polymorphisms altering miRNA target sites, identifies miRNA-related SNPs in GWAS SNPs and eQTLs. BMC Genomics, 2012, 13, 661.	1.2	255
879	Natural selection drives rapid evolution of mouse embryonic heart enhancers. BMC Systems Biology, 2012, 6, S1.	3.0	7
880	Transposable elements reveal a stem cell-specific class of long noncoding RNAs. Genome Biology, 2012, 13, R107.	13.9	462
881	A novel regulatory element between the human FGA and FGG genes. Thrombosis and Haemostasis, 2012, 108, 427-434.	1.8	12
882	Mutational Signatures of De-Differentiation in Functional Non-Coding Regions of Melanoma Genomes. PLoS Genetics, 2012, 8, e1002871.	1.5	11
883	Transcriptional Regulation of N-Acetylglutamate Synthase. PLoS ONE, 2012, 7, e29527.	1.1	26
884	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. PLoS ONE, 2012, 7, e34286.	1.1	8
885	A Selection Index for Gene Expression Evolution and Its Application to the Divergence between Humans and Chimpanzees. PLoS ONE, 2012, 7, e34935.	1.1	15
886	Transcriptional Enhancers in Protein-Coding Exons of Vertebrate Developmental Genes. PLoS ONE, 2012, 7, e35202.	1.1	50
887	Cis-Acting Polymorphisms Affect Complex Traits through Modifications of MicroRNA Regulation Pathways. PLoS ONE, 2012, 7, e36694.	1.1	37
888	Developing and Applying Heterogeneous Phylogenetic Models with XRate. PLoS ONE, 2012, 7, e36898.	1.1	5
889	Evaluation of the Role of SNCA Variants in Survival without Neurological Disease. PLoS ONE, 2012, 7, e42877.	1.1	7
890	Gene Isoform Specificity through Enhancer-Associated Antisense Transcription. PLoS ONE, 2012, 7, e43511.	1.1	27
891	miR-127 Protects Proximal Tubule Cells against Ischemia/Reperfusion: Identification of Kinesin Family Member 3B as miR-127 Target. PLoS ONE, 2012, 7, e44305.	1.1	59
892	Prediction of Conserved Precursors of miRNAs and Their Mature Forms by Integrating Position-Specific Structural Features. PLoS ONE, 2012, 7, e44314.	1.1	12

#	Article	IF	Citations
893	Cooperativity of Stress-Responsive Transcription Factors in Core Hypoxia-Inducible Factor Binding Regions. PLoS ONE, 2012, 7, e45708.	1.1	46
894	Whole Genome Sequencing and a New Bioinformatics Platform Allow for Rapid Gene Identification in D. melanogaster EMS Screens. Biology, 2012, 1, 766-777.	1.3	10
895	Clinical Implications of Human Population Differences in Genome-Wide Rates of Functional Genotypes. Frontiers in Genetics, 2012, 3, 211.	1.1	29
896	Resequencing of the auxiliary GABAB receptor subunit gene KCTD12 in chronic tinnitus. Frontiers in Systems Neuroscience, 2012, 6, 41.	1.2	29
897	Tracing recent adaptations in natural populations of the house mouse. , 0, , 315-333.		4
898	Cloning, expression analysis and sequence prediction of the CCAAT/enhancer-binding protein alpha gene of Qinchuan cattle. Genetics and Molecular Research, 2012, 11, 1651-1661.	0.3	6
899	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
900	Long identical multispecies elements in plant and animal genomes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1183-91.	3.3	43
901	The genomic basis of adaptive evolution in threespine sticklebacks. Nature, 2012, 484, 55-61.	13.7	1,600
902	Bioinformatics for personal genome interpretation. Briefings in Bioinformatics, 2012, 13, 495-512.	3.2	62
903	Deep sequencing of theLRRK2gene in 14,002 individuals reveals evidence of purifying selection and independent origin of the p.Arg1628Pro mutation in Europe. Human Mutation, 2012, 33, 1087-1098.	1.1	24
904	Long Noncoding RNA: Its Physiological and Pathological Roles. DNA and Cell Biology, 2012, 31, S-34-S-41.	0.9	88
905	More than 1000 ultraconserved elements provide evidence that turtles are the sister group of archosaurs. Biology Letters, 2012, 8, 783-786.	1.0	331
906	Ultraconserved Elements Anchor Thousands of Genetic Markers Spanning Multiple Evolutionary Timescales. Systematic Biology, 2012, 61, 717-726.	2.7	983
907	Ultraconserved elements are novel phylogenomic markers that resolve placental mammal phylogeny when combined with species-tree analysis. Genome Research, 2012, 22, 746-754.	2.4	349
908	Integrated genome analysis suggests that most conserved non-coding sequences are regulatory factor binding sites. Nucleic Acids Research, 2012, 40, 7858-7869.	6.5	36
909	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. Genome Biology and Evolution, 2012, 4, 586-601.	1.1	9
910	Analysis of microRNAs and their precursors in bovine early embryonic development. Molecular Human Reproduction, 2012, 18, 425-434.	1.3	92

#	Article	IF	Citations
911	wANNOVAR: annotating genetic variants for personal genomes via the web. Journal of Medical Genetics, 2012, 49, 433-436.	1.5	366
912	The UCSC Archaeal Genome Browser: 2012 update. Nucleic Acids Research, 2012, 40, D646-D652.	6.5	89
913	A map of the cis-regulatory sequences in the mouse genome. Nature, 2012, 488, 116-120.	13.7	1,306
914	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. Nature Biotechnology, 2012, 30, 99-104.	9.4	437
915	Uncovering cis-regulatory sequence requirements for context-specific transcription factor binding. Genome Research, 2012, 22, 2018-2030.	2.4	98
916	Evolutionary Genomics of Colias Phosphoglucose Isomerase (PGI) Introns. Journal of Molecular Evolution, 2012, 74, 96-111.	0.8	7
917	THE QTN PROGRAM AND THE ALLELES THAT MATTER FOR EVOLUTION: ALL THAT'S GOLD DOES NOT GLITTER. Evolution; International Journal of Organic Evolution, 2012, 66, 1-17.	1.1	623
918	Clustering of DNA words and biological function: A proof of principle. Journal of Theoretical Biology, 2012, 297, 127-136.	0.8	22
919	Analysis of genes regulated by the transcription factor LUMAN identifies ApoA4 as a target gene in dendritic cells. Molecular Immunology, 2012, 50, 66-73.	1.0	18
920	Genomeâ€wide identification and initial characterization of bovine long nonâ€coding <scp>RNA</scp>s from <scp>EST</scp> data. Animal Genetics, 2012, 43, 674-682.	0.6	61
921	Genetic diagnosis of neuroacanthocytosis disorders using exome sequencing. Movement Disorders, 2012, 27, 539-543.	2.2	22
922	Phosphoribosylpyrophosphate synthetase superactivity and recurrent infections is caused by a p.Val142Leu mutation in PRSâ€I. American Journal of Medical Genetics, Part A, 2012, 158A, 455-460.	0.7	26
923	Evidence for involvement of GNB1L in autism. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 61-71.	1.1	28
924	Molecular mechanisms of EGF signaling-dependent regulation of pipe, a gene crucial for dorsoventral axis formation in Drosophila. Development Genes and Evolution, 2012, 222, 1-17.	0.4	9
925	Meta-analysis of new genome-wide association studies of colorectal cancer risk. Human Genetics, 2012, 131, 217-234.	1.8	183
926	Mutations within lncRNAs are effectively selected against in fruitfly but not in human. Genome Biology, 2013, 14, R49.	13.9	62
927	Pervasive and dynamic protein binding sites of the mRNA transcriptome in Saccharomyces cerevisiae. Genome Biology, 2013, 14, R13.	13.9	91
928	High-resolution mapping of transcription factor binding sites on native chromatin. Epigenetics and Chromatin, 2013, 6, .	1.8	0

#	Article	IF	Citations
929	Dilated cardiomyopathy: the complexity of a diverse genetic architecture. Nature Reviews Cardiology, 2013, 10, 531-547.	6.1	763
930	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Nature Genetics, 2013, 45, 891-898.	9.4	350
932	Exome Sequencing Analysis: A Guide to Disease Variant Detection. Methods in Molecular Biology, 2013, 1038, 137-158.	0.4	18
933	A Parzen window-based approach for the detection of locally enriched transcription factor binding sites. BMC Bioinformatics, 2013, 14, 26.	1.2	4
934	CpG islands under selective pressure are enriched with H3K4me3, H3K27ac and H3K36me3 histone modifications. BMC Evolutionary Biology, 2013, 13, 145.	3.2	5
935	iSeeRNA: identification of long intergenic non-coding RNA transcripts from transcriptome sequencing data. BMC Genomics, 2013, 14, S7.	1.2	141
936	Selective constraint, background selection, and mutation accumulation variability within and between human populations. BMC Genomics, 2013, 14, 495.	1.2	16
937	Unsupervised genome-wide recognition of local relationship patterns. BMC Genomics, 2013, 14, 347.	1.2	59
938	The genomic signature of trait-associated variants. BMC Genomics, 2013, 14, 108.	1.2	45
939	Repeat-encoded poly-Q tracts show statistical commonalities across species. BMC Genomics, 2013, 14, 76.	1.2	6
940	CpGIMethPred: computational model for predicting methylation status of CpG islands in human genome. BMC Medical Genomics, 2013, 6, S13.	0.7	41
941	Functional dissection of the <scp>PROPEP2</scp> and <scp>PROPEP3</scp> promoters reveals the importance of <scp>WRKY</scp> factors in mediating microbeâ€associated molecular patternâ€induced expression. New Phytologist, 2013, 198, 1165-1177.	3.5	56
942	Computational methodology for ChIPâ€seq analysis. Quantitative Biology, 2013, 1, 54-70.	0.3	24
943	Selection and Adaptation in the Human Genome. Annual Review of Genomics and Human Genetics, 2013, 14, 467-489.	2.5	116
944	Major Histocompatibility Complex Genomics and Human Disease. Annual Review of Genomics and Human Genetics, 2013, 14, 301-323.	2.5	580
945	Extensive Cooperation of Immune Master Regulators IRF3 and NFÎºB in RNA Pol II Recruitment and Pause Release in Human Innate Antiviral Transcription. Cell Reports, 2013, 4, 959-973.	2.9	70
946	A Common Set of DNA Regulatory Elements Shapes Drosophila Appendages. Developmental Cell, 2013, 27, 306-318.	3.1	133
947	Whole-Exome Sequencing Identifies Mutated C12orf57 in Recessive Corpus Callosum Hypoplasia. American Journal of Human Genetics, 2013, 92, 392-400.	2.6	28

#	Article	IF	Citations
948	Mechanistic insights into mutually exclusive splicing in dynamin 1. Bioinformatics, 2013, 29, 2084-2087.	1.8	25
949	Dial M(<scp>RF</scp>) for myogenesis. FEBS Journal, 2013, 280, 3980-3990.	2.2	106
950	Computational prediction of the localization of microRNAs within their pre-miRNA. Nucleic Acids Research, 2013, 41, 7200-7211.	6.5	75
951	Conservation and Functional Element Discovery in 20 Angiosperm Plant Genomes. Molecular Biology and Evolution, 2013, 30, 1729-1744.	3.5	60
952	Exome Sequencing and Genome-Wide Linkage Analysis in 17 Families Illustrate the Complex Contribution of TTN Truncating Variants to Dilated Cardiomyopathy. Circulation: Cardiovascular Genetics, 2013, 6, 144-153.	5.1	95
953	Disclosing the crosstalk among DNA methylation, transcription factors, and histone marks in human pluripotent cells through discovery of DNA methylation motifs. Genome Research, 2013, 23, 2013-2029.	2.4	32
954	Deep conservation ofcis-regulatory elements in metazoans. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130020.	1.8	26
955	Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. Cell, 2013, 155, 1521-1531.	13.5	342
956	Molecular genetic relationships and some issues of systematics of rock lizards of the genus Darevskia (Squamata: Lacertidae) based on locus analysis of SINE-type repeats (Squam1). Russian Journal of Genetics, 2013, 49, 857-869.	0.2	2
957	Analysis of the DNA-Binding Profile and Function of TALE Homeoproteins Reveals Their Specialization and Specific Interactions with Hox Genes/Proteins. Cell Reports, 2013, 3, 1321-1333.	2.9	125
958	Combining in silico prediction and ribosome profiling in a genome-wide search for novel putatively coding sORFs. BMC Genomics, 2013, 14, 648.	1.2	79
959	Joint Linkage and Association Analysis with Exome Sequence Data Implicates SLC25A40 in Hypertriglyceridemia. American Journal of Human Genetics, 2013, 93, 1035-1045.	2.6	36
961	Identifying Rare Variants Associated with Complex Traits via Sequencing. Current Protocols in Human Genetics, 2013, 78, Unit 1.26.	3.5	29
962	miRTCat: a comprehensive map of human and mouse microRNA target sites including non-canonical nucleation bulges. Bioinformatics, 2013, 29, 1898-1899.	1.8	14
963	Chromatin connectivity maps reveal dynamic promoterâ€“enhancer long-range associations. Nature, 2013, 504, 306-310.	13.7	405
964	A practical guide for the functional annotation of genetic variations using SNPnexus. Briefings in Bioinformatics, 2013, 14, 437-447.	3.2	90
965	Virmid: accurate detection of somatic mutations with sample impurity inference. Genome Biology, 2013, 14, R90.	13.9	58
966	PARma: identification of microRNA target sites in AGO-PAR-CLIP data. Genome Biology, 2013, 14, R79.	13.9	53

#	Article	IF	Citations
967	Insights into snoRNA biogenesis and processing from PAR-CLIP of snoRNA core proteins and small RNA sequencing. Genome Biology, 2013, 14, R45.	13.9	129
968	Comprehensive characterization of erythroid-specific enhancers in the genomic regions of human KrÃ¼ppel-like factors. BMC Genomics, 2013, 14, 587.	1.2	32
969	Spatial-temporal targeting of lung-specific mesenchyme by a Tbx4enhancer. BMC Biology, 2013, 11, 111.	1.7	74
970	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. Molecular Cancer, 2013, 12, 140.	7.9	59
971	Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. Nature Genetics, 2013, 45, 1198-1206.	9.4	431
972	Towards Precision Medicine: Advances in Computational Approaches for the Analysis of Human Variants. Journal of Molecular Biology, 2013, 425, 4047-4063.	2.0	122
973	The Imprinted H19 LncRNA Antagonizes Let-7 MicroRNAs. Molecular Cell, 2013, 52, 101-112.	4.5	969
974	eXtasy: variant prioritization by genomic data fusion. Nature Methods, 2013, 10, 1083-1084.	9.0	153
975	Machine learning and genome annotation: a match meant to be?. Genome Biology, 2013, 14, 205.	13.9	72
976	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490
977	Prevalence of Multinucleotide Replacements in Evolution of Primates and Drosophila. Molecular Biology and Evolution, 2013, 30, 1315-1325.	3.5	28
978	The UCSC genome browser and associated tools. Briefings in Bioinformatics, 2013, 14, 144-161.	3.2	736
979	Applications of next-generation sequencing to phylogeography and phylogenetics. Molecular Phylogenetics and Evolution, 2013, 66, 526-538.	1.2	531
980	Analysis of alternative cleavage and polyadenylation by 3â€² region extraction and deep sequencing. Nature Methods, 2013, 10, 133-139.	9.0	386
981	A Recent Evolutionary Change Affects a Regulatory Element in the Human FOXP2 Gene. Molecular Biology and Evolution, 2013, 30, 844-852.	3.5	205
982	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	13.5	1,202
983	Comprehensive meta-analysis of Signal Transducers and Activators of Transcription (STAT) genomic binding patterns discerns cell-specific cis-regulatory modules. BMC Genomics, 2013, 14, 4.	1.2	67
984	A DNA-Centric Protein Interaction Map of Ultraconserved Elements Reveals Contribution of Transcription Factor Binding Hubs to Conservation. Cell Reports, 2013, 5, 531-545.	2.9	26

#	Article	IF	Citations
985	A Comprehensive Nuclear Receptor Network for Breast Cancer Cells. Cell Reports, 2013, 3, 538-551.	2.9	73
986	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. Genome Research, 2013, 23, 1235-1247.	2.4	205
987	Use of comparative genomics approaches to characterize interspecies differences in response to environmental chemicals: Challenges, opportunities, and research needs. Toxicology and Applied Pharmacology, 2013, 271, 372-385.	1.3	29
988	GEnomes Management Application (GEM.app): A New Software Tool for Large-Scale Collaborative Genome Analysis. Human Mutation, 2013, 34, 842-846.	1.1	69
989	Robust shifts in S100a9 expression with aging: A novel mechanism for chronic inflammation. Scientific Reports, 2013, 3, 1215.	1.6	96
990	Conserved non-coding elements and cis regulation: actions speak louder than words. Development (Cambridge), 2013, 140, 1385-1395.	1.2	53
991	A High-Resolution Enhancer Atlas of the Developing Telencephalon. Cell, 2013, 152, 895-908.	13.5	241
992	Designs for Massively Parallel Sequencing Approaches to Identify Causal Mutations in Human Immune Disorders. Methods in Molecular Biology, 2013, 979, 175-187.	0.4	0
993	Genome-wide Analysis Reveals TET- and TDG-Dependent 5-Methylcytosine Oxidation Dynamics. Cell, 2013, 153, 692-706.	13.5	440
994	The Vast, Conserved Mammalian lincRNome. PLoS Computational Biology, 2013, 9, e1002917.	1.5	62
995	Genome-wide inference of natural selection on human transcription factor binding sites. Nature Genetics, 2013, 45, 723-729.	9.4	121
996	Computational Identification of Active Enhancers in Model Organisms. Genomics, Proteomics and Bioinformatics, 2013, 11, 142-150.	3.0	15
997	Dense genotyping of immune-related disease regions identifies 14 new susceptibility loci for juvenile idiopathic arthritis. Nature Genetics, 2013, 45, 664-669.	9.4	337
998	MicroRNA target site identification by integrating sequence and binding information. Nature Methods, 2013, 10, 630-633.	9.0	56
999	New Insights from Existing Sequence Data: Generating Breakthroughs without a Pipette. Molecular Cell, 2013, 49, 605-617.	4.5	12
1000	Population genomics of <scp>P</scp>acific lamprey: adaptive variation in a highly dispersive species. Molecular Ecology, 2013, 22, 2898-2916.	2.0	166
1001	Untranslated Gene Regions and Other Non-coding Elements. SpringerBriefs in Biochemistry and Molecular Biology, 2013, , 1-56.	0.3	4
1002	Reciprocal regulation of Rag expression in thymocytes by the zinc-finger proteins, Zfp608 and Zfp609. Genes and Immunity, 2013, 14, 7-12.	2.2	9

#	Article	IF	Citations
1003	The Evolution of Lineage-Specific Regulatory Activities in the Human Embryonic Limb. Cell, 2013, 154, 185-196.	13.5	202
1004	Cell Engineering with Synthetic Messenger RNA. Methods in Molecular Biology, 2013, 969, 3-28.	0.4	13
1005	Hepatitis B virus X protein (HBx)-related long noncoding RNA (lncRNA) down-regulated expression by HBx (Dreh) inhibits hepatocellular carcinoma metastasis by targeting the intermediate filament protein vimentin. Hepatology, 2013, 57, 1882-1892.	3.6	299
1006	84. Cytokine, 2013, 63, 263.	1.4	0
1007	Structure-aided prediction of mammalian transcription factor complexes in conserved non-coding elements. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130029.	1.8	30
1008	Whole Exome Sequencing Identifies a Causal RBM20 Mutation in a Large Pedigree With Familial Dilated Cardiomyopathy. Circulation: Cardiovascular Genetics, 2013, 6, 317-326.	5.1	57
1009	Many human accelerated regions are developmental enhancers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130025.	1.8	188
1010	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. Science, 2013, 342, 1241006.	6.0	209
1011	Microbiome in Human Health and Disease. Science Progress, 2013, 96, 153-170.	1.0	18
1012	Hyper conserved elements in vertebrate mRNA 3â€²-UTRs reveal a translational network of RNA-binding proteins controlled by HuR. Nucleic Acids Research, 2013, 41, 3201-3216.	6.5	38
1013	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. , 2013, , .		216
1014	Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions. Genome Research, 2013, 23, 777-788.	2.4	203
1015	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. Genome Research, 2013, 23, 2136-2148.	2.4	51
1016	The transcription start site landscape of C. elegans. Genome Research, 2013, 23, 1348-1361.	2.4	58
1017	The million mutation project: A new approach to genetics in Caenorhabditis elegans. Genome Research, 2013, 23, 1749-1762.	2.4	382
1018	Association of polymorphisms and haplotype in the region of TRIT1, MYCL1 and MFSD2A with the risk and clinicopathological features of gastric cancer in a southeast Chinese population. Carcinogenesis, 2013, 34, 1018-1024.	1.3	14
1019	CLIP-based prediction of mammalian microRNA binding sites. Nucleic Acids Research, 2013, 41, e138-e138.	6.5	84
1020	All SNPs Are Not Created Equal: Genome-Wide Association Studies Reveal a Consistent Pattern of Enrichment among Functionally Annotated SNPs. PLoS Genetics, 2013, 9, e1003449.	1.5	268

#	Article	IF	Citations
1021	A Model-Based Analysis of GC-Biased Gene Conversion in the Human and Chimpanzee Genomes. PLoS Genetics, 2013, 9, e1003684.	1.5	74
1022	Contributions of Protein-Coding and Regulatory Change to Adaptive Molecular Evolution in Murid Rodents. PLoS Genetics, 2013, 9, e1003995.	1.5	106
1023	The Conserved Intronic Cleavage and Polyadenylation Site of CstF-77 Gene Imparts Control of 3â€² End Processing Activity through Feedback Autoregulation and by U1 snRNP. PLoS Genetics, 2013, 9, e1003613.	1.5	44
1024	Exome Sequencing Reveals Novel Rare Variants in the Ryanodine Receptor and Calcium Channel Genes in Malignant Hyperthermia Families. Anesthesiology, 2013, 119, 1054-1065.	1.3	56
1025	The rs391957 variant cis-regulating oncogene GRP78 expression contributes to the risk of hepatocellular carcinoma. Carcinogenesis, 2013, 34, 1273-1280.	1.3	33
1026	The Enhancer Landscape during Early Neocortical Development Reveals Patterns of Dense Regulation and Co-option. PLoS Genetics, 2013, 9, e1003728.	1.5	33
1027	Parallel Evolution of Chordate Cis-Regulatory Code for Development. PLoS Genetics, 2013, 9, e1003904.	1.5	16
1028	Analysis of CDS-located miRNA target sites suggests that they can effectively inhibit translation. Genome Research, 2013, 23, 604-615.	2.4	299
1029	Identification of Biologically Relevant Enhancers in Human Erythroid Cells. Journal of Biological Chemistry, 2013, 288, 8433-8444.	1.6	49
1030	Heterogeneous Tempo and Mode of Conserved Noncoding Sequence Evolution among Four Mammalian Orders. Genome Biology and Evolution, 2013, 5, 2330-2343.	1.1	25
1031	The mystery of extreme non-coding conservation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130021.	1.8	71
1032	Microfluidic affinity and ChIP-seq analyses converge on a conserved FOXP2-binding motif in chimp and human, which enables the detection of evolutionarily novel targets. Nucleic Acids Research, 2013, 41, 5991-6004.	6.5	36
1033	Segmenting the human genome based on states of neutral genetic divergence. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14699-14704.	3.3	18
1034	Mapping of the IRF8 Gene Identifies a 3â€²UTR Variant Associated with Risk of Chronic Lymphocytic Leukemia but not Other Common Non-Hodgkin Lymphoma Subtypes. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 461-466.	1.1	13
1035	Genomic Dynamics of Transposable Elements in the Western Clawed Frog (Silurana tropicalis). Genome Biology and Evolution, 2013, 5, 998-1009.	1.1	13
1036	Evolution and diversity of copy number variation in the great ape lineage. Genome Research, 2013, 23, 1373-1382.	2.4	161
1037	OLego: fast and sensitive mapping of spliced mRNA-Seq reads using small seeds. Nucleic Acids Research, 2013, 41, 5149-5163.	6.5	116
1038	Human MicroRNAs Originated from Two Periods at Accelerated Rates in Mammalian Evolution. Molecular Biology and Evolution, 2013, 30, 613-626.	3.5	34

#	Article	IF	Citations
1039	Integrated Analysis of Dysregulated lncRNA Expression in Fetal Cardiac Tissues with Ventricular Septal Defect. PLoS ONE, 2013, 8, e77492.	1.1	41
1040	One size does not fit all: On how Markov model order dictates performance of genomic sequence analyses. Nucleic Acids Research, 2013, 41, 1416-1424.	6.5	23
1041	Non-polyadenylated transcription in embryonic stem cells reveals novel non-coding RNA related to pluripotency and differentiation. Nucleic Acids Research, 2013, 41, 6300-6315.	6.5	28
1042	A Scan for Human-Specific Relaxation of Negative Selection Reveals Unexpected Polymorphism in Proteasome Genes. Molecular Biology and Evolution, 2013, 30, 1808-1815.	3.5	23
1043	Deep Proteome Coverage Based on Ribosome Profiling Aids Mass Spectrometry-based Protein and Peptide Discovery and Provides Evidence of Alternative Translation Products and Near-cognate Translation Initiation Events*. Molecular and Cellular Proteomics, 2013, 12, 1780-1790.	2.5	154
1044	A graphical model method for integrating multiple sources of genome-scale data. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 469-87.	0.2	5
1045	Deciphering the 8q24.21 association for glioma. Human Molecular Genetics, 2013, 22, 2293-2302.	1.4	50
1046	RhesusBase: a knowledgebase for the monkey research community. Nucleic Acids Research, 2013, 41, D892-D905.	6.5	27
1047	Inference of Natural Selection from Interspersed Genomic Elements Based on Polymorphism and Divergence. Molecular Biology and Evolution, 2013, 30, 1159-1171.	3.5	77
1048	Topoisomerase II regulates yeast genes with singular chromatin architectures. Nucleic Acids Research, 2013, 41, 9243-9256.	6.5	14
1049	lncRNome: a comprehensive knowledgebase of human long noncoding RNAs. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat034.	1.4	126
1050	Mutations in gamma adducin are associated with inherited cerebral palsy. Annals of Neurology, 2013, 74, 805-814.	2.8	44
1051	Somatic gain-of-function mutations in PIK3CA in patients with macrodactyly. Human Molecular Genetics, 2013, 22, 444-451.	1.4	144
1052	A yeast oneâ€hybrid and microfluidicsâ€based pipeline to map mammalian gene regulatory networks. Molecular Systems Biology, 2013, 9, 682.	3.2	35
1053	eXtasy simplified-towards opening the black box. , 2013, , .		0
1055	Widespread splicing changes in human brain development and aging. Molecular Systems Biology, 2013, 9, 633.	3.2	183
1056	Î²-Catenin signaling regulates Foxa2 expression during endometrial hyperplasia formation. Oncogene, 2013, 32, 3477-3482.	2.6	43
1057	Self-catalytic DNA Depurination Underlies Human Î²-Globin Gene Mutations at Codon 6 That Cause Anemias and Thalassemias. Journal of Biological Chemistry, 2013, 288, 11581-11589.	1.6	10

#	Article	IF	Citations
1058	Frac-seq reveals isoform-specific recruitment to polyribosomes. Genome Research, 2013, 23, 1615-1623.	2.4	93
1059	Missense mutation in the MEN1 gene discovered through whole exome sequencing co-segregates with familial hyperparathyroidism. Genetical Research, 2013, 95, 114-120.	0.3	11
1060	Novel common and rare genetic determinants of paraoxonase activity: FTO, SERPINA12, and ITGAL. Journal of Lipid Research, 2013, 54, 552-560.	2.0	17
1061	Computational methods to detect conserved non-genic elements in phylogenetically isolated genomes: application to zebrafish. Nucleic Acids Research, 2013, 41, e151-e151.	6.5	84
1062	RNA-seq identified a super-long intergenic transcript functioning in adipogenesis. RNA Biology, 2013, 10, 990-1001.	1.5	31
1064	Population Genomics and Transcriptional Consequences of Regulatory Motif Variation in Globally Diverse Saccharomyces cerevisiae Strains. Molecular Biology and Evolution, 2013, 30, 1605-1613.	3.5	11
1065	Variation at 10p12.2 and 10p14 influences risk of childhood B-cell acute lymphoblastic leukemia and phenotype. Blood, 2013, 122, 3298-3307.	0.6	147
1066	Not Junk After All: Non-Protein-Coding DNA Carries Extensive Biological Information. , 2013, , .		1
1067	Co-binding by YY1 identifies the transcriptionally active, highly conserved set of CTCF-bound regions in primate genomes. Genome Biology, 2013, 14, R148.	13.9	68
1068	Sequence signatures extracted from proximal promoters can be used to predict distal enhancers. Genome Biology, 2013, 14, R117.	13.9	32
1070	Predicting tissue specific transcription factor binding sites. BMC Genomics, 2013, 14, 796.	1.2	25
1071	Analysis of non-synonymous single-nucleotide polymorphisms and population variability of PLD2 gene associated with hypertension. International Journal of Bioinformatics Research and Applications, 2013, 9, 227.	0.1	5
1072	Modulation of Epidermal Transcription Circuits in Psoriasis: New Links between Inflammation and Hyperproliferation. PLoS ONE, 2013, 8, e79253.	1.1	49
1073	Profiling of Androgen Response in Rainbow Trout Pubertal Testis: Relevance to Male Gonad Development and Spermatogenesis. PLoS ONE, 2013, 8, e53302.	1.1	36
1074	A Phylogeny of Birds Based on Over 1,500 Loci Collected by Target Enrichment and High-Throughput Sequencing. PLoS ONE, 2013, 8, e54848.	1.1	287
1075	Bidirectional Promoters as Important Drivers for the Emergence of Species-Specific Transcripts. PLoS ONE, 2013, 8, e57323.	1.1	25
1076	Gene Expression Profile of the Hippocampus of Rats Subjected to Chronic Immobilization Stress. PLoS ONE, 2013, 8, e57621.	1.1	35
1077	cis-Regulatory Complexity within a Large Non-Coding Region in the Drosophila Genome. PLoS ONE, 2013, 8, e60137.	1.1	8

#	Article	IF	Citations
1078	Exome Sequencing of 47 Chinese Families with Cone-Rod Dystrophy: Mutations in 25 Known Causative Genes. PLoS ONE, 2013, 8, e65546.	1.1	52
1079	SIFT Indel: Predictions for the Functional Effects of Amino Acid Insertions/Deletions in Proteins. PLoS ONE, 2013, 8, e77940.	1.1	108
1080	Fine-Mapping an Association of FSHR with Preterm Birth in a Finnish Population. PLoS ONE, 2013, 8, e78032.	1.1	15
1081	Comparison of Ultra-Conserved Elements in Drosophilids and Vertebrates. PLoS ONE, 2013, 8, e82362.	1.1	14
1082	Spastic Paraplegia Type 7 Is Associated with Multiple Mitochondrial DNA Deletions. PLoS ONE, 2014, 9, e86340.	1.1	49
1083	Deep Profiling of the Novel Intermediate-Size Noncoding RNAs in Intraerythrocytic Plasmodium falciparum. PLoS ONE, 2014, 9, e92946.	1.1	14
1084	Studying the System-Level Involvement of MicroRNAs in Parkinson's Disease. PLoS ONE, 2014, 9, e93751.	1.1	21
1085	Characterization of Human Pseudogene-Derived Non-Coding RNAs for Functional Potential. PLoS ONE, 2014, 9, e93972.	1.1	51
1086	Mammalian TBX1 Preferentially Binds and Regulates Downstream Targets Via a Tandem T-site Repeat. PLoS ONE, 2014, 9, e95151.	1.1	33
1087	Drosophila 3â€² UTRs Are More Complex than Protein-Coding Sequences. PLoS ONE, 2014, 9, e97336.	1.1	5
1088	Dynamic Epigenetic Control of Highly Conserved Noncoding Elements. PLoS ONE, 2014, 9, e109326.	1.1	5
1089	Increased Expression of MERTK is Associated with a Unique Form of Canine Retinopathy. PLoS ONE, 2014, 9, e114552.	1.1	7
1090	Genetic Profiling for Risk Reduction in Human Cardiovascular Disease. Genes, 2014, 5, 214-234.	1.0	12
1091	Extensive translation of small Open Reading Frames revealed by Poly-Ribo-Seq. ELife, 2014, 3, e03528.	2.8	286
1092	A novel virus-inducible enhancer of the interferon-Î² gene with tightly linked promoter and enhancer activities. Nucleic Acids Research, 2014, 42, 12537-12554.	6.5	30
1093	The apparent enhancement of CpG transversions in primate lineage is a consequence of multiple replacements. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450011.	0.3	2
1094	Lineage-Specific Conserved Noncoding Sequences of Plant Genomes: Their Possible Role in Nucleosome Positioning. Genome Biology and Evolution, 2014, 6, 2527-2542.	1.1	15
1095	Identifying and mapping cell-type-specific chromatin programming of gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E645-54.	3.3	31

#	Article	IF	Citations
1096	Underreplicated Regions in Drosophila melanogaster Are Enriched with Fast-Evolving Genes and Highly Conserved Noncoding Sequences. Genome Biology and Evolution, 2014, 6, 2050-2060.	1.1	12
1097	Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. Genome Biology, 2014, 15, 512.	3.8	475
1098	De novo prediction of cis-regulatory elements and modules through integrative analysis of a large number of ChIP datasets. BMC Genomics, 2014, 15, 1047.	1.2	11
1099	OncoCis: annotation of cis-regulatory mutations in cancer. Genome Biology, 2014, 15, 485.	3.8	22
1100	Identification of anHMGB3Frameshift Mutation in a Family With an X-linked Colobomatous Microphthalmia Syndrome Using Whole-Genome and X-Exome Sequencing. JAMA Ophthalmology, 2014, 132, 1215.	1.4	21
1101	VAS: a convenient web portal for efficient integration of genomic features with millions of genetic variants. BMC Genomics, 2014, 15, 886.	1.2	1
1102	Application of high-throughput sequencing for studying genomic variations in congenital heart disease. Briefings in Functional Genomics, 2014, 13, 51-65.	1.3	16
1103	FLAGS, frequently mutated genes in public exomes. BMC Medical Genomics, 2014, 7, 64.	0.7	108
1104	Differences in DNA methylation between human neuronal and glial cells are concentrated in enhancers and non-CpG sites. Nucleic Acids Research, 2014, 42, 109-127.	6.5	187
1105	Discovering Functional DNA Elements Using Population Genomic Information: A Proof of Concept Using Human mtDNA. Genome Biology and Evolution, 2014, 6, 1542-1548.	1.1	2
1106	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.	3.3	635
1107	Tissue-Specific RNA-Seq in Human Evoked Inflammation Identifies Blood and Adipose LincRNA Signatures of Cardiometabolic Diseases. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 902-912.	1.1	75
1108	Genome-wide distribution of Auts2 binding localizes with active neurodevelopmental genes. Translational Psychiatry, 2014, 4, e431-e431.	2.4	51
1109	MicroRNA binding sites inC. elegans3â€² UTRs. RNA Biology, 2014, 11, 693-701.	1.5	9
1110	Regulation of the Dynamic Chromatin Architecture of the Epidermal Differentiation Complex Is Mediated by a c-Jun/AP-1-Modulated Enhancer. Journal of Investigative Dermatology, 2014, 134, 2371-2380.	0.3	29
1111	Sex- and Tissue-Specific Functions of Drosophila Doublesex Transcription Factor Target Genes. Developmental Cell, 2014, 31, 761-773.	3.1	122
1112	CHD7 and retinoic acid signaling cooperate to regulate neural stem cell and inner ear development in mouse models of CHARGE syndrome. Human Molecular Genetics, 2014, 23, 434-448.	1.4	57
1113	Biased, Non-equivalent Gene-Proximal and -Distal Binding Motifs of Orphan Nuclear Receptor TR4 in Primary Human Erythroid Cells. PLoS Genetics, 2014, 10, e1004339.	1.5	6

#	Article	IF	Citations
1114	Erasing Errors due to Alignment Ambiguity When Estimating Positive Selection. Molecular Biology and Evolution, 2014, 31, 1979-1993.	3.5	53
1115	The ATXN2-SH2B3 locus is associated with peripheral arterial disease: an electronic medical record-based genome-wide association study. Frontiers in Genetics, 2014, 5, 166.	1.1	40
1116	8.2% of the Human Genome Is Constrained: Variation in Rates of Turnover across Functional Element Classes in the Human Lineage. PLoS Genetics, 2014, 10, e1004525.	1.5	213
1117	Phylogenetic Gaussian Process Model for the Inference of Functionally Important Regions in Protein Tertiary Structures. PLoS Computational Biology, 2014, 10, e1003429.	1.5	21
1118	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481
1119	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. PLoS Genetics, 2014, 10, e1004610.	1.5	105
1120	Tracing the Evolution of Lineage-Specific Transcription Factor Binding Sites in a Birth-Death Framework. PLoS Computational Biology, 2014, 10, e1003771.	1.5	25
1121	The Functional Consequences of Variation in Transcription Factor Binding. PLoS Genetics, 2014, 10, e1004226.	1.5	187
1122	The Role of the 3' Untranslated Region in the Post-Transcriptional Regulation of KLF6 Gene Expression in Hepatocellular Carcinoma. Cancers, 2014, 6, 28-41.	1.7	4
1123	Altered Chromatin Occupancy of Master Regulators Underlies Evolutionary Divergence in the Transcriptional Landscape of Erythroid Differentiation. PLoS Genetics, 2014, 10, e1004890.	1.5	42
1124	Epigenome-Guided Analysis of the Transcriptome of Plaque Macrophages during Atherosclerosis Regression Reveals Activation of the Wnt Signaling Pathway. PLoS Genetics, 2014, 10, e1004828.	1.5	31
1125	Integrating Diverse Datasets Improves Developmental Enhancer Prediction. PLoS Computational Biology, 2014, 10, e1003677.	1.5	149
1126	Approximation to the Distribution of Fitness Effects across Functional Categories in Human Segregating Polymorphisms. PLoS Genetics, 2014, 10, e1004697.	1.5	59
1127	Noncoding origins of anthropoid traits and a new null model of transposon functionalization. Genome Research, 2014, 24, 1469-1484.	2.4	31
1128	Polo-like kinase 4 transcription is activated via CRE and NRF1 elements, repressed by DREAM through CDE/CHR sites and deregulated by HPV E7 protein. Nucleic Acids Research, 2014, 42, 163-180.	6.5	48
1129	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. Cell, 2014, 159, 1511-1523.	13.5	546
1130	The transcription factor p53: Not a repressor, solely an activator. Cell Cycle, 2014, 13, 3037-3058.	1.3	119
1131	Activation of Muscle Enhancers by MyoD and epigenetic modifiers. Journal of Cellular Biochemistry, 2014, 115, n/a-n/a.	1.2	15

#	Article	IF	Citations
1132	TCIRG1-Associated Congenital Neutropenia. Human Mutation, 2014, 35, 824-827.	1.1	35
1133	The role of the interactome in the maintenance of deleterious variability in human populations. Molecular Systems Biology, 2014, 10, 752.	3.2	28
1134	Two Novel Mutations in theBCKDK(Branched-Chain Keto-Acid Dehydrogenase Kinase) Gene Are Responsible for a Neurobehavioral Deficit in Two Pediatric Unrelated Patients. Human Mutation, 2014, 35, 470-477.	1.1	70
1135	Exome Sequencing as a Diagnostic Tool for Pediatricâ€Onset Ataxia. Human Mutation, 2014, 35, 45-49.	1.1	91
1136	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	6.0	300
1137	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
1138	A novel reannotation strategy for dissecting DNA methylation patterns of human long intergenic non-coding RNAs in cancers. Nucleic Acids Research, 2014, 42, 8258-8270.	6.5	40
1139	Human skin color is influenced by an intergenic DNA polymorphism regulating transcription of the nearby BNC2 pigmentation gene. Human Molecular Genetics, 2014, 23, 5750-5762.	1.4	73
1140	Genome-Wide Analysis of Functional and Evolutionary Features of Tele-Enhancers. G3: Genes, Genomes, Genetics, 2014, 4, 579-593.	0.8	3
1141	Approaches to identify genetic variants that influence the risk for onset of fragile X-associated primary ovarian insufficiency (FXPOI): a preliminary study. Frontiers in Genetics, 2014, 5, 260.	1.1	15
1142	Large-scale modeling of condition-specific gene regulatory networks by information integration and inference. Nucleic Acids Research, 2014, 42, e166-e166.	6.5	12
1143	Identification and functional analysis of long non-coding RNAs in mouse cleavage stage embryonic development based on single cell transcriptome data. BMC Genomics, 2014, 15, 845.	1.2	74
1144	Comparative genomic data of the Avian Phylogenomics Project. GigaScience, 2014, 3, 26.	3.3	117
1145	Divergent evolutionary rates in vertebrate and mammalian specific conserved non-coding elements (CNEs) in echolocating mammals. BMC Evolutionary Biology, 2014, 14, 261.	3.2	7
1146	The CHR site: definition and genome-wide identification of a cell cycle transcriptional element. Nucleic Acids Research, 2014, 42, 10331-10350.	6.5	82
1147	Cooperative gene regulation by microRNA pairs and their identification using a computational workflow. Nucleic Acids Research, 2014, 42, 7539-7552.	6.5	72
1148	RBPmap: a web server for mapping binding sites of RNA-binding proteins. Nucleic Acids Research, 2014, 42, W361-W367.	6.5	409
1149	The Catalytic Function of Hormone-Sensitive Lipase is Essential for Fertility in Male Mice. Endocrinology, 2014, 155, 3047-3053.	1.4	12

#	Article	IF	Citations
1150	A New Genome-Wide Method to Track Horizontally Transferred Sequences: Application to Drosophila. Genome Biology and Evolution, 2014, 6, 416-432.	1.1	10
1151	Simultaneous mapping of transcript ends at single-nucleotide resolution and identification of widespread promoter-associated non-coding RNA governed by TATA elements. Nucleic Acids Research, 2014, 42, 3736-3749.	6.5	93
1152	STarMir: a web server for prediction of microRNA binding sites. Nucleic Acids Research, 2014, 42, W114-W118.	6.5	92
1153	Effects of genetic variations on microRNA: targetÂinteractions. Nucleic Acids Research, 2014, 42, 9543-9552.	6.5	45
1154	Plzf as a Candidate Gene Predisposing the Spontaneously Hypertensive Rat to Hypertension, Left Ventricular Hypertrophy, and Interstitial Fibrosis. American Journal of Hypertension, 2014, 27, 99-106.	1.0	25
1155	Characterization of Human Chromosomal Material Exchange with Regard to the Chromosome Translocations Using Next-Generation Sequencing Data. Genome Biology and Evolution, 2014, 6, 3015-3024.	1.1	2
1156	DNA Methylation is Associated with an Increased Level of Conservation at Nondegenerate Nucleotides in Mammals. Molecular Biology and Evolution, 2014, 31, 387-396.	3.5	14
1157	MutPred Splice: machine learning-based prediction of exonic variants that disrupt splicing. Genome Biology, 2014, 15, R19.	13.9	135
1158	Epigenetic modifications are associated with inter-species gene expression variation in primates. Genome Biology, 2014, 15, 547.	3.8	72
1159	Association of Levels of Fasting Glucose and Insulin With Rare Variants at the Chromosome 11p11.2-MADD Locus. Circulation: Cardiovascular Genetics, 2014, 7, 374-382.	5.1	12
1160	A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications. Nucleic Acids Research, 2014, 42, W83-W87.	6.5	6
1161	Noninvasive and quantitative live imaging reveals a potential stressâ€responsive enhancer in the failing heart. FASEB Journal, 2014, 28, 1870-1879.	0.2	9
1162	Regulation of MEIS1 by distal enhancer elements in acute leukemia. Leukemia, 2014, 28, 138-146.	3.3	17
1163	Haplotype structure and positive selection at TLR1. European Journal of Human Genetics, 2014, 22, 551-557.	1.4	20
1164	Development, validation and highâ€throughput analysis of sequence markers in nonmodel species. Molecular Ecology Resources, 2014, 14, 352-360.	2.2	27
1165	MicroRNAs Cooperatively Inhibit a Network of Tumor Suppressor Genes to Promote Pancreatic Tumor Growth and Progression. Gastroenterology, 2014, 146, 268-277.e18.	0.6	141
1166	SIZE DISTRIBUTION OF GENE FAMILIES IN A GENOME. Mathematical Models and Methods in Applied Sciences, 2014, 24, 697-717.	1.7	13
1167	Genome-wide signals of positive selection in human evolution. Genome Research, 2014, 24, 885-895.	2.4	200

#	Article	IF	Citations
1168	Argonaute-Bound Small RNAs from Promoter-Proximal RNA Polymerase II. Cell, 2014, 156, 920-934.	13.5	103
1169	Determining pathogenicity of genetic variants in hypertrophic cardiomyopathy: importance of periodic reassessment. Genetics in Medicine, 2014, 16, 286-293.	1.1	83
1170	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	1.4	222
1171	Single Nucleotide Polymorphisms in MicroRNA Binding Sites of Oncogenes: Implications in Cancer and Pharmacogenomics. OMICS A Journal of Integrative Biology, 2014, 18, 142-154.	1.0	42
1172	Computational Approaches and Resources in Single Amino Acid Substitutions Analysis Toward Clinical Research. Advances in Protein Chemistry and Structural Biology, 2014, 94, 365-423.	1.0	22
1173	Identifying mRNA sequence elements for target recognition by human Argonaute proteins. Genome Research, 2014, 24, 775-785.	2.4	34
1174	Alu elements shape the primate transcriptome by cis-regulation of RNA editing. Genome Biology, 2014, 15, R28.	13.9	97
1175	NRG3 gene is associated with the risk and age at onset of Alzheimer disease. Journal of Neural Transmission, 2014, 121, 183-192.	1.4	24
1176	Emerging trends of long nonâ€coding <scp>RNA</scp>s in gene activation. FEBS Journal, 2014, 281, 34-45.	2.2	38
1177	Evolution of transcription factor binding in metazoans â€" mechanisms and functional implications. Nature Reviews Genetics, 2014, 15, 221-233.	7.7	207
1178	Obesity-associated variants within FTO form long-range functional connections with IRX3. Nature, 2014, 507, 371-375.	13.7	1,079
1179	Laying a solid foundation for Manhattan â€" â€˜setting the functional basis for the post-GWAS eraâ€™. Trends in Genetics, 2014, 30, 140-149.	2.9	84
1180	Genomic tools in acute myeloid leukemia: From the bench to the bedside. Cancer, 2014, 120, 1134-1144.	2.0	21
1181	Recessive mutations in a distal PTF1A enhancer cause isolated pancreatic agenesis. Nature Genetics, 2014, 46, 61-64.	9.4	255
1182	Sequence analysis of bovine C/EBPÎ´ gene and its adipogenic effects on fibroblasts. Molecular Biology Reports, 2014, 41, 251-257.	1.0	12
1183	Patterns of coding variation in the complete exomes of three Neandertals. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6666-6671.	3.3	223
1184	Mitochondrial DNA sequence associations with dementia and amyloid-Î² in elderly African Americans. Neurobiology of Aging, 2014, 35, 442.e1-442.e8.	1.5	27
1185	miR-1, miR-10b, miR-155, and miR-191 are novel regulators of BDNF. Cellular and Molecular Life Sciences, 2014, 71, 4443-4456.	2.4	146

#	Article	IF	Citations
1186	No Gene in the Genome Makes Sense Except in the Light of Evolution. Annual Review of Genomics and Human Genetics, 2014, 15, 71-92.	2.5	19
1187	Contrasting X-Linked and Autosomal Diversity across 14 Human Populations. American Journal of Human Genetics, 2014, 94, 827-844.	2.6	61
1188	Comparative population genomics: power and principles for the inference of functionality. Trends in Genetics, 2014, 30, 133-139.	2.9	48
1189	Genomic Features and Regulatory Roles of Intermediate-Sized Non-Coding RNAs in Arabidopsis. Molecular Plant, 2014, 7, 514-527.	3.9	77
1190	High-resolution mapping of transcription factor binding sites on native chromatin. Nature Methods, 2014, 11, 203-209.	9.0	170
1191	Accurate molecular diagnosis of phenylketonuria and tetrahydrobiopterin-deficient hyperphenylalaninemias using high-throughput targeted sequencing. European Journal of Human Genetics, 2014, 22, 528-534.	1.4	36
1192	The evolution of lncRNA repertoires and expression patterns in tetrapods. Nature, 2014, 505, 635-640.	13.7	898
1193	Peroxisome Proliferator-activated Receptor Î³ Regulates Genes Involved in Insulin/Insulin-like Growth Factor Signaling and Lipid Metabolism during Adipogenesis through Functionally Distinct Enhancer Classes. Journal of Biological Chemistry, 2014, 289, 708-722.	1.6	39
1194	A general framework for estimating the relative pathogenicity of human genetic variants. Nature Genetics, 2014, 46, 310-315.	9.4	5,167
1195	Identification of expressed and conserved human noncoding RNAs. Rna, 2014, 20, 236-251.	1.6	47
1196	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. Science, 2014, 346, 1007-1012.	6.0	244
1197	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. Blood, 2014, 123, 1927-1937.	0.6	169
1198	Targeted Analysis of Whole Genome Sequence Data to Diagnose Genetic Cardiomyopathy. Circulation: Cardiovascular Genetics, 2014, 7, 751-759.	5.1	53
1199	The RIDL hypothesis: transposable elements as functional domains of long noncoding RNAs. Rna, 2014, 20, 959-976.	1.6	246
1200	N-terminal Proteomics and Ribosome Profiling Provide a Comprehensive View of the Alternative Translation Initiation Landscape in Mice and Men. Molecular and Cellular Proteomics, 2014, 13, 1245-1261.	2.5	123
1201	Long non-coding RNA and microRNAs might act in regulating the expression of BARD1 mRNAs. International Journal of Biochemistry and Cell Biology, 2014, 54, 356-367.	1.2	73
1202	Exome Sequencing Identifies a Novel Frameshift Mutation ofMYO6as the Cause of Autosomal Dominant Nonsyndromic Hearing Loss in a Chinese Family. Annals of Human Genetics, 2014, 78, 410-423.	0.3	10
1203	The Most Deeply Conserved Noncoding Sequences in Plants Serve Similar Functions to Those in Vertebrates Despite Large Differences in Evolutionary Rates. Plant Cell, 2014, 26, 946-961.	3.1	38

#	Article	IF	Citations
1204	A homolog of lariat-debranching enzyme modulates turnover of branched RNA. Rna, 2014, 20, 1337-1348.	1.6	34
1205	Widespread contribution of transposable elements to the innovation of gene regulatory networks. Genome Research, 2014, 24, 1963-1976.	2.4	408
1206	A survey of tools for variant analysis of next-generation genome sequencing data. Briefings in Bioinformatics, 2014, 15, 256-278.	3.2	480
1207	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
1208	Translation of Small Open Reading Frames within Unannotated RNA Transcripts in Saccharomyces cerevisiae. Cell Reports, 2014, 7, 1858-1866.	2.9	150
1209	The genomic substrate for adaptive radiation in African cichlid fish. Nature, 2014, 513, 375-381.	13.7	874
1210	Exploring the genesis and functions of Human Accelerated Regions sheds light on their role in human evolution. Current Opinion in Genetics and Development, 2014, 29, 15-21.	1.5	108
1211	5mC Oxidation by Tet2 Modulates Enhancer Activity and Timing of Transcriptome Reprogramming during Differentiation. Molecular Cell, 2014, 56, 286-297.	4.5	285
1212	Conservation in first introns is positively associated with the number of exons within genes and the presence of regulatory epigenetic signals. BMC Genomics, 2014, 15, 526.	1.2	66
1213	Identification of cis-regulatory modules encoding temporal dynamics during development. BMC Genomics, 2014, 15, 534.	1.2	10
1214	Evaluation of gene-based association tests for analyzing rare variants using Genetic Analysis Workshop 18 data. BMC Proceedings, 2014, 8, S9.	1.8	7
1215	Genetic Analysis Workshop 18 single-nucleotide variant prioritization based on protein impact, sequence conservation, and gene annotation. BMC Proceedings, 2014, 8, S11.	1.8	10
1216	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
1217	Recurrent duplications of the annexin A1 gene (ANXA1) in autism spectrum disorders. Molecular Autism, 2014, 5, 28.	2.6	13
1218	glbase: a framework for combining, analyzing and displaying heterogeneous genomic and high-throughput sequencing data. Cell Regeneration, 2014, 3, 3:1.	1.1	79
1219	Candidate genes and functional noncoding variants identified in a canine model of obsessive-compulsive disorder. Genome Biology, 2014, 15, R25.	13.9	78
1220	GluA2 mRNA distribution and regulation by miR-124 in hippocampal neurons. Molecular and Cellular Neurosciences, 2014, 61, 1-12.	1.0	46
1221	Developmental transcriptome analysis of human erythropoiesis. Human Molecular Genetics, 2014, 23, 4528-4542.	1.4	45

#	Article	IF	Citations
1222	Identification and characterization of long intergenic non-coding RNAs related to mouse liver development. Molecular Genetics and Genomics, 2014, 289, 1225-1235.	1.0	28
1223	Identifying microRNA targets in different gene regions. BMC Bioinformatics, 2014, 15, S4.	1.2	112
1224	Multiscale representation of genomic signals. Nature Methods, 2014, 11, 689-694.	9.0	31
1225	Genomic Landscape of Human, Bat, and Ex Vivo DNA Transposon Integrations. Molecular Biology and Evolution, 2014, 31, 1816-1832.	3.5	30
1226	Inference of Transcriptional Networks in Arabidopsis through Conserved Noncoding Sequence Analysis. Plant Cell, 2014, 26, 2729-2745.	3.1	57
1227	Menzerathâ€“Altmann law in mammalian exons reflects the dynamics of gene structure evolution. Computational Biology and Chemistry, 2014, 53, 134-143.	1.1	9
1228	Phevor Combines Multiple Biomedical Ontologies for Accurate Identification of Disease-Causing Alleles in Single Individuals and Small Nuclear Families. American Journal of Human Genetics, 2014, 94, 599-610.	2.6	175
1229	Border patrol: Insights into the unique role of perlecan/heparan sulfate proteoglycan 2 at cell and tissue borders. Matrix Biology, 2014, 34, 64-79.	1.5	137
1230	Transcriptional Network Analysis in Muscle Reveals AP-1 as a Partner of PGC-1Î± in the Regulation of the Hypoxic Gene Program. Molecular and Cellular Biology, 2014, 34, 2996-3012.	1.1	32
1231	Conserved regions of the DMD 3â€² UTR regulate translation and mRNA abundance in cultured myotubes. Neuromuscular Disorders, 2014, 24, 693-706.	0.3	4
1232	Common features of microRNA target prediction tools. Frontiers in Genetics, 2014, 5, 23.	1.1	356
1233	Evaluating the Accuracy and Efficiency of Multiple Sequence Alignment Methods. Evolutionary Bioinformatics, 2014, 10, EBO.S19199.	0.6	37
1234	Multiple conserved regulatory domains promote Fezf2 expression in the developing cerebral cortex. Neural Development, 2014, 9, 6.	1.1	21
1235	Global transcriptome analysis and enhancer landscape of human primary T follicular helper and T effector lymphocytes. Blood, 2014, 124, 3719-3729.	0.6	55
1236	Functional Annotation of Putative Regulatory Elements at Cancer Susceptibility Loci. Cancer Informatics, 2014, 13s2, CIN.S13789.	0.9	6
1237	P2-030: INVESTIGATING THE ROLE OF CLU, PICALM, AND CR1 IN ALZHEIMER'S DISEASE. , 2014, 10, P481-P481.		0
1238	cis MEP: an integrated repository of genomic epigenetic profiles and cis-regulatory modules in Drosophila. BMC Systems Biology, 2014, 8, S8.	3.0	9
1239	Population Genetic Simulations of Complex Phenotypes with Implications for Rare Variant Association Tests. Genetic Epidemiology, 2015, 39, 35-44.	0.6	16

#	Article	IF	Citations
1240	The achaeteâ€scute complex in Diptera: patterns of noncoding sequence evolution. Journal of Evolutionary Biology, 2015, 28, 1770-1781.	0.8	7
1241	An ensemble SVM model for the accurate prediction of non-canonical MicroRNA targets. , 2015, , .		12
1242	The conservation and signatures of lincRNAs in Mareksâ€™s disease of chicken. Scientific Reports, 2015, 5, 15184.	1.6	69
1243	The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. Scientific Reports, 2015, 5, 15065.	1.6	24
1244	Systematically Prioritizing Functional Differentially Methylated Regions (fDMRs) by Integrating Multi-omics Data in Colorectal Cancer. Scientific Reports, 2015, 5, 12789.	1.6	6
1245	An alignment-free method to find and visualise rearrangements between pairs of DNA sequences. Scientific Reports, 2015, 5, 10203.	1.6	27
1246	A novel DNA sequence motif in human and mouse genomes. Scientific Reports, 2015, 5, 10444.	1.6	0
1247	A deeper confusion. Evolution: Education and Outreach, 2015, 8, .	0.3	0
1248	BALR-6 regulates cell growth and cell survival in B-lymphoblastic leukemia. Molecular Cancer, 2015, 14, 214.	7.9	29
1249	MtiBase: a database for decoding microRNA target sites located within CDS and 5â€²UTR regions from CLIP-Seq and expression profile datasets. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav102.	1.4	23
1250	Problems with the nested granularity of feature domains in bioinformatics: the eXtasy case. BMC Bioinformatics, 2015, 16, S2.	1.2	5
1251	Using epigenomics data to predict gene expression in lung cancer. BMC Bioinformatics, 2015, 16, S10.	1.2	39
1252	MicroRNA target prediction using thermodynamic and sequence curves. BMC Genomics, 2015, 16, 999.	1.2	28
1253	Functionally conserved enhancers with divergent sequences in distant vertebrates. BMC Genomics, 2015, 16, 882.	1.2	18
1254	Genome-wide predictors of NF-ÎºB recruitment and transcriptional activity. BioData Mining, 2015, 8, 37.	2.2	14
1255	Comparative genomics of Steinernema reveals deeply conserved gene regulatory networks. Genome Biology, 2015, 16, 200.	3.8	77
1256	miRGate: a curated database of human, mouse and rat miRNAâ€“mRNA targets. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav035.	1.4	87
1257	Whole exome sequencing identifies rare protein-coding variants in BehÃ§et's disease. Arthritis and Rheumatology, 2015, 68, n/a-n/a.	2.9	9

#	Article	IF	Citations
1258	An Empirical Prior Improves Accuracy for Bayesian Estimation of Transcription Factor Binding Site Frequencies within Gene Promoters. Bioinformatics and Biology Insights, 2015, 9S4, BBI.S29330.	1.0	2
1259	Unusual Novel SnoRNA-Like RNAs in Drosophila melanogaster. Non-coding RNA, 2015, 1, 139-150.	1.3	3
1260	Pain-related stress during the Neonatal Intensive Care Unit stay and SLC6A4 methylation in very preterm infants. Frontiers in Behavioral Neuroscience, 2015, 9, 99.	1.0	78
1261	Dendritic targeting of short and long 3â€² UTR BDNF mRNA is regulated by BDNF or NT-3 and distinct sets of RNA-binding proteins. Frontiers in Molecular Neuroscience, 2015, 8, 62.	1.4	39
1262	Translational Activation of Oskar mRNA: Reevaluation of the Role and Importance of a 5' Regulatory Element. PLoS ONE, 2015, 10, e0125849.	1.1	6
1263	Long Noncoding RNA Expression during Human B-Cell Development. PLoS ONE, 2015, 10, e0138236.	1.1	80
1264	Genome-Wide Detection and Analysis of Multifunctional Genes. PLoS Computational Biology, 2015, 11, e1004467.	1.5	36
1265	Identification of High-Impact cis-Regulatory Mutations Using Transcription Factor Specific Random Forest Models. PLoS Computational Biology, 2015, 11, e1004590.	1.5	21
1266	YAP1 Exerts Its Transcriptional Control via TEAD-Mediated Activation of Enhancers. PLoS Genetics, 2015, 11, e1005465.	1.5	296
1267	Conserved piRNA Expression from a Distinct Set of piRNA Cluster Loci in Eutherian Mammals. PLoS Genetics, 2015, 11, e1005652.	1.5	73
1268	c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280.	1.1	20
1269	Handling Permutation in Sequence Comparison: Genome-Wide Enhancer Prediction in Vertebrates by a Novel Non-Linear Alignment Scoring Principle. PLoS ONE, 2015, 10, e0141487.	1.1	1
1270	Analysis of the Entire Ryanodine Receptor type 1 and Alpha 1 Subunit of the Dihydropyridine Receptor (CACNA1S) Coding Regions for Variants Associated with Malignant Hyperthermia in Australian Families. Anaesthesia and Intensive Care, 2015, 43, 157-166.	0.2	30
1271	Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility. Epigenetics and Chromatin, 2015, 8, 16.	1.8	100
1272	Genome-wide features of neuroendocrine regulation in Drosophila by the basic helix-loop-helix transcription factor DIMMED. Nucleic Acids Research, 2015, 43, 2199-2215.	6.5	23
1274	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. Human Genetics, 2015, 134, 823-835.	1.8	133
1275	Gene Regulatory Networks. , 2015, , 41-77.		5
1276	Genomic landscape of rat strain and substrain variation. BMC Genomics, 2015, 16, 357.	1.2	84

#	Article	IF	Citations
1277	Genome-wide ultraconserved elements exhibit higher phylogenetic informativeness than traditional gene markers in percomorph fishes. Molecular Phylogenetics and Evolution, 2015, 92, 140-146.	1.2	68
1278	Sequential data selection for predicting the pathogenic effects of sequence variation. , 2015, , .		1
1279	Finding smORFs: getting closer. Genome Biology, 2015, 16, 189.	3.8	24
1280	Systematic analysis of the Hmga2 3â€² UTR identifies many independent regulatory sequences and a novel interaction between distal sites. Rna, 2015, 21, 1346-1360.	1.6	36
1281	Functional Variants in DPYSL2 Sequence Increase Risk of Schizophrenia and Suggest a Link to mTOR Signaling. G3: Genes, Genomes, Genetics, 2015, 5, 61-72.	0.8	39
1282	Selection Against Maternal microRNA Target Sites in Maternal Transcripts. G3: Genes, Genomes, Genetics, 2015, 5, 2199-2207.	0.8	26
1283	Competition between DNA methylation and transcription factors determines binding of NRF1. Nature, 2015, 528, 575-579.	13.7	401
1284	Hypoxia-induced gene expression results from selective mRNA partitioning to the endoplasmic reticulum. Nucleic Acids Research, 2015, 43, 3219-3236.	6.5	38
1285	Integrating motif, DNA accessibility and gene expression data to build regulatory maps in an organism. Nucleic Acids Research, 2015, 43, 3998-4012.	6.5	36
1286	Assessing the impact of mutations found in next generation sequencing data over human signaling pathways. Nucleic Acids Research, 2015, 43, W270-W275.	6.5	16
1287	Splicing of many human genes involves sites embedded within introns. Nucleic Acids Research, 2015, 43, 4721-4732.	6.5	31
1288	ADCY5 -related dyskinesia. Neurology, 2015, 85, 2026-2035.	1.5	163
1289	Functional Genomics Analysis of Big Data Identifies Novel Peroxisome Proliferatorâ€“Activated Receptor Î³ Target Single Nucleotide Polymorphisms Showing Association With Cardiometabolic Outcomes. Circulation: Cardiovascular Genetics, 2015, 8, 842-851.	5.1	1
1290	Singleâ€“base pair differences in a shared motif determine differential Rhodopsin expression. Science, 2015, 350, 1258-1261.	6.0	49
1291	Identification of Lineage-SpecificCis-Regulatory Modules Associated with Variation in Transcription Factor Binding and Chromatin Activity Using Ornsteinâ€“Uhlenbeck Models. Molecular Biology and Evolution, 2015, 32, 2441-2455.	3.5	11
1292	Predicting chromatin organization using histone marks. Genome Biology, 2015, 16, 162.	3.8	98
1293	Predicting RAD-seq Marker Numbers across the Eukaryotic Tree of Life. Genome Biology and Evolution, 2015, 7, 3207-3225.	1.1	36
1294	Identifying transcriptional cisâ€regulatory modules in animal genomes. Wiley Interdisciplinary Reviews: Developmental Biology, 2015, 4, 59-84.	5.9	54

#	Article	IF	Citations
1295	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. Bioinformatics, 2015, 31, 17-24.	1.8	39
1296	Identification and Computational Analysis of Gene Regulatory Elements. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083642.	0.2	7
1297	Genomic Perspectives of Transcriptional Regulation in Forebrain Development. Neuron, 2015, 85, 27-47.	3.8	136
1298	Genome-wide discovery of human splicing branchpoints. Genome Research, 2015, 25, 290-303.	2.4	222
1299	A Distinct Vitreo-retinal Dystrophy with Early-onset Cataract from RecessiveKCNJ13Mutations. Ophthalmic Genetics, 2015, 36, 79-84.	0.5	25
1300	Identification of 4438 novel lincRNAs involved in mouse pre-implantation embryonic development. Molecular Genetics and Genomics, 2015, 290, 685-697.	1.0	24
1301	Target enrichment of ultraconserved elements from arthropods provides a genomic perspective on relationships among <scp>H</scp>ymenoptera. Molecular Ecology Resources, 2015, 15, 489-501.	2.2	244
1302	Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. Cell Cycle, 2015, 14, 1148-1155.	1.3	14
1303	Evolution of Darwinâ€™s finches and their beaks revealed by genome sequencing. Nature, 2015, 518, 371-375.	13.7	766
1304	A composite enhancer regulates p63 gene expression in epidermal morphogenesis and in keratinocyte differentiation by multiple mechanisms. Nucleic Acids Research, 2015, 43, 862-874.	6.5	30
1305	Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimerâ€™s disease. Nature, 2015, 518, 365-369.	13.7	526
1306	C2H2 zinc finger proteins greatly expand the human regulatory lexicon. Nature Biotechnology, 2015, 33, 555-562.	9.4	271
1307	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	5.8	73
1308	Using the plurality of codon positions to identify deleterious variants in human exomes. Bioinformatics, 2015, 31, 301-305.	1.8	3
1309	A long non-coding RNA links calreticulin-mediated immunogenic cell removal to RB1 transcription. Oncogene, 2015, 34, 5046-5054.	2.6	39
1310	RBFOX and PTBP1 proteins regulate the alternative splicing of micro-exons in human brain transcripts. Genome Research, 2015, 25, 1-13.	2.4	187
1311	MIWI and piRNA-mediated cleavage of messenger RNAs in mouse testes. Cell Research, 2015, 25, 193-207.	5.7	266
1312	A method for calculating probabilities of fitness consequences for point mutations across the human genome. Nature Genetics, 2015, 47, 276-283.	9.4	247

#	Article	IF	Citations
1313	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression. Genome Research, 2015, 25, 544-557.	2.4	74
1314	Sparse expression bases in cancer reveal tumor drivers. Nucleic Acids Research, 2015, 43, 1332-1344.	6.5	27
1315	The Genome 10K Project: A Way Forward. Annual Review of Animal Biosciences, 2015, 3, 57-111.	3.6	294
1316	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. Nature Communications, 2015, 6, 6178.	5.8	186
1317	Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. Nature Communications, 2015, 6, 6315.	5.8	73
1318	Prioritizing genes for X-linked diseases using population exome data. Human Molecular Genetics, 2015, 24, 599-608.	1.4	18
1319	Whole-genome sequence of the Tibetan frog Nanorana parkeri and the comparative evolution of tetrapod genomes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1257-62.	3.3	159
1320	Genome-wide CIITA-binding profile identifies sequence preferences that dictate function versus recruitment. Nucleic Acids Research, 2015, 43, 3128-3142.	6.5	28
1321	An integrative analysis of TFBS-clustered regions reveals new transcriptional regulation models on the accessible chromatin landscape. Scientific Reports, 2015, 5, 8465.	1.6	41
1322	Running spell-check to identify regulatory variants. Nature Genetics, 2015, 47, 853-855.	9.4	5
1323	MIR retrotransposon sequences provide insulators to the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4428-37.	3.3	104
1324	Discovery, Annotation, and Functional Analysis of Long Noncoding RNAs Controlling Cell-Cycle Gene Expression and Proliferation in Breast Cancer Cells. Molecular Cell, 2015, 59, 698-711.	4.5	179
1325	Systematic Screening of Promoter Regions Pinpoints Functional Cis-Regulatory Mutations in a Cutaneous Melanoma Genome. Molecular Cancer Research, 2015, 13, 1218-1226.	1.5	29
1326	Tissue Expression Pattern of PMK-2 p38 MAPK Is Established by the miR-58 Family in C. elegans. PLoS Genetics, 2015, 11, e1004997.	1.5	36
1327	College of American Pathologists' Laboratory Standards for Next-Generation Sequencing Clinical Tests. Archives of Pathology and Laboratory Medicine, 2015, 139, 481-493.	1.2	315
1328	Large-scale genomics unveil polygenic architecture of human cortical surface area. Nature Communications, 2015, 6, 7549.	5.8	30
1329	A post-transcriptional mechanism pacing expression of neural genes with precursor cell differentiation status. Nature Communications, 2015, 6, 7576.	5.8	36
1330	Animal Models in Biomedical Research. , 2015, , 1497-1534.		11

#	Article	IF	Citations
1331	Highly Constrained Intergenic Drosophila Ultraconserved Elements Are Candidate ncRNAs. Genome Biology and Evolution, 2015, 7, 689-698.	1.1	16
1332	A single nucleotide polymorphism associated with isolated cleft lip and palate, thyroid cancer and hypothyroidism alters the activity of an oral epithelium and thyroid enhancer near FOXE1. Human Molecular Genetics, 2015, 24, 3895-3907.	1.4	36
1333	GenomeCons: a web server for manipulating multiple genome sequence alignments and their consensus sequences. Bioinformatics, 2015, 31, 1293-1295.	1.8	3
1334	Re-annotation of presumed noncoding disease/trait-associated genetic variants by integrative analyses. Scientific Reports, 2015, 5, 9453.	1.6	13
1335	Difference in microRNA expression and editing profile of lung tissues from different pig breeds related to immune responses to HP-PRRSV. Scientific Reports, 2015, 5, 9549.	1.6	43
1336	Pan-cancer transcriptome analysis reveals long noncoding RNAs with conserved function. RNA Biology, 2015, 12, 628-642.	1.5	85
1337	Allele-specific transcriptional regulation of IRF4 in melanocytes is mediated by chromatin looping of the intronic rs12203592 enhancer to the IRF4 promoter. Human Molecular Genetics, 2015, 24, 2649-2661.	1.4	47
1338	Efficient representation of uncertainty in multiple sequence alignments using directed acyclic graphs. BMC Bioinformatics, 2015, 16, 108.	1.2	16
1339	The recently identified modifier of murine metastable epialleles, Rearranged L-Myc Fusion, is involved in maintaining epigenetic marks at CpG island shores and enhancers. BMC Biology, 2015, 13, 21.	1.7	16
1340	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. Genome Biology, 2015, 16, 14.	3.8	165
1341	Psoriasis drug development and GWAS interpretation through in silico analysis of transcription factor binding sites. Clinical and Translational Medicine, 2015, 4, 13.	1.7	40
1342	Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. Genetics, 2015, 200, 295-308.	1.2	44
1343	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	9.4	384
1344	SRSF2 Mutations Contribute to Myelodysplasia by Mutant-Specific Effects on Exon Recognition. Cancer Cell, 2015, 27, 617-630.	7.7	449
1345	Structural imprints in vivo decode RNA regulatory mechanisms. Nature, 2015, 519, 486-490.	13.7	639
1346	A Novel Promoter Mutation (HBB: c.-75G>T) Was Identified as a Cause of Î²+-Thalassemia. Hemoglobin, 2015, 39, 115-120.	0.4	4
1347	Discovering short linear protein motif based on selective training of profile hidden Markov models. Journal of Theoretical Biology, 2015, 377, 75-84.	0.8	5
1348	The RCSB Protein Data Bank: views of structural biology for basic and applied research and education. Nucleic Acids Research, 2015, 43, D345-D356.	6.5	461

#	Article	IF	Citations
1349	Splicing predictions reliably classify different types of alternative splicing. Rna, 2015, 21, 813-823.	1.6	22
1350	Feather Development Genes and Associated Regulatory Innovation Predate the Origin of Dinosauria. Molecular Biology and Evolution, 2015, 32, 23-28.	3.5	57
1351	Identification of a Nonsynonymous Polymorphism in the SVEP1 Gene Associated With Altered Clinical Outcomes in Septic Shock*. Critical Care Medicine, 2015, 43, 101-108.	0.4	29
1352	MiR-203 Involves in Neuropathic Pain Development and Represses Rap1a Expression in Nerve Growth Factor Differentiated Neuronal PC12 Cells. Clinical Journal of Pain, 2015, 31, 36-43.	0.8	32
1353	A lncRNA regulates alternative splicing via establishment of a splicing-specific chromatin signature. Nature Structural and Molecular Biology, 2015, 22, 370-376.	3.6	229
1354	Genomic approaches for understanding the genetics of complex disease. Genome Research, 2015, 25, 1432-1441.	2.4	75
1355	Genomic approaches to studying human-specific developmental traits. Development (Cambridge), 2015, 142, 3100-3112.	1.2	26
1356	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. Carcinogenesis, 2015, 36, 1314-1326.	1.3	15
1357	Diving deeper to predict noncoding sequence function. Nature Methods, 2015, 12, 925-926.	9.0	4
1358	Proximal Regulatory Elements with Emphasis on CpG Rich Regions. , 2015, , 285-296.		0
1359	microRNA-185 modulates low density lipoprotein receptor expression as a key posttranscriptional regulator. Atherosclerosis, 2015, 243, 523-532.	0.4	60
1360	Detection and characterization of small insertion and deletion genetic variants in modern layer chicken genomes. BMC Genomics, 2015, 16, 562.	1.2	10
1361	The identification of cis-regulatory elements: A review from a machine learning perspective. BioSystems, 2015, 138, 6-17.	0.9	51
1362	RNA-Seq analysis identifies genes associated with differential reproductive success under drought-stress in accessions of wild barley Hordeum spontaneum. BMC Plant Biology, 2015, 15, 134.	1.6	62
1363	Extensive identification and analysis of conserved small ORFs in animals. Genome Biology, 2015, 16, 179.	3.8	180
1364	Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. Nature Genetics, 2015, 47, 1393-1401.	9.4	202
1365	Combined serial analysis of gene expression and transcription factor binding site prediction identifies novel-candidate-target genes of Nr2e1 in neocortex development. BMC Genomics, 2015, 16, 545.	1.2	9
1366	Identification of linc-NeD125, a novel long non coding RNA that hosts miR-125b-1 and negatively controls proliferation of human neuroblastoma cells. RNA Biology, 2015, 12, 1323-1337.	1.5	23

#	Article	IF	Citations
1367	Mutations in DCHS1 cause mitral valve prolapse. Nature, 2015, 525, 109-113.	13.7	150
1368	A Simulation Approach for Change-Points on Phylogenetic Trees. Journal of Computational Biology, 2015, 22, 10-24.	0.8	2
1369	The interplay between DNA methylation and sequence divergence in recent human evolution. Nucleic Acids Research, 2015, 43, 8204-8214.	6.5	67
1370	Trends in genome dynamics among major orders of insects revealed through variations in protein families. BMC Genomics, 2015, 16, 583.	1.2	5
1371	Assessing Recent Selection and Functionality at Long Noncoding RNA Loci in the Mouse Genome. Genome Biology and Evolution, 2015, 7, 2432-2444.	1.1	12
1372	Evolution of the unspliced transcriptome. BMC Evolutionary Biology, 2015, 15, 166.	3.2	7
1373	Predicting effects of noncoding variants with deep learningâ€“based sequence model. Nature Methods, 2015, 12, 931-934.	9.0	1,714
1374	Absence of canonical marks of active chromatin in developmentally regulated genes. Nature Genetics, 2015, 47, 1158-1167.	9.4	75
1375	miR-92a Corrects CD34+ Cell Dysfunction in Diabetes by Modulating Core Circadian Genes Involved in Progenitor Differentiation. Diabetes, 2015, 64, 4226-4237.	0.3	27
1376	Functional classification of 15 million SNPs detected from diverse chicken populations. DNA Research, 2015, 22, 205-217.	1.5	40
1377	Modeling Human Severe Combined Immunodeficiency and Correction by CRISPR/Cas9-Enhanced Gene Targeting. Cell Reports, 2015, 12, 1668-1677.	2.9	95
1378	Comparative Analysis of Gene Regulatory Networks: From Network Reconstruction to Evolution. Annual Review of Cell and Developmental Biology, 2015, 31, 399-428.	4.0	170
1379	Scrutinizing the FTO locus: compelling evidence for a complex, long-range regulatory context. Human Genetics, 2015, 134, 1183-1193.	1.8	22
1380	Genomic variant annotation and prioritization with ANNOVAR and wANNOVAR. Nature Protocols, 2015, 10, 1556-1566.	5.5	727
1381	Rare k-mer DNA: Identification of sequence motifs and prediction of CpG island and promoter. Journal of Theoretical Biology, 2015, 387, 88-100.	0.8	13
1382	Why the DNA self-depurination mechanism operates in HB-Î² but not in Î²-globin paralogs HB-Î´, HB-É›1, HB-Î³1 and HB-Î³2. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 778, 11-17.	0.4	1
1383	Inferring Selective Constraint from Population Genomic Data Suggests Recent Regulatory Turnover in the Human Brain. Genome Biology and Evolution, 2015, 7, 3511-3528.	1.1	25
1384	A 3â€² untranslated region variant in FMR1 eliminates neuronal activity-dependent translation of FMRP by disrupting binding of the RNA-binding protein HuR. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6553-61.	3.3	33

#	Article	IF	Citations
1385	U2AF1 mutations alter splice site recognition in hematological malignancies. Genome Research, 2015, 25, 14-26.	2.4	238
1386	Mutations in IFT172 cause isolated retinal degeneration and Bardetâ€“Biedl syndrome. Human Molecular Genetics, 2015, 24, 230-242.	1.4	136
1387	The tempo and mode of New World monkey evolution and biogeography in the context of phylogenomic analysis. Molecular Phylogenetics and Evolution, 2015, 82, 386-399.	1.2	66
1388	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. Genome Research, 2015, 25, 257-267.	2.4	94
1389	Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression. Briefings in Bioinformatics, 2015, 16, 393-412.	3.2	58
1390	Current trend of annotating single nucleotide variation in humans â€“ A case study on SNVrap. Methods, 2015, 79-80, 32-40.	1.9	12
1391	Design and application of a target capture sequencing of exons and conserved non-coding sequences for the rat. BMC Genomics, 2016, 17, 593.	1.2	12
1392	Hierarchical Map of Orthologous Genomic Regions Reconstructed from Two Closely Related Genomes: Cucumber Case Study. Plant Genome, 2016, 9, plantgenome2015.10.0099.	1.6	1
1393	Transcriptional Interference Promotes Rapid Expression Divergence ofDrosophilaNested Genes. Genome Biology and Evolution, 2016, 8, 3149-3158.	1.1	8
1394	Identifying and functionally characterizing tissue-specific and ubiquitously expressed human lncRNAs. Oncotarget, 2016, 7, 7120-7133.	0.8	114
1395	Cluster Analysis of p53 Binding Site Sequences Reveals Subsets with Different Functions. Cancer Informatics, 2016, 15, CIN.S39968.	0.9	1
1396	A new view of transcriptome complexity and regulation through the lens of local splicing variations. ELife, 2016, 5, e11752.	2.8	385
1397	Does conservation account for splicing patterns?. BMC Genomics, 2016, 17, 787.	1.2	15
1398	Tools for Sequence-Based miRNA Target Prediction: What to Choose?. International Journal of Molecular Sciences, 2016, 17, 1987.	1.8	353
1399	Conservation of the Exon-Intron Structure of Long Intergenic Non-Coding RNA Genes in Eutherian Mammals. Life, 2016, 6, 27.	1.1	18
1400	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. BMC Bioinformatics, 2016, 17, 404.	1.2	100
1401	Association of polymorphisms in genes of factors involved in regulation of splicing of cystic fibrosis transmembrane conductance regulator mRNA with acute respiratory distress syndrome in children with pneumonia. Critical Care, 2016, 20, 281.	2.5	6
1402	Disruption of an Evolutionarily Novel Synaptic Expression Pattern in Autism. PLoS Biology, 2016, 14, e1002558.	2.6	73

#	Article	IF	Citations
1403	Bat Accelerated Regions Identify a Bat Forelimb Specific Enhancer in the HoxD Locus. PLoS Genetics, 2016, 12, e1005738.	1.5	51
1404	Downstream Antisense Transcription Predicts Genomic Features That Define the Specific Chromatin Environment at Mammalian Promoters. PLoS Genetics, 2016, 12, e1006224.	1.5	15
1405	Linking Core Promoter Classes to Circadian Transcription. PLoS Genetics, 2016, 12, e1006231.	1.5	7
1406	Coordinately Co-opted Multiple Transposable Elements Constitute an Enhancer for wnt5a Expression in the Mammalian Secondary Palate. PLoS Genetics, 2016, 12, e1006380.	1.5	47
1407	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. PLoS ONE, 2016, 11, e0157521.	1.1	8
1408	A Novel HRAS Mutation Independently Contributes to Left Ventricular Hypertrophy in a Family with a Known MYH7 Mutation. PLoS ONE, 2016, 11, e0168501.	1.1	13
1409	Long Noncoding RNA Identification: Comparing Machine Learning Based Tools for Long Noncoding Transcripts Discrimination. BioMed Research International, 2016, 2016, 1-14.	0.9	1,176
1410	NovelRP1L1Variants and Genotypeâ€“Photoreceptor Microstructural Phenotype Associations in Cohort of Japanese Patients With Occult Macular Dystrophy. , 2016, 57, 4837.		54
1411	A comprehensive characterization of rare mitochondrial DNA variants in neuroblastoma. Oncotarget, 2016, 7, 49246-49258.	0.8	25
1412	Sequencing of Genes Involved in the Movement of Calcium across Human Skeletal Muscle Sarcoplasmic Reticulum: Continuing the Search for Genes Associated with Malignant Hyperthermia. Anaesthesia and Intensive Care, 2016, 44, 762-768.	0.2	12
1413	Ancient hybridization and genomic stabilization in a swordtail fish. Molecular Ecology, 2016, 25, 2661-2679.	2.0	91
1414	Functional annotation of noncoding variants and prioritization of cancer-associated lncRNAs in lung cancer. Oncology Letters, 2016, 12, 222-230.	0.8	8
1415	Complex mode of inheritance in holoprosencephaly revealed by whole exome sequencing. Clinical Genetics, 2016, 89, 659-668.	1.0	36
1416	Gene-specific patterns of expression variation across organs and species. Genome Biology, 2016, 17, 151.	3.8	89
1417	dbNSFP v3.0: A One-Stop Database of Functional Predictions and Annotations for Human Nonsynonymous and Splice-Site SNVs. Human Mutation, 2016, 37, 235-241.	1.1	845
1418	Reconstruction and applications of consensus yeast metabolic network based on <scp>RNA</scp> sequencing. FEBS Open Bio, 2016, 6, 264-275.	1.0	4
1419	Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096.	1.4	344
1420	dbWGFP: a database and web server of human whole-genome single nucleotide variants and their functional predictions. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw024.	1.4	27

#	Article	IF	Citations
1421	NPInter v3.0: an upgraded database of noncoding RNA-associated interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw057.	1.4	130
1422	Identifying and annotating human bifunctional RNAs reveals their versatile functions. Science China Life Sciences, 2016, 59, 981-992.	2.3	16
1423	PEDLA: predicting enhancers with a deep learning-based algorithmic framework. Scientific Reports, 2016, 6, 28517.	1.6	88
1424	A comprehensive collection of annotations to interpret sequence variation in human mitochondrial transfer RNAs. BMC Bioinformatics, 2016, 17, 338.	1.2	12
1425	VARPRISM: incorporating variant prioritization in tests of de novo mutation association. Genome Medicine, 2016, 8, 91.	3.6	7
1426	Human adaptation and population differentiation in the light of ancient genomes. Nature Communications, 2016, 7, 10775.	5.8	36
1427	Complex Selection on Human Polyadenylation Signals Revealed by Polymorphism and Divergence Data. Genome Biology and Evolution, 2016, 8, 1971-1979.	1.1	6
1428	Purifying selection shapes the coincident SNP distribution of primate coding sequences. Scientific Reports, 2016, 6, 27272.	1.6	5
1429	Non-Coding Loss-of-Function Variation in Human Genomes. Human Heredity, 2016, 81, 78-87.	0.4	16
1430	Secondary structure impacts patterns of selection in human lncRNAs. BMC Biology, 2016, 14, 60.	1.7	43
1431	Unsupervised Learning in Genome Informatics. , 2016, , 405-448.		4
1432	Controlling for Phylogenetic Relatedness and Evolutionary Rates Improves the Discovery of Associations Between Speciesâ€™ Phenotypic and Genomic Differences. Molecular Biology and Evolution, 2016, 33, 2135-2150.	3.5	74
1433	Targeted capture and resequencing of 1040 genes reveal environmentally driven functional variation in grey wolves. Molecular Ecology, 2016, 25, 357-379.	2.0	47
1434	Segregation of a rare TTC3 variant in an extended family with late-onset Alzheimer disease. Neurology: Genetics, 2016, 2, e41.	0.9	41
1435	Identifying cell-specific microRNA transcriptional start sites. Bioinformatics, 2016, 32, 2403-2410.	1.8	18
1436	Functional Conservation of the Glide/Gcm Regulatory Network Controlling Glia, Hemocyte, and Tendon Cell Differentiation in Drosophila. Genetics, 2016, 202, 191-219.	1.2	18
1437	Poly(A) code analyses reveal key determinants for tissue-specific mRNA alternative polyadenylation. Rna, 2016, 22, 813-821.	1.6	17
1438	A beak size locus in Darwinâ€™s finches facilitated character displacement during a drought. Science, 2016, 352, 470-474.	6.0	206

#	Article	IF	Citations
1439	A widespread sequence-specific mRNA decay pathway mediated by hnRNPs A1 and A2/B1. Genes and Development, 2016, 30, 1070-1085.	2.7	46
1440	Genomic Flatlining in the Endangered Island Fox. Current Biology, 2016, 26, 1183-1189.	1.8	201
1441	STarMirDB: A database of microRNA binding sites. RNA Biology, 2016, 13, 554-560.	1.5	49
1442	Evolution of Gene Regulation in Humans. Annual Review of Genomics and Human Genetics, 2016, 17, 45-67.	2.5	52
1443	Origin and evolution of developmental enhancers in the mammalian neocortex. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2617-26.	3.3	95
1444	Separating the wheat from the chaff: systematic identification of functionally relevant noncoding variants in ADHD. Molecular Psychiatry, 2016, 21, 1589-1598.	4.1	7
1445	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33
1446	A systematic, large-scale comparison of transcription factor binding site models. BMC Genomics, 2016, 17, 388.	1.2	15
1447	Congenital dilated cardiomyopathy caused by biallelic mutations in Filamin C. European Journal of Human Genetics, 2016, 24, 1792-1796.	1.4	36
1448	LncRNA and mRNA expression profiles of glioblastoma multiforme (GBM) reveal the potential roles of lncRNAs in GBM pathogenesis. Tumor Biology, 2016, 37, 14537-14552.	0.8	34
1449	STarMir Tools for Prediction of microRNA Binding Sites. Methods in Molecular Biology, 2016, 1490, 73-82.	0.4	29
1450	Genome wide predictions of miRNA regulation by transcription factors. Bioinformatics, 2016, 32, i746-i754.	1.8	9
1451	Evolution of the Insertion-Deletion Mutation Rate Across the Tree of Life. G3: Genes, Genomes, Genetics, 2016, 6, 2583-2591.	0.8	89
1452	Chromatin structureâ€“based prediction of recurrent noncoding mutations in cancer. Nature Genetics, 2016, 48, 1321-1326.	9.4	29
1453	Selective Sweeps across Twenty Millions Years of Primate Evolution. Molecular Biology and Evolution, 2016, 33, 3065-3074.	3.5	28
1454	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. American Journal of Human Genetics, 2016, 99, 877-885.	2.6	1,555
1455	Novel regional age-associated DNA methylation changes within human common disease-associated loci. Genome Biology, 2016, 17, 193.	3.8	29
1456	Disruption of promoter memory by synthesis of a long noncoding RNA. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9575-9580.	3.3	21

#	Article	IF	Citations
1457	Screening of CD96 and ASXL1 in 11 patients with Opitz C or Bohringâ€“Opitz syndromes. American Journal of Medical Genetics, Part A, 2016, 170, 24-31.	0.7	13
1458	Variants in the genes DCTN 2 , DNAH 10 , LRIG 3, and MYO 1A are associated with intermediate Charcotâ€“Marieâ€“Tooth disease in a Norwegian family. Acta Neurologica Scandinavica, 2016, 134, 67-75.	1.0	12
1459	A position-specific 3â€²UTR sequence that accelerates mRNA decay. RNA Biology, 2016, 13, 1075-1077.	1.5	27
1460	Systematic Analysis of Long Noncoding RNAs in the Senescence-accelerated Mouse Prone 8 Brain Using RNA Sequencing. Molecular Therapy - Nucleic Acids, 2016, 5, e343.	2.3	40
1461	Lineageâ€specific genomics: Frequent birth and death in the human genome. BioEssays, 2016, 38, 654-663.	1.2	4
1462	AnnoLnc: a web server for systematically annotating novel human lncRNAs. BMC Genomics, 2016, 17, 931.	1.2	51
1463	Ciliary dyslexia candidate genes DYX1C1 and DCDC2 are regulated by Regulatory Factor X (RFX) transcription factors through Xâ€box promoter motifs. FASEB Journal, 2016, 30, 3578-3587.	0.2	28
1464	The ChIP-Seq tools and web server: a resource for analyzing ChIP-seq and other types of genomic data. BMC Genomics, 2016, 17, 938.	1.2	25
1465	Characterization of long non-coding RNA transcriptome in high-energy diet induced nonalcoholic steatohepatitis minipigs. Scientific Reports, 2016, 6, 30709.	1.6	29
1466	Multiple myeloma risk variant at 7p15.3 creates an IRF4-binding site and interferes with CDCA7L expression. Nature Communications, 2016, 7, 13656.	5.8	32
1467	Genetic Predisposition to Chronic Lymphocytic Leukemia Is Mediated by a BMF Super-Enhancer Polymorphism. Cell Reports, 2016, 16, 2061-2067.	2.9	58
1468	Truncating and missense PPM1D mutations in earlyâ€onset and/or familial/hereditary prostate cancer patients. Genes Chromosomes and Cancer, 2016, 55, 954-961.	1.5	15
1469	Genetic drift, selection and the evolution of the mutation rate. Nature Reviews Genetics, 2016, 17, 704-714.	7.7	648
1470	Comprehensive computational analysis of chromosome 11. , 2016, , .		0
1471	Targeted Resequencing of Deafness Genes Reveals a FounderMYO15AVariant in Northeastern Brazil. Annals of Human Genetics, 2016, 80, 327-331.	0.3	17
1472	Pedigree based DNA sequencing pipeline for germline genomes of cancer families. Hereditary Cancer in Clinical Practice, 2016, 14, 16.	0.6	7
1473	A catalog of hemizygous variation in 127 22q11 deletion patients. Human Genome Variation, 2016, 3, 15065.	0.4	8
1474	Neural specificity of the RNA binding protein Elav is achieved by post-transcriptional repression in non-neural tissues. Development (Cambridge), 2016, 143, 4474-4485.	1.2	16

#	Article	IF	Citations
1475	Prioritization of non-coding disease-causing variants and long non-coding RNAs in liver cancer. Oncology Letters, 2016, 12, 3987-3994.	0.8	8
1476	M-CAP eliminates a majority of variants of uncertain significance in clinical exomes at high sensitivity. Nature Genetics, 2016, 48, 1581-1586.	9.4	654
1477	Deciphering Variability of PKD1 and PKD2 in an Italian Cohort of 643 Patients with Autosomal Dominant Polycystic Kidney Disease (ADPKD). Scientific Reports, 2016, 6, 30850.	1.6	28
1478	Emergence of the Noncoding Cancer Genome: A Target of Genetic and Epigenetic Alterations. Cancer Discovery, 2016, 6, 1215-1229.	7.7	81
1479	Evolutionary origin and functional divergence of totipotent cell homeobox genes in eutherian mammals. BMC Biology, 2016, 14, 45.	1.7	37
1480	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. Genome Biology, 2016, 17, 211.	3.8	101
1481	An Efficient Cache-oblivious Parallel Viterbi Algorithm. Lecture Notes in Computer Science, 2016, , 574-587.	1.0	1
1482	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. Genome Medicine, 2016, 8, 55.	3.6	51
1483	Identification of the Photoreceptor Transcriptional Co-Repressor SAMD11 as Novel Cause of Autosomal Recessive Retinitis Pigmentosa. Scientific Reports, 2016, 6, 35370.	1.6	13
1484	Analyses of Long Non-Coding RNA and mRNA profiling using RNA sequencing during the pre-implantation phases in pig endometrium. Scientific Reports, 2016, 6, 20238.	1.6	150
1485	Genome-wide identification of Drosophila dorso-ventral enhancers by differential histone acetylation analysis. Genome Biology, 2016, 17, 196.	3.8	54
1486	Joint mouseâ€“human phenome-wide association to test gene function and disease risk. Nature Communications, 2016, 7, 10464.	5.8	190
1487	A method for identification of highly conserved elements and evolutionary analysis of superphylum Alveolata. BMC Bioinformatics, 2016, 17, 385.	1.2	9
1488	Differential long non-coding RNA and mRNA expression in differentiated human glioblastoma stem cells. Molecular Medicine Reports, 2016, 14, 2067-2076.	1.1	7
1489	Global inference of disease-causing single nucleotide variants from exome sequencing data. BMC Bioinformatics, 2016, 17, 468.	1.2	4
1490	Predicting the recurrence of noncoding regulatory mutations in cancer. BMC Bioinformatics, 2016, 17, 492.	1.2	10
1491	DIVAN: accurate identification of non-coding disease-specific risk variants using multi-omics profiles. Genome Biology, 2016, 17, 252.	3.8	67
1492	Identification and preliminary characterization of chemosensory perception-associated proteins in the melon fly Bactrocera cucurbitae using RNA-seq. Scientific Reports, 2016, 6, 19112.	1.6	29

#	Article	IF	Citations
1493	Characterizing the roles of long non-coding RNA in rat alcohol preference. , 2016, , .		0
1494	Tools for Predicting the Functional Impact of Nonsynonymous Genetic Variation. Genetics, 2016, 203, 635-647.	1.2	84
1495	Seqinspector: position-based navigation through the ChIP-seq data landscape to identify gene expression regulators. BMC Bioinformatics, 2016, 17, 85.	1.2	15
1496	Predicting regulatory variants with composite statistic. Bioinformatics, 2016, 32, 2729-2736.	1.8	40
1497	Analysis of Long Noncoding RNAs in RNA-Seq Data. , 2016, , 143-174.		0
1498	Purifying Selection on Exonic Splice Enhancers in Intronless Genes. Molecular Biology and Evolution, 2016, 33, 1396-1418.	3.5	21
1499	Ataxia-Pancytopenia Syndrome Is Caused by Missense Mutations in SAMD9L. American Journal of Human Genetics, 2016, 98, 1146-1158.	2.6	136
1500	New Peptides Under the s(ORF)ace of the Genome. Trends in Biochemical Sciences, 2016, 41, 665-678.	3.7	82
1501	Combinatorial Gene Regulatory Functions Underlie Ultraconserved Elements in Drosophila. Molecular Biology and Evolution, 2016, 33, 2294-2306.	3.5	18
1502	Genome-wide analysis of long non-coding RNAs at early stage of skin pigmentation in goats (Capra) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	139
1503	High-throughput discovery of post-transcriptional cis-regulatory elements. BMC Genomics, 2016, 17, 177.	1.2	41
1504	Protein-structure-guided discovery of functional mutations across 19 cancer types. Nature Genetics, 2016, 48, 827-837.	9.4	128
1505	Coding exon-structure aware realigner (CESAR) utilizes genome alignments for accurate comparative gene annotation. Nucleic Acids Research, 2016, 44, e103-e103.	6.5	47
1506	Overlapping cell population expression profiling and regulatory inference in C. elegans. BMC Genomics, 2016, 17, 159.	1.2	6
1507	The Cellular and Molecular Landscapes of the Developing Human Central Nervous System. Neuron, 2016, 89, 248-268.	3.8	571
1508	Genomic determinants of somatic copy number alterations across human cancers. Human Molecular Genetics, 2016, 25, 1019-1030.	1.4	10
1509	267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. Molecular Biology and Evolution, 2016, 33, 1205-1218.	3.5	78
1510	Search for new loci and low-frequency variants influencing glioma risk by exome-array analysis. European Journal of Human Genetics, 2016, 24, 717-724.	1.4	8

#	Article	IF	Citations
1511	Massively parallel cis-regulatory analysis in the mammalian central nervous system. Genome Research, 2016, 26, 238-255.	2.4	106
1512	Detecting actively translated open reading frames in ribosome profiling data. Nature Methods, 2016, 13, 165-170.	9.0	368
1513	Where does transcription start? 5â€²-RACE adapted to next-generation sequencing. Nucleic Acids Research, 2016, 44, 2628-2645.	6.5	21
1514	Testing for Ancient Selection Using Cross-population Allele Frequency Differentiation. Genetics, 2016, 202, 733-750.	1.2	101
1515	The UCSC Genome Browser database: 2016 update. Nucleic Acids Research, 2016, 44, D717-D725.	6.5	376
1516	CEGAâ€”a catalog of conserved elements from genomic alignments. Nucleic Acids Research, 2016, 44, D96-D100.	6.5	18
1517	Developing maps of fitness consequences for plant genomes. Current Opinion in Plant Biology, 2016, 30, 101-107.	3.5	13
1518	UCSC Data Integrator and Variant Annotation Integrator. Bioinformatics, 2016, 32, 1430-1432.	1.8	78
1519	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	13.7	392
1520	Alternative splicing modulated by genetic variants demonstrates accelerated evolution regulated by highly conserved proteins. Genome Research, 2016, 26, 440-450.	2.4	50
1521	Research Resource: Genetic Labeling of Human Islet Alpha Cells. Molecular Endocrinology, 2016, 30, 248-253.	3.7	6
1522	Transcriptome-scale RNase-footprinting of RNA-protein complexes. Nature Biotechnology, 2016, 34, 410-413.	9.4	49
1523	Analysis of computational footprinting methods for DNase sequencing experiments. Nature Methods, 2016, 13, 303-309.	9.0	141
1524	Predicting transcription factor site occupancy using DNA sequence intrinsic and cell-type specific chromatin features. BMC Bioinformatics, 2016, 17, 4.	1.2	42
1525	Association of the IGF1 gene with fasting insulin levels. European Journal of Human Genetics, 2016, 24, 1337-1343.	1.4	5
1526	Modeling the combined effect of RNA-binding proteins and microRNAs in post-transcriptional regulation. Nucleic Acids Research, 2016, 44, e83-e83.	6.5	30
1527	cnvScan: a CNV screening and annotation tool to improve the clinical utility of computational CNV prediction from exome sequencing data. BMC Genomics, 2016, 17, 51.	1.2	24
1528	Shadow Enhancers Are Pervasive Features of Developmental Regulatory Networks. Current Biology, 2016, 26, 38-51.	1.8	212

#	Article	IF	Citations
1529	Active DNA demethylation at enhancers during the vertebrate phylotypic period. Nature Genetics, 2016, 48, 417-426.	9.4	210
1530	A comprehensive overview of lncRNA annotation resources. Briefings in Bioinformatics, 2017, 18, bbw015.	3.2	122
1531	Gene regulatory mechanisms underpinning prostate cancer susceptibility. Nature Genetics, 2016, 48, 387-397.	9.4	119
1532	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. Nature Genetics, 2016, 48, 427-437.	9.4	545
1533	A novelHSD17B10mutation impairing the activities of the mitochondrial RNase P complex causes X-linked intractable epilepsy and neurodevelopmental regression. RNA Biology, 2016, 13, 477-485.	1.5	42
1534	Machine Learning in Genomic Medicine: A Review of Computational Problems and Data Sets. Proceedings of the IEEE, 2016, 104, 176-197.	16.4	186
1535	â€œReverse Genomicsâ€•Predicts Function of Human Conserved Noncoding Elements. Molecular Biology and Evolution, 2016, 33, 1358-1369.	3.5	55
1536	CLIPSeqToolsâ€”a novel bioinformatics CLIP-seq analysis suite. Rna, 2016, 22, 1-9.	1.6	49
1537	Exome sequencing identifies rare variants in multiple genes in atrioventricular septal defect. Genetics in Medicine, 2016, 18, 189-198.	1.1	39
1538	Dense genotyping of immune-related loci in idiopathic inflammatory myopathies confirms HLA alleles as the strongest genetic risk factor and suggests different genetic background for major clinical subgroups. Annals of the Rheumatic Diseases, 2016, 75, 1558-1566.	0.5	127
1539	Mapping the Transcriptome-Wide Landscape of RBP Binding Sites Using gPAR-CLIP-seq: Bioinformatic Analysis. Methods in Molecular Biology, 2016, 1361, 91-104.	0.4	3
1540	Interpreting functional effects of coding variants: challenges in proteome-scale prediction, annotation and assessment. Briefings in Bioinformatics, 2016, 17, 841-862.	3.2	23
1541	Analysis of the genes responsible for steroid-resistant nephrotic syndrome and/or focal segmental glomerulosclerosis in Japanese patients by whole-exome sequencing analysis. Journal of Human Genetics, 2016, 61, 137-141.	1.1	21
1542	The p53-p21-DREAM-CDE/CHR pathway regulates G₂/M cell cycle genes. Nucleic Acids Research, 2016, 44, 164-174.	6.5	318
1543	Sequence capture of ultraconserved elements from bird museum specimens. Molecular Ecology Resources, 2016, 16, 1189-1203.	2.2	206
1544	Hepatic Long Intergenic Noncoding RNAs: High Promoter Conservation and Dynamic, Sex-Dependent Transcriptional Regulation by Growth Hormone. Molecular and Cellular Biology, 2016, 36, 50-69.	1.1	39
1545	Methods for distinguishing between protein-coding and long noncoding RNAs and the elusive biological purpose of translation of long noncoding RNAs. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 31-40.	0.9	82
1546	Decoding Crucial LncRNAs Implicated in Neurogenesis and Neurological Disorders. Stem Cells and Development, 2017, 26, 541-553.	1.1	16

#	Article	IF	Citations
1547	Antisense transcription of the myotonic dystrophy locus yields low-abundant RNAs with and without (CAG)n repeat. RNA Biology, 2017, 14, 1374-1388.	1.5	25
1548	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. Cell, 2017, 168, 442-459.e20.	13.5	432
1549	The PRC2-binding long non-coding RNAs in human and mouse genomes are associated with predictive sequence features. Scientific Reports, 2017, 7, 41669.	1.6	13
1550	The rice paradox: Multiple origins but single domestication in Asian rice. Molecular Biology and Evolution, 2017, 34, msx049.	3.5	178
1551	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	1.1	39
1552	Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal promoters. Genome Research, 2017, 27, 553-566.	2.4	32
1553	Identification of Cadherin 2 (CDH2) Mutations in Arrhythmogenic Right Ventricular Cardiomyopathy. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	123
1554	Cell Type-Specific Epigenomic Analysis Reveals a Uniquely Closed Chromatin Architecture in Mouse Rod Photoreceptors. Scientific Reports, 2017, 7, 43184.	1.6	71
1555	cis -Acting Complex-Trait-Associated lincRNA Expression Correlates with Modulation of Chromosomal Architecture. Cell Reports, 2017, 18, 2280-2288.	2.9	67
1556	An atlas of human long non-coding RNAs with accurate 5â€² ends. Nature, 2017, 543, 199-204.	13.7	898
1557	Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. Nature Communications, 2017, 8, 14229.	5.8	61
1558	Calculating Higher-Order Moments of Phylogenetic Stochastic Mapping Summaries in Linear Time. Journal of Computational Biology, 2017, 24, 377-399.	0.8	1
1559	Conserved effect of aging on DNA methylation and association with EZH2 polycomb protein in mice and humans. Mechanisms of Ageing and Development, 2017, 162, 27-37.	2.2	38
1560	Chemosensory adaptations of the mountain fly Drosophila nigrosparsa (Insecta: Diptera) through genomicsâ€™ and structural biologyâ€™s lenses. Scientific Reports, 2017, 7, 43770.	1.6	21
1561	Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder. Nature Neuroscience, 2017, 20, 602-611.	7.1	691
1562	Genome-wide identification and functional prediction of cold and/or drought-responsive lncRNAs in cassava. Scientific Reports, 2017, 7, 45981.	1.6	126
1563	Differential Gene Expression in the Human Brain Is Associated with Conserved, but Not Accelerated, Noncoding Sequences. Molecular Biology and Evolution, 2017, 34, 1217-1229.	3.5	10
1564	Defining Functional Genic Regions in the Human Genome through Integration of Biochemical, Evolutionary, and Genetic Evidence. Molecular Biology and Evolution, 2017, 34, 1788-1798.	3.5	8

#	Article	IF	Citations
1565	Flicr , a long noncoding RNA, modulates Foxp3 expression and autoimmunity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3472-E3480.	3.3	141
1566	DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. Genome Biology, 2017, 18, 67.	3.8	361
1567	Clinical, Molecular, and Computational Analysis in Patients With a Novel Double Mutation and a New Synonymous Variant in MeCP2: Report of the First Missense Mutation Within the AT-hook1 Cluster in Rett Syndrome. Journal of Child Neurology, 2017, 32, 694-703.	0.7	8
1568	Variants in the host genome may inhibit tumour growth in devil facial tumours: evidence from genome-wide association. Scientific Reports, 2017, 7, 423.	1.6	56
1569	Role of the LF-SINEâ€“Derived Distal ISL1 Enhancer in Patients with Classic Bladder Exstrophy. Journal of Pediatric Genetics, 2017, 06, 169-173.	0.3	3
1570	The identification and functional annotation of RNA structures conserved in vertebrates. Genome Research, 2017, 27, 1371-1383.	2.4	71
1571	Whole exome sequencing identification of novel candidate genes in patients with proliferative diabetic retinopathy. Vision Research, 2017, 139, 168-176.	0.7	33
1572	Evolutionary re-wiring of p63 and the epigenomic regulatory landscape in keratinocytes and its potential implications on species-specific gene expression and phenotypes. Nucleic Acids Research, 2017, 45, 8208-8224.	6.5	39
1573	Evolutionary acquisition of promoter-associated non-coding RNA (pancRNA) repertoires diversifies species-dependent gene activation mechanisms in mammals. BMC Genomics, 2017, 18, 285.	1.2	23
1574	Systematic identification and characterization of cardiac long intergenic noncoding RNAs in zebrafish. Scientific Reports, 2017, 7, 1250.	1.6	12
1575	MicroRNAs, Regulatory Networks, and Comorbidities: Decoding Complex Systems. Methods in Molecular Biology, 2017, 1580, 281-295.	0.4	2
1576	The Molecular Revolution in Cutaneous Biology: EDC and Locus Control. Journal of Investigative Dermatology, 2017, 137, e101-e104.	0.3	23
1577	Inferring Trees. Methods in Molecular Biology, 2017, 1525, 349-377.	0.4	5
1578	Upgrading short-read animal genome assemblies to chromosome level using comparative genomics and a universal probe set. Genome Research, 2017, 27, 875-884.	2.4	97
1579	Cloning and characterization of adipogenin and its overexpression enhances fat accumulation of bovine myosatellite cells. Gene, 2017, 601, 27-35.	1.0	7
1580	Identification of non-coding and coding RNAs in porcine endometrium. Genomics, 2017, 109, 43-50.	1.3	33
1581	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. Systematic Biology, 2017, 66, 1028-1044.	2.7	46
1582	Using high-resolution variant frequencies to empower clinical genome interpretation. Genetics in Medicine, 2017, 19, 1151-1158.	1.1	355

#	Article	IF	Citations
1583	Genome urbanization: clusters of topologically co-regulated genes delineate functional compartments in the genome of Saccharomyces cerevisiae. Nucleic Acids Research, 2017, 45, 5818-5828.	6.5	22
1584	A new promoter element associated with daily time keeping in Drosophila. Nucleic Acids Research, 2017, 45, 6459-6470.	6.5	6
1585	Mutation Spectrum in the CACNA1A Gene in 49 Patients with Episodic Ataxia. Scientific Reports, 2017, 7, 2514.	1.6	36
1586	A RAB27A duplication in several cases of Griscelli syndrome type 2: An explanation for cases lacking a genetic diagnosis. Human Mutation, 2017, 38, 1355-1359.	1.1	9
1587	Repeated divergent selection on pigmentation genes in a rapid finch radiation. Science Advances, 2017, 3, e1602404.	4.7	148
1588	Evolutionary Footprints Reveal Insights into Plant MicroRNA Biogenesis. Plant Cell, 2017, 29, 1248-1261.	3.1	69
1589	chainCleaner improves genome alignment specificity and sensitivity. Bioinformatics, 2017, 33, 1596-1603.	1.8	33
1590	Identification of genetic variants affecting vitamin D receptor binding and associations with autoimmune disease. Human Molecular Genetics, 2017, 26, 2164-2176.	1.4	27
1591	A combined sequence and structure based method for discovering enriched motifs in RNA from in vivo binding data. Methods, 2017, 118-119, 73-81.	1.9	13
1592	BiRen: predicting enhancers with a deep-learning-based model using the DNA sequence alone. Bioinformatics, 2017, 33, 1930-1936.	1.8	121
1593	Identification of long non-coding transcripts with feature selection: a comparative study. BMC Bioinformatics, 2017, 18, 187.	1.2	21
1594	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. Nature Genetics, 2017, 49, 618-624.	9.4	299
1595	A novel method for in silico identification of regulatory SNPs in human genome. Journal of Theoretical Biology, 2017, 415, 84-89.	0.8	6
1596	Comparative analyses of super-enhancers reveal conserved elements in vertebrate genomes. Genome Research, 2017, 27, 259-268.	2.4	39
1597	Deep sequencing of natural and experimental populations of Drosophila melanogaster reveals biases in the spectrum of new mutations. Genome Research, 2017, 27, 1988-2000.	2.4	45
1598	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. Nature Genetics, 2017, 49, 1705-1713.	9.4	107
1599	Analyses of long non-coding RNAs and mRNA profiling through RNA sequencing of MDBK cells at different stages of bovine viral diarrhea virus infection. Research in Veterinary Science, 2017, 115, 508-516.	0.9	34
1600	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	13.7	229

#	Article	IF	Citations
1601	SMARCB1 is required for widespread BAF complexâ€“mediated activation of enhancers and bivalent promoters. Nature Genetics, 2017, 49, 1613-1623.	9.4	207
1602	Overexpressed somatic alleles are enriched in functional elements in Breast Cancer. Scientific Reports, 2017, 7, 8287.	1.6	3
1603	Understanding Sequence Conservation With Deep Learning. , 2017, , .		4
1604	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	9.4	456
1605	Ultraconserved Sequences Associated with HoxD Cluster Have Strong Repression Activity. Genome Biology and Evolution, 2017, 9, 2134-2139.	1.1	6
1606	Regulation by 3â€²-Untranslated Regions. Annual Review of Genetics, 2017, 51, 171-194.	3.2	426
1607	Transposable elements are the primary source of novelty in primate gene regulation. Genome Research, 2017, 27, 1623-1633.	2.4	197
1608	The Schistosoma mansoni genome encodes thousands of long non-coding RNAs predicted to be functional at different parasite life-cycle stages. Scientific Reports, 2017, 7, 10508.	1.6	48
1609	CScape: a tool for predicting oncogenic single-point mutations in the cancer genome. Scientific Reports, 2017, 7, 11597.	1.6	52
1610	Increased alignment sensitivity improves the usage of genome alignments for comparative gene annotation. Nucleic Acids Research, 2017, 45, 8369-8377.	6.5	50
1611	m6aViewer: software for the detection, analysis, and visualization of N⁶-methyladenosine peaks from m⁶A-seq/ME-RIP sequencing data. Rna, 2017, 23, 1493-1501.	1.6	34
1612	Assessment of imprinting- and genetic variation-dependent monoallelic expression using reciprocal allele descendants between human family trios. Scientific Reports, 2017, 7, 7038.	1.6	10
1613	Transcriptional mechanisms that control expression of the macrophage colony-stimulating factor receptor locus. Clinical Science, 2017, 131, 2161-2182.	1.8	66
1614	The Ground State and Evolution of Promoter Region Directionality. Cell, 2017, 170, 889-898.e10.	13.5	77
1615	Cis-regulatory elements explain most of the mRNA stability variation across genes in yeast. Rna, 2017, 23, 1648-1659.	1.6	63
1616	Comparative Genomics as a Foundation for Evo-Devo Studies in Birds. Methods in Molecular Biology, 2017, 1650, 11-46.	0.4	15
1617	Genetic Gastric Cancer Susceptibility in the International Clinical Cancer Genomics Community Research Network. Cancer Genetics, 2017, 216-217, 111-119.	0.2	42
1618	Settling the score: variant prioritization and Mendelian disease. Nature Reviews Genetics, 2017, 18, 599-612.	7.7	213

#	Article	IF	Citations
1619	Gene expression reversal toward pre-adult levels in the aging human brain and age-related loss of cellular identity. Scientific Reports, 2017, 7, 5894.	1.6	35
1620	A transcribed enhancer dictates mesendoderm specification in pluripotency. Nature Communications, 2017, 8, 1806.	5.8	56
1621	Evolutionary recruitment of flexible Esrp-dependent splicing programs into diverse embryonic morphogenetic processes. Nature Communications, 2017, 8, 1799.	5.8	40
1622	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	7.1	122
1623	Estimating the prevalence of functional exonic splice regulatory information. Human Genetics, 2017, 136, 1059-1078.	1.8	26
1624	Genome-wide analysis of long noncoding RNA profiling in PRRSV-infected PAM cells by RNA sequencing. Scientific Reports, 2017, 7, 4952.	1.6	29
1625	Soft Sweeps Are the Dominant Mode of Adaptation in the Human Genome. Molecular Biology and Evolution, 2017, 34, 1863-1877.	3.5	164
1626	FlyExpress 7: An Integrated Discovery Platform To Study Coexpressed Genes Usingin SituHybridization Images inDrosophila. G3: Genes, Genomes, Genetics, 2017, 7, 2791-2797.	0.8	4
1627	Solving the master equation for Indels. BMC Bioinformatics, 2017, 18, 255.	1.2	17
1628	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	3.6	27
1629	Genome annotation for clinical genomic diagnostics: strengths and weaknesses. Genome Medicine, 2017, 9, 49.	3.6	51
1630	ConTra v3: a tool to identify transcription factor binding sites across species, update 2017. Nucleic Acids Research, 2017, 45, W490-W494.	6.5	97
1631	Altered SOX9 genital tubercle enhancer region in hypospadias. Journal of Steroid Biochemistry and Molecular Biology, 2017, 170, 28-38.	1.2	10
1632	Calpain 12 Function Revealed through the Study of an Atypical Case of Autosomal Recessive Congenital Ichthyosis. Journal of Investigative Dermatology, 2017, 137, 385-393.	0.3	19
1633	In Silico Prediction of Deleteriousness for Nonsynonymous and Splice-Altering Single Nucleotide Variants in the Human Genome. Methods in Molecular Biology, 2017, 1498, 191-197.	0.4	17
1634	3DSNP: a database for linking human noncoding SNPs to their three-dimensional interacting genes. Nucleic Acids Research, 2017, 45, D643-D649.	6.5	90
1635	The mRNA transportome of the BicD/Egl transport machinery. RNA Biology, 2017, 14, 73-89.	1.5	35
1636	A novel amyotrophic lateral sclerosis mutation in OPTN induces ER stress and Golgi fragmentation in vitro. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2017, 18, 126-133.	1.1	24

#	Article	IF	Citations
1637	EFHC1 variants in juvenile myoclonic epilepsy: reanalysis according to NHGRI and ACMG guidelines for assigning disease causality. Genetics in Medicine, 2017, 19, 144-156.	1.1	34
1638	LncVar: a database of genetic variation associated with long non-coding genes. Bioinformatics, 2017, 33, 112-118.	1.8	33
1639	Genomic distribution and estimation of nucleotide diversity in natural populations: perspectives from the collared flycatcher (Ficedula albicollis) genome. Molecular Ecology Resources, 2017, 17, 586-597.	2.2	38
1640	POSTAR: a platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. Nucleic Acids Research, 2017, 45, D104-D114.	6.5	115
1641	Evolutionary clues in <scp>lncRNAs</scp>. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1376.	3.2	60
1642	CeNDR, theCaenorhabditis elegansnatural diversity resource. Nucleic Acids Research, 2017, 45, D650-D657.	6.5	287
1643	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. Nature Genetics, 2017, 49, 10-16.	9.4	307
1644	Promoter-enhancer interactions identified from Hi-C data using probabilistic models and hierarchical topological domains. Nature Communications, 2017, 8, 2237.	5.8	126
1645	Prediction of human miRNA target genes using computationally reconstructed ancestral mammalian sequences. Nucleic Acids Research, 2017, 45, 556-566.	6.5	34
1646	Discovering the 3â€² UTR-mediated regulation of alpha-synuclein. Nucleic Acids Research, 2017, 45, 12888-12903.	6.5	32
1647	Beyond <scp>SNP</scp>s: how to detect selection on transposable element insertions. Methods in Ecology and Evolution, 2017, 8, 728-737.	2.2	23
1648	Conserved non-coding elements: developmental gene regulation meets genome organization. Nucleic Acids Research, 2017, 45, 12611-12624.	6.5	75
1649	Identification and characterization of conserved lncRNAs in human and rat brain. BMC Bioinformatics, 2017, 18, 489.	1.2	22
1650	Identification of potential cancer-related pseudogenes in lung adenocarcinoma based on ceRNA hypothesis. Oncotarget, 2017, 8, 59036-59047.	0.8	21
1651	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. BMC Genomics, 2017, 18, 724.	1.2	71
1652	Ancient human miRNAs are more likely to have broad functions and disease associations than young miRNAs. BMC Genomics, 2017, 18, 672.	1.2	11
1653	X Chromosome Evolution in Cetartiodactyla. Genes, 2017, 8, 216.	1.0	24
1654	Resources for Interpreting Variants in Precision Genomic Oncology Applications. Frontiers in Oncology, 2017, 7, 214.	1.3	18

#	Article	IF	Citations
1655	Genome-Wide Analysis of mRNA and Long Noncoding RNA Profiles in Chronic Actinic Dermatitis. BioMed Research International, 2017, 2017, 1-15.	0.9	8
1656	Systematic Identification and Molecular Characteristics of Long Noncoding RNAs in Pig Tissues. BioMed Research International, 2017, 2017, 1-9.	0.9	28
1657	Mapping cell type-specific transcriptional enhancers using high affinity, lineage-specific Ep300 bioChIP-seq. ELife, 2017, 6, .	2.8	50
1658	Rare, Potentially Pathogenic Variants in ZNF469 Are Not Enriched in Keratoconus in a Large Australian Cohort of European Descent. , 2017, 58, 6248.		13
1659	Identification of breast cancer associated variants that modulate transcription factor binding. PLoS Genetics, 2017, 13, e1006761.	1.5	37
1660	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. PLoS Computational Biology, 2017, 13, e1005720.	1.5	17
1661	Dynamic hyper-editing underlies temperature adaptation in Drosophila. PLoS Genetics, 2017, 13, e1006931.	1.5	51
1662	High rate of adaptation of mammalian proteins that interact with Plasmodium and related parasites. PLoS Genetics, 2017, 13, e1007023.	1.5	37
1663	Using DIVAN to assess disease/trait-associated single nucleotide variants in genome-wide scale. BMC Research Notes, 2017, 10, 530.	0.6	10
1664	Evaluation of in silico algorithms for use with ACMG/AMP clinical variant interpretation guidelines. Genome Biology, 2017, 18, 225.	3.8	185
1665	Variant Ranker: a web-tool to rank genomic data according to functional significance. BMC Bioinformatics, 2017, 18, 341.	1.2	21
1666	An integrative approach to predicting the functional effects of small indels in non-coding regions of the human genome. BMC Bioinformatics, 2017, 18, 442.	1.2	34
1667	CERENKOV. , 2017, , .		3
1668	Functional 5â€² UTR motif discovery with LESMoN: Local Enrichment of Sequence Motifs in biological Networks. Nucleic Acids Research, 2017, 45, 10415-10427.	6.5	9
1669	Omicseq: a web-based search engine for exploring omics datasets. Nucleic Acids Research, 2017, 45, W445-W452.	6.5	11
1670	Single-base resolution map of evolutionary constraints and annotation of conserved elements across major grass genomes. Genome Biology and Evolution, 2018, 10, 473-488.	1.1	11
1671	Dissecting super-enhancer hierarchy based on chromatin interactions. Nature Communications, 2018, 9, 943.	5.8	179
1672	Accelerated Evolution in Distinctive Species Reveals Candidate Elements for Clinically Relevant Traits, Including Mutation and Cancer Resistance. Cell Reports, 2018, 22, 2742-2755.	2.9	30

#	Article	IF	Citations
1673	Regulatory integration of Hox factor activity with Tbox factors in limb development. Development (Cambridge), 2018, 145, .	1.2	21
1674	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. Nature Communications, 2018, 9, 859.	5.8	126
1675	Discovery of coding regions in the human genome by integrated proteogenomics analysis workflow. Nature Communications, 2018, 9, 903.	5.8	108
1676	Most human introns are recognized via multiple and tissue-specific branchpoints. Genes and Development, 2018, 32, 577-591.	2.7	95
1677	The G protein-coupled receptor GPR34 â€“ The past 20â€¯years of a grownup. , 2018, 189, 71-88.		29
1678	Wholeâ€exome sequencing reveals a novel missense mutation in the MARS gene related to a rare Charcotâ€Marieâ€Tooth neuropathy type 2U. Journal of the Peripheral Nervous System, 2018, 23, 138-142.	1.4	14
1679	Point-of-care whole-exome sequencing of idiopathic male infertility. Genetics in Medicine, 2018, 20, 1365-1373.	1.1	105
1680	Physiological and Genetic Adaptations to Diving in Sea Nomads. Cell, 2018, 173, 569-580.e15.	13.5	129
1681	Filtering nucleotide sites by phylogenetic signal to noise ratio increases confidence in the Neoaves phylogeny generated from ultraconserved elements. Molecular Phylogenetics and Evolution, 2018, 126, 116-128.	1.2	19
1682	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
1683	G-Anchor: a novel approach for whole-genome comparative mapping utilizing evolutionary conserved DNA sequences. GigaScience, 2018, 7, .	3.3	3
1684	m6ASNP: a tool for annotating genetic variants by m6A function. GigaScience, 2018, 7, .	3.3	36
1685	VarCards: an integrated genetic and clinical database for coding variants in the human genome. Nucleic Acids Research, 2018, 46, D1039-D1048.	6.5	148
1686	Modelâ€based detection and analysis of introgressed Neanderthal ancestry in modern humans. Molecular Ecology, 2018, 27, 3873-3888.	2.0	67
1687	CommonVWFsequence variants associated with higher VWF and FVIII are less frequent in subjects diagnosed with type 1 VWD. Research and Practice in Thrombosis and Haemostasis, 2018, 2, 390-398.	1.0	5
1688	Inference of the human polyadenylation code. Bioinformatics, 2018, 34, 2889-2898.	1.8	26
1689	Widespread enhancer activation via ERÎ± mediates estrogen response in vivo during uterine development. Nucleic Acids Research, 2018, 46, 5487-5503.	6.5	25
1690	Allele-specific SHAPE-MaP assessment of the effects of somatic variation and protein binding on mRNA structure. Rna, 2018, 24, 513-528.	1.6	20

#	Article	IF	Citations
1691	A phenotype centric benchmark of variant prioritisation tools. Npj Genomic Medicine, 2018, 3, 5.	1.7	39
1692	Aminode: Identification of Evolutionary Constraints in the Human Proteome. Scientific Reports, 2018, 8, 1357.	1.6	35
1693	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. GigaScience, 2018, 7, 1-17.	3.3	27
1694	miR-328 mediates a metabolic shift in colon cancer cells by targeting SLC2A1/GLUT1. Clinical and Translational Oncology, 2018, 20, 1161-1167.	1.2	41
1695	Combined annotationâ€dependent depletion score for BRCA1/2 variants in patients with breast and/or ovarian cancer. Cancer Science, 2018, 109, 453-461.	1.7	17
1696	Highâ€throughput identification of <scp>RNA</scp> nuclear enrichment sequences. EMBO Journal, 2018, 37, .	3.5	99
1697	Rules governing the mechanism of epigenetic reprogramming memory. Epigenomics, 2018, 10, 149-174.	1.0	10
1698	Incorporation of a skeletal muscle-specific enhancer in the regulatory region of Igf1 upregulates IGF1 expression and induces skeletal muscle hypertrophy. Scientific Reports, 2018, 8, 2781.	1.6	12
1699	Comparative Genomics in Drosophila. Methods in Molecular Biology, 2018, 1704, 433-450.	0.4	1
1700	Phylogenomics. Methods in Molecular Biology, 2018, 1704, 103-187.	0.4	15
1701	Disease-causing mutations in the promoter and enhancer of the ornithine transcarbamylase gene. Human Mutation, 2018, 39, 527-536.	1.1	37
1702	Principles and methods of in-silico prioritization of non-coding regulatory variants. Human Genetics, 2018, 137, 15-30.	1.8	37
1703	Evolutionary expansion of DNA hypomethylation in the mammalian germline genome. Genome Research, 2018, 28, 145-158.	2.4	30
1704	A benchmark study of scoring methods for non-coding mutations. Bioinformatics, 2018, 34, 1635-1641.	1.8	21
1705	Supervised Machine Learning for Population Genetics: A New Paradigm. Trends in Genetics, 2018, 34, 301-312.	2.9	356
1706	Light in the darkness: New perspective on lanternfish relationships and classification using genomic and morphological data. Molecular Phylogenetics and Evolution, 2018, 121, 71-85.	1.2	32
1707	Human Accelerated Regions and Other Human-Specific Sequence Variations in the Context of Evolution and Their Relevance for Brain Development. Genome Biology and Evolution, 2018, 10, 166-188.	1.1	61
1708	GxGrare: gene-gene interaction analysis method for rare variants from high-throughput sequencing data. BMC Systems Biology, 2018, 12, 19.	3.0	7

#	Article	IF	Citations
1709	SPAR: small RNA-seq portal for analysis of sequencing experiments. Nucleic Acids Research, 2018, 46, W36-W42.	6.5	22
1710	Widespread intronic polyadenylation diversifies immune cell transcriptomes. Nature Communications, 2018, 9, 1716.	5.8	117
1711	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	9.4	235
1712	GenomicScores: seamless access to genomewide position-specific scores from R and Bioconductor. Bioinformatics, 2018, 34, 3208-3210.	1.8	22
1713	Divergence of Noncoding Regulatory Elements Explains Geneâ€“Phenotype Differences between Human and Mouse Orthologous Genes. Molecular Biology and Evolution, 2018, 35, 1653-1667.	3.5	12
1714	Long non-coding RNAs involved in the regulatory network during porcine pre-implantation embryonic development and iPSC induction. Scientific Reports, 2018, 8, 6649.	1.6	29
1715	DeFine: deep convolutional neural networks accurately quantify intensities of transcription factor-DNA binding and facilitate evaluation of functional non-coding variants. Nucleic Acids Research, 2018, 46, e69-e69.	6.5	89
1716	DNA Conformation Induces Adaptable Binding by Tandem Zinc Finger Proteins. Cell, 2018, 173, 221-233.e12.	13.5	52
1717	Loss of the Hematopoietic Stem Cell Factor GATA2 in the Osteogenic Lineage Impairs Trabecularization and Mechanical Strength of Bone. Molecular and Cellular Biology, 2018, 38, .	1.1	14
1718	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. Population Genomics, 2018, , 361-425.	0.2	6
1719	Conserved and species-specific transcription factor co-binding patterns drive divergent gene regulation in human and mouse. Nucleic Acids Research, 2018, 46, 1878-1894.	6.5	12
1720	De novo mutations in regulatory elements in neurodevelopmental disorders. Nature, 2018, 555, 611-616.	13.7	232
1721	Chromium disrupts chromatin organization and CTCF access to its cognate sites in promoters of differentially expressed genes. Epigenetics, 2018, 13, 363-375.	1.3	21
1722	Disrupting the three-dimensional regulatory topology of the Pitx1 locus results in overtly normal development. Development (Cambridge), 2018, 145, .	1.2	14
1723	The spectrum of genetic variants in hereditary pancreatic cancer includes Fanconi anemia genes. Familial Cancer, 2018, 17, 235-245.	0.9	29
1724	Exome Sequencing Identifies a Novel Nonsense Mutation of MYO6 as the Cause of Deafness in a Brazilian Family. Annals of Human Genetics, 2018, 82, 23-34.	0.3	9
1725	m6AVar: a database of functional variants involved in m6A modification. Nucleic Acids Research, 2018, 46, D139-D145.	6.5	181
1726	MGA repository: a curated data resource for ChIP-seq and other genome annotated data. Nucleic Acids Research, 2018, 46, D175-D180.	6.5	17

#	Article	IF	Citations
1727	mirTrans: a resource of transcriptional regulation on microRNAs for human cell lines. Nucleic Acids Research, 2018, 46, D168-D174.	6.5	18
1728	Mitochondrial mutations in human cancer: Curation of translation. RNA Biology, 2018, 15, 62-69.	1.5	17
1729	Monoallelic and biallelic CREB3L1 variant causes mild and severe osteogenesis imperfecta, respectively. Genetics in Medicine, 2018, 20, 411-419.	1.1	47
1730	Combined immunodeficiency and atopy caused by a dominant negative mutation in caspase activation and recruitment domain family member 11 (CARD11). Journal of Allergy and Clinical Immunology, 2018, 141, 1818-1830.e2.	1.5	93
1731	The Long Noncoding RNA LnRPT Is Regulated by PDGF-BB and Modulates the Proliferation of Pulmonary Artery Smooth Muscle Cells. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 181-193.	1.4	52
1732	Variants in chondroitin sulfate metabolism genes in thrombotic storm. Thrombosis Research, 2018, 161, 43-51.	0.8	5
1733	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression. Nature Ecology and Evolution, 2018, 2, 152-163.	3.4	131
1734	Natural selection beyond genes: Identification and analyses of evolutionarily conserved elements in the genome of the collared flycatcher (Ficedula albicollis). Molecular Ecology, 2018, 27, 476-492.	2.0	19
1735	Characterizing mRNA Sequence Motifs in the 3â€²-UTR Using GFP Reporter Constructs. Methods in Molecular Biology, 2018, 1720, 77-88.	0.4	0
1736	Mining for Small Translated ORFs. Journal of Proteome Research, 2018, 17, 1-11.	1.8	54
1737	Transposable Element Mediated Innovation in Gene Regulatory Landscapes of Cells: Reâ€Visiting the â€œGeneâ€Batteryâ€•Model. BioEssays, 2018, 40, 1700155.	1.2	39
1738	A microRNA feedback loop regulates global microRNA abundance during aging. Rna, 2018, 24, 159-172.	1.6	37
1739	Contemporary genetic testing in inherited cardiac disease. Journal of Cardiovascular Medicine, 2018, 19, 1-11.	0.6	48
1740	Invisible cities: segregated domains in the yeast genome with distinct structural and functional attributes. Current Genetics, 2018, 64, 247-258.	0.8	10
1741	Who Are We?. , 2018, , 195-214.		0
1742	Identification and characterization of novel conserved RNA structures in Drosophila. BMC Genomics, 2018, 19, 899.	1.2	6
1743	Borders of Cis-Regulatory DNA Sequences Preferentially Harbor the Divergent Transcription Factor Binding Motifs in the Human Genome. Frontiers in Genetics, 2018, 9, 571.	1.1	4
1744	Dichotomy in redundant enhancers points to presence of initiators of gene regulation. BMC Genomics, 2018, 19, 947.	1.2	5

#	Article	IF	Citations
1745	dbCPM: a manually curated database for exploring the cancer passenger mutations. Briefings in Bioinformatics, 2018, , .	3.2	10
1746	A multi-omic atlas of the human frontal cortex for aging and Alzheimerâ€™s disease research. Scientific Data, 2018, 5, 180142.	2.4	357
1747	Small non-coding RNA expression in mouse nephrogenic mesenchymal progenitors. Scientific Data, 2018, 5, 180218.	2.4	5
1748	Detection of long nonâ€“coding RNA homology, a comparative study on alignment and alignmentâ€“free metrics. BMC Bioinformatics, 2018, 19, 407.	1.2	31
1749	Expression profiling of lncRNAs and mRNAs reveals regulation of muscle growth in the Pacific abalone, Haliotis discus hannai. Scientific Reports, 2018, 8, 16839.	1.6	13
1750	Sendai Virus Infection Induces Expression of Novel RNAs in Human Cells. Scientific Reports, 2018, 8, 16815.	1.6	5
1751	The genome of the tegu lizardSalvator merianae: combining Illumina, PacBio, and optical mapping data to generate a highly contiguous assembly. GigaScience, 2018, 7, .	3.3	23
1752	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892.	2.6	30
1753	Competition among Aedes aegypti larvae. PLoS ONE, 2018, 13, e0202455.	1.1	18
1754	Amphioxus functional genomics and the origins of vertebrate gene regulation. Nature, 2018, 564, 64-70.	13.7	224
1755	Neomorphic PDGFRA extracellular domain driver mutations are resistant to PDGFRA targeted therapies. Nature Communications, 2018, 9, 4583.	5.8	44
1756	Genome-wide maps of distal gene regulatory enhancers active in the human placenta. PLoS ONE, 2018, 13, e0209611.	1.1	7
1757	Whole-genome sequencing in a family with twin boys with autism and intellectual disability suggests multimodal polygenic risk. Journal of Physical Education and Sports Management, 2018, 4, a003285.	0.5	11
1758	Functional characterization of theZEB2regulatory landscape. Human Molecular Genetics, 2019, 28, 1487-1497.	1.4	16
1759	Split-inducing indels in phylogenomic analysis. Algorithms for Molecular Biology, 2018, 13, 12.	0.3	11
1760	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	6.0	234
1761	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
1762	Analyses of long non-coding RNA and mRNA profiling in the spleen of diarrheic piglets caused by Clostridium perfringens type C. PeerJ, 2018, 6, e5997.	0.9	21

#	Article	IF	Citations
1763	The conservation landscape of the human ribosomal RNA gene repeats. PLoS ONE, 2018, 13, e0207531.	1.1	55
1764	Ice ages and butterflyfishes: Phylogenomics elucidates the ecological and evolutionary history of reef fishes in an endemism hotspot. Ecology and Evolution, 2018, 8, 10989-11008.	0.8	8
1765	Eukaryote Genomes. Computational Biology, 2018, , 221-240.	0.1	0
1766	Challenging popular tools for the annotation of genetic variations with a real case, pathogenic mutations of lysosomal alpha-galactosidase. BMC Bioinformatics, 2018, 19, 433.	1.2	8
1767	Comparative Genomics of Pineapple and Other Angiosperm Genomes. Plant Genetics and Genomics: Crops and Models, 2018, , 131-153.	0.3	0
1768	Computational Methods for the Pharmacogenetic Interpretation of Next Generation Sequencing Data. Frontiers in Pharmacology, 2018, 9, 1437.	1.6	62
1769	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. Nature Genetics, 2018, 50, 1600-1607.	9.4	132
1770	REforge associates transcription factor binding site divergence in regulatory elements with phenotypic differences between species. Molecular Biology and Evolution, 2018, 35, 3027-3040.	3.5	12
1771	HOXA9 Reprograms the Enhancer Landscape to Promote Leukemogenesis. Cancer Cell, 2018, 34, 643-658.e5.	7.7	94
1772	Evidence that RNA Viruses Drove Adaptive Introgression between Neanderthals and Modern Humans. Cell, 2018, 175, 360-371.e13.	13.5	164
1773	Exhaustive non-synonymous variants functionality prediction enables high resolution characterization of the neurofibromin architecture. EBioMedicine, 2018, 36, 508-516.	2.7	1
1774	Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. PLoS Genetics, 2018, 14, e1007640.	1.5	20
1775	Accurate annotation of accessible chromatin in mouse and human primordial germ cells. Cell Research, 2018, 28, 1077-1089.	5.7	17
1776	Extensive Structural Differences of Closely Related 3â€² mRNA Isoforms: Links to Pab1 Binding and mRNA Stability. Molecular Cell, 2018, 72, 849-861.e6.	4.5	30
1777	Vertebrate Genomes. Computational Biology, 2018, , 247-272.	0.1	0
1779	Geneâ€specific criteria for PTEN variant curation: Recommendations from the ClinGen PTEN Expert Panel. Human Mutation, 2018, 39, 1581-1592.	1.1	123
1780	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	5.8	43
1781	Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse. BMC Bioinformatics, 2018, 19, 373.	1.2	10

#	Article	IF	Citations
1782	Syndromic hearing loss molecular diagnosis: Application of massive parallel sequencing. Hearing Research, 2018, 370, 181-188.	0.9	6
1783	A neural network based model effectively predicts enhancers from clinical ATAC-seq samples. Scientific Reports, 2018, 8, 16048.	1.6	23
1784	N-Acetylglutamate Synthase Deficiency Due to a Recurrent Sequence Variant in the N-acetylglutamate Synthase Enhancer Region. Scientific Reports, 2018, 8, 15436.	1.6	7
1785	A Bayesian framework for efficient and accurate variant prediction. PLoS ONE, 2018, 13, e0203553.	1.1	12
1786	A panâ€cancer atlas of cancer hallmarkâ€associated candidate driver lnc<scp>RNA</scp>s. Molecular Oncology, 2018, 12, 1980-2005.	2.1	20
1787	Functional Characterization of a GGPPS Variant Identified in Atypical Femoral Fracture Patients and Delineation of the Role of GGPPS in Bone-Relevant Cell Types. Journal of Bone and Mineral Research, 2018, 33, 2091-2098.	3.1	21
1788	Pairs of Adjacent Conserved Noncoding Elements Separated by Conserved Genomic Distances Act as Cis-Regulatory Units. Genome Biology and Evolution, 2018, 10, 2535-2550.	1.1	1
1789	Enhancer-Promoter Interactions and Their Role in theÂControl of Epidermal Differentiation. Contributions To Management Science, 2018, , 231-262.	0.4	0
1790	Systematic Identification of Non-coding RNAs. Advances in Experimental Medicine and Biology, 2018, 1094, 9-18.	0.8	13
1791	A sequence-based, deep learning model accurately predicts RNA splicing branchpoints. Rna, 2018, 24, 1647-1658.	1.6	59
1792	CDH23 Methylation Status and Presbycusis Risk in Elderly Women. Frontiers in Aging Neuroscience, 2018, 10, 241.	1.7	21
1793	Association of CDKAL1 Polymorphisms with Early-Onset Atopic Dermatitis in Koreans. Annals of Dermatology, 2018, 30, 276.	0.3	3
1794	The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. PLoS Genetics, 2018, 14, e1007579.	1.5	17
1795	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. PLoS Genetics, 2018, 14, e1007588.	1.5	18
1796	Recessive Spondylocarpotarsal Synostosis Syndrome Due to Compound Heterozygosity for Variants in MYH3. American Journal of Human Genetics, 2018, 102, 1115-1125.	2.6	18
1797	Systematic pan-cancer analysis of somatic allele frequency. Scientific Reports, 2018, 8, 7735.	1.6	21
1798	Conserved Noncoding Elements Influence the Transposable Element Landscape in Drosophila. Genome Biology and Evolution, 2018, 10, 1533-1545.	1.1	14
1799	Analysis of Genetic Variation Indicates DNA Shape Involvement in Purifying Selection. Molecular Biology and Evolution, 2018, 35, 1958-1967.	3.5	14

#	Article	IF	Citations
1800	Assessing the functional association of intronic miRNAs with their host genes. Rna, 2018, 24, 991-1004.	1.6	43
1801	Genome-scale identification of transcription factors that mediate an inflammatory network during breast cellular transformation. Nature Communications, 2018, 9, 2068.	5.8	24
1802	De Novo Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. Neuron, 2018, 99, 302-314.e4.	3.8	112
1803	Next-generation museum genomics: Phylogenetic relationships among palpimanoid spiders using sequence capture techniques (Araneae: Palpimanoidea). Molecular Phylogenetics and Evolution, 2018, 127, 907-918.	1.2	65
1804	Islet Long Noncoding RNAs: A Playbook for Discovery and Characterization. Diabetes, 2018, 67, 1461-1470.	0.3	26
1805	The helicase Ded1p controls use of near-cognate translation initiation codons in 5â€² UTRs. Nature, 2018, 559, 130-134.	13.7	143
1806	Human demographic history has amplified the effects of background selection across the genome. PLoS Genetics, 2018, 14, e1007387.	1.5	71
1807	Marked Diversity of Unique Cortical Enhancers Enables Neuron-Specific Tools by Enhancer-Driven Gene Expression. Current Biology, 2018, 28, 2103-2114.e5.	1.8	66
1808	Coding variants in NOD-like receptors: An association study on risk and survival of colorectal cancer. PLoS ONE, 2018, 13, e0199350.	1.1	6
1809	Analyses of mRNA structure dynamics identify embryonic gene regulatory programs. Nature Structural and Molecular Biology, 2018, 25, 677-686.	3.6	90
1810	High resolution annotation of zebrafish transcriptome using long-read sequencing. Genome Research, 2018, 28, 1415-1425.	2.4	69
1811	Pan-Cancer Analysis Reveals the Functional Importance of Protein Lysine Modification in Cancer Development. Frontiers in Genetics, 2018, 9, 254.	1.1	39
1812	Brain activation patterns following a cooperation opportunity in a highly social cichlid fish. Physiology and Behavior, 2018, 195, 37-47.	1.0	21
1813	High-Resolution Single-Cell DNA Methylation Measurements Reveal Epigenetically Distinct Hematopoietic Stem Cell Subpopulations. Stem Cell Reports, 2018, 11, 578-592.	2.3	79
1814	Post-translational buffering leads to convergent protein expression levels between primates. Genome Biology, 2018, 19, 83.	3.8	33
1815	An MTF1 binding site disrupted by a homozygous variant in the promoter of ATP7B likely causes Wilson Disease. European Journal of Human Genetics, 2018, 26, 1810-1818.	1.4	15
1816	Transcriptome Reveals Long Non-coding RNAs and mRNAs Involved in Primary Wool Follicle Induction in Carpet Sheep Fetal Skin. Frontiers in Physiology, 2018, 9, 446.	1.3	72
1817	An Updated Functional Annotation of Protein-Coding Genes in the Cucumber Genome. Frontiers in Plant Science, 2018, 9, 325.	1.7	2

#	Article	IF	Citations
1818	An Evolutionary Mechanism for the Generation of Competing RNA Structures Associated with Mutually Exclusive Exons. Genes, 2018, 9, 356.	1.0	14
1819	Performance evaluation of pathogenicity-computation methods for missense variants. Nucleic Acids Research, 2018, 46, 7793-7804.	6.5	168
1820	Genome-wide analysis of differentially expressed profiles of mRNAs, lncRNAs and circRNAs during Cryptosporidium baileyi infection. BMC Genomics, 2018, 19, 356.	1.2	26
1821	The Role of Phylogenetically Conserved Elements in Shaping Patterns of Human Genomic Diversity. Molecular Biology and Evolution, 2018, 35, 2284-2295.	3.5	5
1822	A genome-wide assessment of conserved SNP alleles reveals a panel of regulatory SNPs relevant to the peripheral nerve. BMC Genomics, 2018, 19, 311.	1.2	3
1823	Micropeptides Encoded in Transcripts Previously Identified as Long Noncoding RNAs: A New Chapter in Transcriptomics and Proteomics. Frontiers in Genetics, 2018, 9, 144.	1.1	83
1824	Genome-Wide Analysis of Long Non-Coding RNAs in Potato and Their Potential Role in Tuber Sprouting Process. International Journal of Molecular Sciences, 2018, 19, 101.	1.8	22
1825	A Novel Long Non-Coding RNA in the hTERT Promoter Region Regulates hTERT Expression. Non-coding RNA, 2018, 4, 1.	1.3	28
1826	Systematic Analysis of Long Non-Coding RNAs and mRNAs in the Ovaries of Duroc Pigs During Different Follicular Stages Using RNA Sequencing. International Journal of Molecular Sciences, 2018, 19, 1722.	1.8	40
1827	Strategies to Annotate and Characterize Long Noncoding RNAs: Advantages and Pitfalls. Trends in Genetics, 2018, 34, 704-721.	2.9	86
1828	The asymmetrically segregating lncRNA cherub is required for transforming stem cells into malignant cells. ELife, 2018, 7, .	2.8	28
1829	Prioritization and functional assessment of noncoding variants associated with complex diseases. Genome Medicine, 2018, 10, 53.	3.6	33
1830	Analysis of causal effect of APOA5 variants on premature coronary artery disease. Annals of Human Genetics, 2018, 82, 437-447.	0.3	8
1831	Genome-wide maps of ribosomal occupancy provide insights into adaptive evolution and regulatory roles of uORFs during Drosophila development. PLoS Biology, 2018, 16, e2003903.	2.6	77
1832	Comprehensive analysis of coding-lncRNA gene co-expression network uncovers conserved functional lncRNAs in zebrafish. BMC Genomics, 2018, 19, 112.	1.2	36
1833	Identification of Gossypium hirsutum long non-coding RNAs (lncRNAs) under salt stress. BMC Plant Biology, 2018, 18, 23.	1.6	142
1834	Using more native-like language acquisition processes in the foreign language classroom. Cogent Education, 2018, 5, 1429134.	0.6	1
1835	RNA editing in nascent RNA affects pre-mRNA splicing. Genome Research, 2018, 28, 812-823.	2.4	107

#	Article	IF	Citations
1836	Characterization of a novel Drosophila melanogaster cisâ€regulatory module that drives gene expression to the larval tracheal system and adult thoracic musculature. Genesis, 2018, 56, e23222.	0.8	1
1837	Rat BodyMap transcriptomes reveal unique circular RNA features across tissue types and developmental stages. Rna, 2018, 24, 1443-1456.	1.6	50
1838	Genome Wide Identification of Novel Long Non-coding RNAs and Their Potential Associations With Milk Proteins in Chinese Holstein Cows. Frontiers in Genetics, 2018, 9, 281.	1.1	30
1839	A piRNA utilizes HILI and HIWI2 mediated pathway to down-regulate ferritin heavy chain 1 mRNA in human somatic cells. Nucleic Acids Research, 2018, 46, 10635-10648.	6.5	27
1840	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. Scientific Reports, 2018, 8, 11635.	1.6	30
1841	A Network of Noncoding Regulatory RNAs Acts in the Mammalian Brain. Cell, 2018, 174, 350-362.e17.	13.5	485
1842	Enrichment-Based Proteogenomics Identifies Microproteins, Missing Proteins, and Novel smORFs in Saccharomyces cerevisiae. Journal of Proteome Research, 2018, 17, 2335-2344.	1.8	35
1843	Genetic Network Complexity Shapes Background-Dependent Phenotypic Expression. Trends in Genetics, 2018, 34, 578-586.	2.9	35
1844	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
1845	Taking a bite out of nutrition and arbovirus infection. PLoS Neglected Tropical Diseases, 2018, 12, e0006247.	1.3	31
1846	Natural re-colonization and admixture of wolves (Canis lupus) in the US Pacific Northwest: challenges for the protection and management of rare and endangered taxa. Heredity, 2019, 122, 133-149.	1.2	13
1847	LncFinder: an integrated platform for long non-coding RNA identification utilizing sequence intrinsic composition, structural information and physicochemical property. Briefings in Bioinformatics, 2019, 20, 2009-2027.	3.2	98
1848	Implementing precision cancer medicine in the genomic era. Seminars in Cancer Biology, 2019, 55, 16-27.	4.3	24
1849	Landscape of the long non-coding RNA transcriptome in human heart. Briefings in Bioinformatics, 2019, 20, 1812-1825.	3.2	17
1851	Genome Informatics. , 2019, , 178-194.		0
1852	Genome Annotation. , 2019, , 195-209.		3
1853	Detecting and Annotating Rare Variants. , 2019, , 388-399.		4
1854	dbCID: a manually curated resource for exploring the driver indels in human cancer. Briefings in Bioinformatics, 2019, 20, 1925-1933.	3.2	11

#	Article	IF	Citations
1855	A Bioinformatics Toolkit: In Silico Tools and Online Resources for Investigating Genetic Variation. Seminars in Thrombosis and Hemostasis, 2019, 45, 674-684.	1.5	1
1856	Saturation mutagenesis of twenty disease-associated regulatory elements at single base-pair resolution. Nature Communications, 2019, 10, 3583.	5.8	152
1857	Beyond the Exome: The Non-coding Genome and Enhancers in Neurodevelopmental Disorders and Malformations of Cortical Development. Frontiers in Cellular Neuroscience, 2019, 13, 352.	1.8	53
1858	Challenges in funding and developing genomic software: roots and remedies. Genome Biology, 2019, 20, 147.	3.8	21
1860	Phylogenomic Reconstruction of the Neotropical Poison Frogs (Dendrobatidae) and Their Conservation. Diversity, 2019, 11, 126.	0.7	23
1861	Novel Genes Associated with the Development of Carotid Paragangliomas. Molecular Biology, 2019, 53, 547-559.	0.4	9
1862	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. Nature Communications, 2019, 10, 3072.	5.8	53
1863	Identifying Cancer Driver lncRNAs Bridged by Functional Effectors through Integrating Multi-omics Data in Human Cancers. Molecular Therapy - Nucleic Acids, 2019, 17, 362-373.	2.3	30
1864	Selection Acting on Genomes. Methods in Molecular Biology, 2019, 1910, 373-397.	0.4	9
1865	Systematic discovery of conservation states for single-nucleotide annotation of the human genome. Communications Biology, 2019, 2, 248.	2.0	15
1866	VIPdb, a genetic Variant Impact Predictor Database. Human Mutation, 2019, 40, 1202-1214.	1.1	24
1867	Benchmark and integration of resources for the estimation of human transcription factor activities. Genome Research, 2019, 29, 1363-1375.	2.4	552
1868	Networks of mRNA Processing and Alternative Splicing Regulation in Health and Disease. Advances in Experimental Medicine and Biology, 2019, 1157, 1-27.	0.8	9
1869	Predicting functional long non-coding RNAs validated by low throughput experiments. RNA Biology, 2019, 16, 1555-1564.	1.5	6
1870	An integrative genomic analysis of the Longshanks selection experiment for longer limbs in mice. ELife, 2019, 8, .	2.8	58
1871	A Kinetic Map of the Homomeric Voltage-Gated Potassium Channel (Kv) Family. Frontiers in Cellular Neuroscience, 2019, 13, 358.	1.8	70
1872	Estimation of allele-specific fitness effects across human protein-coding sequences and implications for disease. Genome Research, 2019, 29, 1310-1321.	2.4	24
1873	Single-base mapping of m ⁶ A by an antibody-independent method. Science Advances, 2019, 5, eaax0250.	4.7	270

#	Article	IF	Citations
1874	RegulationSpotter: annotation and interpretation of extratranscriptic DNA variants. Nucleic Acids Research, 2019, 47, W106-W113.	6.5	17
1875	Precise Prediction of Calpain Cleavage Sites and Their Aberrance Caused by Mutations in Cancer. Frontiers in Genetics, 2019, 10, 715.	1.1	26
1876	Recapitulation and Reversal of Schizophrenia-Related Phenotypes in Setd1a-Deficient Mice. Neuron, 2019, 104, 471-487.e12.	3.8	79
1877	Comparative Genomic Characterization of the Multimammate Mouse Mastomys coucha. Molecular Biology and Evolution, 2019, 36, 2805-2812.	3.5	6
1878	Strategies for the Identification of Bioactive Neuropeptides in Vertebrates. Frontiers in Neuroscience, 2019, 13, 948.	1.4	11
1879	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. Cell, 2019, 179, 750-771.e22.	13.5	174
1880	Contribution of retrotransposition to developmental disorders. Nature Communications, 2019, 10, 4630.	5.8	43
1881	Evaluating Chromatin Accessibility Differences Across Multiple Primate Species Using a Joint Modeling Approach. Genome Biology and Evolution, 2019, 11, 3035-3053.	1.1	12
1882	Convolutional neural network model to predict causal risk factors that share complex regulatory features. Nucleic Acids Research, 2019, 47, e146-e146.	6.5	6
1883	A novel LAMP2 p.G93R mutation associated with mild Danon disease presenting with familial hypertrophic cardiomyopathy. Molecular Genetics & Genomic Medicine, 2019, 7, e00941.	0.6	9
1884	Gene4Denovo: an integrated database and analytic platform for de novo mutations in humans. Nucleic Acids Research, 2020, 48, D913-D926.	6.5	41
1885	Retrotransposons spread potential cis-regulatory elements during mammary gland evolution. Nucleic Acids Research, 2019, 47, 11551-11562.	6.5	17
1886	WormBase: a modern Model Organism Information Resource. Nucleic Acids Research, 2020, 48, D762-D767.	6.5	213
1887	A reference map of murine cardiac transcription factor chromatin occupancy identifies dynamic and conserved enhancers. Nature Communications, 2019, 10, 4907.	5.8	100
1888	A-to-I RNA editing contributes to the persistence of predicted damaging mutations in populations. Genome Research, 2019, 29, 1766-1776.	2.4	5
1889	NPInter v4.0: an integrated database of ncRNA interactions. Nucleic Acids Research, 2020, 48, D160-D165.	6.5	106
1890	PlantRegMap: charting functional regulatory maps in plants. Nucleic Acids Research, 2020, 48, D1104-D1113.	6.5	333
1891	Missense Pathogenic variants in KIF4A Affect Dental Morphogenesis Resulting in X-linked Taurodontism, Microdontia and Dens-Invaginatus. Frontiers in Genetics, 2019, 10, 800.	1.1	7

#	Article	IF	Citations
1892	The Caenorhabditis elegans Transgenic Toolbox. Genetics, 2019, 212, 959-990.	1.2	118
1893	Predicting Functional Effects of Synonymous Variants: A Systematic Review and Perspectives. Frontiers in Genetics, 2019, 10, 914.	1.1	67
1894	SalMotifDB: a tool for analyzing putative transcription factor binding sites in salmonid genomes. BMC Genomics, 2019, 20, 694.	1.2	13
1895	Deciphering epigenomic code for cell differentiation using deep learning. BMC Genomics, 2019, 20, 709.	1.2	7
1896	Considerable Synteny and Sequence Similarity of Primate Chromosomal Region VIIq31. Cytogenetic and Genome Research, 2019, 158, 88-97.	0.6	0
1897	Rapidly evolving protointrons in Saccharomyces genomes revealed by a hungry spliceosome. PLoS Genetics, 2019, 15, e1008249.	1.5	16
1898	Comparative analysis demonstrates cell type-specific conservation of SOX9 targets between mouse and chicken. Scientific Reports, 2019, 9, 12560.	1.6	22
1899	GRAM: A GeneRAlized Model to predict the molecular effect of a non-coding variant in a cell-type specific manner. PLoS Genetics, 2019, 15, e1007860.	1.5	1
1900	Comprehensive analysis of long noncoding RNA (lncRNA)-chromatin interactions reveals lncRNA functions dependent on binding diverse regulatory elements. Journal of Biological Chemistry, 2019, 294, 15613-15622.	1.6	32
1901	Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. Clinica Chimica Acta, 2019, 498, 38-46.	0.5	38
1902	Immediate and deferred epigenomic signatures of in vivo neuronal activation in mouse hippocampus. Nature Neuroscience, 2019, 22, 1718-1730.	7.1	114
1903	Evolutionary characteristics of intergenic transcribed regions indicate rare novel genes and widespread noisy transcription in the Poaceae. Scientific Reports, 2019, 9, 12122.	1.6	3
1904	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19398-19408.	3.3	99
1905	A Unique Epigenomic Landscape Defines Human Erythropoiesis. Cell Reports, 2019, 28, 2996-3009.e7.	2.9	41
1906	Widespread cis-regulatory convergence between the extinct Tasmanian tiger and gray wolf. Genome Research, 2019, 29, 1648-1658.	2.4	18
1907	Extracting phylogenetic signal from phylogenomic data: Higher-level relationships of the nightbirds (Strisores). Molecular Phylogenetics and Evolution, 2019, 141, 106611.	1.2	11
1908	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research, 2019, 47, 10597-10611.	6.5	39
1909	Annotation of Variant Data from High-Throughput DNA Sequencing from Tumor Specimens: Filtering Strategies to Identify Driver Mutations. Methods in Molecular Biology, 2019, 1908, 49-60.	0.4	1

#	Article	IF	Citations
1910	Localizing and Classifying Adaptive Targets with Trend Filtered Regression. Molecular Biology and Evolution, 2019, 36, 252-270.	3.5	31
1911	Experimental validation of in silico predicted RAD locus frequencies using genomic resources and short read data from a model marine mammal. BMC Genomics, 2019, 20, 72.	1.2	4
1912	Mining for missed sORF-encoded peptides. Expert Review of Proteomics, 2019, 16, 257-266.	1.3	38
1913	VARIFIâ€"Web-Based Automatic Variant Identification, Filtering and Annotation of Amplicon Sequencing Data. Journal of Personalized Medicine, 2019, 9, 10.	1.1	1
1914	Biological relevance of computationally predicted pathogenicity of noncoding variants. Nature Communications, 2019, 10, 330.	5.8	44
1915	Innovative strategies for annotating the â€œrelationSNPâ€•between variants and molecular phenotypes. BioData Mining, 2019, 12, 10.	2.2	6
1916	Pathogenic and likely pathogenic variants in PALB2, CHEK2, and other known breast cancer susceptibility genes among 1054 BRCAâ€•negative Hispanics with breast cancer. Cancer, 2019, 125, 2829-2836.	2.0	43
1917	Genetic Contexts Characterize Dynamic Histone Modification Patterns Among Cell Types. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 698-710.	2.2	1
1918	Metaâ€•analysis of massively parallel reporter assays enables prediction of regulatory function across cell types. Human Mutation, 2019, 40, 1299-1313.	1.1	15
1919	Non-neutral evolution of H3.3-encoding genes occurs without alterations in protein sequence. Scientific Reports, 2019, 9, 8472.	1.6	10
1920	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	6.0	266
1921	Genome-wide enhancer annotations differ significantly in genomic distribution, evolution, and function. BMC Genomics, 2019, 20, 511.	1.2	38
1922	SIRT7 mediates L1 elements transcriptional repression and their association with the nuclear lamina. Nucleic Acids Research, 2019, 47, 7870-7885.	6.5	55
1923	HMMRATAC: a Hidden Markov ModeleR for ATAC-seq. Nucleic Acids Research, 2019, 47, e91-e91.	6.5	67
1924	Searching for Sympatric Speciation in the Genomic Era. BioEssays, 2019, 41, e1900047.	1.2	61
1925	Prediction of genes and protein-protein interaction networking for miR-221-5p using bioinformatics analysis. Gene Reports, 2019, 16, 100426.	0.4	2
1926	Integrating natural history collections and comparative genomics to study the genetic architecture of convergent evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180248.	1.8	32
1927	A massively parallel 3â€² UTR reporter assay reveals relationships between nucleotide content, sequence conservation, and mRNA destabilization. Genome Research, 2019, 29, 896-906.	2.4	34

#	Article	IF	Citations
1928	Transcriptome analysis reveals lncRNAâ€mediated complex regulatory network response to DNA damage in the liver tissue of Rattus norvegicus. Journal of Cellular Physiology, 2019, 234, 23216-23231.	2.0	6
1929	Evolution of Mechanisms that Control Mating in Drosophila Males. Cell Reports, 2019, 27, 2527-2536.e4.	2.9	23
1930	Integrative Analyses of Long Non-coding RNA and mRNA Involved in Piglet Ileum Immune Response to Clostridium perfringens Type C Infection. Frontiers in Cellular and Infection Microbiology, 2019, 9, 130.	1.8	40
1931	Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts. Nature Medicine, 2019, 25, 911-919.	15.2	221
1932	Rate variation in the evolution of non-coding DNA associated with social evolution in bees. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180247.	1.8	22
1933	Long non-coding RNA and MicroRNA profiling provides comprehensive insight into non-coding RNA involved host immune responses in ALV-J-infected chicken primary macrophage. Developmental and Comparative Immunology, 2019, 100, 103414.	1.0	10
1934	Reverse geneâ€“environment interaction approach to identify variants influencing body-mass index in humans. Nature Metabolism, 2019, 1, 630-642.	5.1	14
1935	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. Frontiers in Genetics, 2019, 10, 309.	1.1	28
1936	Molecular footprint of Medawarâ€™s mutation accumulation process in mammalian aging. Aging Cell, 2019, 18, e12965.	3.0	15
1937	CAGI 5 splicing challenge: Improved exon skipping and intron retention predictions with MMSplice. Human Mutation, 2019, 40, 1243-1251.	1.1	10
1938	Characterizing human genomic coevolution in locus-gene regulatory interactions. BioData Mining, 2019, 12, 8.	2.2	0
1939	Integration of multiple epigenomic marks improves prediction of variant impact in saturation mutagenesis reporter assay. Human Mutation, 2019, 40, 1280-1291.	1.1	46
1940	Removal of alleles by genome editing (RAGE) against deleterious load. Genetics Selection Evolution, 2019, 51, 14.	1.2	44
1941	Fitness Landscape of the Fission Yeast Genome. Molecular Biology and Evolution, 2019, 36, 1612-1623.	3.5	12
1942	GenePy - a score for estimating gene pathogenicity in individuals using next-generation sequencing data. BMC Bioinformatics, 2019, 20, 254.	1.2	21
1943	Genetics and evidence for balancing selection of a sex-linked colour polymorphism in a songbird. Nature Communications, 2019, 10, 1852.	5.8	47
1944	A novel missense variant in IDH3A causes autosomal recessive retinitis pigmentosa. Ophthalmic Genetics, 2019, 40, 177-181.	0.5	10
1945	Functional characterization of 3D protein structures informed by human genetic diversity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8960-8965.	3.3	33

#	Article	IF	Citations
1946	Gene expression differences between matched pairs of ovarian cancer patient tumors and patient-derived xenografts. Scientific Reports, 2019, 9, 6314.	1.6	33
1947	Effects of Xiaoyaosan on the Hippocampal Gene Expression Profile in Rats Subjected to Chronic Immobilization Stress. Frontiers in Psychiatry, 2019, 10, 178.	1.3	7
1948	Evidence that alternative transcriptional initiation is largely nonadaptive. PLoS Biology, 2019, 17, e3000197.	2.6	46
1949	Low plasma adropin concentrations increase risks of weight gain and metabolic dysregulation in response to a high-sugar diet in male nonhuman primates. Journal of Biological Chemistry, 2019, 294, 9706-9719.	1.6	45
1950	Novel potential causative genes in carotid paragangliomas. BMC Medical Genetics, 2019, 20, 48.	2.1	4
1951	Quantification and discovery of sequence determinants of proteinâ€perâ€mRNA amount inÂ29Âhuman tissues. Molecular Systems Biology, 2019, 15, e8513.	3.2	63
1952	Transcriptomic Analysis of Coding Genes and Non-Coding RNAs Reveals Complex Regulatory Networks Underlying the Black Back and White Belly Coat Phenotype in Chinese Wuzhishan Pigs. Genes, 2019, 10, 201.	1.0	6
1953	Making Sense of the Epigenome Using Data Integration Approaches. Frontiers in Pharmacology, 2019, 10, 126.	1.6	58
1954	TFforge utilizes large-scale binding site divergence to identify transcriptional regulators involved in phenotypic differences. Nucleic Acids Research, 2019, 47, e19-e19.	6.5	8
1955	MMSplice: modular modeling improves the predictions of genetic variant effects on splicing. Genome Biology, 2019, 20, 48.	3.8	140
1956	Evolution of replication origins in vertebrate genomes: rapid turnover despite selective constraints. Nucleic Acids Research, 2019, 47, 5114-5125.	6.5	10
1957	Functional characterization of CHEK2 variants in a Saccharomyces cerevisiae system. Human Mutation, 2019, 40, 631-648.	1.1	34
1958	Volatile Evolution of Long Non-Coding RNA Repertoire in Retinal Pigment Epithelium: Insights from Comparison of Bovine and Human RNA Expression Profiles. Genes, 2019, 10, 205.	1.0	10
1959	Carrier frequency estimation of Zellweger spectrum disorder using ExAC database and bioinformatics tools. Genetics in Medicine, 2019, 21, 1969-1976.	1.1	10
1960	Magic roundabout is an endothelial-specific ohnolog of ROBO1 which neo-functionalized to an essential new role in angiogenesis. PLoS ONE, 2019, 14, e0208952.	1.1	7
1961	New insights into the pathogenicity of non-synonymous variants through multi-level analysis. Scientific Reports, 2019, 9, 1667.	1.6	40
1962	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. Molecular Biology and Evolution, 2019, 36, 1086-1100.	3.5	39
1963	A Syndromic Neurodevelopmental Disorder Caused by Mutations in SMARCD1, a Core SWI/SNF Subunit Needed for Context-Dependent Neuronal Gene Regulation in Flies. American Journal of Human Genetics, 2019, 104, 596-610.	2.6	32

#	Article	IF	Citations
1964	Characterizing variants of unknown significance in rhodopsin: A functional genomics approach. Human Mutation, 2019, 40, 1127-1144.	1.1	22
1965	Sfold Tools for MicroRNA Target Prediction. Methods in Molecular Biology, 2019, 1970, 31-42.	0.4	10
1966	Mutational load in carotid body tumor. BMC Medical Genomics, 2019, 12, 39.	0.7	12
1967	ALPK1 missense pathogenic variant in five families leads to ROSAH syndrome, an ocular multisystem autosomal dominant disorder. Genetics in Medicine, 2019, 21, 2103-2115.	1.1	28
1968	Predicting enhancers in mammalian genomes using supervised hidden Markov models. BMC Bioinformatics, 2019, 20, 157.	1.2	12
1969	Approaches to functionally validate candidate genetic variants involved in colorectal cancer predisposition. Molecular Aspects of Medicine, 2019, 69, 27-40.	2.7	5
1970	Convergent regulatory evolution and loss of flight in paleognathous birds. Science, 2019, 364, 74-78.	6.0	189
1971	Transcriptome sequencing profiles reveal lncRNAs may involve in breast cancer (ER/PR positive type) by interaction with RAS associated genes. Pathology Research and Practice, 2019, 215, 152405.	1.0	15
1972	GC-biased gene conversion conceals the prediction of the nearly neutral theory in avian genomes. Genome Biology, 2019, 20, 5.	3.8	37
1973	Analysis of long non-coding RNA and mRNA expression in bovine macrophages brings up novel aspects of Mycobacterium avium subspecies paratuberculosis infections. Scientific Reports, 2019, 9, 1571.	1.6	24
1974	Epigenomic analysis reveals DNA motifs regulating histone modifications in human and mouse. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3668-3677.	3.3	35
1975	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. Genome Biology, 2019, 20, 30.	3.8	61
1976	S-CAP extends pathogenicity prediction to genetic variants that affect RNA splicing. Nature Genetics, 2019, 51, 755-763.	9.4	56
1977	NCBoost classifies pathogenic non-coding variants in Mendelian diseases through supervised learning on purifying selection signals in humans. Genome Biology, 2019, 20, 32.	3.8	47
1978	Comprehensive sequencing of the myocilin gene in a selected cohort of severe primary open-angle glaucoma patients. Scientific Reports, 2019, 9, 3100.	1.6	8
1979	CERENKOV2: improved detection of functional noncoding SNPs using data-space geometric features. BMC Bioinformatics, 2019, 20, 63.	1.2	5
1980	Significant Strain Variation in the Mutation Spectra of Inbred Laboratory Mice. Molecular Biology and Evolution, 2019, 36, 865-874.	3.5	23
1981	WHISTLE: a high-accuracy map of the human N6-methyladenosine (m6A) epitranscriptome predicted using a machine learning approach. Nucleic Acids Research, 2019, 47, e41-e41.	6.5	177

#	Article	IF	Citations
1982	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589.	2.4	39
1983	Using zebrafish to study skeletal genomics. Bone, 2019, 126, 37-50.	1.4	55
1984	Data Mining Approaches for Understanding of Regulation of Expression of the Urea Cycle Genes. , 2019, , .		0
1985	Evolution of Exons and the Exonâ€“Intron Structure of Long Intergenic Noncoding RNA Genes in Placental Mammals. Biology Bulletin Reviews, 2019, 9, 491-502.	0.3	1
1986	Transposable elements as genetic accelerators of evolution: contribution to genome size, gene regulatory network rewiring and morphological innovation. Genes and Genetic Systems, 2019, 94, 269-281.	0.2	34
1987	Exploration of CTCF post-translation modifications uncovers Serine-224 phosphorylation by PLK1 at pericentric regions during the G2/M transition. ELife, 2019, 8, .	2.8	18
1988	Recapitulation-like developmental transitions of chromatin accessibility in vertebrates. Zoological Letters, 2019, 5, 33.	0.7	24
1989	Filling in the Gaps: Adopting Ultraconserved Elements Alongside COI to Strengthen Metabarcoding Studies. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	2
1990	Application of Computational Biology and Artificial Intelligence Technologies in Cancer Precision Drug Discovery. BioMed Research International, 2019, 2019, 1-15.	0.9	42
1991	Analysis of five deep-sequenced trio-genomes of the Peninsular Malaysia Orang Asli and North Borneo populations. BMC Genomics, 2019, 20, 842.	1.2	3
1992	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	1.7	109
1993	Intra-VÎº Cluster Recombination Shapes the Ig Kappa Locus Repertoire. Cell Reports, 2019, 29, 4471-4481.e6.	2.9	9
1995	SyntDB:Âdefining orthologues of human long noncoding RNAs across primates. Nucleic Acids Research, 2019, 48, D238-D245.	6.5	16
1996	A de novo EGR2 variant, c.1232Aâ€‰>â€‰G p.Asp411Gly, causes severe early-onset Charcot-Marie-Tooth Neuropathy Type 3 (Dejerine-Sottas Neuropathy). Scientific Reports, 2019, 9, 19336.	1.6	4
1997	RepeatFiller newly identifies megabases of aligning repetitive sequences and improves annotations of conserved non-exonic elements. GigaScience, 2019, 8, .	3.3	22
1998	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. Genome Research, 2019, 29, 2073-2087.	2.4	52
1999	The impact of genetic adaptation on chimpanzee subspecies differentiation. PLoS Genetics, 2019, 15, e1008485.	1.5	15
2000	Parallel Accelerated Evolution in Distant Hibernators Reveals Candidate Cis Elements and Genetic Circuits Regulating Mammalian Obesity. Cell Reports, 2019, 29, 2608-2620.e4.	2.9	8

#	Article	IF	Citations
2001	Insight into genetic regulation of miRNA in mouse brain. BMC Genomics, 2019, 20, 849.	1.2	4
2002	VPOT: A Customizable Variant Prioritization Ordering Tool for Annotated Variants. Genomics, Proteomics and Bioinformatics, 2019, 17, 540-545.	3.0	10
2003	Machine Learning Approaches for the Prioritization of Genomic Variants Impacting Pre-mRNA Splicing. Cells, 2019, 8, 1513.	1.8	41
2004	TMRS: an algorithm for computing the time to the most recent substitution event from a multiple alignment column. Algorithms for Molecular Biology, 2019, 14, 23.	0.3	3
2005	Multiple selective sweeps of ancient polymorphisms in and around LTÎ± located in the MHC class III region on chromosome 6. BMC Evolutionary Biology, 2019, 19, 218.	3.2	5
2006	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	1.7	27
2007	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
2008	3â€² UTRs Regulate Protein Functions by Providing a Nurturing Niche during Protein Synthesis. Cold Spring Harbor Symposia on Quantitative Biology, 2019, 84, 95-104.	2.0	8
2009	What Are 3â€² UTRs Doing?. Cold Spring Harbor Perspectives in Biology, 2019, 11, a034728.	2.3	298
2010	CADD: predicting the deleteriousness of variants throughout the human genome. Nucleic Acids Research, 2019, 47, D886-D894.	6.5	2,360
2011	PhastWeb: a web interface for evolutionary conservation scoring of multiple sequence alignments using phastCons and phyloP. Bioinformatics, 2019, 35, 2320-2322.	1.8	44
2012	HmtVar: a new resource for human mitochondrial variations and pathogenicity data. Nucleic Acids Research, 2019, 47, D1202-D1210.	6.5	58
2013	A Multiplexed Assay for Exon Recognition Reveals that an Unappreciated Fraction of Rare Genetic Variants Cause Large-Effect Splicing Disruptions. Molecular Cell, 2019, 73, 183-194.e8.	4.5	88
2014	A neuronal enhancer network upstream of MEF2C is compromised in patients with Rett-like characteristics. Human Molecular Genetics, 2019, 28, 818-827.	1.4	14
2015	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. Genes Chromosomes and Cancer, 2019, 58, 191-199.	1.5	117
2016	Cell-Type-Specific Profiling of Alternative Translation Identifies Regulated Protein Isoform Variation in the Mouse Brain. Cell Reports, 2019, 26, 594-607.e7.	2.9	61
2017	Ancient exapted transposable elements promote nuclear enrichment of human long noncoding RNAs. Genome Research, 2019, 29, 208-222.	2.4	64
2018	A map of direct TFâ€“DNA interactions in the human genome. Nucleic Acids Research, 2019, 47, e21-e21.	6.5	72

#	Article	IF	Citations
2019	Branch Point Selection in RNA Splicing Using Deep Learning. IEEE Access, 2019, 7, 1800-1807.	2.6	46
2020	ncRNA Editing: Functional Characterization and Computational Resources. Methods in Molecular Biology, 2019, 1912, 133-174.	0.4	20
2021	Exploiting regulatory heterogeneity to systematically identify enhancers with high accuracy. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 900-908.	3.3	20
2022	Limits of long-term selection against Neandertal introgression. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1639-1644.	3.3	151
2023	A quantitative framework for characterizing the evolutionary history of mammalian gene expression. Genome Research, 2019, 29, 53-63.	2.4	78
2024	Functional Conservation of a Developmental Switch in Mammals since the Jurassic Age. Molecular Biology and Evolution, 2019, 36, 39-53.	3.5	2
2025	Framework for microRNA variant annotation and prioritization using human population and disease datasets. Human Mutation, 2019, 40, 73-89.	1.1	18
2026	A dedicated target capture approach reveals variable genetic markers across microâ€•and macroâ€•evolutionary time scales in palms. Molecular Ecology Resources, 2019, 19, 221-234.	2.2	42
2027	Genome-wide differential expression of long noncoding RNAs and mRNAs in ovarian follicles of two different chicken breeds. Genomics, 2019, 111, 1395-1403.	1.3	26
2028	De novopattern discovery enables robust assessment of functional consequences of non-coding variants. Bioinformatics, 2019, 35, 1453-1460.	1.8	15
2029	An optimized prediction framework to assess the functional impact of pharmacogenetic variants. Pharmacogenomics Journal, 2019, 19, 115-126.	0.9	109
2030	New GJA8 variants and phenotypes highlight its critical role in a broad spectrum of eye anomalies. Human Genetics, 2019, 138, 1027-1042.	1.8	38
2031	Evolutionary perspectives on polygenic selection, missing heritability, and GWAS. Human Genetics, 2020, 139, 5-21.	1.8	37
2032	Identification of novel loci associated with infant cognitive ability. Molecular Psychiatry, 2020, 25, 3010-3019.	4.1	6
2033	Comparative Transcriptomics Analyses across Species, Organs, and Developmental Stages Reveal Functionally Constrained lncRNAs. Molecular Biology and Evolution, 2020, 37, 240-259.	3.5	30
2034	The Clinical Genome and Ancestry Report: An interactive web application for prioritizing clinically implicated variants from genome sequencing data with ancestry composition. Human Mutation, 2020, 41, 387-396.	1.1	0
2035	Matching whole genomes to rare genetic disorders: Identification of potential causative variants using phenotypeâ€weighted knowledge in the CAGI SickKids5 clinical genomes challenge. Human Mutation, 2020, 41, 347-362.	1.1	4
2036	Impact of Mutation Rate and Selection at Linked Sites on DNA Variation across the Genomes of Humans and Other Homininae. Genome Biology and Evolution, 2020, 12, 3550-3561.	1.1	18

#	Article	IF	Citations
2037	Constitutively bound CTCF sites maintain 3D chromatin architecture and long-range epigenetically regulated domains. Nature Communications, 2020, 11, 54.	5.8	72
2038	RNA isoform screens uncover the essentiality and tumor-suppressor activity of ultraconserved poison exons. Nature Genetics, 2020, 52, 84-94.	9.4	70
2039	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. Nature Communications, 2020, 11, 27.	5.8	23
2040	Pathogenicity Reclassification of RPE65 Missense Variants Related to Leber Congenital Amaurosis and Early-Onset Retinal Dystrophy. Genes, 2020, 11, 24.	1.0	14
2041	Genome-wide evolution analysis reveals low CpG contents of fast-evolving genes and identifies antiviral microRNAs. Journal of Genetics and Genomics, 2020, 47, 49-60.	1.7	4
2042	Dataset on the formation of Thioredoxin interacting protein (Txnip) containing redox sensitive high molecular weight nucleoprotein complexes. Data in Brief, 2020, 28, 104893.	0.5	1
2043	Exploring a Drosophila Transcription Factor Interaction Network to Identify Cis-Regulatory Modules. Journal of Computational Biology, 2020, 27, 1313-1328.	0.8	0
2044	A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. Molecular Cell, 2020, 77, 352-367.e8.	4.5	48
2045	Whatâ€™s the target: understanding two decades of in silico microRNA-target prediction. Briefings in Bioinformatics, 2020, 21, 1999-2010.	3.2	35
2047	A novel mutation in gene of PRPS1 in a young Chinese woman with X-linked gout: a case report and review of the literature. Clinical Rheumatology, 2020, 39, 949-956.	1.0	6
2048	InMeRF: prediction of pathogenicity of missense variants by individual modeling for each amino acid substitution. NAR Genomics and Bioinformatics, 2020, 2, lqaa038.	1.5	16
2049	Conserved Patterns in Developmental Processes and Phases, Rather than Genes, Unite the Highly Divergent Bilateria. Life, 2020, 10, 182.	1.1	2
2050	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. Scientific Data, 2020, 7, 326.	2.4	40
2051	Immunohistochemistry and Mutation Analysis of SDHx Genes in Carotid Paragangliomas. International Journal of Molecular Sciences, 2020, 21, 6950.	1.8	13
2052	Tissue-specific usage of transposable element-derived promoters in mouse development. Genome Biology, 2020, 21, 255.	3.8	55
2053	Genome-wide analysis of differentially expressed mRNAs, lncRNAs, and circRNAs in chicken bursae of Fabricius during infection with very virulent infectious bursal disease virus. BMC Genomics, 2020, 21, 724.	1.2	8
2054	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. Science, 2020, 370, 208-214.	6.0	41
2055	Cancer Predisposition Genes in Cancer-Free Families. Cancers, 2020, 12, 2770.	1.7	2

#	Article	IF	Citations
2056	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. PLoS Genetics, 2020, 16, e1009027.	1.5	7
2057	Giant Island Mice Exhibit Widespread Gene Expression Changes in Key Metabolic Organs. Genome Biology and Evolution, 2020, 12, 1277-1301.	1.1	1
2058	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	9.4	174
2059	Reorganized 3D Genome Structures Support Transcriptional Regulation in Mouse Spermatogenesis. IScience, 2020, 23, 101034.	1.9	36
2060	Unified inference of missense variant effects and gene constraints in the human genome. PLoS Genetics, 2020, 16, e1008922.	1.5	17
2061	Regulation, diversity and function of MECP2 exon and 3â€²UTR isoforms. Human Molecular Genetics, 2020, 29, R89-R99.	1.4	9
2062	â€˜There and Back Againâ€™â€”Forward Genetics and Reverse Phenotyping in Pulmonary Arterial Hypertension. Genes, 2020, 11, 1408.	1.0	11
2063	Prediction of driver variants in the cancer genome via machine learning methodologies. Briefings in Bioinformatics, 2021, 22, .	3.2	13
2064	Genome-Wide Analysis Reveals Changes in Long Noncoding RNAs in the Differentiation of Canine BMSCs into Insulin-Producing Cells. International Journal of Molecular Sciences, 2020, 21, 5549.	1.8	5
2065	VEPAD - Predicting the effect of variants associated with Alzheimer's disease using machine learning. Computers in Biology and Medicine, 2020, 124, 103933.	3.9	14
2066	Informing patients about their mutation tests: CDKN2A c.256G>A in melanoma as an example. Hereditary Cancer in Clinical Practice, 2020, 18, 15.	0.6	3
2067	Dynamic changes in the epigenomic landscape regulate human organogenesis and link to developmental disorders. Nature Communications, 2020, 11, 3920.	5.8	17
2068	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. Haematologica, 2021, 106, 2613-2623.	1.7	12
2069	Molecular diagnosis of epileptic encephalopathy of the first year of life applying a customized gene panel in a group of Argentinean patients. Epilepsy and Behavior, 2020, 111, 107322.	0.9	4
2070	Reinterpreting sheep muscle strandâ€specific RNA sequencing data showing extensive 3â€²UTR extensions. Animal Genetics, 2020, 51, 788-798.	0.6	0
2071	Intrinsic transcriptomic sex differences in human endothelial cells at birth and in adults are associated with coronary artery disease targets. Scientific Reports, 2020, 10, 12367.	1.6	39
2072	Cross-species analysis of enhancer logic using deep learning. Genome Research, 2020, 30, 1815-1834.	2.4	65
2073	MISTIC: A prediction tool to reveal disease-relevant deleterious missense variants. PLoS ONE, 2020, 15, e0236962.	1.1	26

#	Article	IF	Citations
2074	Chronic lymphocytic leukemia (CLL) risk is mediated by multiple enhancer variants within CLL risk loci. Human Molecular Genetics, 2020, 29, 2761-2774.	1.4	6
2075	Divergence, gene flow, and speciation in eight lineages of transâ€Beringian birds. Molecular Ecology, 2020, 29, 3526-3542.	2.0	18
2076	The RNA exosome shapes the expression of key protein-coding genes. Nucleic Acids Research, 2020, 48, 8509-8528.	6.5	12
2077	SOX10-regulated promoter use defines isoform-specific gene expression in Schwann cells. BMC Genomics, 2020, 21, 549.	1.2	13
2078	Promoter CpG Density Predicts Downstream Gene Loss-of-Function Intolerance. American Journal of Human Genetics, 2020, 107, 487-498.	2.6	12
2079	Novel Compound Heterozygous Mutations in CRTAP Cause Rare Autosomal Recessive Osteogenesis Imperfecta. Frontiers in Genetics, 2020, 11, 897.	1.1	4
2080	Identification of Edible Short- and Long-Horned Grasshoppers and Their Host Plants in East Africa. Journal of Economic Entomology, 2020, 113, 2150-2162.	0.8	8
2081	Ancient RNA virus epidemics through the lens of recent adaptation in human genomes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190575.	1.8	37
2082	The First Report of Biallelic Missense Mutations in the SFRP4 Gene Causing Pyle Disease in Two Siblings. Frontiers in Genetics, 2020, 11, 593407.	1.1	8
2083	A new homozygous HERC1 gain-of-function variant in MDFPMR syndrome leads to mTORC1 hyperactivation and reduced autophagy during cell catabolism. Molecular Genetics and Metabolism, 2020, 131, 126-134.	0.5	6
2084	Implication of a new function of human tDNAs in chromatin organization. Scientific Reports, 2020, 10, 17440.	1.6	6
2085	Background Selection Does Not Mimic the Patterns of Genetic Diversity Produced by Selective Sweeps. Genetics, 2020, 216, 499-519.	1.2	41
2086	Evaluating the informativeness of deep learning annotations for human complex diseases. Nature Communications, 2020, 11, 4703.	5.8	21
2087	Transcription factor expression defines subclasses of developing projection neurons highly similar to single-cell RNA-seq subtypes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25074-25084.	3.3	23
2088	Scratch2, a Snail Superfamily Member, Is Regulated by miR-125b. Frontiers in Cell and Developmental Biology, 2020, 8, 769.	1.8	2
2089	Inter-embryo gene expression variability recapitulates the hourglass pattern of evo-devo. BMC Biology, 2020, 18, 129.	1.7	23
2090	Genotypeâ€“phenotype correlation of 33 patients with maple syrup urine disease. American Journal of Medical Genetics, Part A, 2020, 182, 2486-2500.	0.7	6
2091	CAPICE: a computational method for Consequence-Agnostic Pathogenicity Interpretation of Clinical Exome variations. Genome Medicine, 2020, 12, 75.	3.6	30

#	Article	IF	Citations
2092	m6A Reader: Epitranscriptome Target Prediction and Functional Characterization of N6-Methyladenosine (m6A) Readers. Frontiers in Cell and Developmental Biology, 2020, 8, 741.	1.8	31
2093	Transphyletic conservation of nitric oxide synthase regulation in cephalochordates and tunicates. Development Genes and Evolution, 2020, 230, 329-338.	0.4	3
2094	Learning the properties of adaptive regions with functional data analysis. PLoS Genetics, 2020, 16, e1008896.	1.5	16
2095	Integrated analysis of lncRNA, miRNA and mRNA reveals novel insights into the fertility regulation of large white sows. BMC Genomics, 2020, 21, 636.	1.2	11
2096	A human-specific VNTR in the TRIB3 promoter causes gene expression variation between individuals. PLoS Genetics, 2020, 16, e1008981.	1.5	13
2097	PINCER: improved CRISPR/Cas9 screening by efficient cleavage at conserved residues. Nucleic Acids Research, 2020, 48, 9462-9477.	6.5	6
2098	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	9.4	146
2099	Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations. Nature Communications, 2020, 11, 6168.	5.8	1
2100	Mutation Frequency in Main Susceptibility Genes Among Patients With Head and Neck Paragangliomas. Frontiers in Genetics, 2020, 11, 614908.	1.1	16
2101	An Overview of Genomics, Phylogenomics and Proteomics Approaches in Ascomycota. Life, 2020, 10, 356.	1.1	12
2102	dbNSFP v4: a comprehensive database of transcript-specific functional predictions and annotations for human nonsynonymous and splice-site SNVs. Genome Medicine, 2020, 12, 103.	3.6	300
2103	Toward an Evolutionarily Appropriate Null Model: Jointly Inferring Demography and Purifying Selection. Genetics, 2020, 215, 173-192.	1.2	119
2104	The Evolution of Human Cancer Gene Duplications acrossÂMammals. Molecular Biology and Evolution, 2020, 37, 2875-2886.	3.5	31
2105	Opposite regulation of piRNAs, rRNAs and miRNAs in the blood after subarachnoid hemorrhage. Journal of Molecular Medicine, 2020, 98, 887-896.	1.7	2
2106	Cistrome Data Browser and Toolkit: analyzing human and mouse genomic data using compendia of ChIPâ€seq and chromatin accessibility data. Quantitative Biology, 2020, 8, 267-276.	0.3	11
2107	Reconsidering proteomic diversity with functional investigation of small ORFs and alternative ORFs. Experimental Cell Research, 2020, 393, 112057.	1.2	37
2108	Challenges in the diagnosis and discovery of rare genetic disorders using contemporary sequencing technologies. Briefings in Functional Genomics, 2020, 19, 243-258.	1.3	27
2109	Identifying branch-specific positive selection throughout the regulatory genome using an appropriate proxy neutral. BMC Genomics, 2020, 21, 359.	1.2	10

#	Article	IF	Citations
2110	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. Nature Communications, 2020, 11, 2653.	5.8	17
2111	Population genetic models of GERP scores suggest pervasive turnover of constrained sites across mammalian evolution. PLoS Genetics, 2020, 16, e1008827.	1.5	65
2112	Long non-coding RNAs in the alkaline stress response in sugar beet (Beta vulgaris L.). BMC Plant Biology, 2020, 20, 227.	1.6	13
2113	DNA steganography: hiding undetectable secret messages within the single nucleotide polymorphisms of a genome and detecting mutation-induced errors. Microbial Cell Factories, 2020, 19, 128.	1.9	12
2114	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	13.7	194
2115	A Germline Mutation in the POT1 Gene Is a Candidate for Familial Non-Medullary Thyroid Cancer. Cancers, 2020, 12, 1441.	1.7	24
2116	Alternative UNC13D Promoter Encodes a Functional Munc13-4 Isoform Predominantly Expressed in Lymphocytes and Platelets. Frontiers in Immunology, 2020, 11, 1154.	2.2	2
2117	Machine learning and deep learning for the advancement of epigenomics. , 2020, , 217-237.		0
2118	LEAP: Using machine learning to support variant classification in a clinical setting. Human Mutation, 2020, 41, 1079-1090.	1.1	23
2119	Therapeutic base editing of human hematopoietic stem cells. Nature Medicine, 2020, 26, 535-541.	15.2	196
2120	Computational identification of cell-specific variable regions in ChIP-seq data. Nucleic Acids Research, 2020, 48, e53-e53.	6.5	4
2121	Long noncoding RNA and messenger RNA abnormalities in pediatric sepsis: a preliminary study. BMC Medical Genomics, 2020, 13, 36.	0.7	9
2122	m7GHub: deciphering the location, regulation and pathogenesis of internal mRNA N7-methylguanosine (m7G) sites in human. Bioinformatics, 2020, 36, 3528-3536.	1.8	85
2123	Locally acting transcription factors regulate p53-dependent cis-regulatory element activity. Nucleic Acids Research, 2020, 48, 4195-4213.	6.5	16
2124	Mammalian Alternative Translation Initiation Is Mostly Nonadaptive. Molecular Biology and Evolution, 2020, 37, 2015-2028.	3.5	13
2125	An Evolutionary Trace method defines functionally important bases and sites common to RNA families. PLoS Computational Biology, 2020, 16, e1007583.	1.5	2
2126	Exploring 3D chromatin contacts in gene regulation: The evolution of approaches for the identification of functional enhancer-promoter interaction. Computational and Structural Biotechnology Journal, 2020, 18, 558-570.	1.9	37
2127	Identification of Familial Hodgkin Lymphoma Predisposing Genes Using Whole Genome Sequencing. Frontiers in Bioengineering and Biotechnology, 2020, 8, 179.	2.0	12

#	Article	IF	Citations
2128	Phylogenetics is the New Genetics (for Most of Biodiversity). Trends in Ecology and Evolution, 2020, 35, 415-425.	4.2	72
2129	Phylogenetic Modeling of Regulatory Element Turnover Based on Epigenomic Data. Molecular Biology and Evolution, 2020, 37, 2137-2152.	3.5	14
2130	LIST-S2: taxonomy based sorting of deleterious missense mutations across species. Nucleic Acids Research, 2020, 48, W154-W161.	6.5	46
2131	Genome-Wide Identification and Analysis of Enhancer-Regulated microRNAs Across 31 Human Cancers. Frontiers in Genetics, 2020, 11, 644.	1.1	4
2132	Exploration of Long Non-coding RNAs and Circular RNAs in Porcine Milk Exosomes. Frontiers in Genetics, 2020, 11, 652.	1.1	25
2133	A Chromatin Accessibility Atlas of the Developing Human Telencephalon. Cell, 2020, 182, 754-769.e18.	13.5	69
2134	Targeted sequencing of genes associated with the mismatch repair pathway in patients with endometrial cancer. PLoS ONE, 2020, 15, e0235613.	1.1	4
2135	Epigenetics for Clinicians from the Perspective of Pediatric Rheumatic Diseases. Current Rheumatology Reports, 2020, 22, 46.	2.1	5
2136	pCADD: SNV prioritisation in Sus scrofa. Genetics Selection Evolution, 2020, 52, 4.	1.2	21
2137	An inferred fitness consequence map of the rice genome. Nature Plants, 2020, 6, 119-130.	4.7	20
2138	In the presence of population structure: From genomics to candidate genes underlying local adaptation. Ecology and Evolution, 2020, 10, 1889-1904.	0.8	17
2139	EEF1A2 mutations in epileptic encephalopathy/intellectual disability: Understanding the potential mechanism of phenotypic variation. Epilepsy and Behavior, 2020, 105, 106955.	0.9	11
2140	Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex. Nature Communications, 2020, 11, 1001.	5.8	147
2141	Phylogenomic analysis of trichomycterid catfishes (Teleostei: Siluriformes) inferred from ultraconserved elements. Scientific Reports, 2020, 10, 2697.	1.6	45
2142	Setup and Validation of a Targeted Next-Generation Sequencing Approach for the Diagnosis of Lysosomal Storage Disorders. Journal of Molecular Diagnostics, 2020, 22, 488-502.	1.2	15
2143	Unmasking Retinitis Pigmentosa complex cases by a whole genome sequencing algorithm based on open-access tools: hidden recessive inheritance and potential oligogenic variants. Journal of Translational Medicine, 2020, 18, 73.	1.8	23
2144	Inferring the transcriptional regulatory mechanism of signalâ€dependent gene expression via an integrative computational approach. FEBS Letters, 2020, 594, 1477-1496.	1.3	3
2145	A genome alignment of 120 mammals highlights ultraconserved element variability and placenta-associated enhancers. GigaScience, 2020, 9, .	3.3	29

#	Article	IF	Citations
2146	Genome-wide analysis of mRNAs and lncRNAs in Mycoplasma bovis infected and non-infected bovine mammary gland tissues. Molecular and Cellular Probes, 2020, 50, 101512.	0.9	17
2147	Enhancerâ€“gene maps in the human and zebrafish genomes using evolutionary linkage conservation. Nucleic Acids Research, 2020, 48, 2357-2371.	6.5	32
2148	A transcriptome-wide antitermination mechanism sustaining identity of embryonic stem cells. Nature Communications, 2020, 11, 361.	5.8	20
2149	Towards a comprehensive catalogue of validated and target-linked human enhancers. Nature Reviews Genetics, 2020, 21, 292-310.	7.7	229
2150	Reducing the structure bias of RNA-Seq reveals a large number of non-annotated non-coding RNA. Nucleic Acids Research, 2020, 48, 2271-2286.	6.5	29
2151	Independent Transposon Exaptation Is a Widespread Mechanism of Redundant Enhancer Evolution in the Mammalian Genome. Genome Biology and Evolution, 2020, 12, 1-17.	1.1	14
2152	From reads to insight: a hitchhikerâ€™s guide to ATAC-seq data analysis. Genome Biology, 2020, 21, 22.	3.8	268
2153	High Mobility Group A (HMGA): Chromatin Nodes Controlled by a Knotty miRNA Network. International Journal of Molecular Sciences, 2020, 21, 717.	1.8	6
2154	The Expression of Decidual Protein Induced by Progesterone (DEPP) Is Controlled by Three Distal Consensus Hypoxia Responsive Element (HRE) in Hypoxic Retinal Epithelial Cells. Genes, 2020, 11, 111.	1.0	3
2155	Parallel Genetic Origin of Foot Feathering in Birds. Molecular Biology and Evolution, 2020, 37, 2465-2476.	3.5	19
2156	Genetic Architecture of Gene Expression in European and African Americans: An eQTL Mapping Study in GENOA. American Journal of Human Genetics, 2020, 106, 496-512.	2.6	56
2157	A spontaneous missense mutation in the chromodomain helicase DNAâ€bbinding protein 8 (CHD8) gene: a novel association with congenital myasthenic syndrome. Neuropathology and Applied Neurobiology, 2020, 46, 588-601.	1.8	6
2158	PIANO: A Web Server for Pseudouridine-Site (Î¨) Identification and Functional Annotation. Frontiers in Genetics, 2020, 11, 88.	1.1	30
2159	Comprehensive History of CSP Genes: Evolution, Phylogenetic Distribution and Functions. Genes, 2020, 11, 413.	1.0	22
2160	An Improved Phenotype-Driven Tool for Rare Mendelian Variant Prioritization: Benchmarking Exomiser on Real Patient Whole-Exome Data. Genes, 2020, 11, 460.	1.0	42
2161	Tumour characteristics provide evidence for germline mismatch repair missense variant pathogenicity. Journal of Medical Genetics, 2020, 57, 62-69.	1.5	11
2162	CScape-somatic: distinguishing driver and passenger point mutations in the cancer genome. Bioinformatics, 2020, 36, 3637-3644.	1.8	19
2163	Evolutionary Dynamics of the SKN-1 â†' MED â†' END-1,3 Regulatory Gene Cascade inCaenorhabditisEndoderm Specification. G3: Genes, Genomes, Genetics, 2020, 10, 333-356.	0.8	14

#	Article	IF	Citations
2164	A novel PCDH19 missense mutation, c.812G>A (p.Gly271Asp), identified using wholeâ€exome sequencing in a Chinese family with epilepsy female restricted mental retardation syndrome. Molecular Genetics & Genomic Medicine, 2020, 8, e1234.	0.6	5
2165	Transposable elements contribute to cell and species-specific chromatin looping and gene regulation in mammalian genomes. Nature Communications, 2020, 11, 1796.	5.8	82
2166	Prot2HG: a database of protein domains mapped to the human genome. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	17
2167	Stable intronic sequence RNAs (sisRNAs) are selected regions in introns with distinct properties. BMC Genomics, 2020, 21, 287.	1.2	3
2168	PredCID: prediction of driver frameshift indels in human cancer. Briefings in Bioinformatics, 2021, 22, .	3.2	29
2169	Modes of genetic adaptations underlying functional innovations in the rumen. Science China Life Sciences, 2021, 64, 1-21.	2.3	19
2170	A systematic evaluation of bioinformatics tools for identification of long noncoding RNAs. Rna, 2021, 27, 80-98.	1.6	19
2171	Integration of multiomic annotation data to prioritize and characterize inflammation and immuneâ€related risk variants in squamous cell lung cancer. Genetic Epidemiology, 2021, 45, 99-114.	0.6	7
2172	Genetic Variation and Hybridization in Evolutionary Radiations of Cichlid Fishes. Annual Review of Animal Biosciences, 2021, 9, 55-79.	3.6	24
2173	OncoVar: an integrated database and analysis platform for oncogenic driver variants in cancers. Nucleic Acids Research, 2021, 49, D1289-D1301.	6.5	64
2174	ZNF410ÂUniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. Molecular Cell, 2021, 81, 239-254.e8.	4.5	48
2175	Biallelic ZNF335 mutations cause basal ganglia abnormality with progressive cerebral/cerebellar atrophy. Journal of Neurogenetics, 2021, 35, 23-28.	0.6	2
2176	m6A-Atlas: a comprehensive knowledgebase for unraveling theN6-methyladenosine (m6A) epitranscriptome. Nucleic Acids Research, 2021, 49, D134-D143.	6.5	185
2177	Recapitulating Evolutionary Divergence in a SingleCis-Regulatory Element Is Sufficient to Cause Expression Changes of the Lens GeneTdrd7. Molecular Biology and Evolution, 2021, 38, 380-392.	3.5	4
2178	DeepRibSt: a multi-feature convolutional neural network for predicting ribosome stalling. Multimedia Tools and Applications, 2021, 80, 17239-17255.	2.6	1
2179	An Ensemble Framework for Improving the Prediction of Deleterious Synonymous Mutation. IEEE Transactions on Circuits and Systems for Video Technology, 2022, 32, 2603-2611.	5.6	6
2180	The Great Pond Snail (Lymnaea stagnalis) as a Model of Aging and Age-Related Memory Impairment: An Overview. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 975-982.	1.7	8
2181	GPCards: An integrated database of genotypeâ€“phenotype correlations in human genetic diseases. Computational and Structural Biotechnology Journal, 2021, 19, 1603-1611.	1.9	5

#	Article	IF	Citations
2182	ACES: Analysis of Conservation with an Extensive list of Species. Bioinformatics, 2021, 37, 3920-3922.	1.8	0
2183	Mitochondrial gene expression in single cells shape pancreatic beta cells' sub-populations and explain variation in insulin pathway. Scientific Reports, 2021, 11, 466.	1.6	9
2185	Identifying LncRNA-Encoded Short Peptides Using Optimized Hybrid Features and Ensemble Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2873-2881.	1.9	3
2187	Illuminating lncRNA Function Through Target Prediction. Methods in Molecular Biology, 2021, 2372, 263-295.	0.4	3
2189	Probing the aggregated effects of purifying selection per individual on 1,380 medical phenotypes in the UK Biobank. PLoS Genetics, 2021, 17, e1009337.	1.5	2
2190	Positive Selection in Human Populations: Practical Aspects and Current Knowledge. Evolutionary Studies, 2021, , 29-65.	0.2	1
2191	Evolutionary conservation and divergence of the human brain transcriptome. Genome Biology, 2021, 22, 52.	3.8	28
2192	Genetic variant effect prediction by supervised nonnegative matrix tri-factorization. Molecular Omics, 2021, 17, 740-751.	1.4	1
2193	Integrating Evolutionary Genetics to Medical Genomics: Evolutionary Approaches to Investigate Disease-Causing Variants. , 0, , .		0
2194	Online Genomic Resources and Bioinformatics Tools Available for Epigenetics and Non-coding RNA. , 2021, , 306-328.		0
2195	Whole Exome Sequencing Identifies APCDD1 and HDAC5 Genes as Potentially Cancer Predisposing in Familial Colorectal Cancer. International Journal of Molecular Sciences, 2021, 22, 1837.	1.8	6
2196	A Mini-review of Computational Approaches to Predict Functions and Findings of Novel Micro Peptides. Current Bioinformatics, 2021, 15, 1027-1035.	0.7	2
2197	Evolution of Conserved Noncoding Sequences inArabidopsis thaliana. Molecular Biology and Evolution, 2021, 38, 2692-2703.	3.5	14
2198	Genetic Mechanisms Underlying Cortical Evolution in Mammals. Frontiers in Cell and Developmental Biology, 2021, 9, 591017.	1.8	15
2199	The Genomes of Two Billfishes Provide Insights into the Evolution of Endothermy in Teleosts. Molecular Biology and Evolution, 2021, 38, 2413-2427.	3.5	15
2200	Life-Threatening Influenza, Hemophagocytic Lymphohistiocytosis and Probable Vaccine-Strain Varicella in a Novel Case of Homozygous STAT2 Deficiency. Frontiers in Immunology, 2020, 11, 624415.	2.2	21
2201	CADD-Spliceâ€"improving genome-wide variant effect prediction using deep learning-derived splice scores. Genome Medicine, 2021, 13, 31.	3.6	375
2202	Comparative genomics of Chlamydomonas. Plant Cell, 2021, 33, 1016-1041.	3.1	46

#	Article	IF	Citations
2205	Next Generation Exome Sequencing of Pediatric Asthma Identifies Rare and Novel Variants in Candidate Genes. Disease Markers, 2021, 2021, 1-10.	0.6	6
2207	Motif-Raptor: a cell type-specific and transcription factor centric approach for post-GWAS prioritization of causal regulators. Bioinformatics, 2021, 37, 2103-2111.	1.8	5
2208	Revisiting sORFs: overcoming challenges to identify and characterize functional microproteins. FEBS Journal, 2022, 289, 53-74.	2.2	57
2209	Structure-Based Approaches to Classify the Functional Impact of ZBTB18 Missense Variants in Health and Disease. ACS Chemical Neuroscience, 2021, 12, 979-989.	1.7	4
2211	Eliminating Target Anopheles Proteins to Non-Target Organisms based on Posterior Probability Algorithm. Advances in Science, Technology and Engineering Systems, 2021, 6, 710-718.	0.4	0
2212	New Insights Into Mitochondrial DNA Reconstruction and Variant Detection in Ancient Samples. Frontiers in Genetics, 2021, 12, 619950.	1.1	6
2213	The Impact of Purifying and Background Selection on the Inference of Population History: Problems and Prospects. Molecular Biology and Evolution, 2021, 38, 2986-3003.	3.5	56
2214	Whole Genome Sequencing Prioritizes CHEK2, EWSR1, and TIAM1 as Possible Predisposition Genes for Familial Non-Medullary Thyroid Cancer. Frontiers in Endocrinology, 2021, 12, 600682.	1.5	13
2215	Topologically associating domain boundaries that are stable across diverse cell types are evolutionarily constrained and enriched for heritability. American Journal of Human Genetics, 2021, 108, 269-283.	2.6	117
2216	Predicting dynamic cellular proteinâ€“RNA interactions by deep learning using in vivo RNA structures. Cell Research, 2021, 31, 495-516.	5.7	64
2217	Derepression of retroelements in acute myeloid leukemia with 3q aberrations. Haematologica, 2021, 106, 2269-2273.	1.7	0
2218	Ultraconservation of enhancers is not ultranecessary. Nature Genetics, 2021, 53, 429-430.	9.4	1
2219	Evolutionary Constraint on Visual and Nonvisual Mammalian Opsins. Journal of Biological Rhythms, 2021, 36, 109-126.	1.4	22
2220	Genetic-variant hotspots and hotspot clusters in the human genome facilitating adaptation while increasing instability. Human Genomics, 2021, 15, 19.	1.4	9
2221	Prioritizing non-coding regions based on human genomic constraint and sequence context with deep learning. Nature Communications, 2021, 12, 1504.	5.8	40
2222	A transcription-centric model of SNP-age interaction. PLoS Genetics, 2021, 17, e1009427.	1.5	7
2224	Comprehensive profiling of circular RNAs with nanopore sequencing and CIRI-long. Nature Biotechnology, 2021, 39, 836-845.	9.4	108
2227	Exploring Common Therapeutic Targets for Neurodegenerative Disorders Using Transcriptome Study. Frontiers in Genetics, 2021, 12, 639160.	1.1	11

#	Article	IF	Citations
2228	A conserved role for the ALS-linked splicing factor SFPQ in repression of pathogenic cryptic last exons. Nature Communications, 2021, 12, 1918.	5.8	10
2231	Rapid speciation via the evolution of pre-mating isolation in the IberÃ¡ Seedeater. Science, 2021, 371, .	6.0	44
2232	Mutations of Intrinsically Disordered Protein Regions Can Drive Cancer but Lack Therapeutic Strategies. Biomolecules, 2021, 11, 381.	1.8	26
2233	Ultra-conserved sequences in the genomes of highly diverse Anopheles mosquitoes, with implications for malaria vector control. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
2234	Does Saccharomyces cerevisiae Require Specific Post-Translational Silencing against Leaky Translation of Hac1up?. Microorganisms, 2021, 9, 620.	1.6	1
2236	Ultraconserved enhancer function does not require perfect sequence conservation. Nature Genetics, 2021, 53, 521-528.	9.4	39
2237	African lungfish genome sheds light on the vertebrate water-to-land transition. Cell, 2021, 184, 1362-1376.e18.	13.5	99
2240	Genomic Basis of Striking Fin Shapes and Colors in the Fighting Fish. Molecular Biology and Evolution, 2021, 38, 3383-3396.	3.5	33
2241	Genomic insights into population history and biological adaptation in Oceania. Nature, 2021, 592, 583-589.	13.7	100
2242	Human-lineage-specific genomic elements are associated with neurodegenerative disease and APOE transcript usage. Nature Communications, 2021, 12, 2076.	5.8	9
2243	Amplicon genome fishing (AGF): a rapid and efficient method for sequencing target cis-regulatory regions in nonmodel organisms. Molecular Genetics and Genomics, 2021, 296, 527-539.	1.0	0
2244	Conservation of Aging and Cancer Epigenetic Signatures across Human and Mouse. Molecular Biology and Evolution, 2021, 38, 3415-3435.	3.5	5
2245	usDSM: a novel method for deleterious synonymous mutation prediction using undersampling scheme. Briefings in Bioinformatics, 2021, 22, .	3.2	12
2248	Prediction of diseaseâ€associated functional variants in noncoding regions through a comprehensive analysis by integrating datasets and features. Human Mutation, 2021, 42, 667-684.	1.1	0
2250	The Impact of the FKBP5 Gene Polymorphisms on the Relationship between Traumatic Life Events and Psychotic-Like Experiences in Non-Clinical Adults. Brain Sciences, 2021, 11, 561.	1.1	3
2251	Monoallelic and bi-allelic variants in NCDN cause neurodevelopmental delay, intellectual disability, and epilepsy. American Journal of Human Genetics, 2021, 108, 739-748.	2.6	15
2252	CytoTalk: De novo construction of signal transduction networks using single-cell transcriptomic data. Science Advances, 2021, 7, .	4.7	51
2253	EEF1D facilitates milk lipid synthesis by regulation of PI3Kâ€Akt signaling in mammals. FASEB Journal, 2021, 35, e21455.	0.2	9

#	Article	IF	Citations
2254	Repeated mutation of a developmental enhancer contributed to human thermoregulatory evolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
2255	Interactions between PDA-associated polymorphisms and genetic ancestry alter ductus arteriosus gene expression. Pediatric Research, 2021, , .	1.1	0
2256	A Novel Low-Risk Germline Variant in the SH2 Domain of the SRC Gene Affects Multiple Pathways in Familial Colorectal Cancer. Journal of Personalized Medicine, 2021, 11, 262.	1.1	0
2257	Functional and structural basis of extreme conservation in vertebrate 5â€² untranslated regions. Nature Genetics, 2021, 53, 729-741.	9.4	17
2259	Conserved long-range base pairings are associated with pre-mRNA processing of human genes. Nature Communications, 2021, 12, 2300.	5.8	27
2261	TAD boundary and strength prediction by integrating sequence and epigenetic profile information. Briefings in Bioinformatics, 2021, 22, .	3.2	11
2262	Cancer LncRNA Census 2 (CLC2): an enhanced resource reveals clinical features of cancer lncRNAs. NAR Cancer, 2021, 3, zcab013.	1.6	21
2263	The Translational Machine: A novel machineâ€learning approach to illuminate complex genetic architectures. Genetic Epidemiology, 2021, 45, 485-536.	0.6	0
2264	Enhancer viruses for combinatorial cell-subclass-specific labeling. Neuron, 2021, 109, 1449-1464.e13.	3.8	93
2265	A distal Foxp3 enhancer enables interleukin-2 dependent thymic Treg cell lineage commitment for robust immune tolerance. Immunity, 2021, 54, 931-946.e11.	6.6	46
2266	Modeling the Evolutionary Architectures of Transcribed Human Enhancer Sequences Reveals Distinct Origins, Functions, and Associations with Human Trait Variation. Molecular Biology and Evolution, 2021, 38, 3681-3696.	3.5	7
2267	Missense and truncating variants in CHD5 in a dominant neurodevelopmental disorder with intellectual disability, behavioral disturbances, and epilepsy. Human Genetics, 2021, 140, 1109-1120.	1.8	18
2268	Epigenomic profiling of primate lymphoblastoid cell lines reveals the evolutionary patterns of epigenetic activities in gene regulatory architectures. Nature Communications, 2021, 12, 3116.	5.8	19
2269	SARS-CoV-2 gene content and COVID-19 mutation impact by comparing 44 Sarbecovirus genomes. Nature Communications, 2021, 12, 2642.	5.8	136
2270	Single nucleus multi-omics regulatory landscape of the murine pituitary. Nature Communications, 2021, 12, 2677.	5.8	38
2272	Cardiac cell typeâ€“specific gene regulatory programs and disease risk association. Science Advances, 2021, 7, .	4.7	63
2273	Learning a genome-wide score of humanâ€“mouse conservation at the functional genomics level. Nature Communications, 2021, 12, 2495.	5.8	12
2274	dSPRINT: predicting DNA, RNA, ion, peptide and small molecule interaction sites within protein domains. Nucleic Acids Research, 2021, 49, e78-e78.	6.5	5

#	Article	IF	Citations
2275	Elephant Genomes Reveal Accelerated Evolution in Mechanisms Underlying Disease Defenses. Molecular Biology and Evolution, 2021, 38, 3606-3620.	3.5	33
2276	Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. Nucleic Acids Research, 2021, 49, 5705-5725.	6.5	10
2277	Integrated genomic analysis reveals key features of long undecoded transcript isoform-based gene repression. Molecular Cell, 2021, 81, 2231-2245.e11.	4.5	20
2278	ExTraMapper: exon- and transcript-level mappings for orthologous gene pairs. Bioinformatics, 2021, 37, 3412-3420.	1.8	3
2279	Alternative splicing during mammalian organ development. Nature Genetics, 2021, 53, 925-934.	9.4	93
2283	The pluripotent stem cell-specific transcript ESRG is dispensable for human pluripotency. PLoS Genetics, 2021, 17, e1009587.	1.5	20
2284	Identification and Classification of Rare Variants in NPC1 and NPC2 in Quebec. Scientific Reports, 2021, 11, 10344.	1.6	2
2285	Self-selection of evolutionary strategies: adaptive versus non-adaptive forces. Heliyon, 2021, 7, e06997.	1.4	4
2286	The landscape and driver potential of site-specific hotspots across cancer genomes. Npj Genomic Medicine, 2021, 6, 33.	1.7	8
2288	ConsRM: collection and large-scale prediction of the evolutionarily conserved RNA methylation sites, with implications for the functional epitranscriptome. Briefings in Bioinformatics, 2021, 22, .	3.2	34
2289	Chromosomeâ€level assembly of southern catfish (silurus meridionalis) provides insights into visual adaptation to nocturnal and benthic lifestyles. Molecular Ecology Resources, 2021, 21, 1575-1592.	2.2	20
2290	Toward comprehensive functional analysis of gene lists weighted by gene essentiality scores. Bioinformatics, 2021, 37, 4399-4404.	1.8	9
2291	Genome-enabled discovery of evolutionary divergence in brains and behavior. Scientific Reports, 2021, 11, 13016.	1.6	5
2293	Annotation of snoRNA abundance across human tissues reveals complex snoRNA-host gene relationships. Genome Biology, 2021, 22, 172.	3.8	28
2294	Computational Tools to Assess the Functional Consequences of Rare and Noncoding Pharmacogenetic Variability. Clinical Pharmacology and Therapeutics, 2021, 110, 626-636.	2.3	16
2295	Vitamin D decreases silencer methylation to downregulate renin gene expression. Gene, 2021, 786, 145623.	1.0	3
2297	Functional differences between TSHR alleles associate with variation in spawning season in Atlantic herring. Communications Biology, 2021, 4, 795.	2.0	5
2298	C. elegans detects toxicity of traumatic brain injury generated tau. Neurobiology of Disease, 2021, 153, 105330.	2.1	5

#	Article	IF	Citations
2301	SnoRNA copy regulation affects family size, genomic location and family abundance levels. BMC Genomics, 2021, 22, 414.	1.2	12
2303	Pan-cancer characterization of long non-coding RNA and DNA methylation mediated transcriptional dysregulation. EBioMedicine, 2021, 68, 103399.	2.7	25
2304	Shifting epigenetic contexts influence regulatory variation and disease risk. Aging, 2021, 13, 15699-15749.	1.4	2
2305	Genetics of white color and iridophoroma in â€œLemon Frostâ€•leopard geckos. PLoS Genetics, 2021, 17, e1009580.	1.5	13
2306	Single-nucleotide conservation state annotation of the SARS-CoV-2 genome. Communications Biology, 2021, 4, 698.	2.0	2
2307	UniBind: maps of high-confidence direct TF-DNA interactions across nine species. BMC Genomics, 2021, 22, 482.	1.2	36
2308	Assessing conservation of alternative splicing with evolutionary splicing graphs. Genome Research, 2021, 31, 1462-1473.	2.4	8
2309	Yeast Ssd1 is a non-enzymatic member of the RNase II family with an alternative RNA recognition site. Nucleic Acids Research, 2022, 50, 2923-2937.	6.5	13
2312	Genome of PeÅŸtera Muierii skull shows high diversity and low mutational load in pre-glacial Europe. Current Biology, 2021, 31, 2973-2983.e9.	1.8	18
2313	Highly contiguous assemblies of 101 drosophilid genomes. ELife, 2021, 10, .	2.8	108
2316	Efficacy of computational predictions of the functional effect of idiosyncratic pharmacogenetic variants. PeerJ, 2021, 9, e11774.	0.9	2
2317	Brutonâ€™s Tyrosine Kinase and Its Isoforms in Cancer. Frontiers in Cell and Developmental Biology, 2021, 9, 668996.	1.8	20
2318	Long Non-coding RNA Signatures Associated With Liver Aging in Senescence-Accelerated Mouse Prone 8 Model. Frontiers in Cell and Developmental Biology, 2021, 9, 698442.	1.8	3
2323	Impact of Genetic Variation in Gene Regulatory Sequences: A Population Genomics Perspective. Frontiers in Genetics, 2021, 12, 660899.	1.1	2
2324	ETS1, ELK1, and ETV4 Transcription Factors Regulate Angiopoietin-1 Signaling and the Angiogenic Response in Endothelial Cells. Frontiers in Physiology, 2021, 12, 683651.	1.3	9
2325	Transcription factor RFX7 governs a tumor suppressor network in response to p53 and stress. Nucleic Acids Research, 2021, 49, 7437-7456.	6.5	17
2326	Differential usage of transcriptional repressor Zeb2 enhancers distinguishes adult and embryonic hematopoiesis. Immunity, 2021, 54, 1417-1432.e7.	6.6	17
2328	Transcriptional reprogramming by oxidative stress occurs within a predefined chromatin accessibility landscape. Free Radical Biology and Medicine, 2021, 171, 319-331.	1.3	6

#	Article	IF	Citations
2329	MitoPhen database: a human phenotype ontology-based approach to identify mitochondrial DNA diseases. Nucleic Acids Research, 2021, 49, 9686-9695.	6.5	14
2330	Cis-regulatory variants affect gene expression dynamics in yeast. ELife, 2021, 10, .	2.8	6
2331	PNPT1, MYO15A, PTPRQ, and SLC12A2â€associated genetic and phenotypic heterogeneity among hearing impaired assortative mating families in Southern India. Annals of Human Genetics, 2022, 86, 1-13.	0.3	5
2332	Open chromatin in grapevine marks candidate CREs and with other chromatin features correlates with gene expression. Plant Journal, 2021, 107, 1631-1647.	2.8	17
2333	An ancient viral epidemic involving host coronavirus interacting genes more than 20,000 years ago in East Asia. Current Biology, 2021, 31, 3504-3514.e9.	1.8	71
2334	New mechanistic insights to PLOD1-mediated human vascular disease. Translational Research, 2022, 239, 1-17.	2.2	8
2336	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. Cell, 2021, 184, 4168-4185.e21.	13.5	203
2337	A domain damage index to prioritizing the pathogenicity of missense variants. Human Mutation, 2021, 42, 1503-1517.	1.1	0
2338	TERA-Seq: true end-to-end sequencing of native RNA molecules for transcriptome characterization. Nucleic Acids Research, 2021, 49, e115-e115.	6.5	18
2339	Decoding disease: from genomes to networks to phenotypes. Nature Reviews Genetics, 2021, 22, 774-790.	7.7	46
2343	Developmental and evolutionary dynamics of cis-regulatory elements in mouse cerebellar cells. Science, 2021, 373, .	6.0	51
2344	Evolution of host use in fungivorous ciid beetles (Coleoptera: Ciidae): Molecular phylogeny focusing on Japanese taxa. Molecular Phylogenetics and Evolution, 2021, 162, 107197.	1.2	9
2345	Genome sequencing data analysis for rare disease gene discovery. Briefings in Bioinformatics, 2022, 23, .	3.2	6
2346	The noncoding genome and hearing loss. Human Genetics, 2022, 141, 323-333.	1.8	7
2348	Improved pathogenicity prediction for rare human missense variants. American Journal of Human Genetics, 2021, 108, 1891-1906.	2.6	51
2350	Trends in the Application of â€œOmicsâ€•to Ecotoxicology and Stress Ecology. Genes, 2021, 12, 1481.	1.0	22
2351	G-quadruplexes in genomes of viruses infecting eukaryotes or prokaryotes are under different selection pressures from hosts. Journal of Genetics and Genomics, 2022, 49, 20-29.	1.7	6
2352	Genetic architecture of autism spectrum disorder: Lessons from large-scale genomic studies. Neuroscience and Biobehavioral Reviews, 2021, 128, 244-257.	2.9	31

#	Article	IF	Citations
2355	Circular RNA repertoires are associated with evolutionarily young transposable elements. ELife, 2021, 10, .	2.8	14
2356	ERÎ± is an RNA-binding protein sustaining tumor cell survival and drug resistance. Cell, 2021, 184, 5215-5229.e17.	13.5	76
2357	Developmental and temporal characteristics of clonal sperm mosaicism. Cell, 2021, 184, 4772-4783.e15.	13.5	27
2358	An enhanced variant effect predictor based on a deep generative model and the Born-Again Networks. Scientific Reports, 2021, 11, 19127.	1.6	7
2359	Noncoding sequence variants define a novel regulatory element in the first intron of the N â€acetylglutamate synthase gene. Human Mutation, 2021, 42, 1624-1636.	1.1	3
2360	Identification of Two de novo Variants of CACNA1A in Pediatric Chinese Patients With Paroxysmal Tonic Upgaze. Frontiers in Pediatrics, 2021, 9, 722105.	0.9	3
2361	Conserved and species-specific chromatin remodeling and regulatory dynamics during mouse and chicken limb bud development. Nature Communications, 2021, 12, 5685.	5.8	6
2362	Evidence for a functional interaction of WNT10A and EBF1 in male-pattern baldness. PLoS ONE, 2021, 16, e0256846.	1.1	6
2365	VannoPortal: multiscale functional annotation of human genetic variants for interrogating molecular mechanism of traits and diseases. Nucleic Acids Research, 2022, 50, D1408-D1416.	6.5	31
2366	Revealing modifier variations characterizations for elucidating the genetic basis of human phenotypic variations. Human Genetics, 2021, , 1.	1.8	3
2368	Productive visualization of high-throughput sequencing data using the SeqCode open portable platform. Scientific Reports, 2021, 11, 19545.	1.6	9
2370	dbMCS: A Database for Exploring the Mutation Markers of Anti-Cancer Drug Sensitivity. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 4229-4237.	3.9	3
2371	Human IRES Atlas: an integrative platform for studying IRES-driven translational regulation in humans. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	21
2372	Giant lungfish genome elucidates the conquest of land by vertebrates. Nature, 2021, 590, 284-289.	13.7	132
2374	Fluoxetine ameliorates depressive symptoms by regulating lncRNA expression in the mouse hippocampus. Zoological Research, 2021, 42, 28-42.	0.9	10
2375	Genome-wide phylogenetic study of Percomorpha providing robust support for previous molecular classification. Marine and Freshwater Research, 2021, 72, 1387.	0.7	0
2376	LncRNAs and Available Databases. Methods in Molecular Biology, 2021, 2348, 3-26.	0.4	10
2377	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. Nature Structural and Molecular Biology, 2021, 28, 152-161.	3.6	172

#	Article	IF	Citations
2381	New Methods for Detecting Lineage-Specific Selection. Lecture Notes in Computer Science, 2006, , 190-205.	1.0	158
2382	Efficient Enumeration of Phylogenetically Informative Substrings. Lecture Notes in Computer Science, 2006, , 248-264.	1.0	1
2383	Controlling Size When Aligning Multiple Genomic Sequences with Duplications. Lecture Notes in Computer Science, 2006, , 138-149.	1.0	4
2384	Ordering Partially Assembled Genomes Using Gene Arrangements. Lecture Notes in Computer Science, 2006, , 113-128.	1.0	10
2385	Finding Maximum Likelihood Indel Scenarios. Lecture Notes in Computer Science, 2006, , 171-185.	1.0	4
2386	Regulatory Motif Analysis. , 2009, , 137-163.		6
2387	Population Genomics on the Fly: Recent Advances in Drosophila. Methods in Molecular Biology, 2020, 2090, 357-396.	0.4	17
2388	Population Genomics in the Great Apes. Methods in Molecular Biology, 2020, 2090, 453-463.	0.4	4
2389	Metagenomics of the Human Body. , 2011, , .		18
2391	Approaches for Classifying DNA Variants Found by Sanger Sequencing in a Medical Genetics Laboratory. Methods in Molecular Biology, 2014, 1168, 227-250.	0.4	3
2392	Analysis of Genomic DNA with the UCSC Genome Browser. Methods in Molecular Biology, 2009, 537, 277-301.	0.4	8
2393	Comparative Analysis and Visualization of Genomic Sequences Using VISTA Browser and Associated Computational Tools. Methods in Molecular Biology, 2007, 395, 3-16.	0.4	17
2394	Comparative Genomic Analysis Using the UCSC Genome Browser. Methods in Molecular Biology, 2007, 395, 17-33.	0.4	23
2395	Sequence Segmentation. Methods in Molecular Biology, 2008, 452, 207-229.	0.4	9
2396	Algorithms and Methods for Correlating Experimental Results with Annotation Databases. Methods in Molecular Biology, 2010, 593, 315-340.	0.4	2
2397	On-Line Viterbi Algorithm for Analysis of Long Biological Sequences. Lecture Notes in Computer Science, 2007, , 240-251.	1.0	8
2398	A Fast, Alignment-Free, Conservation-Based Method for Transcription Factor Binding Site Discovery. , 2008, , 98-111.		10
2399	Mining of cis-Regulatory Motifs Associated with Tissue-Specific Alternative Splicing. Lecture Notes in Computer Science, 2009, , 260-271.	1.0	3

#	Article	IF	Citations
2400	Identification of Specific Genomic Regions Responsible for the Invasivity of Neisseria Meningitidis. Studies in Classification, Data Analysis, and Knowledge Organization, 2010, , 491-499.	0.1	2
2403	Reconstruction of enhancerâ€“target networks in 935 samples of human primary cells, tissues and cell lines. Nature Genetics, 2017, 49, 1428-1436.	9.4	194
2405	Evolutionary and phylogenetic significance of platypus microsatellites conserved in mammalian and other vertebrate genomes. Australian Journal of Zoology, 2009, 57, 175.	0.6	8
2406	Massively parallel discovery of human-specific substitutions that alter enhancer activity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	67
2407	AI-Driver: an ensemble method for identifying driver mutations in personal cancer genomes. NAR Genomics and Bioinformatics, 2020, 2, lqaa084.	1.5	19
2408	ConsHMM Atlas: conservation state annotations for major genomes and human genetic variation. NAR Genomics and Bioinformatics, 2020, 2, lqaa104.	1.5	4
2513	Nonconserved Long Intergenic Noncoding RNAs Associate With Complex Cardiometabolic Disease Traits. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 501-511.	1.1	8
2514	A misplaced lncRNA causes brachydactyly in humans. Journal of Clinical Investigation, 2012, 122, 3990-4002.	3.9	108
2515	Most â€œDark Matterâ€•Transcripts Are Associated With Known Genes. PLoS Biology, 2010, 8, e1000371.	2.6	377
2516	Alternative Splicing of RNA Triplets Is Often Regulated and Accelerates Proteome Evolution. PLoS Biology, 2012, 10, e1001229.	2.6	93
2517	Signatures of hostâ€“pathogen evolutionary conflict reveal MISTRâ€”A conserved MItochondrial STress Response network. PLoS Biology, 2020, 18, e3001045.	2.6	20
2518	Erosion of Conserved Binding Sites in Personal Genomes Points to Medical Histories. PLoS Computational Biology, 2016, 12, e1004711.	1.5	7
2519	PredictSNP2: A Unified Platform for Accurately Evaluating SNP Effects by Exploiting the Different Characteristics of Variants in Distinct Genomic Regions. PLoS Computational Biology, 2016, 12, e1004962.	1.5	149
2520	Genomic Selective Constraints in Murids. PLoS Genetics, 2005, preprint, e204.	1.5	1
2521	Whole-Genome Cartography of Estrogen ReceptorÎ± Binding Sites. PLoS Genetics, 2005, preprint, e87.	1.5	1
2522	Adaptive evolution of conserved non-coding elements in mammals. PLoS Genetics, 2005, preprint, e147.	1.5	2
2523	Repair-Mediated Duplication by Capture of Proximal Chromosomal DNA Has Shaped Vertebrate Genome Evolution. PLoS Genetics, 2009, 5, e1000469.	1.5	16
2524	Widespread Genomic Signatures of Natural Selection in Hominid Evolution. PLoS Genetics, 2009, 5, e1000471.	1.5	398

#	Article	IF	Citations
2525	Human Developmental Enhancers Conserved between Deuterostomes and Protostomes. PLoS Genetics, 2012, 8, e1002852.	1.5	55
2526	3â€™UTR Shortening Potentiates MicroRNA-Based Repression of Pro-differentiation Genes in Proliferating Human Cells. PLoS Genetics, 2016, 12, e1005879.	1.5	77
2527	Utilizing the Dog Genome in the Search for Novel Candidate Genes Involved in Glioma Developmentâ€"Genome Wide Association Mapping followed by Targeted Massive Parallel Sequencing Identifies a Strongly Associated Locus. PLoS Genetics, 2016, 12, e1006000.	1.5	54
2528	Determining the Effect of Natural Selection on Linked Neutral Divergence across Species. PLoS Genetics, 2016, 12, e1006199.	1.5	49
2529	Mutation Rate Variation is a Primary Determinant of the Distribution of Allele Frequencies in Humans. PLoS Genetics, 2016, 12, e1006489.	1.5	63
2530	The Zic family homologue Odd-paired regulates Alk expression in Drosophila. PLoS Genetics, 2017, 13, e1006617.	1.5	15
2531	Parallel reorganization of protein function in the spindle checkpoint pathway through evolutionary paths in the fitness landscape that appear neutral in laboratory experiments. PLoS Genetics, 2017, 13, e1006735.	1.5	9
2532	Recurrent promoter mutations in melanoma are defined by an extended context-specific mutational signature. PLoS Genetics, 2017, 13, e1006773.	1.5	67
2533	Loss of the Caenorhabditis elegans pocket protein LIN-35 reveals MuvB's innate function as the repressor of DREAM target genes. PLoS Genetics, 2017, 13, e1007088.	1.5	28
2534	The Cis-regulatory Logic of the Mammalian Photoreceptor Transcriptional Network. PLoS ONE, 2007, 2, e643.	1.1	133
2535	Predicted Functional RNAs within Coding Regions Constrain Evolutionary Rates of Yeast Proteins. PLoS ONE, 2008, 3, e1559.	1.1	15
2536	VILIP-1 Downregulation in Non-Small Cell Lung Carcinomas: Mechanisms and Prediction of Survival. PLoS ONE, 2008, 3, e1698.	1.1	29
2537	Nucleotide Sequence Variation within the PI3K p85 Alpha Gene Associates with Alcohol Risk Drinking Behaviour in Adolescents. PLoS ONE, 2008, 3, e1769.	1.1	15
2538	Probabilistic Inference of Transcription Factor Binding from Multiple Data Sources. PLoS ONE, 2008, 3, e1820.	1.1	42
2539	Comparative Analysis of mRNA Targets for Human PUF-Family Proteins Suggests Extensive Interaction with the miRNA Regulatory System. PLoS ONE, 2008, 3, e3164.	1.1	254
2540	Novel Exon of Mammalian ADAR2 Extends Open Reading Frame. PLoS ONE, 2009, 4, e4225.	1.1	40
2541	Efficient Double Fragmentation ChIP-seq Provides Nucleotide Resolution Protein-DNA Binding Profiles. PLoS ONE, 2010, 5, e15092.	1.1	39
2542	A Systematic Enhancer Screen Using Lentivector Transgenesis Identifies Conserved and Non-Conserved Functional Elements at the Olig1 and Olig2 Locus. PLoS ONE, 2010, 5, e15741.	1.1	25

#	Article	IF	Citations
2543	Evolutionary Dynamics of the Ty3/Gypsy LTR Retrotransposons in the Genome of Anopheles gambiae. PLoS ONE, 2011, 6, e16328.	1.1	15
2544	Chromosome Conformation Capture Uncovers Potential Genome-Wide Interactions between Human Conserved Non-Coding Sequences. PLoS ONE, 2011, 6, e17634.	1.1	19
2545	Algebraic Distribution of Segmental Duplication Lengths in Whole-Genome Sequence Self-Alignments. PLoS ONE, 2011, 6, e18464.	1.1	19
2546	SNPs Occur in Regions with Less Genomic Sequence Conservation. PLoS ONE, 2011, 6, e20660.	1.1	57
2547	A High Resolution Genome-Wide Scan of HNF4Î± Recognition Sites Infers a Regulatory Gene Network in Colon Cancer. PLoS ONE, 2011, 6, e21667.	1.1	17
2548	Comparative Analysis of Human Protein-Coding and Noncoding RNAs between Brain and 10 Mixed Cell Lines by RNA-Seq. PLoS ONE, 2011, 6, e28318.	1.1	27
2549	A Mammalian Conserved Element Derived from SINE Displays Enhancer Properties Recapitulating Satb2 Expression in Early-Born Callosal Projection Neurons. PLoS ONE, 2011, 6, e28497.	1.1	49
2550	microPIR: An Integrated Database of MicroRNA Target Sites within Human Promoter Sequences. PLoS ONE, 2012, 7, e33888.	1.1	34
2551	Linking the Epigenome to the Genome: Correlation of Different Features to DNA Methylation of CpG Islands. PLoS ONE, 2012, 7, e35327.	1.1	29
2552	Relating the Disease Mutation Spectrum to the Evolution of the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR). PLoS ONE, 2012, 7, e42336.	1.1	12
2553	Bovine ncRNAs Are Abundant, Primarily Intergenic, Conserved and Associated with Regulatory Genes. PLoS ONE, 2012, 7, e42638.	1.1	64
2554	29 Mammalian Genomes Reveal Novel Exaptations of Mobile Elements for Likely Regulatory Functions in the Human Genome. PLoS ONE, 2012, 7, e43128.	1.1	60
2555	Mechanisms of Dietary Response in Mice and Primates: A Role for EGR1 in Regulating the Reaction to Human-Specific Nutritional Content. PLoS ONE, 2012, 7, e43915.	1.1	3
2556	Discovery and Characterization of Human Exonic Transcriptional Regulatory Elements. PLoS ONE, 2012, 7, e46098.	1.1	14
2557	PPARG Binding Landscapes in Macrophages Suggest a Genome-Wide Contribution of PU.1 to Divergent PPARG Binding in Human and Mouse. PLoS ONE, 2012, 7, e48102.	1.1	20
2558	Nuclear RNA Sequencing of the Mouse Erythroid Cell Transcriptome. PLoS ONE, 2012, 7, e49274.	1.1	35
2559	Large-Scale Screens of miRNA-mRNA Interactions Unveiled That the 3â€²UTR of a Gene Is Targeted by Multiple miRNAs. PLoS ONE, 2013, 8, e68204.	1.1	57
2560	Long Non-Coding RNA Expression Profiling of Mouse Testis during Postnatal Development. PLoS ONE, 2013, 8, e75750.	1.1	142

#	Article	IF	Citations
2561	Sebnif: An Integrated Bioinformatics Pipeline for the Identification of Novel Large Intergenic Noncoding RNAs (lincRNAs) - Application in Human Skeletal Muscle Cells. PLoS ONE, 2014, 9, e84500.	1.1	21
2562	Otx2 ChIP-seq Reveals Unique and Redundant Functions in the Mature Mouse Retina. PLoS ONE, 2014, 9, e89110.	1.1	54
2563	A Comparison of the Rest Complex Binding Patterns in Embryonic Stem Cells and Epiblast Stem Cells. PLoS ONE, 2014, 9, e95374.	1.1	15
2564	Conserved Noncoding Elements Follow Power-Law-Like Distributions in Several Genomes as a Result of Genome Dynamics. PLoS ONE, 2014, 9, e95437.	1.1	27
2565	Systematic Identification and Characterization of RNA Editing in Prostate Tumors. PLoS ONE, 2014, 9, e101431.	1.1	15
2566	Purifying Selection in Deeply Conserved Human Enhancers Is More Consistent than in Coding Sequences. PLoS ONE, 2014, 9, e103357.	1.1	9
2567	Hybrid Mice Reveal Parent-of-Origin and Cis- and Trans-Regulatory Effects in the Retina. PLoS ONE, 2014, 9, e109382.	1.1	22
2568	Allele Frequencies of Variants in Ultra Conserved Elements Identify Selective Pressure on Transcription Factor Binding. PLoS ONE, 2014, 9, e110692.	1.1	6
2569	Selective MicroRNA-Offset RNA Expression in Human Embryonic Stem Cells. PLoS ONE, 2015, 10, e0116668.	1.1	25
2570	Functional Implications of Human-Specific Changes in Great Ape microRNAs. PLoS ONE, 2016, 11, e0154194.	1.1	12
2571	Prediction and Quantification of Splice Events from RNA-Seq Data. PLoS ONE, 2016, 11, e0156132.	1.1	102
2572	Genome-Wide Analysis of Long Noncoding RNAs and Their Responses to Drought Stress in Cotton (Gossypium hirsutum L.). PLoS ONE, 2016, 11, e0156723.	1.1	109
2573	Technical Evaluation: Identification of Pathogenic Mutations in PKD1 and PKD2 in Patients with Autosomal Dominant Polycystic Kidney Disease by Next-Generation Sequencing and Use of a Comprehensive New Classification System. PLoS ONE, 2016, 11, e0166288.	1.1	28
2574	CRISPR-FOCUS: A web server for designing focused CRISPR screening experiments. PLoS ONE, 2017, 12, e0184281.	1.1	16
2575	SEQscoring: a tool to facilitate the interpretation of data generated with next generation sequencing technologies. EMBnet Journal, 2011, 17, 38.	0.2	8
2576	MUC5B and Idiopathic Pulmonary Fibrosis. Annals of the American Thoracic Society, 2015, 12, S193-S199.	1.5	67
2577	Prevention of dsRNAâ€induced interferon signaling by AGO1x is linked to breast cancer cell proliferation. EMBO Journal, 2020, 39, e103922.	3.5	22
2578	Alternative splicing coupled mRNA decay shapes the temperatureâ€dependent transcriptome. EMBO Reports, 2020, 21, e51369.	2.0	28

#	Article	IF	Citations
2579	miR146a-mediated targeting of FANCM during inflammation compromises genome integrity. Oncotarget, 2016, 7, 45976-45994.	0.8	9
2580	Dysregulated long intergenic non-coding RNA modules contribute to heart failure. Oncotarget, 2016, 7, 59676-59690.	0.8	22
2581	Systematically characterizing dysfunctional long intergenic non-coding RNAs in multiple brain regions of major psychosis. Oncotarget, 2016, 7, 71087-71098.	0.8	43
2582	High throughput estimation of functional cell activities reveals disease mechanisms and predicts relevant clinical outcomes. Oncotarget, 2017, 8, 5160-5178.	0.8	66
2583	Renal oncocytoma characterized by the defective complex I of the respiratory chain boosts the synthesis of the ROS scavenger glutathione. Oncotarget, 2017, 8, 105882-105904.	0.8	32
2584	The single-nucleotide polymorphisms in CHD5 affect the prognosis of patients with hepatocellular carcinoma. Oncotarget, 2018, 9, 13222-13230.	0.8	7
2585	Indirect p53-dependent transcriptional repression ofSurvivin, CDC25C,andPLK1genes requires the cyclin-dependent kinase inhibitor p21/CDKN1A and CDE/CHR promoter sites binding the DREAM complex. Oncotarget, 2015, 6, 41402-41417.	0.8	48
2586	Sox9: A Master Regulator of the Pancreatic Program. Review of Diabetic Studies, 2014, 11, 51-83.	0.5	77
2588	The role of genomics and genetics in pulmonary arterial hypertension. Global Cardiology Science & Practice, 2020, 2020, e202013.	0.3	5
2589	An Overview of Computational Tools of Nucleic Acid Binding Site Prediction for Site-specific Proteins and Nucleases. Protein and Peptide Letters, 2020, 27, 370-384.	0.4	2
2590	The Roles of Long Non-coding RNA in Osteoporosis. Current Stem Cell Research and Therapy, 2020, 15, 639-645.	0.6	12
2591	Identification of target sequences for association studies - analysis of the pig <i>FABP3</i> and <i>FABP4</i> loci using comparative genomics methods. Journal of Animal and Feed Sciences, 2008, 17, 191-201.	0.4	5
2592	Conserved sequences identify the closest living relatives of primates. Zoological Research, 2019, 40, 532-540.	0.9	8
2593	OrthReg: a tool to predict <i>cis</i>-regulatory elements based on cross-species orthologous sequence conservation. Zoological Research, 2020, 41, 471-475.	0.9	3
2594	Expression of miR-145-5p During Chondrogenesis of Mesenchymal Stem Cells. Stem Cell & Regenerative Medicine, 2017, 1, 1-10.	0.1	3
2595	Whole exome sequencing identifies genomic alterations in proximal and distal colorectal cancer. Bulletin of the Geological Society of Malaysia, 2019, 2, .	0.5	1
2596	Identification of microRNAs in human circulating monocytes of postmenopausal osteoporotic Mexican-Mestizo women: A pilot study. Experimental and Therapeutic Medicine, 2017, 14, 5464-5472.	0.8	13
2597	Is Whole Exome Sequencing Clinically Practical in the Management of Pediatric Crohn's Disease?. Gut and Liver, 2015, 9, 767.	1.4	10

#	Article	IF	Citations
2598	A global change in RNA polymerase II pausing during the Drosophila midblastula transition. ELife, 2013, 2, e00861.	2.8	126
2599	Many lncRNAs, 5â€™UTRs, and pseudogenes are translated and some are likely to express functional proteins. ELife, 2015, 4, e08890.	2.8	439
2600	Evidence for a common evolutionary rate in metazoan transcriptional networks. ELife, 2015, 4, .	2.8	26
2601	Striking circadian neuron diversity and cycling of Drosophila alternative splicing. ELife, 2018, 7, .	2.8	24
2602	Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences. ELife, 2018, 7, .	2.8	121
2603	Genome-wide quantification of the effects of DNA methylation on human gene regulation. ELife, 2018, 7, .	2.8	96
2604	Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, .	2.8	58
2605	DAZL mediates a broad translational program regulating expansion and differentiation of spermatogonial progenitors. ELife, 2020, 9, .	2.8	28
2606	Systematic identification of cis-regulatory variants that cause gene expression differences in a yeast cross. ELife, 2020, 9, .	2.8	18
2607	Positive selection within the genomes of SARS-CoV-2 and other Coronaviruses independent of impact on protein function. PeerJ, 2020, 8, e10234.	0.9	49
2608	Ultraconserved elements (UCEs) illuminate the population genomics of a recent, high-latitude avian speciation event. PeerJ, 2018, 6, e5735.	0.9	31
2609	VaRank: a simple and powerful tool for ranking genetic variants. PeerJ, 2015, 3, e796.	0.9	80
2610	m5C-Atlas: a comprehensive database for decoding and annotating the 5-methylcytosine (m5C) epitranscriptome. Nucleic Acids Research, 2022, 50, D196-D203.	6.5	53
2611	AnnoLnc: A One-Stop Portal to Systematically Annotate Novel Human Long Noncoding RNAs. Methods in Molecular Biology, 2021, 2254, 111-131.	0.4	1
2612	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	13.7	95
2613	Positive selection in noncoding genomic regions of vocal learning birds is associated with genes implicated in vocal learning and speech functions in humans. Genome Research, 2021, 31, 2035-2049.	2.4	16
2614	lncRNA cytoskeleton regulator RNA (CYTOR): Diverse functions in metabolism, inflammation and tumorigenesis, and potential applications in precision oncology. Genes and Diseases, 2023, 10, 415-429.	1.5	9
2615	Detecting Selection in Multiple Populations by Modeling Ancestral Admixture Components. Molecular Biology and Evolution, 2022, 39, .	3.5	24

#	Article	IF	Citations
2616	Novel and Annotated Long Noncoding RNAs Associated with Ischemia in the Human Heart. International Journal of Molecular Sciences, 2021, 22, 11324.	1.8	4
2617	Genome-wide oscillations in G + C density and sequence conservation. Genome Research, 2021, 31, 2050-2057.	2.4	1
2618	Comprehensive multi-omics integration identifies differentially active enhancers during human brain development with clinical relevance. Genome Medicine, 2021, 13, 162.	3.6	9
2619	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. Genome Biology, 2021, 22, 282.	3.8	8
2621	A phylogenomic perspective on the evolutionary history of the stonefly genus Suwallia (Plecoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Evolution, 2022, 166, 107320.	1.2	3
2622	Prediction methods for microRNA targets in bilaterian animals: Toward a better understanding by biologists. Computational and Structural Biotechnology Journal, 2021, 19, 5811-5825.	1.9	6
2624	Exploration of weighting schemes based on allele frequency and annotation for weighted burden association analysis of complex phenotypes. Gene, 2022, 809, 146039.	1.0	5
2625	Decreased recent adaptation at human mendelian disease genes as a possible consequence of interference between advantageous and deleterious variants. ELife, 2021, 10, .	2.8	13
2627	Global properties of regulatory sequences are predicted by transcription factor recognition mechanisms. Genome Biology, 2021, 22, 285.	3.8	3
2628	A macaque's-eye view of human insertions and deletions: differences in mechanisms. PLoS Computational Biology, 2005, preprint, e176.	1.5	2
2629	Genome Organization and Gene Expression Shape the Distribution of Transposable Elements in the Euchromatin of Drosophila Melanogaster. PLoS Genetics, 2005, preprint, e210.	1.5	0
2630	Identification and characterization of cell type-specific and ubiquitous chromatin regulatory structures in the human genome. PLoS Genetics, 2005, preprint, e136.	1.5	0
2637	Direct detection of hemophilia B F9 gene mutation using multiplex PCR and conformation sensitive gel electrophoresis. Korean Journal of Pediatrics, 2010, 53, 397.	1.9	0
2638	Mapping Association between Long-Range Cis-Regulatory Regions and Their Target Genes Using Comparative Genomics. Lecture Notes in Computer Science, 2010, , 216-227.	1.0	0
2640	PSAR: Measuring Multiple Sequence Alignment Reliability by Probabilistic Sampling. Lecture Notes in Computer Science, 2011, , 134-135.	1.0	0
2643	Generation of Functional Long Noncoding RNA Through Transcription and Natural Selection. , 2012, , 151-174.		0
2644	Molecular cloning, expression analysis and sequence prediction of CCAAT/enhancer-binding protein beta gene of Qinchuan cattle. African Journal of Biotechnology, 2011, 10, .	0.3	0
2645	The Contributions of RET Noncoding Variation to Hirschsprung Disease. , 2012, , 169-194.		0

#	Article	IF	Citations
2646	A single nucleotide polymorphism in the promoter region of the mink tumor necrosis factor-alpha gene. , 2012, , 300-304.		0
2647	Bioinformatic Tools for the Search of Disease-Associated Variations. , 2012, , 1-25.		0
2648	MicroRNA Target Prediction. , 2013, , 1335-1335.		0
2649	Eukaryote Genomes. Computational Biology, 2013, , 193-222.	0.1	0
2651	Topics in Computational Genomics. , 2013, , 69-100.		0
2652	Emerging Technologies to Study Long Non-coding RNAs. , 2013, , 163-195.		0
2655	Cryptosporidium: Current State of Genomics and Systems Biological Research. , 2014, , 327-344.		1
2656	Bioinformatics Approaches to the Study of MicroRNAs. , 2014, , 165-245.		0
2658	Computational Prediction of microRNAs and their Targets. Journal of Proteomics and Bioinformatics, 2014, 07, .	0.4	2
2659	The Role of Genome Sequencing in the Identification of Novel Therapeutic Targets. Journal of Glycomics & Lipidomics, 2014, 04, .	0.4	2
2682	Whole exome and genome sequencing for Mendelian immune disorders: from molecular diagnostics to new disease variant and gene discovery. LymphoSign Journal, 0, , .	0.1	1
2687	Sequencing Strategies. , 2017, , 61-80.		0
2706	A Multiplexed Assay for Exon Recognition Reveals That an Unappreciated Fraction of Rare Genetic Variants Cause Large-Effect Disruptions to Splicing. SSRN Electronic Journal, 0, , .	0.4	0
2707	Novel Genetic Loci Affecting Facial Shape Variation in Humans. SSRN Electronic Journal, 0, , .	0.4	0
2746	Development and Genome Sequence of a Laboratory-Inbred Miniature Pig Facilitate Study of Human Diabetic Disease. SSRN Electronic Journal, 0, , .	0.4	0
2790	Functional annotation of de novo variants from healthy individuals. Genomics and Informatics, 2019, 17, e46.	0.4	1
2810	Phylogenetic Manifold Regularization: A semi-supervised approach to predict transcription factor binding sites. , 2020, , .		0
2811	Improving Prediction Accuracy of Microarray Cancer Data with Non-negative Matrix Factorization and Its Variant. , 2020, , .		0

#	Article	IF	Citations
2815	Genome-wide DNA-binding profile of SRY-box transcription factor 3 (SOX3) in mouse testes. Reproduction, Fertility and Development, 2020, 32, 1260.	0.1	1
2816	Association ofDOCK8,IL17RA, andKLK12Polymorphisms with Atopic Dermatitis in Koreans. Annals of Dermatology, 2020, 32, 197.	0.3	4
2832	Genome-wide CRISPR interference screen identifies long non-coding RNA loci required for differentiation and pluripotency. PLoS ONE, 2021, 16, e0252848.	1.1	12
2834	A Hidden Structural Variation in a Known IRD Gene: A Cautionary Tale of Two New Disease Candidate Genes. Journal of Physical Education and Sports Management, 2021, , mcs.a006131.	0.5	0
2835	BTLA Expression in CLL: Epigenetic Regulation and Impact on CLL B Cell Proliferation and Ability to IL-4 Production. Cells, 2021, 10, 3009.	1.8	5
2837	In-Depth Annotation of the Drosophila Bithorax-Complex Reveals the Presence of Several Alternative ORFs That Could Encode for Motif-Rich Peptides. Cells, 2021, 10, 2983.	1.8	0
2841	Generation of Functional Long Noncoding RNA Through Transcription and Natural Selection. , 2012, , 151-174.		0
2850	dbCNS: A New Database for Conserved Noncoding Sequences. Molecular Biology and Evolution, 2021, 38, 1665-1676.	3.5	3
2854	A low affinity cis-regulatory BMP response element restricts target gene activation to subsets of Drosophila neurons. ELife, 2020, 9, .	2.8	3
2855	Identification of Wnt/Î²-catenin modulated genes in the developing retina. Molecular Vision, 2012, 18, 645-56.	1.1	11
2856	Accelerated evolution of constraint elements for hematophagic adaptation in mosquitoes. Zoological Research, 2015, 36, 320-7.	0.6	0
2857	IDIOPATHIC PULMONARY FIBROSIS IS A COMPLEX GENETIC DISORDER. Transactions of the American Clinical and Climatological Association, 2016, 127, 34-45.	0.9	23
2858	Expression of miR-145-5p During Chondrogenesis of Mesenchymal Stem Cells. Journal of Stem Cell Research, 2017, 1, 1-10.	0.0	3
2859	Accelerated Evolution of the Regulatory Sequences of Brain Development in the Human Genome. Molecules and Cells, 2020, 43, 331-339.	1.0	3
2860	Mutation saturation for fitness effects at human CpG sites. ELife, 2021, 10, .	2.8	23
2863	Pseudoexon activation in disease by nonâ€splice site deep intronic sequence variation â€" wild type pseudoexons constitute highâ€risk sites in the human genome. Human Mutation, 2022, 43, 103-127.	1.1	17
2864	Prediction of functional microexons by transfer learning. BMC Genomics, 2021, 22, 855.	1.2	1
2865	Massively parallel analysis of human 3â€² UTRs reveals that AU-rich element length and registration predict mRNA destabilization. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	17

#	Article	IF	Citations
2866	Master lineage transcription factors anchor trans mega transcriptional complexes at highly accessible enhancer sites to promote long-range chromatin clustering and transcription of distal target genes. Nucleic Acids Research, 2021, 49, 12196-12210.	6.5	7
2867	Nonâ€coding regulatory elements: Potential roles in disease and the case of epilepsy. Neuropathology and Applied Neurobiology, 2022, 48, .	1.8	14
2868	Estimated prevalence of Niemannâ€“Pick type C disease in Quebec. Scientific Reports, 2021, 11, 22621.	1.6	5
2870	Perfect and imperfect views of ultraconserved sequences. Nature Reviews Genetics, 2022, 23, 182-194.	7.7	16
2872	Mutant alleles differentially shape fitness and other complex traits in cattle. Communications Biology, 2021, 4, 1353.	2.0	6
2873	FoxO-KLF15 pathway switches the flow of macronutrients under the control of insulin. IScience, 2021, 24, 103446.	1.9	6
2874	SMAD4 target genes are part of a transcriptional network that integrates the response to BMP and SHH signaling during early limb bud patterning. Development (Cambridge), 2021, 148, .	1.2	4
2875	Computational Methods and Approaches in Pharmacogenomic Research. , 2022, , 53-83.		1
2876	Overcoming constraints on the detection of recessive selection in human genes from population frequency data. American Journal of Human Genetics, 2022, 109, 33-49.	2.6	5
2877	SegAlign: A Scalable GPU-Based Whole Genome Aligner. , 2020, , .		8
2878	Impact of CpG Islands on lncRNA Conservation. Biology Bulletin Reviews, 2021, 11, 533-543.	0.3	0
2879	Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. Cell Reports, 2022, 38, 110280.	2.9	18
2880	Integration of single-cell transcriptomes and chromatin landscapes reveals regulatory programs driving pharyngeal organ development. Nature Communications, 2022, 13, 457.	5.8	22
2881	Variant pathogenic prediction by locus variability: the importance of the current picture of evolution. European Journal of Human Genetics, 2022, 30, 555-559.	1.4	3
2882	Prediction and analysis of functional RNA structures within the integrative genomics viewer. NAR Genomics and Bioinformatics, 2022, 4, lqab127.	1.5	5
2883	Small Open Reading Frames, How to Find Them and Determine Their Function. Frontiers in Genetics, 2021, 12, 796060.	1.1	10
2884	Clinical severity prediction in children with osteogenesis imperfecta caused by COL1A1/2 defects. Osteoporosis International, 2022, , 1.	1.3	5
2885	Finding and Characterizing Repeats in Plant Genomes. Methods in Molecular Biology, 2022, 2443, 327-385.	0.4	2

#	Article	IF	Citations
2886	A comparison on predicting functional impact of genomic variants. NAR Genomics and Bioinformatics, 2022, 4, lqab122.	1.5	12
2887	StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants. American Journal of Human Genetics, 2022, 109, 195-209.	2.6	29
2889	Whole-Exome Sequencing Identifies a Novel Germline Variant in PTK7 Gene in Familial Colorectal Cancer. International Journal of Molecular Sciences, 2022, 23, 1295.	1.8	2
2891	Universal annotation of the human genome through integration of over a thousand epigenomic datasets. Genome Biology, 2022, 23, 9.	3.8	39
2892	Regulation of retinal amacrine cell generation by miR-216b and Foxn3. Development (Cambridge), 2022, 149, .	1.2	3
2893	Evaluating the relevance of sequence conservation in the prediction of pathogenic missense variants. Human Genetics, 2022, 141, 1649-1658.	1.8	3
2894	Haplotype-based inference of the distribution of fitness effects. Genetics, 2022, 220, .	1.2	1
2896	OUP accepted manuscript. Briefings in Bioinformatics, 2022, 23, .	3.2	5
2897	Genome-wide analysis and functional annotation of chromatin-enriched noncoding RNAs in rice during somatic cell regeneration. Genome Biology, 2022, 23, 28.	3.8	13
2898	N 6-methyladenosine enhances post-transcriptional gene regulation by microRNAs. Bioinformatics Advances, 2022, 2, vbab046.	0.9	2
2899	Screening and functional validation of lipid metabolism-related lncRNA-46546 based on the transcriptome analysis of early embryonic muscle tissue in chicken. Animal Bioscience, 2023, 36, 175-190.	0.8	3
2900	Functional and comparative genomics reveals conserved noncoding sequences in the nitrogenâ€fixing clade. New Phytologist, 2022, 234, 634-649.	3.5	2
2901	Heterozygous calcyclin-binding protein/Siah1-interacting protein (CACYBP/SIP) gene pathogenic variant linked to a dominant family with paucity of interlobular bile duct. Journal of Human Genetics, 2022, , .	1.1	0
2902	Distinct transcription kinetics of pluripotent cell states. Molecular Systems Biology, 2022, 18, e10407.	3.2	4
2904	regCNN: identifying Drosophila genome-wide cis-regulatory modules via integrating the local patterns in epigenetic marks and transcription factor binding motifs. Computational and Structural Biotechnology Journal, 2022, 20, 296-308.	1.9	9
2905	A Compound Heterozygous Mutation in Calpain 1 Identifies a New Genetic Cause for Spinal Muscular Atrophy Type 4 (SMA4). Frontiers in Genetics, 2021, 12, 801253.	1.1	1
2906	Functional Validation of Osteoporosis Genetic Findings Using Small Fish Models. Genes, 2022, 13, 279.	1.0	11
2907	Enhancerâ€“silencer transitions in the human genome. Genome Research, 2022, 32, 437-448.	2.4	17

#	Article	IF	Citations
2908	Understanding the constitutive presentation of MHC class I immunopeptidomes in primary tissues. IScience, 2022, 25, 103768.	1.9	16
2909	Prevalence of Choroidal Abnormalities and Lisch Nodules in Children Meeting Clinical and Molecular Diagnosis of Neurofibromatosis Type 1. Translational Vision Science and Technology, 2022, 11, 10.	1.1	4
2910	A mammalian methylation array for profiling methylation levels at conserved sequences. Nature Communications, 2022, 13, 783.	5.8	93
2912	Analysis of missense variants in the human genome reveals widespread gene-specific clustering and improves prediction of pathogenicity. American Journal of Human Genetics, 2022, 109, 457-470.	2.6	29
2914	Discovery of genomic loci of the human cerebral cortex using genetically informed brain atlases. Science, 2022, 375, 522-528.	6.0	31
2915	Further delineation of familial polycystic ovary syndrome (PCOS) via <scp>wholeâ€exome</scp> sequencing: <scp>PCOS</scp>â€related rare <scp>FBN3</scp> and <scp>FN1</scp> gene variants are identified. Journal of Obstetrics and Gynaecology Research, 2022, 48, 1202-1211.	0.6	9
2916	Computational Assessment of the Expression-Modulating Potential for Non-Coding Variants. Genomics, Proteomics and Bioinformatics, 2023, 21, 662-673.	3.0	3
2918	Computational Resources for the Interpretation of Variations in Cancer. Advances in Experimental Medicine and Biology, 2022, 1361, 177-198.	0.8	2
2919	High-quality reference genomes of swallowtail butterflies provide insights into their coloration evolution. Zoological Research, 2022, 43, 367-379.	0.9	6
2920	A framework to score the effects of structural variants in health and disease. Genome Research, 2022, 32, 766-777.	2.4	17
2922	DVPred: a disease-specific prediction tool for variant pathogenicity classification for hearing loss. Human Genetics, 2022, 141, 401-411.	1.8	6
2925	HyperChIP: identification of hypervariable signals across ChIP-seq or ATAC-seq samples. Genome Biology, 2022, 23, 62.	3.8	1
2926	Multi-Omic Analysis in a Metabolic Syndrome Porcine Model Implicates Arachidonic Acid Metabolism Disorder as a Risk Factor for Atherosclerosis. Frontiers in Nutrition, 2022, 9, 807118.	1.6	5
2928	A novel variant in <scp>UBE3A</scp> in a family with multigenerational intellectual disability and developmental delay. Molecular Genetics & Genomic Medicine, 2022, , e1883.	0.6	1
2929	Analysis of recent shared ancestry in a familial cohort identifies coding and noncoding autism spectrum disorder variants. Npj Genomic Medicine, 2022, 7, 13.	1.7	18
2930	Machine-learning of complex evolutionary signals improves classification of SNVs. NAR Genomics and Bioinformatics, 2022, 4, lqac025.	1.5	4
2931	The GRN concept as a guide for evolutionary developmental biology. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2023, 340, 92-104.	0.6	4
2932	Paleozoic Protein Fossils Illuminate the Evolution of Vertebrate Genomes and Transposable Elements. Molecular Biology and Evolution, 2022, 39, .	3.5	7

#	Article	IF	Citations
2933	Four novel candidate causal variants for deficient homozygous haplotypes in Holstein cattle. Scientific Reports, 2022, 12, 5435.	1.6	6
2935	TADAâ€"a machine learning tool for functional annotation-based prioritisation of pathogenic CNVs. Genome Biology, 2022, 23, 67.	3.8	4
2936	RevUP: an online scoring system for regulatory variants implicated in rare diseases. Bioinformatics, 2022, 38, 2664-2666.	1.8	0
2937	In Silico Assessment of Probe-Capturing Strategies and Effectiveness in the Spider Sub-Lineage Araneoidea (Order: Araneae). Diversity, 2022, 14, 184.	0.7	4
2938	ENNGene: an Easy Neural Network model building tool for Genomics. BMC Genomics, 2022, 23, 248.	1.2	7
2939	Short open reading frames (sORFs) and microproteins: an update on their identification and validation measures. Journal of Biomedical Science, 2022, 29, 19.	2.6	21
2941	InsuLock: A Weakly Supervised Learning Approach for Accurate Insulator Prediction, and Variant Impact Quantification. Genes, 2022, 13, 621.	1.0	1
2942	Contiguously hydrophobic sequences are functionally significant throughout the human exome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2116267119.	3.3	1
2943	An expanded phenotype centric benchmark of variant prioritisation tools. Human Mutation, 2022, 43, 539-546.	1.1	9
2944	A comprehensive WGS-based pipeline for the identification of new candidate genes in inherited retinal dystrophies. Npj Genomic Medicine, 2022, 7, 17.	1.7	7
2945	Single-nuclei isoform RNA sequencing unlocks barcoded exon connectivity in frozen brain tissue. Nature Biotechnology, 2022, 40, 1082-1092.	9.4	52
2946	Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. Npj Genomic Medicine, 2022, 7, 18.	1.7	14
2947	A multi-dimensional integrative scoring framework for predicting functional variants in the human genome. American Journal of Human Genetics, 2022, 109, 446-456.	2.6	18
2948	Using an Unsupervised Clustering Model to Detect the Early Spread of SARS-CoV-2 Worldwide. Genes, 2022, 13, 648.	1.0	1
2949	Heteroplasmic mitochondrial DNA variants in cardiovascular diseases. PLoS Genetics, 2022, 18, e1010068.	1.5	19
2950	Phylogenomic analysis of the Neotropical fish subfamily Characinae using ultraconserved elements (Teleostei: Characidae). Molecular Phylogenetics and Evolution, 2022, 171, 107462.	1.2	5
2951	A comprehensive and bias-free evaluation of genomic variant clinical interpretation tools. , 2021, , .		0
2952	Functional Constraints on Insect Immune System Components Govern Their Evolutionary Trajectories. Molecular Biology and Evolution, 2022, 39, .	3.5	3

#	Article	IF	Citations
2955	A predominant enhancer co-amplified with the SOX2 oncogene is necessary and sufficient for its expression in squamous cancer. Nature Communications, 2021, 12, 7139.	5.8	12
2957	Reverse Genetic Screen for Deleterious Recessive Variants in the Local Simmental Cattle Population of Switzerland. Animals, 2021, 11, 3535.	1.0	2
2958	Co-existing TP53 and ARID1A mutations promote aggressive endometrial tumorigenesis. PLoS Genetics, 2021, 17, e1009986.	1.5	24
2959	Integration of high-resolution promoter profiling assays reveals novel, cell typeâ€“specific transcription start sites across 115 human cell and tissue types. Genome Research, 2022, 32, 389-402.	2.4	8
2961	RegVar: Tissue-Specific Prioritization of Non-Coding Regulatory Variants. Genomics, Proteomics and Bioinformatics, 2023, 21, 385-395.	3.0	2
2962	Predicting deleterious missense genetic variants via integrative supervised nonnegative matrix tri-factorization. Scientific Reports, 2021, 11, 23747.	1.6	0
2963	Common Features in lncRNA Annotation and Classification: A Survey. Non-coding RNA, 2021, 7, 77.	1.3	13
2964	Unsupervised clustering analysis of SARS-Cov-2 population structure reveals six major subtypes at early stage across the world. , 2021, , .		0
2965	Mining massive genomic data of two Swiss Braunvieh cattle populations reveals six novel candidate variants that impair reproductive success. Genetics Selection Evolution, 2021, 53, 95.	1.2	5
2966	The Small Open Reading Frameâ€Encoded Peptides: Advances in Methodologies and Functional Studies. ChemBioChem, 2022, 23, .	1.3	4
2967	A functionally impaired missense variant identified in French Canadian families implicates FANCI as a candidate ovarian cancer-predisposing gene. Genome Medicine, 2021, 13, 186.	3.6	12
2968	Integrated Analysis of the ceRNA Network and M-7474 Function in Testosterone-Mediated Fat Deposition in Pigs. Genes, 2022, 13, 668.	1.0	2
2969	Inferring mammalian tissue-specific regulatory conservation by predicting tissue-specific differences in open chromatin. BMC Genomics, 2022, 23, 291.	1.2	8
2970	Proximal and Distal Regions of Pathogenic Th17 Related Chromatin Loci Are Sequentially Accessible During Pathogenicity of Th17. Frontiers in Immunology, 2022, 13, 864314.	2.2	3
2971	Cell-Selective Adeno-Associated Virus-Mediated SCN1A Gene Regulation Therapy Rescues Mortality and Seizure Phenotypes in a Dravet Syndrome Mouse Model and Is Well Tolerated in Nonhuman Primates. Human Gene Therapy, 2022, 33, 579-597.	1.4	33
2972	Connecting high-resolution 3D chromatin organization with epigenomics. Nature Communications, 2022, 13, 2054.	5.8	9
2973	Life-threatening viral disease in a novel form of autosomal recessive IFNAR2 deficiency in the Arctic. Journal of Experimental Medicine, 2022, 219, .	4.2	33
2976	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants. Plant Genome, 2022, 15, e20204.	1.6	5

#	Article	IF	Citations
2978	Multidimensional chromatin profiling of zebrafish pancreas to uncover and investigate disease-relevant enhancers. Nature Communications, 2022, 13, 1945.	5.8	5
2980	Genetic Association of rs1021188 and DNA Methylation Signatures of TNFSF11 in the Risk of Conductive Hearing Loss. Frontiers in Medicine, 2022, 9, 870244.	1.2	0
3109	Systematic annotation of conservation states provides insights into regulatory regions in rice. Journal of Genetics and Genomics, 2022, 49, 1127-1137.	1.7	3
3112	Tandem Exon Duplications Expanding the Alternative Splicing Repertoire. , 2022, 14, 73-81.		0
3113	Genome interpretation using in silico predictors of variant impact. Human Genetics, 2022, 141, 1549-1577.	1.8	26
3114	Classification of non-coding variants with high pathogenic impact. PLoS Genetics, 2022, 18, e1010191.	1.5	15
3115	Inferring Potential Cancer Driving Synonymous Variants. Genes, 2022, 13, 778.	1.0	1
3116	Rapid Intraspecies Evolution of Fitness Effects of Yeast Genes. Genome Biology and Evolution, 2022, 14, .	1.1	2
3117	Integrating convolution and self-attention improves language model of human genome for interpreting non-coding regions at base-resolution. Nucleic Acids Research, 2022, 50, e81-e81.	6.5	13
3118	Pediatric Pan-Central Nervous System Tumor Methylome Analyses Reveal Immune-Related LncRNAs. Frontiers in Immunology, 2022, 13, .	2.2	4
3119	Whole exome sequencing identifies novel germline variants of SLC15A4 gene as potentially cancer predisposing in familial colorectal cancer. Molecular Genetics and Genomics, 2022, , 1.	1.0	1
3122	Rapid Molecular Diagnosis of Genetically Inherited Neuromuscular Disorders Using Next-Generation Sequencing Technologies. Journal of Clinical Medicine, 2022, 11, 2750.	1.0	3
3123	Cancer-related micropeptides encoded by ncRNAs: Promising drug targets and prognostic biomarkers. Cancer Letters, 2022, 547, 215723.	3.2	17
3124	Expression and Potential Biomarkers of Regulators for M7G RNA Modification in Gliomas. Frontiers in Neurology, 2022, 13, .	1.1	13
3125	The critically endangered vaquita is not doomed to extinction by inbreeding depression. Science, 2022, 376, 635-639.	6.0	49
3126	3â€²untranslated regions of tumor suppressor genes evolved specific features to favor cancer resistance. Oncogene, 2022, , .	2.6	0
3127	Phylogeny of NF-YA trans-activation splicing isoforms in vertebrate evolution. Genomics, 2022, 114, 110390.	1.3	4
3128	MiRLog and dbmiR: Prioritization and functional annotation tools to study human microRNA sequence variants. Human Mutation, 2022, , .	1.1	1

#	Article	IF	Citations
3129	Bioinformatics for the Origin and Evolution of Viruses. Advances in Experimental Medicine and Biology, 2022, 1368, 53-71.	0.8	2
3130	Revealing the novel complexity of plant long non-coding RNA by strand-specific and whole transcriptome sequencing for evolutionarily representative plant species. BMC Genomics, 2022, 23, 381.	1.2	3
3135	Clinical description and genetic analysis of a novel familial skeletal dysplasia characterized by high bone mass and lucent bone lesions. Bone, 2022, 161, 116450.	1.4	2
3136	Genomic signatures of the evolution of a diurnal lifestyle in Strigiformes. G3: Genes, Genomes, Genetics, 0, , .	0.8	3
3138	tiRNAs: Insights into Their Biogenesis, Functions, and Future Applications in Livestock Research. Non-coding RNA, 2022, 8, 37.	1.3	1
3140	pop-1/TCF, ref-2/ZIC and T-box factors regulate the development of anterior cells in the C.Âelegans embryo. Developmental Biology, 2022, 489, 34-46.	0.9	1
3141	Machine-Learning Prospects for Detecting Selection Signatures Using Population Genomics Data. Journal of Computational Biology, 2022, 29, 943-960.	0.8	9
3142	PHACT: Phylogeny-Aware Computing of Tolerance for Missense Mutations. Molecular Biology and Evolution, 2022, 39, .	3.5	3
3143	Prediction of Neurodevelopmental Disorders Based on De Novo Coding Variation. Journal of Autism and Developmental Disorders, 2023, 53, 963-976.	1.7	2
3147	DIRECT-NET: An efficient method to discover cis-regulatory elements and construct regulatory networks from single-cell multiomics data. Science Advances, 2022, 8, .	4.7	21
3149	Evolution of transcription factor binding through sequence variations and turnover of binding sites. Genome Research, 2022, 32, 1099-1111.	2.4	13
3151	Identification of the Core Promoter and Variants Regulating Chicken CCKAR Expression. Genes, 2022, 13, 1083.	1.0	1
3152	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	9.4	61
3153	Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome. Genome Biology, 2022, 23, .	3.8	14
3154	Microbiome-associated human genetic variants impact phenome-wide disease risk. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
3155	Identification and functional annotation of long intergenic non-coding RNAs in Brassicaceae. Plant Cell, 2022, 34, 3233-3260.	3.1	22
3156	TSABL: Trait Specific Annotation Based Locus predictor. BMC Genomics, 2022, 23, .	1.2	0
3157	The 3D mutational constraint on amino acid sites in the human proteome. Nature Communications, 2022, 13, .	5.8	15

#	Article	IF	Citations
3158	scEpiLock: A Weakly Supervised Learning Framework for cis-Regulatory Element Localization and Variant Impact Quantification for Single-Cell Epigenetic Data. Biomolecules, 2022, 12, 874.	1.8	0
3161	Molecular evolutionary trends and biosynthesis pathways in the Oribatida revealed by the genome of Archegozetes longisetosus. Acarologia, 2022, 62, 532-573.	0.2	3
3163	A high-resolution map of human RNA translation. Molecular Cell, 2022, 82, 2885-2899.e8.	4.5	37
3164	Changes in the Mucosa-Associated Microbiome and Transcriptome across Gut Segments Are Associated with Obesity in a Metabolic Syndrome Porcine Model. Microbiology Spectrum, 2022, 10, .	1.2	11
3166	Identification and functional analysis of <scp>N6</scp>â€methyladenine (<scp>m⁶A</scp>)â€related <scp>lncRNA</scp> across 33 cancer types. Cancer Medicine, 2023, 12, 2104-2116.	1.3	3
3167	The evolutionary history of human spindle genes includes back-and-forth gene flow with Neandertals. ELife, 0, 11, .	2.8	12
3168	Non-coding de novo mutations in chromatin interactions are implicated in autism spectrum disorder. Molecular Psychiatry, 2022, 27, 4680-4694.	4.1	9
3169	Variant Annotation and Functional Prediction: SnpEff. Methods in Molecular Biology, 2022, , 289-314.	0.4	47
3170	Whole genome sequencing and inheritance-based variant filtering as a tool for unraveling missing heritability in pediatric cancer. Pediatric Hematology and Oncology, 2023, 40, 326-340.	0.3	0
3171	Investigation of rumen long noncoding RNA before and after weaning in cattle. BMC Genomics, 2022, 23, .	1.2	2
3172	Aggregated Genomic Data as Cohort-Specific Allelic Frequencies can Boost Variants and Genes Prioritization in Non-Solved Cases of Inherited Retinal Dystrophies. International Journal of Molecular Sciences, 2022, 23, 8431.	1.8	4
3173	Extreme purifying selection against point mutations in the human genome. Nature Communications, 2022, 13, .	5.8	14
3174	Bridging between Mouse and Human Enhancer-Promoter Long-Range Interactions in Neural Stem Cells, to Understand Enhancer Function in Neurodevelopmental Disease. International Journal of Molecular Sciences, 2022, 23, 7964.	1.8	3
3175	X-CAP improves pathogenicity prediction of stopgain variants. Genome Medicine, 2022, 14, .	3.6	0
3177	Early-onset diabetes involving three consecutive generations had different clinical features from age-matched type 2 diabetes without a family history in China. Endocrine, 0, , .	1.1	0
3180	Transcription-coupled and epigenome-encoded mechanisms direct H3K4 methylation. Nature Communications, 2022, 13, .	5.8	17
3182	A paternal bias in germline mutation is widespread in amniotes and can arise independently of cell division numbers. ELife, 0, 11, .	2.8	20
3183	Multi-hallmark long noncoding RNA maps reveal non-small cell lung cancer vulnerabilities. Cell Genomics, 2022, 2, 100171.	3.0	9

#	Article	IF	Citations
3185	mvPPT: A Highly Efficient and Sensitive Pathogenicity Prediction Tool for Missense Variants. Genomics, Proteomics and Bioinformatics, 2023, 21, 414-426.	3.0	2
3186	A cross-disorder dosage sensitivity map of the human genome. Cell, 2022, 185, 3041-3055.e25.	13.5	117
3187	A regulatory network of Sox and Six transcription factors initiate a cell fate transformation during hearing regeneration in adult zebrafish. Cell Genomics, 2022, 2, 100170.	3.0	13
3188	Unsupervised clustering of SARS-CoV-2 using deep convolutional autoencoder. Journal of Engineering and Applied Science, 2022, 69, .	0.8	6
3189	AnFiSA: An open-source computational platform for the analysis of sequencing data for rare genetic disease. Journal of Biomedical Informatics, 2022, 133, 104174.	2.5	0
3190	Clinical significance of genetic variation in hypertrophic cardiomyopathy: comparison of computational tools to prioritize missense variants. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	5
3192	A single WNT enhancer drives specification and regeneration of the Drosophila wing. Nature Communications, 2022, 13, .	5.8	12
3193	Short open reading frame genes in innate immunity: from discovery to characterization. Trends in Immunology, 2022, 43, 741-756.	2.9	9
3196	Systematic analysis of inheritance pattern determination in genes that cause rare neurodevelopmental diseases. Frontiers in Genetics, 0, 13, .	1.1	5
3199	TVAR: assessing tissue-specific functional effects of non-coding variants with deep learning. Bioinformatics, 2022, 38, 4697-4704.	1.8	4
3200	High-throughput identification of RNA localization elements in neuronal cells. Nucleic Acids Research, 2022, 50, 10626-10642.	6.5	18
3201	Diverse ancestry whole-genome sequencing association study identifies TBX5 and PTK7 as susceptibility genes for posterior urethral valves. ELife, 0, 11, .	2.8	5
3202	Monsoon boosted radiation of the endemic East Asian carps. Science China Life Sciences, 2023, 66, 563-578.	2.3	4
3203	Building integrative functional maps of gene regulation. Human Molecular Genetics, 0, , .	1.4	2
3208	Detecting associated genes for complex traits shared across East Asian and European populations under the framework of composite null hypothesis testing. Journal of Translational Medicine, 2022, 20, .	1.8	5
3209	Evolution of stickleback spines through independent cis-regulatory changes at HOXDB. Nature Ecology and Evolution, 2022, 6, 1537-1552.	3.4	8
3212	RMDisease V2.0: an updated database of genetic variants that affect RNA modifications with disease and trait implication. Nucleic Acids Research, 2023, 51, D1388-D1396.	6.5	23
3213	Computational approaches for predicting variant impact: An overview from resources, principles to applications. Frontiers in Genetics, 0, 13, .	1.1	11

#	Article	IF	Citations
3214	Diagnosis of a Single-Nucleotide Variant in Whole-Exome Sequencing Data for Patients With Inherited Diseases: Machine Learning Study Using Artificial Intelligence Variant Prioritization. JMIR Bioinformatics and Biotechnology, 2022, 3, e37701.	0.4	0
3215	snoDB 2.0: an enhanced interactive database, specializing in human snoRNAs. Nucleic Acids Research, 2023, 51, D291-D296.	6.5	10
3217	Physiological intron retaining transcripts in the cytoplasm abound during human motor neurogenesis. Genome Research, 0, , .	2.4	2
3218	The conservation of human functional variants and their effects across livestock species. Communications Biology, 2022, 5, .	2.0	6
3219	Functional characterization of enhancer activity during a long terminal repeat's evolution. Genome Research, 0, , .	2.4	4
3220	Broad-scale variation in human genetic diversity levels is predicted by purifying selection on coding and non-coding elements. ELife, 0, 12, .	2.8	12
3222	Inferring and perturbing cell fate regulomes in human brain organoids. Nature, 2023, 621, 365-372.	13.7	71
3224	A new molecular mechanism supports that blue-greenish egg color evolved independently across chicken breeds. Poultry Science, 2022, 101, 102223.	1.5	3
3225	Unveiling the functional and evolutionary landscape of RNA editing in chicken using genomics and transcriptomics. Zoological Research, 2022, 43, 1011-1022.	0.9	0
3226	Uncovering the Relationship between Tissue-Specific TF-DNA Binding and Chromatin Features through a Transformer-Based Model. Genes, 2022, 13, 1952.	1.0	5
3228	Sex differences in interindividual gene expression variability across human tissues. , 2022, 1, .		5
3229	Deep cis-regulatory homology of the butterfly wing pattern ground plan. Science, 2022, 378, 304-308.	6.0	23
3230	MetaRNN: differentiating rare pathogenic and rare benign missense SNVs and InDels using deep learning. Genome Medicine, 2022, 14, .	3.6	28
3232	Pervasive translation of small open reading frames in plant long non-coding RNAs. Frontiers in Plant Science, 0, 13, .	1.7	4
3234	Diverse environmental perturbations reveal the evolution and context-dependency of genetic effects on gene expression levels. Genome Research, 0, , .	2.4	6
3235	Profiling subcellular localization of nuclear-encoded mitochondrial gene products in zebrafish. Life Science Alliance, 2023, 6, e202201514.	1.3	2
3240	Systematic analysis and prediction of genes associated with monogenic disorders on human chromosome X. Nature Communications, 2022, 13, .	5.8	14
3241	An integrative analysis of lncRNAs and mRNAs highlights the potential roles of lncRNAs in the process of follicle selection in Taihang chickens. Theriogenology, 2023, 195, 122-130.	0.9	1

#	Article	IF	Citations
3242	Comprehensive analysis of mRNA-lncRNA co-expression profiles in mouse brain during infection with Toxoplasma gondii. Acta Tropica, 2023, 237, 106722.	0.9	2
3243	Distinct chromosomal â€œnichesâ€•in the genome of‹i›Saccharomyces cerevisiae‹/i›provide the background for genomic innovation and shape the fate of gene duplicates. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	1
3244	NPInter v5.0: ncRNA interaction database in a new era. Nucleic Acids Research, 2023, 51, D232-D239.	6.5	11
3245	Predicting functional effect of missense variants using graph attention neural networks. Nature Machine Intelligence, 2022, 4, 1017-1028.	8.3	15
3246	Mosaic patterns of selection in genomic regions associated with diverse human traits. PLoS Genetics, 2022, 18, e1010494.	1.5	1
3248	Complementary evolution of coding and noncoding sequence underlies mammalian hairlessness. ELife, 0, 11, .	2.8	13
3249	Chromosome-level genome assembly of the Muscovy duck provides insight into fatty liver susceptibility. Genomics, 2022, 114, 110518.	1.3	2
3250	Rare tandem repeat expansions associate with genes involved in synaptic and neuronal signaling functions in schizophrenia. Molecular Psychiatry, 2023, 28, 475-482.	4.1	10
3252	UTRdb 2.0: a comprehensive, expert curated catalog of eukaryotic mRNAs untranslated regions. Nucleic Acids Research, 2023, 51, D337-D344.	6.5	4
3253	IntroVerse: a comprehensive database of introns across human tissues. Nucleic Acids Research, 2023, 51, D167-D178.	6.5	5
3256	Mendelian Disorders in an Interstitial Cystitis/Bladder Pain Syndrome Cohort. Genetics & Genomics Next, 2023, 4, .	0.8	1
3257	African Suid Genomes Provide Insights into the Local Adaptation to Diverse African Environments. Molecular Biology and Evolution, 2022, 39, .	3.5	9
3258	Ribo-uORF: a comprehensive data resource of upstream open reading frames (uORFs) based on ribosome profiling. Nucleic Acids Research, 2023, 51, D248-D261.	6.5	6
3259	Insights on variant analysis in silico tools for pathogenicity prediction. Frontiers in Genetics, 0, 13, .	1.1	17
3260	Genetic analysis and clinical features of three Chinese patients with Oguchi disease. Documenta Ophthalmologica, 2023, 146, 17-32.	1.0	2
3261	Complexity of enhancer networks predicts cell identity and disease genes revealed by single-cell multi-omics analysis. Briefings in Bioinformatics, 2023, 24, .	3.2	2
3262	Whole exome sequencing identifies two novel variants in PHEX and DMP1 in Malaysian children with hypophosphatemic rickets. Italian Journal of Pediatrics, 2022, 48, .	1.0	1
3263	An NKX-COUP-TFII morphogenetic code directs mucosal endothelial addressin expression. Nature Communications, 2022, 13, .	5.8	4

#	Article	IF	Citations
3264	Is Evolutionary Conservation a Useful Predictor for Cancer Long Noncoding RNAs? Insights from the Cancer LncRNA Census 3. Non-coding RNA, 2022, 8, 82.	1.3	1
3265	DisCanVis: Visualizing integrated structural and functional annotations to better understand the effect of cancer mutations located within disordered proteins. Protein Science, 2023, 32, .	3.1	1
3266	De novo birth of functional microproteins in the human lineage. Cell Reports, 2022, 41, 111808.	2.9	31
3268	CRAG: de novo characterization of cell-free DNA fragmentation hotspots in plasma whole-genome sequencing. Genome Medicine, 2022, 14, .	3.6	6
3272	Single-cell chromatin accessibility identifies enhancer networks driving gene expression during spinal cord development in mouse. Developmental Cell, 2022, 57, 2761-2775.e6.	3.1	6
3273	Analysis approaches for the identification and prediction of N ⁶ -methyladenosine sites. Epigenetics, 2023, 18, .	1.3	2
3274	Boosting tissue-specific prediction of active cis-regulatory regions through deep learning and Bayesian optimization techniques. BMC Bioinformatics, 2022, 23, .	1.2	2
3275	Rapid Targeted Sequencing Using Dried Blood Spot Samples for Patients With Suspected Actionable Genetic Diseases. Annals of Laboratory Medicine, 2023, 43, 280-289.	1.2	4
3276	HARs: History, Functions, and Role in the Evolution and Pathogenesis of Human Diseases. Cell and Tissue Biology, 2022, 16, 499-512.	0.2	1
3277	Human ERG oncoprotein represses a Drosophila LIM domain binding proteinâ€"coding gene Chip. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	0
3278	Transcription factor Ap2b regulates the mouse autosomal recessive polycystic kidney disease genes, Pkhd1 and Cys1. Frontiers in Molecular Biosciences, 0, 9, .	1.6	1
3279	Therapeutic adenine base editing of human hematopoietic stem cells. Nature Communications, 2023, 14, .	5.8	16
3280	An atlas of transcribed human cardiac promoters and enhancers reveals an important role of regulatory elements in heart failure. , 2023, 2, 58-75.		7
3281	MARVEL: an integrated alternative splicing analysis platform for single-cell RNA sequencing data. Nucleic Acids Research, 2023, 51, e29-e29.	6.5	6
3282	Functional genomics provide key insights to improve the diagnostic yield of hereditary ataxia. Brain, 2023, 146, 2869-2884.	3.7	4
3283	A Multi-Omics Approach Reveals Features That Permit Robust and Widespread Regulation of IFN-Inducible Antiviral Effectors. Journal of Immunology, 2022, 209, 1930-1941.	0.4	0
3284	mRNA transport, translation, and decay in adult mammalian central nervous system axons. Neuron, 2023, 111, 650-668.e4.	3.8	16
3285	Investigation of Rare Non-Coding Variants in Familial Multiple Myeloma. Cells, 2023, 12, 96.	1.8	2

#	Article	IF	Citations
3286	Long-term Small Population Size, Deleterious Variation, and Altitude Adaptation in the Ethiopian Wolf, a Severely Endangered Canid. Molecular Biology and Evolution, 2023, 40, .	3.5	9
3289	How does precursor RNA structure influence RNA processing and gene expression?. Bioscience Reports, 2023, 43, .	1.1	1
3290	Enhancers for Selective Targeting. Neuromethods, 2023, , 169-184.	0.2	0
3291	Deciphering Hierarchical Chromatin Domains and Preference of Genomic Position Forming Boundaries in Single Mouse Embryonic Stem Cells. Advanced Science, 2023, 10, .	5.6	3
3292	A chromosome-level reference genome and pangenome for barn swallow population genomics. Cell Reports, 2023, 42, 111992.	2.9	4
3293	Molecular Genetic Characteristics of FANCI, a Proposed New Ovarian Cancer Predisposing Gene. Genes, 2023, 14, 277.	1.0	3
3294	The epigenetic basis of evolution. Progress in Biophysics and Molecular Biology, 2023, 178, 57-69.	1.4	7
3295	Characterization of Two Transposable Elements and an Ultra-Conserved Element Isolated in the Genome of Zootoca vivipara (Squamata, Lacertidae). Life, 2023, 13, 637.	1.1	1
3297	An ASO therapy for Angelman syndrome that targets an evolutionarily conserved region at the start of the UBE3A-AS transcript. Science Translational Medicine, 2023, 15, .	5.8	10
3299	Comparative genomics analyses reveal sequence determinants underlying interspecies variations in injury-responsive enhancers. BMC Genomics, 2023, 24, .	1.2	1
3300	HTLV-1 bZIP factor impairs DNA mismatch repair system. Biochemical and Biophysical Research Communications, 2023, 657, 43-49.	1.0	1
3301	Multidimensional conservation analysis decodes the expression of conserved long noncoding RNAs. Life Science Alliance, 2023, 6, e202302002.	1.3	0
3303	Human-specific genetics: new tools to explore the molecular and cellular basis of human evolution. Nature Reviews Genetics, 2023, 24, 687-711.	7.7	21
3305	The Foundational Data Initiative for Parkinson Disease: Enabling efficient translation from genetic maps to mechanism. Cell Genomics, 2023, 3, 100261.	3.0	12
3308	254. Successful trio-based reverse genetic screen in an endangered local cattle breed. , 2022, , .		0
3309	Model performance and interpretability of semi-supervised generative adversarial networks to predict oncogenic variants with unlabeled data. BMC Bioinformatics, 2023, 24, .	1.2	5
3310	Explainable AI for Estimating Pathogenicity of Genetic Variants Using Large-Scale Knowledge Graphs. Cancers, 2023, 15, 1118.	1.7	1
3313	Screening of lncRNA profiles during intramuscular adipogenic differentiation in longissimus dorsi and semitendinosus muscles in pigs. Animal Biotechnology, 2023, 34, 4616-4626.	0.7	2

#	Article	IF	Citations
3317	Protein domains provide a new layer of information for classifying human variations in rare diseases. Frontiers in Bioinformatics, 0, 3, .	1.0	2
3318	Detection and characterization of constitutive replication origins defined by DNA polymerase epsilon. BMC Biology, 2023, 21, .	1.7	2
3319	Assessing the impacts of various factors on circular RNA reliability. Life Science Alliance, 2023, 6, e202201793.	1.3	3
3320	Identification of clade-wide putative cis-regulatory elements from conserved non-coding sequences in Cucurbitaceae genomes. Horticulture Research, 2023, 10, .	2.9	1
3321	Gene expression variability across cells and species shapes the relationship between renal resident macrophages and infiltrated macrophages. BMC Bioinformatics, 2023, 24, .	1.2	2
3322	Three amphioxus reference genomes reveal gene and chromosome evolution of chordates. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	11
3323	Genetic analyses of DNA repair pathway associated genes implicate new candidate cancer predisposing genes in ancestrally defined ovarian cancer cases. Frontiers in Oncology, 0, 13, .	1.3	1
3327	Fine-mapping and candidate gene analysis of the Mcgy1 locus responsible for gynoecy in bitter gourd (Momordica spp.). Theoretical and Applied Genetics, 2023, 136, .	1.8	3
3328	Convergent and complementary selection shaped gains and losses of eusociality in sweat bees. Nature Ecology and Evolution, 2023, 7, 557-569.	3.4	9
3329	PredDSMC: A predictor for driver synonymous mutations in human cancers. Frontiers in Genetics, 0, 14, .	1.1	0
3330	Regulatory Potential of SNP Markers in Genes of DNA Repair Systems. Molecular Biology, 2023, 57, 19-38.	0.4	1
3331	The EN-TEx resource of multi-tissue personal epigenomesÂ& variant-impact models. Cell, 2023, 186, 1493-1511.e40.	13.5	13
3332	Assessment of pathogenic variation in gynecologic cancer genes in a national cohort. Scientific Reports, 2023, 13, .	1.6	0
3333	miR-6087 Might Regulate Cell Cycleâ€“Related mRNAs During Cardiomyogenesis of hESCs. Bioinformatics and Biology Insights, 2023, 17, 117793222311619.	1.0	0
3334	Mutational scans reveal differential evolvability of Drosophila promoters and enhancers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2023, 378, .	1.8	2
3335	The expansion of agriculture has shaped the recent evolutionary history of a specialized squash pollinator. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	7
3336	Epicardioid single-cell genomics uncovers principles of human epicardium biology in heart development and disease. Nature Biotechnology, 2023, 41, 1787-1800.	9.4	10
3338	Analysis of the P.Âlividus sea urchin genome highlights contrasting trends of genomic and regulatory evolution in deuterostomes. Cell Genomics, 2023, 3, 100295.	3.0	11

#	Article	IF	Citations
3339	A multi-omics atlas of the human retina at single-cell resolution. Cell Genomics, 2023, 3, 100298.	3.0	10
3340	PredinID: Predicting Pathogenic Inframe Indels in Human Through Graph Convolution Neural Network With Graph Sampling Technique. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 3226-3233.	1.9	0
3342	Dynamic changes in P300 enhancers and enhancer-promoter contacts control mouse cardiomyocyte maturation. Developmental Cell, 2023, 58, 898-914.e7.	3.1	3
3469	Computational approaches for identifying disease-causing mutations in proteins. Advances in Protein Chemistry and Structural Biology, 2024, , 141-171.	1.0	0
3486	Hybrid heuristics: for the repetition-free longest common subsequence problem with index-gene. , 2023, , .		0