

A promoter-level mammalian expression atlas

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Cis-Acting Locus. , 2013, , 9-11.		0
2	Lymphotoxin \hat{I}^2 Receptor Signaling Induces IL-8 Production in Human Bronchial Epithelial Cells. PLoS ONE, 2014, 9, e114791.	1.1	16
3	Alternative Forms of Y-Box Binding Protein 1 and YB-1 mRNA. PLoS ONE, 2014, 9, e104513.	1.1	6
4	Ceruloplasmin Is a Novel Adipokine Which Is Overexpressed in Adipose Tissue of Obese Subjects and in Obesity-Associated Cancer Cells. PLoS ONE, 2014, 9, e80274.	1.1	50
5	Genetic and Epigenetic Control of RKIP Transcription. Critical Reviews in Oncogenesis, 2014, 19, 417-430.	0.2	10
6	A simple metric of promoter architecture robustly predicts expression breadth of human genes suggesting that most transcription factors are positive regulators. Genome Biology, 2014, 15, 413.	3.8	20
7	Approaches for establishing the function of regulatory genetic variants involved in disease. Genome Medicine, 2014, 6, 92.	3.6	34
8	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5289-5294.	3.3	111
9	OncoCis: annotation of cis-regulatory mutations in cancer. Genome Biology, 2014, 15, 485.	3.8	22
10	A transient disruption of fibroblastic transcriptional regulatory network facilitates trans-differentiation. Nucleic Acids Research, 2014, 42, 8905-8913.	6.5	35
11	A genome-wide association study identifies susceptibility loci for ossification of the posterior longitudinal ligament of the spine. Nature Genetics, 2014, 46, 1012-1016.	9.4	115
12	De-repressing LncRNA-Targeted Genes to Upregulate Gene Expression: Focus on Small Molecule Therapeutics. Molecular Therapy - Nucleic Acids, 2014, 3, e196.	2.3	63
13	Characterisation of a Novel Fc Conjugate of Macrophage Colony-stimulating Factor. Molecular Therapy, 2014, 22, 1580-1592.	3.7	88
14	Differential methylation in CN-AML preferentially targets non-CGI regions and is dictated by DNMT3A mutational status and associated with predominant hypomethylation of HOX genes. Epigenetics, 2014, 9, 1108-1119.	1.3	74
15	Variation and constraints in species-specific promoter sequences. Journal of Theoretical Biology, 2014, 363, 357-366.	0.8	1
16	UCbase 2.0: ultraconserved sequences database (2014 update). Database: the Journal of Biological Databases and Curation, 2014, 2014, bau062-bau062.	1.4	19
17	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. PLoS Genetics, 2014, 10, e1004610.	1.5	105
18	Identification of TNF- \hat{A} -Responsive Promoters and Enhancers in the Intestinal Epithelial Cell Model Caco-2. DNA Research, 2014, 21, 569-583.	1.5	12

#	ARTICLE	IF	CITATIONS
19	The Evolution of Human Cells in Terms of Protein Innovation. <i>Molecular Biology and Evolution</i> , 2014, 31, 1364-1374.	3.5	13
21	Conserved Higher-Order Chromatin Regulates NMDA Receptor Gene Expression and Cognition. <i>Neuron</i> , 2014, 84, 997-1008.	3.8	76
22	Transcriptomic analysis of mononuclear phagocyte differentiation and activation. <i>Immunological Reviews</i> , 2014, 262, 74-84.	2.8	62
23	Explaining the correlations among properties of mammalian promoters. <i>Nucleic Acids Research</i> , 2014, 42, 4823-4832.	6.5	7
24	Retinal transcriptome profiling at transcription start sites: a cap analysis of gene expression early after axonal injury. <i>BMC Genomics</i> , 2014, 15, 982.	1.2	26
25	The DEK oncoprotein binds to highly and ubiquitously expressed genes with a dual role in their transcriptional regulation. <i>Molecular Cancer</i> , 2014, 13, 215.	7.9	29
26	SuRFing the genomics wave: an R package for prioritising SNPs by functionality. <i>Genome Medicine</i> , 2014, 6, 79.	3.6	15
27	Multiple novel promoter-architectures revealed by decoding the hidden heterogeneity within the genome. <i>Nucleic Acids Research</i> , 2014, 42, 12388-12403.	6.5	14
28	Mast cell transcriptome elucidation: what are the implications for allergic disease in the clinic and where do we go next?. <i>Expert Review of Clinical Immunology</i> , 2014, 10, 977-980.	1.3	10
29	Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. <i>BMC Genomics</i> , 2014, 15, 729.	1.2	46
30	Protection of CpG islands against de novo DNA methylation during oogenesis is associated with the recognition site of E2f1 and E2f2. <i>Epigenetics and Chromatin</i> , 2014, 7, 26.	1.8	30
31	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
32	A catalogue of human gene activity. <i>Nature Reviews Genetics</i> , 2014, 15, 290-290.	7.7	0
33	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014, 24, 708-717.	2.4	99
34	Targeting the host immune response to fight infection. <i>Science</i> , 2014, 344, 807-808.	6.0	30
35	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	9.4	271
36	Mice in the ENCODE spotlight. <i>Nature</i> , 2014, 515, 346-347.	13.7	11
37	Nuclear stability and transcriptional directionality separate functionally distinct RNA species. <i>Nature Communications</i> , 2014, 5, 5336.	5.8	165

#	ARTICLE	IF	CITATIONS
38	Rare and low-frequency variants in human common diseases and other complex traits. <i>Journal of Medical Genetics</i> , 2014, 51, 705-714.	1.5	29
39	Specific Mesothelial Signature Marks the Heterogeneity of Mesenchymal Stem Cells From High-Grade Serous Ovarian Cancer. <i>Stem Cells</i> , 2014, 32, 2998-3011.	1.4	16
40	Genetic Networks Governing Heart Development. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014, 4, a013839-a013839.	2.9	46
41	Gene coexpression measures in large heterogeneous samples using count statistics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16371-16376.	3.3	29
42	Homeostasis in the mononuclear phagocyte system. <i>Trends in Immunology</i> , 2014, 35, 358-367.	2.9	153
43	Longitudinal Analysis of DNA Methylation in CD34+ Hematopoietic Progenitors in Myelodysplastic Syndrome. <i>Stem Cells Translational Medicine</i> , 2014, 3, 1188-1198.	1.6	7
44	Evolutionary dynamics of coding and non-coding transcriptomes. <i>Nature Reviews Genetics</i> , 2014, 15, 734-748.	7.7	209
45	Opportunity for Selection in Human Health. <i>Advances in Genetics</i> , 2014, 87, 1-70.	0.8	5
46	Design and development of exome capture sequencing for the domestic pig (<i>Sus scrofa</i>). <i>BMC Genomics</i> , 2014, 15, 550.	1.2	24
47	The devil in the details of RNA-seq. <i>Nature Biotechnology</i> , 2014, 32, 882-884.	9.4	35
48	Bringing RNA-seq closer to the clinic. <i>Nature Biotechnology</i> , 2014, 32, 884-885.	9.4	21
49	RNA sequencing: from tag-based profiling to resolving complete transcript structure. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 3537-3551.	2.4	33
50	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , 2014, 15, 119.	1.2	214
51	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. <i>BMC Genomics</i> , 2014, 15, 120.	1.2	17
52	RECLU: a pipeline to discover reproducible transcriptional start sites and their alternative regulation using capped analysis of gene expression (CAGE). <i>BMC Genomics</i> , 2014, 15, 269.	1.2	61
53	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 73-83.	0.5	39
55	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , 2014, 15, 1177.	1.2	10
56	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014, 123, e58-e67.	0.6	175

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58	Orthology-driven mapping of bidirectional promoters in human and mouse genomes. BMC Bioinformatics, 2014, 15, S1.	1.2	9
59	Identification of long noncoding <scp>RNA</scp>s dysregulated in the midbrain of human cocaine abusers. Journal of Neurochemistry, 2015, 135, 50-59.	2.1	38
60	Two novel DNA motifs are essential for BACE1 gene transcription. Scientific Reports, 2014, 4, 6864.	1.6	11
61	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. Molecular Systems Biology, 2015, 11, 852.	3.2	305
62	Insights into the Transcriptional Architecture of Behavioral Plasticity in the Honey Bee Apis mellifera. Scientific Reports, 2015, 5, 11136.	1.6	59
63	SOXE transcription factors form selective dimers on non-compact DNA motifs through multifaceted interactions between dimerization and high-mobility group domains. Scientific Reports, 2015, 5, 10398.	1.6	65
64	CGGBP1 is an indispensable protein with ubiquitous cytoprotective functions. Upsala Journal of Medical Sciences, 2015, 120, 219-232.	0.4	18
65	Comprehensive comparative homeobox gene annotation in human and mouse. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	12
66	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. Cell Reports, 2015, 13, 1493-1504.	2.9	46
67	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. American Journal of Human Genetics, 2015, 97, 139-152.	2.6	122
68	Disease-associated variants in different categories of disease located in distinct regulatory elements. BMC Genomics, 2015, 16, S3.	1.2	41
69	Many obesity-associated SNPs strongly associate with DNA methylation changes at proximal promoters and enhancers. Genome Medicine, 2015, 7, 103.	3.6	124
70	Multilayered, Hyaluronic Acid-Based Hydrogel Formulations Suitable for Automated 3D High Throughput Drug Screening of Cancer Stromal Cell Cocultures. Advanced Healthcare Materials, 2015, 4, 1664-1674.	3.9	47
71	Detecting shifts in gene regulatory networks during time-course experiments at single-time-point temporal resolution. Journal of Bioinformatics and Computational Biology, 2015, 13, 1543002.	0.3	3
72	Systematic noise degrades gene co-expression signals but can be corrected. BMC Bioinformatics, 2015, 16, 309.	1.2	50
73	Identification and annotation of conserved promoters and macrophage-expressed genes in the pig genome. BMC Genomics, 2015, 16, 970.	1.2	22
74	GenomicInteractions: An R/Bioconductor package for manipulating and investigating chromatin interaction data. BMC Genomics, 2015, 16, 963.	1.2	56
75	Exploring the cellular basis of human disease through a large-scale mapping of deleterious genes to cell types. Genome Medicine, 2015, 7, 95.	3.6	13

#	ARTICLE	IF	CITATIONS
76	What Does Genetics Tell Us About Age-Related Macular Degeneration?. Annual Review of Vision Science, 2015, 1, 73-96.	2.3	21
77	EpiFactors: a comprehensive database of human epigenetic factors and complexes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav067.	1.4	226
78	DENDb: database of integrated human enhancers. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav085.	1.4	51
79	Characterization of regulatory sequences in alternative promoters of hypermethylated genes associated with tumor resistance to cisplatin. Molecular and Clinical Oncology, 2015, 3, 408-414.	0.4	1
80	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and ChIP-seq Data in the TC-YIK Cell Line. Frontiers in Genetics, 2015, 6, 331.	1.1	13
81	The Many Alternative Faces of Macrophage Activation. Frontiers in Immunology, 2015, 6, 370.	2.2	281
82	Expression analysis of the long non-coding RNA antisense to Uchl1 (AS Uchl1) during dopaminergic cells' differentiation in vitro and in neurochemical models of Parkinson's disease. Frontiers in Cellular Neuroscience, 2015, 9, 114.	1.8	112
83	SINEUPs are modular antisense long non-coding RNAs that increase synthesis of target proteins in cells. Frontiers in Cellular Neuroscience, 2015, 9, 174.	1.8	81
84	Discovery of Molecular Markers to Discriminate Corneal Endothelial Cells in the Human Body. PLoS ONE, 2015, 10, e0117581.	1.1	28
85	Long Noncoding RNA Expression during Human B-Cell Development. PLoS ONE, 2015, 10, e0138236.	1.1	80
86	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. PLoS Biology, 2015, 13, e1002315.	2.6	32
87	Assessment of mTOR-Dependent Translational Regulation of Interferon Stimulated Genes. PLoS ONE, 2015, 10, e0133482.	1.1	21
88	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. PLoS ONE, 2015, 10, e0144176.	1.1	1
89	Tor Signaling Regulates Transcription of Amino Acid Permeases through a GATA Transcription Factor Caf1 in Fission Yeast. PLoS ONE, 2015, 10, e0144677.	1.1	15
90	PVT1: A Rising Star among Oncogenic Long Noncoding RNAs. BioMed Research International, 2015, 2015, 1-10.	0.9	191
91	The DDBJ Japanese Genotype-phenotype Archive for genetic and phenotypic human data. Nucleic Acids Research, 2015, 43, D18-D22.	6.5	57
92	Expression of mouse Dab2ip transcript variants and gene methylation during brain development. Gene, 2015, 568, 19-24.	1.0	2
93	Genetic Engineering for Microalgae Strain Improvement in Relation to Biocrude Production Systems. Biofuel and Biorefinery Technologies, 2015, , 191-249.	0.1	8

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94	Biomass and Biofuels from Microalgae. <i>Biofuel and Biorefinery Technologies</i> , 2015, , .	0.1	33
95	Western Blotting. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	16
96	Meta-analysis identifies seven susceptibility loci involved in the atopic march. <i>Nature Communications</i> , 2015, 6, 8804.	5.8	148
97	Strategies for fine-mapping complex traits. <i>Human Molecular Genetics</i> , 2015, 24, R111-R119.	1.4	191
98	EvoTol: a protein-sequence based evolutionary intolerance framework for disease-gene prioritization. <i>Nucleic Acids Research</i> , 2015, 43, e33-e33.	6.5	33
99	Core Promoter Plasticity Between Maize Tissues and Genotypes Contrasts with Predominance of Sharp Transcription Initiation Sites. <i>Plant Cell</i> , 2015, 27, 3309-3320.	3.1	65
100	Exome Sequencing: Current and Future Perspectives. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1543-1550.	0.8	165
101	Multifaceted roles of 5' regulatory region of the cancer associated gene B4GALT1 and its comparison with the gene family. <i>International Journal of Oncology</i> , 2015, 47, 1393-1404.	1.4	30
102	Modeling transcriptional regulation. <i>Nature Genetics</i> , 2015, 47, 1-1.	9.4	47
103	DBTSS as an integrative platform for transcriptome, epigenome and genome sequence variation data. <i>Nucleic Acids Research</i> , 2015, 43, D87-D91.	6.5	46
104	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
105	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	13.7	201
106	Enhancer Evolution across 20 Mammalian Species. <i>Cell</i> , 2015, 160, 554-566.	13.5	671
107	Identification of altered cis-regulatory elements in human disease. <i>Trends in Genetics</i> , 2015, 31, 67-76.	2.9	99
108	Alternative mRNA transcription, processing, and translation: insights from RNA sequencing. <i>Trends in Genetics</i> , 2015, 31, 128-139.	2.9	283
109	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015, 6, 5903.	5.8	73
110	Relationships of RNA Polymerase II Genetic Interactors to Transcription Start Site Usage Defects and Growth in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 21-33.	0.8	13
111	Molecular and Genetic Properties of Tumors Associated with Local Immune Cytolytic Activity. <i>Cell</i> , 2015, 160, 48-61.	13.5	2,948

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112	The statistical geometry of transcriptome divergence in cell-type evolution and cancer. <i>Nature Communications</i> , 2015, 6, 6066.	5.8	49
113	Messenger RNA processing is altered in autosomal dominant leukodystrophy. <i>Human Molecular Genetics</i> , 2015, 24, 2746-2756.	1.4	27
114	Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. <i>Journal of Virology</i> , 2015, 89, 2448-2452.	1.5	6
115	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015, 12, 339-342.	9.0	155
116	Lynch Syndrome Associated with Two <i>MLH1</i> Promoter Variants and Allelic Imbalance of <i>MLH1</i> Expression. <i>Human Mutation</i> , 2015, 36, 622-630.	1.1	26
117	Kinesins and Cancer. , 2015, , .		16
118	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687
119	Improved tagmentation-based whole-genome bisulfite sequencing for input DNA from less than 100 mammalian cells. <i>Epigenomics</i> , 2015, 7, 47-56.	1.0	17
120	Creating reference gene annotation for the mouse C57BL6/J genome assembly. <i>Mammalian Genome</i> , 2015, 26, 366-378.	1.0	182
121	Destabilization of the human epigenome: consequences of foreign DNA insertions. <i>Epigenomics</i> , 2015, 7, 745-755.	1.0	15
122	A Call for Systematic Research on Solute Carriers. <i>Cell</i> , 2015, 162, 478-487.	13.5	457
123	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015, 25, 1546-1557.	2.4	55
124	DNA entropy reveals a significant difference in complexity between housekeeping and tissue specific gene promoters. <i>Computational Biology and Chemistry</i> , 2015, 58, 19-24.	1.1	6
125	Systematic Screening of Promoter Regions Pinpoints Functional <i>Cis</i> -Regulatory Mutations in a Cutaneous Melanoma Genome. <i>Molecular Cancer Research</i> , 2015, 13, 1218-1226.	1.5	29
126	Genomic modulators of gene expression in human neutrophils. <i>Nature Communications</i> , 2015, 6, 7545.	5.8	120
127	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. <i>Nature Immunology</i> , 2015, 16, 933-941.	7.0	148
128	The role of DNA methylation in directing the functional organization of the cancer epigenome. <i>Genome Research</i> , 2015, 25, 467-477.	2.4	90
129	Genome-wide study of correlations between genomic features and their relationship with the regulation of gene expression. <i>DNA Research</i> , 2015, 22, 109-119.	1.5	18

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130	Coexpression networks identify brain region-specific enhancer RNAs in the human brain. <i>Nature Neuroscience</i> , 2015, 18, 1168-1174.	7.1	79
131	Leveraging Functional-Annotation Data in Trans-ethnic Fine-Mapping Studies. <i>American Journal of Human Genetics</i> , 2015, 97, 260-271.	2.6	186
132	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676
133	Novel Transcription Factor Variants through RNA-Sequencing: The Importance of Being "Alternative". <i>International Journal of Molecular Sciences</i> , 2015, 16, 1755-1771.	1.8	8
134	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004217.	1.5	22
135	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015, 47, 569-576.	9.4	738
136	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 638-648.	1.5	59
137	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015, 43, e51-e51.	6.5	194
138	Analysis of tandem E-box motifs within human Complement receptor 2 (CR2/CD21) promoter reveals cell specific roles for RP58, E2A, USF and localized chromatin accessibility. <i>International Journal of Biochemistry and Cell Biology</i> , 2015, 64, 107-119.	1.2	4
139	Retinoic acid potentiates inflammatory cytokines in human mast cells: Identification of mast cells as prominent constituents of the skin retinoid network. <i>Molecular and Cellular Endocrinology</i> , 2015, 406, 49-59.	1.6	25
140	Ubiquitous L1 Mosaicism in Hippocampal Neurons. <i>Cell</i> , 2015, 161, 228-239.	13.5	292
141	A novel myogenic function residing in the 5' non-coding region of Insulin receptor substrate-1 (Irs-1) transcript. <i>BMC Cell Biology</i> , 2015, 16, 8.	3.0	8
142	Age-associated DNA methylation changes in immune genes, histone modifiers and chromatin remodeling factors within 5 years after birth in human blood leukocytes. <i>Clinical Epigenetics</i> , 2015, 7, 34.	1.8	65
143	Unraveling the association between mRNA expressions and mutant phenotypes in a genome-wide assessment of mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4707-4712.	3.3	23
144	The Ensembl Regulatory Build. <i>Genome Biology</i> , 2015, 16, 56.	3.8	382
145	Regulatory genomics: Combined experimental and computational approaches. <i>Russian Journal of Genetics</i> , 2015, 51, 334-352.	0.2	8
146	Principles of Long Noncoding RNA Evolution Derived from Direct Comparison of Transcriptomes in 17 Species. <i>Cell Reports</i> , 2015, 11, 1110-1122.	2.9	565
147	The core promoter: At the heart of gene expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 1116-1131.	0.9	140

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148	Genetic similarity between cancers and comorbid Mendelian diseases identifies candidate driver genes. <i>Nature Communications</i> , 2015, 6, 7033.	5.8	32
149	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	6.0	1,127
150	Neighboring Genes Show Correlated Evolution in Gene Expression. <i>Molecular Biology and Evolution</i> , 2015, 32, 1748-1766.	3.5	126
151	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015, 97, 985-995.	1.5	23
152	DEEP: a general computational framework for predicting enhancers. <i>Nucleic Acids Research</i> , 2015, 43, e6-e6.	6.5	124
153	The Landscape of long noncoding RNA classification. <i>Trends in Genetics</i> , 2015, 31, 239-251.	2.9	942
154	A transcriptional perspective on human macrophage biology. <i>Seminars in Immunology</i> , 2015, 27, 44-50.	2.7	33
155	Genome-wide analysis of core promoter structures in <i>Schizosaccharomyces pombe</i> with DeepCAGE. <i>RNA Biology</i> , 2015, 12, 525-537.	1.5	50
156	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
157	Does every transcript originate from a gene?. <i>Annals of the New York Academy of Sciences</i> , 2015, 1341, 136-148.	1.8	8
158	Functional genomics bridges the gap between quantitative genetics and molecular biology. <i>Genome Research</i> , 2015, 25, 1427-1431.	2.4	63
159	Discovering Genes Essential to the Hypothalamic Regulation of Human Reproduction Using a Human Disease Model: Adjusting to Life in the "Omics" Era. <i>Endocrine Reviews</i> , 2015, 36, 603-621.	8.9	69
160	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982.	6.5	54
161	ElemeNT: a computational tool for detecting core promoter elements. <i>Transcription</i> , 2015, 6, 41-50.	1.7	66
162	TET2 repression by androgen hormone regulates global hydroxymethylation status and prostate cancer progression. <i>Nature Communications</i> , 2015, 6, 8219.	5.8	93
163	A global analysis of the complex landscape of isoforms and regulatory networks of p63 in human cells and tissues. <i>BMC Genomics</i> , 2015, 16, 584.	1.2	52
164	The identification of cis-regulatory elements: A review from a machine learning perspective. <i>BioSystems</i> , 2015, 138, 6-17.	0.9	51
165	Assessing the translational landscape of myogenic differentiation by ribosome profiling. <i>Nucleic Acids Research</i> , 2015, 43, 4408-4428.	6.5	43

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166	SINEUPs: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. <i>RNA Biology</i> , 2015, 12, 771-779.	1.5	84
167	Candidate gene analysis and exome sequencing confirm LBX1 as a susceptibility gene for idiopathic scoliosis. <i>Spine Journal</i> , 2015, 15, 2239-2246.	0.6	53
168	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015, 43, 6787-6798.	6.5	94
169	Evolution of the unspliced transcriptome. <i>BMC Evolutionary Biology</i> , 2015, 15, 166.	3.2	7
170	Massively parallel high-order combinatorial genetics in human cells. <i>Nature Biotechnology</i> , 2015, 33, 952-961.	9.4	50
171	Expression Specificity of Disease-Associated lncRNAs: Toward Personalized Medicine. <i>Current Topics in Microbiology and Immunology</i> , 2015, 394, 237-258.	0.7	33
172	CRB3A Controls the Morphology and Cohesion of Cancer Cells through Ehm2/p114RhoGEF-Dependent Signaling. <i>Molecular and Cellular Biology</i> , 2015, 35, 3423-3435.	1.1	19
173	Complexity of Mammalian Transcriptome Analyzed by RNA Deep Sequencing. , 2015, , 3-22.		2
174	Scrutinizing the FTO locus: compelling evidence for a complex, long-range regulatory context. <i>Human Genetics</i> , 2015, 134, 1183-1193.	1.8	22
175	Host-directed drug therapy for tuberculosis. <i>Nature Chemical Biology</i> , 2015, 11, 748-751.	3.9	44
176	Deciphering H3K4me3 broad domains associated with gene-regulatory networks and conserved epigenomic landscapes in the human brain. <i>Translational Psychiatry</i> , 2015, 5, e679-e679.	2.4	57
177	Significant expansion of the REST/NRSF cistrome in human versus mouse embryonic stem cells: potential implications for neural development. <i>Nucleic Acids Research</i> , 2015, 43, 5730-5743.	6.5	35
178	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. <i>Genome Research</i> , 2015, 25, 1812-1824.	2.4	49
179	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015, 26, 391-402.	1.0	96
180	Risk of childhood asthma is associated with CpG-site polymorphisms, regional DNA methylation and mRNA levels at the GSDMB/ORMDL3 locus. <i>Human Molecular Genetics</i> , 2015, 24, 875-890.	1.4	66
181	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015, 43, D662-D669.	6.5	1,145
182	Biomechanisms of Comorbidity: Reviewing Integrative Analyses of Multi-omics Datasets and Electronic Health Records. <i>Yearbook of Medical Informatics</i> , 2016, 25, 194-206.	0.8	3
183	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. <i>ELife</i> , 2016, 5, .	2.8	609

#	ARTICLE	IF	CITATIONS
184	Global Intersection of Long Non-Coding RNAs with Processed and Unprocessed Pseudogenes in the Human Genome. <i>Frontiers in Genetics</i> , 2016, 7, 26.	1.1	29
185	What Is the Impact of mRNA 5' TL Heterogeneity on Translational Start Site Selection and the Mammalian Cellular Phenotype?. <i>Frontiers in Genetics</i> , 2016, 7, 156.	1.1	12
186	E2 Regulates Epigenetic Signature on Neuroglobin Enhancer-Promoter in Neuronal Cells. <i>Frontiers in Cellular Neuroscience</i> , 2016, 10, 147.	1.8	13
187	TCF/LEF Transcription Factors: An Update from the Internet Resources. <i>Cancers</i> , 2016, 8, 70.	1.7	111
188	Role of Non-Coding RNAs in the Transgenerational Epigenetic Transmission of the Effects of Reprotoxicants. <i>International Journal of Molecular Sciences</i> , 2016, 17, 452.	1.8	33
189	Comprehensive promoter level expression quantitative trait loci analysis of the human frontal lobe. <i>Genome Medicine</i> , 2016, 8, 65.	3.6	20
190	Influence of Rotational Nucleosome Positioning on Transcription Start Site Selection in Animal Promoters. <i>PLoS Computational Biology</i> , 2016, 12, e1005144.	1.5	24
191	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, .	1.4	24
192	Evidence for genetic regulation of the human parieto-occipital 10 Hz rhythmic activity. <i>European Journal of Neuroscience</i> , 2016, 44, 1963-1971.	1.2	20
193	Integrative analysis with ChIP-seq advances the limits of transcript quantification from RNA-seq. <i>Genome Research</i> , 2016, 26, 1124-1133.	2.4	19
194	A comprehensive analysis of 3' end sequencing data sets reveals novel polyadenylation signals and the repressive role of heterogeneous ribonucleoprotein C on cleavage and polyadenylation. <i>Genome Research</i> , 2016, 26, 1145-1159.	2.4	196
195	Phenotypic variability in human skin mast cells. <i>Experimental Dermatology</i> , 2016, 25, 434-439.	1.4	37
196	Ensembl regulation resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav119.	1.4	45
197	Gene-specific patterns of expression variation across organs and species. <i>Genome Biology</i> , 2016, 17, 151.	3.8	89
198	Heat*seq: an interactive web tool for high-throughput sequencing experiment comparison with public data. <i>Bioinformatics</i> , 2016, 32, 3354-3356.	1.8	20
199	Fibroblast VEGF receptor 1 expression as molecular target in periodontitis. <i>Journal of Clinical Periodontology</i> , 2016, 43, 128-137.	2.3	16
200	Whole genome sequence analysis of serum amino acid levels. <i>Genome Biology</i> , 2016, 17, 237.	3.8	17
201	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	5.8	142

#	ARTICLE	IF	CITATIONS
202	Autosomal recessive retinitis pigmentosa with homozygous rhodopsin mutation E150K and non-coding cis-regulatory variants in CRX-binding regions of SAMD7. <i>Scientific Reports</i> , 2016, 6, 21307.	1.6	16
203	Gene-specific correlation of <i>scn</i> RNA and protein levels in human cells and tissues. <i>Molecular Systems Biology</i> , 2016, 12, 883.	3.2	347
204	Novel biomarkers that assist in accurate discrimination of squamous cell carcinoma from adenocarcinoma of the lung. <i>BMC Cancer</i> , 2016, 16, 760.	1.1	40
205	Epigenetic Regulation of Myeloid Cells. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	20
206	Detecting Sources of Transcriptional Heterogeneity in Large-Scale RNA-Seq Data Sets. <i>Genetics</i> , 2016, 204, 1391-1396.	1.2	11
207	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. <i>Nucleic Acids Research</i> , 2017, 45, gkw973.	6.5	30
208	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. <i>Scientific Reports</i> , 2016, 6, 38575.	1.6	4
209	Endogenous retroviral promoter exaptation in human cancer. <i>Mobile DNA</i> , 2016, 7, 24.	1.3	178
210	Transcriptional Regulation and Macrophage Differentiation. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	35
211	The human PRD-like homeobox gene <i>LEUTX</i> has a central role in embryo genome activation. <i>Development (Cambridge)</i> , 2016, 143, 3459-3469.	1.2	42
212	Pervasive isoform-specific translational regulation via alternative transcription start sites in mammals. <i>Molecular Systems Biology</i> , 2016, 12, 875.	3.2	83
213	Transcriptome analysis of periodontitis-associated fibroblasts by CAGE sequencing identified <i>DLX5</i> and <i>RUNX2</i> long variant as novel regulators involved in periodontitis. <i>Scientific Reports</i> , 2016, 6, 33666.	1.6	18
214	Discovering Genes Essential to the Hypothalamic Regulation of Human Reproduction Using a Human Disease Model: Adjusting to Life in the Omics Era. <i>Endocrine Reviews</i> , 2016, 2016, 4-22.	8.9	33
215	Synthetic long non-coding RNAs [SINEUPs] rescue defective gene expression in vivo. <i>Scientific Reports</i> , 2016, 6, 27315.	1.6	37
216	DeepEnhancer: Predicting enhancers by convolutional neural networks. , 2016, , .		9
217	Gene expression signatures of human cell and tissue longevity. <i>Npj Aging and Mechanisms of Disease</i> , 2016, 2, 16014.	4.5	40
218	Genetic and environmental risk factors for atherosclerosis regulate transcription of phosphatase and actin regulating gene <i>PHACTR1</i> . <i>Atherosclerosis</i> , 2016, 250, 95-105.	0.4	39
219	Parallel computation of genome-scale RNA secondary structure to detect structural constraints on human genome. <i>BMC Bioinformatics</i> , 2016, 17, 203.	1.2	30

#	ARTICLE	IF	CITATIONS
220	DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , 2016, 129, 2573-85.	1.2	15
221	Integrated pathway-based transcription regulation network mining and visualization based on gene expression profiles. <i>Journal of Biomedical Informatics</i> , 2016, 61, 194-202.	2.5	6
222	Landscape and Dynamics of Transcription Initiation in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2016, 14, 2463-2475.	2.9	51
223	Differential DNA repair underlies mutation hotspots at active promoters in cancer genomes. <i>Nature</i> , 2016, 532, 259-263.	13.7	195
224	Long Non-coding RNAs in Human Disease. <i>Current Topics in Microbiology and Immunology</i> , 2016, , .	0.7	4
225	Contribution of Heritability and Epigenetic Factors to Skeletal Muscle Mass Variation in United Kingdom Twins. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 2450-2459.	1.8	42
226	Towards understanding pre-mRNA splicing mechanisms and the role of SR proteins. <i>Gene</i> , 2016, 587, 107-119.	1.0	46
227	G72 primate-specific gene: a still enigmatic element in psychiatric disorders. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2029-2039.	2.4	31
228	Differential DNA methylation patterns of homeobox genes in proximal and distal colon epithelial cells. <i>Physiological Genomics</i> , 2016, 48, 257-273.	1.0	6
229	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016, 26, 705-716.	2.4	33
230	Long noncoding RNAs in B-cell development and activation. <i>Blood</i> , 2016, 128, e10-e19.	0.6	115
231	Promoter Architecture and Sex-Specific Gene Expression in <i>Daphnia pulex</i> . <i>Genetics</i> , 2016, 204, 593-612.	1.2	20
233	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. <i>Journal of Biomedical Semantics</i> , 2016, 7, 44.	0.9	201
234	Global transcript structure resolution of high gene density genomes through multi-platform data integration. <i>Nucleic Acids Research</i> , 2016, 44, e145-e145.	6.5	96
235	Expression of FBN1 during adipogenesis: Relevance to the lipodystrophy phenotype in Marfan syndrome and related conditions. <i>Molecular Genetics and Metabolism</i> , 2016, 119, 174-185.	0.5	29
236	Datasets of genes coexpressed with FBN1 in mouse adipose tissue and during human adipogenesis. <i>Data in Brief</i> , 2016, 8, 851-857.	0.5	3
237	WOMEN IN CANCER THEMATIC REVIEW: Diverse functions of DNA methylation: implications for prostate cancer and beyond. <i>Endocrine-Related Cancer</i> , 2016, 23, T169-T178.	1.6	8
238	An inducible long noncoding RNA amplifies DNA damage signaling. <i>Nature Genetics</i> , 2016, 48, 1370-1376.	9.4	195

#	ARTICLE	IF	CITATIONS
239	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. <i>Journal of Virology</i> , 2016, 90, 10811-10822.	1.5	27
240	Tissue Specificity of Gene Expression. <i>Current Genetic Medicine Reports</i> , 2016, 4, 163-169.	1.9	5
241	De Novo Mutations in DENR Disrupt Neuronal Development and Link Congenital Neurological Disorders to Faulty mRNA Translation Re-initiation. <i>Cell Reports</i> , 2016, 15, 2251-2265.	2.9	30
242	CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. <i>Genome Biology</i> , 2016, 17, 201.	3.8	24
243	IL-4 and human skin mast cells revisited: reinforcement of a pro-allergic phenotype upon prolonged exposure. <i>Archives of Dermatological Research</i> , 2016, 308, 665-670.	1.1	22
244	A Survey of the Computational Methods for Enhancers and Enhancer-target Predictions. , 2016, , 3-27.		1
245	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. <i>American Journal of Human Genetics</i> , 2016, 99, 366-374.	2.6	68
246	Integrative analysis of human omics data using biomolecular networks. <i>Molecular BioSystems</i> , 2016, 12, 2953-2964.	2.9	33
247	Isoforms of the Erythropoietin receptor in dopaminergic neurons of the <i>Substantia Nigra</i> . <i>Journal of Neurochemistry</i> , 2016, 139, 596-609.	2.1	11
248	Epigenetic memory: A macrophage perspective. <i>Seminars in Immunology</i> , 2016, 28, 359-367.	2.7	49
249	Prediction of kinase-specific phosphorylation sites through an integrative model of protein context and sequence. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1599-1608.	1.1	16
250	The canine era: the rise of a biomedical model. <i>Animal Genetics</i> , 2016, 47, 519-527.	0.6	44
251	Ubiquitously expressed genes participate in cell-specific functions via alternative promoter usage. <i>EMBO Reports</i> , 2016, 17, 1304-1313.	2.0	26
252	Functional annotation of the cell immunoglobulin mucin family in birds. <i>Immunology</i> , 2016, 148, 287-303.	2.0	16
253	BAR Domain-Containing FAM92 Proteins Interact with Chibby1 To Facilitate Ciliogenesis. <i>Molecular and Cellular Biology</i> , 2016, 36, 2668-2680.	1.1	38
254	The Adipose Transcriptional Response to Insulin Is Determined by Obesity, Not Insulin Sensitivity. <i>Cell Reports</i> , 2016, 16, 2317-2326.	2.9	35
255	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , 2016, 48, 1142-1150.	9.4	196
256	Lineage-specific genomics: Frequent birth and death in the human genome. <i>BioEssays</i> , 2016, 38, 654-663.	1.2	4

#	ARTICLE	IF	CITATIONS
257	Patterns of ribosomal protein expression specify normal and malignant human cells. <i>Genome Biology</i> , 2016, 17, 236.	3.8	171
259	Yeast Polyphosphatases PPX1 and PPN1: Properties, Functions, and Localization. , 2016, , 15-33.		1
260	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , 2016, 6, 37324.	1.6	32
261	Ciliary dyslexia candidate genes <i>DYX1C1</i> and <i>DCDC2</i> are regulated by Regulatory Factor X (RFX) transcription factors through X-box promoter motifs. <i>FASEB Journal</i> , 2016, 30, 3578-3587.	0.2	28
263	Critical Updates to the Leukemia Stem Cell Model. , 2016, , 101-119.		2
264	Heralding a new paradigm in 3D tumor modeling. <i>Biomaterials</i> , 2016, 108, 197-213.	5.7	127
265	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). <i>Nature Protocols</i> , 2016, 11, 1455-1476.	5.5	392
266	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. <i>Nature Genetics</i> , 2016, 48, 984-994.	9.4	75
267	Long Non-coding RNAs and Their Roles in Non-small-cell Lung Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 280-288.	3.0	100
268	Early B-cell factor 1 (EBF1) is critical for transcriptional control of SLAMF1 gene in human B cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1259-1268.	0.9	20
269	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). <i>Nature Communications</i> , 2016, 7, 12339.	5.8	69
270	CisMapper: predicting regulatory interactions from transcription factor ChIP-seq data. <i>Nucleic Acids Research</i> , 2016, 45, gkw956.	6.5	23
271	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. <i>Nature Communications</i> , 2016, 7, 11778.	5.8	68
272	Characterization and target genes of nine human PRD-like homeobox domain genes expressed exclusively in early embryos. <i>Scientific Reports</i> , 2016, 6, 28995.	1.6	33
273	The state of play in higher eukaryote gene annotation. <i>Nature Reviews Genetics</i> , 2016, 17, 758-772.	7.7	74
274	Identification of antisense long noncoding RNAs that function as SINEUPs in human cells. <i>Scientific Reports</i> , 2016, 6, 33605.	1.6	58
275	Computational identification of putative lincRNAs in mouse embryonic stem cell. <i>Scientific Reports</i> , 2016, 6, 34892.	1.6	3
276	Discriminative identification of transcriptional responses of promoters and enhancers after stimulus. <i>Nucleic Acids Research</i> , 2017, 45, gkw1015.	6.5	3

#	ARTICLE	IF	CITATIONS
277	Precision Modulation of Neurodegenerative Disease-Related Gene Expression in Human iPSC-Derived Neurons. <i>Scientific Reports</i> , 2016, 6, 28420.	1.6	67
278	PAX6 MiniPromoters drive restricted expression from rAAV in the adult mouse retina. <i>Molecular Therapy - Methods and Clinical Development</i> , 2016, 3, 16051.	1.8	17
279	Chromosome conformation elucidates regulatory relationships in developing human brain. <i>Nature</i> , 2016, 538, 523-527.	13.7	507
280	The HSA21 gene EURL/C21ORF91 controls neurogenesis within the cerebral cortex and is implicated in the pathogenesis of Down Syndrome. <i>Scientific Reports</i> , 2016, 6, 29514.	1.6	22
281	Full transcription of the chloroplast genome in photosynthetic eukaryotes. <i>Scientific Reports</i> , 2016, 6, 30135.	1.6	51
282	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. <i>Npj Genomic Medicine</i> , 2016, 1, .	1.7	19
283	R-spondin 2 promotes acetylcholine receptor clustering at the neuromuscular junction via Lgr5. <i>Scientific Reports</i> , 2016, 6, 28512.	1.6	24
284	Mammalian Brain Development is Accompanied by a Dramatic Increase in Bipolar DNA Methylation. <i>Scientific Reports</i> , 2016, 6, 32298.	1.6	13
285	Evolutionary hallmarks of the human proteome: chasing the age and coregulation of protein-coding genes. <i>BMC Genomics</i> , 2016, 17, 725.	1.2	4
286	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. <i>Genome Medicine</i> , 2016, 8, 129.	3.6	137
287	Opening up the blackbox: an interpretable deep neural network-based classifier for cell-type specific enhancer predictions. <i>BMC Systems Biology</i> , 2016, 10, 54.	3.0	25
288	eRFSVM: a hybrid classifier to predict enhancers-integrating random forests with support vector machines. <i>Hereditas</i> , 2016, 153, 6.	0.5	5
289	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw105.	1.4	64
290	Seqinspector: position-based navigation through the ChIP-seq data landscape to identify gene expression regulators. <i>BMC Bioinformatics</i> , 2016, 17, 85.	1.2	15
291	Regulation of tracheal antimicrobial peptide gene expression in airway epithelial cells of cattle. <i>Veterinary Research</i> , 2016, 47, 44.	1.1	15
292	Transcriptome Profiling Strategies. , 2016, , 69-104.		0
293	Mechanisms of Gene Regulation. , 2016, , .		15
294	Genetic heterogeneity in autism: From single gene to a pathway perspective. <i>Neuroscience and Biobehavioral Reviews</i> , 2016, 68, 442-453.	2.9	46

#	ARTICLE	IF	CITATIONS
295	Mapping the Genome. , 2016, , 109-125.		0
296	Precursors of tRNAs are stabilized by methylguanosine cap structures. <i>Nature Chemical Biology</i> , 2016, 12, 648-655.	3.9	52
297	CAGEd-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , 2016, 32, 2858-2860.	1.8	13
298	An atlas of gene expression and gene co-regulation in the human retina. <i>Nucleic Acids Research</i> , 2016, 44, 5773-5784.	6.5	65
299	Hidden heterogeneity of transcription factor binding sites: A case study of SF-1. <i>Computational Biology and Chemistry</i> , 2016, 64, 19-32.	1.1	6
300	Genomic sequencing of a dyslexia susceptibility haplotype encompassing ROBO1. <i>Journal of Neurodevelopmental Disorders</i> , 2016, 8, 4.	1.5	8
301	Regulation of LRRK2 promoter activity and gene expression by Sp1. <i>Molecular Brain</i> , 2016, 9, 33.	1.3	19
302	Bacurd1/Kctd13 and Bacurd2/Tnfaip1 are interacting partners to Rnd proteins which influence the long-term positioning and dendritic maturation of cerebral cortical neurons. <i>Neural Development</i> , 2016, 11, 7.	1.1	27
303	C9orf72 is differentially expressed in the central nervous system and myeloid cells and consistently reduced in C9orf72, MAPT and GRN mutation carriers. <i>Acta Neuropathologica Communications</i> , 2016, 4, 37.	2.4	58
304	High-throughput functional comparison of promoter and enhancer activities. <i>Genome Research</i> , 2016, 26, 1023-1033.	2.4	114
305	Ligand cluster-based protein network and ePlatton, a multi-target ligand finder. <i>Journal of Cheminformatics</i> , 2016, 8, 23.	2.8	1
306	In Silico Functional Annotation of Genomic Variation. <i>Current Protocols in Human Genetics</i> , 2016, 88, 6.15.1-6.15.17.	3.5	20
307	Optimizing sgRNA position markedly improves the efficiency of CRISPR/dCas9-mediated transcriptional repression. <i>Nucleic Acids Research</i> , 2016, 44, e141-e141.	6.5	118
308	Reinforcing the association between distal <i>1q43</i> CNVs and structural brain disorder: A case of a complex <i>1q43</i> CNV and a review of the literature. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 458-467.	1.1	23
309	nanoCAGE reveals 5' UTR features that define specific modes of translation of functionally related MTOR-sensitive mRNAs. <i>Genome Research</i> , 2016, 26, 636-648.	2.4	177
310	High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. <i>Nature Genetics</i> , 2016, 48, 323-330.	9.4	219
311	Precision control of recombinant gene transcription for CHO cell synthetic biology. <i>Biotechnology Advances</i> , 2016, 34, 492-503.	6.0	29
312	Enhancer Turnover Is Associated with a Divergent Transcriptional Response to Glucocorticoid in Mouse and Human Macrophages. <i>Journal of Immunology</i> , 2016, 196, 813-822.	0.4	89

#	ARTICLE	IF	CITATIONS
313	Promoter architectures and developmental gene regulation. <i>Seminars in Cell and Developmental Biology</i> , 2016, 57, 11-23.	2.3	53
314	Deep Feature Selection: Theory and Application to Identify Enhancers and Promoters. <i>Journal of Computational Biology</i> , 2016, 23, 322-336.	0.8	118
315	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. <i>Trends in Genetics</i> , 2016, 32, 76-88.	2.9	87
316	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016, 48, 331-335.	9.4	263
317	A human haploid gene trap collection to study lncRNAs with unusual RNA biology. <i>RNA Biology</i> , 2016, 13, 196-220.	1.5	1
318	Spell Checking Nature: Versatility of CRISPR/Cas9 for Developing Treatments for Inherited Disorders. <i>American Journal of Human Genetics</i> , 2016, 98, 90-101.	2.6	86
319	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016, 76, 216-226.	0.4	80
320	Enhancer scanning to locate regulatory regions in genomic loci. <i>Nature Protocols</i> , 2016, 11, 46-60.	5.5	14
321	Expression Atlas update— an integrated database of gene and protein expression in humans, animals and plants. <i>Nucleic Acids Research</i> , 2016, 44, D746-D752.	6.5	526
322	Identification and analysis of mouse non-coding RNA using transcriptome data. <i>Science China Life Sciences</i> , 2016, 59, 589-603.	2.3	10
323	Optimal design of gene knockout experiments for gene regulatory network inference. <i>Bioinformatics</i> , 2016, 32, 875-883.	1.8	29
324	DTIE, a novel core promoter element that directs start site selection in TATA-less genes. <i>Nucleic Acids Research</i> , 2016, 44, 1080-1094.	6.5	31
325	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016, 44, 3233-3252.	6.5	31
326	Clonal Dynamics In Vivo of Virus Integration Sites of T Cells Expressing a Safety Switch. <i>Molecular Therapy</i> , 2016, 24, 736-745.	3.7	11
327	Roles, Functions, and Mechanisms of Long Non-coding RNAs in Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 42-54.	3.0	789
328	Birth and upgrowth of the Hox topological domains during evolution. <i>Nature Genetics</i> , 2016, 48, 227-228.	9.4	0
329	Enabling direct fate conversion with network biology. <i>Nature Genetics</i> , 2016, 48, 226-227.	9.4	3
330	The E3 ubiquitin ligase RNF144B is LPS-inducible in human, but not mouse, macrophages and promotes inducible IL-1 β expression. <i>Journal of Leukocyte Biology</i> , 2016, 100, 155-161.	1.5	16

#	ARTICLE	IF	CITATIONS
331	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016, 48, 510-518.	9.4	617
332	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
333	Tissue-specific regulatory circuits reveal variable modular perturbations across complex diseases. <i>Nature Methods</i> , 2016, 13, 366-370.	9.0	306
334	Genome-wide identification and characterization of transcription start sites and promoters in the tunicate <i>Ciona intestinalis</i> . <i>Genome Research</i> , 2016, 26, 140-150.	2.4	13
335	The life history of retrocopies illuminates the evolution of new mammalian genes. <i>Genome Research</i> , 2016, 26, 301-314.	2.4	104
336	Chromatin and RNA Maps Reveal Regulatory Long Noncoding RNAs in Mouse. <i>Molecular and Cellular Biology</i> , 2016, 36, 809-819.	1.1	75
337	HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2016, 44, D116-D125.	6.5	215
338	Next Generation Sequencing's™ General Information about the Technology, Possibilities, and Limitations. , 2016, , 1-18.		5
339	Whole-genome bisulfite sequencing maps from multiple human tissues reveal novel CpG islands associated with tissue-specific regulation. <i>Human Molecular Genetics</i> , 2016, 25, 69-82.	1.4	44
340	Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , 2016, 17, 603-615.	3.2	46
341	The Primary Auditory Neurons of the Mammalian Cochlea. <i>Springer Handbook of Auditory Research</i> , 2016, , .	0.3	20
342	Functional Analyses of Transcription Factor Binding Sites that Differ between Present-Day and Archaic Humans. <i>Molecular Biology and Evolution</i> , 2016, 33, 316-322.	3.5	19
343	Advances in long noncoding RNAs: identification, structure prediction and function annotation. <i>Briefings in Functional Genomics</i> , 2016, 15, 38-46.	1.3	111
344	Translational issues for human corneal endothelial tissue engineering. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2017, 11, 2425-2442.	1.3	37
345	Antisense transcription of the myotonic dystrophy locus yields low-abundant RNAs with and without (CAG) _n repeat. <i>RNA Biology</i> , 2017, 14, 1374-1388.	1.5	25
346	Mapping eQTLs with RNA-seq reveals novel susceptibility genes, non-coding RNAs and alternative-splicing events in systemic lupus erythematosus. <i>Human Molecular Genetics</i> , 2017, 26, ddw417.	1.4	39
347	Practical Approaches for Whole-Genome Sequence Analysis of Heart- and Blood-Related Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 205-215.	2.6	50
348	Alternative intronic promoters in development and disease. <i>Protoplasma</i> , 2017, 254, 1201-1206.	1.0	14

#	ARTICLE	IF	CITATIONS
349	DEIVA: a web application for interactive visual analysis of differential gene expression profiles. <i>BMC Genomics</i> , 2017, 18, 47.	1.2	41
350	Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal promoters. <i>Genome Research</i> , 2017, 27, 553-566.	2.4	32
351	Data resources for human functional genomics. <i>Current Opinion in Systems Biology</i> , 2017, 1, 75-79.	1.3	5
352	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
353	Single-cell mRNA isoform diversity in the mouse brain. <i>BMC Genomics</i> , 2017, 18, 126.	1.2	70
354	Seek and destroy: targeted adeno-associated viruses for gene delivery to hepatocellular carcinoma. <i>Drug Delivery</i> , 2017, 24, 289-299.	2.5	18
355	Middle East Respiratory Syndrome. <i>New England Journal of Medicine</i> , 2017, 376, 584-594.	13.9	351
356	Promoter shape varies across populations and affects promoter evolution and expression noise. <i>Nature Genetics</i> , 2017, 49, 550-558.	9.4	74
357	High-confidence coding and noncoding transcriptome maps. <i>Genome Research</i> , 2017, 27, 1050-1062.	2.4	58
358	De novo RNA sequence assembly during in vivo inflammatory stress reveals hundreds of unannotated lincRNAs in human blood CD14 ⁺ monocytes and in adipose tissue. <i>Physiological Genomics</i> , 2017, 49, 287-305.	1.0	9
359	Synapses in the spotlight with synthetic optogenetics. <i>EMBO Reports</i> , 2017, 18, 677-692.	2.0	41
360	Computational identification of mutually exclusive transcriptional drivers dysregulating metastatic microRNAs in prostate cancer. <i>Nature Communications</i> , 2017, 8, 14917.	5.8	16
361	Gene Regulatory Elements, Major Drivers of Human Disease. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 45-63.	2.5	115
362	A mouse tissue transcription factor atlas. <i>Nature Communications</i> , 2017, 8, 15089.	5.8	90
363	Proteogenomic analysis reveals alternative splicing and translation as part of the abscisic acid response in <i>Arabidopsis</i> seedlings. <i>Plant Journal</i> , 2017, 91, 518-533.	2.8	156
364	Identification of active miRNA promoters from nuclear run-on RNA sequencing. <i>Nucleic Acids Research</i> , 2017, 45, e121-e121.	6.5	32
365	Comparative transcriptomics in human and mouse. <i>Nature Reviews Genetics</i> , 2017, 18, 425-440.	7.7	168
366	Methylation of <i>avpr1a</i> in the cortex of wild prairie voles: effects of CpG position and polymorphism. <i>Royal Society Open Science</i> , 2017, 4, 160646.	1.1	16

#	ARTICLE	IF	CITATIONS
367	The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. <i>Methods in Molecular Biology</i> , 2017, 1611, 199-217.	0.4	23
368	Systematic identification and characterization of cardiac long intergenic noncoding RNAs in zebrafish. <i>Scientific Reports</i> , 2017, 7, 1250.	1.6	12
369	Normalized long read RNA sequencing in chicken reveals transcriptome complexity similar to human. <i>BMC Genomics</i> , 2017, 18, 323.	1.2	129
370	Transcriptional signatures of steroid hormones in the striatal neurons and astrocytes. <i>BMC Neuroscience</i> , 2017, 18, 37.	0.8	39
371	Protein Function Prediction. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	15
372	Genome Annotation. <i>Methods in Molecular Biology</i> , 2017, 1525, 107-121.	0.4	3
373	Relatively frequent switching of transcription start sites during cerebellar development. <i>BMC Genomics</i> , 2017, 18, 461.	1.2	27
374	The essentiality of non-coding RNAs in cell reprogramming. <i>Non-coding RNA Research</i> , 2017, 2, 74-82.	2.4	18
375	Genome-wide characterization of mammalian promoters with distal enhancer functions. <i>Nature Genetics</i> , 2017, 49, 1073-1081.	9.4	222
376	Chromatin-enriched lncRNAs can act as cell-type specific activators of proximal gene transcription. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 596-603.	3.6	70
377	High-resolution promoter map of human limbal epithelial cells cultured with keratinocyte growth factor and rho kinase inhibitor. <i>Scientific Reports</i> , 2017, 7, 2845.	1.6	9
378	Alternative TSSs are co-regulated in single cells in the mouse brain. <i>Molecular Systems Biology</i> , 2017, 13, 930.	3.2	23
379	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. <i>Trends in Genetics</i> , 2017, 33, 464-478.	2.9	181
380	The Landscape of Isoform Switches in Human Cancers. <i>Molecular Cancer Research</i> , 2017, 15, 1206-1220.	1.5	208
381	Super-Enhancers and Broad H3K4me3 Domains Form Complex Gene Regulatory Circuits Involving Chromatin Interactions. <i>Scientific Reports</i> , 2017, 7, 2186.	1.6	70
382	Systems-wide Studies Uncover Commander, a Multiprotein Complex Essential to Human Development. <i>Cell Systems</i> , 2017, 4, 483-494.	2.9	44
383	Autoregulation of MBNL1 function by exon 1 exclusion from MBNL1 transcript. <i>Nucleic Acids Research</i> , 2017, 45, 1760-1775.	6.5	52
384	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	2.6	131

#	ARTICLE	IF	CITATIONS
385	Inflammation-associated DNA methylation patterns in epithelium of ulcerative colitis. <i>Epigenetics</i> , 2017, 12, 591-606.	1.3	40
386	RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections. <i>Nucleic Acids Research</i> , 2017, 45, e119-e119.	6.5	96
387	Can We Predict Gene Expression by Understanding Proximal Promoter Architecture?. <i>Trends in Biotechnology</i> , 2017, 35, 530-546.	4.9	18
388	A class of circadian long non-coding RNAs mark enhancers modulating long-range circadian gene regulation. <i>Nucleic Acids Research</i> , 2017, 45, 5720-5738.	6.5	39
389	Functional dissection of NEAT1 using genome editing reveals substantial localization of the NEAT1_1 isoform outside paraspeckles. <i>Rna</i> , 2017, 23, 872-881.	1.6	114
390	Epigenomic Promoter Alterations Amplify Gene Isoform and Immunogenic Diversity in Gastric Adenocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 630-651.	7.7	48
391	Interplay between genetic and epigenetic mechanisms in rheumatoid arthritis. <i>Epigenomics</i> , 2017, 9, 493-504.	1.0	23
393	Identification of Gene Transcription Start Sites and Enhancers Responding to Pulmonary Carbon Nanotube Exposure <i>in Vivo</i> . <i>ACS Nano</i> , 2017, 11, 3597-3613.	7.3	23
394	Crosstalks between Raf-kinase inhibitor protein and cancer stem cell transcription factors (Oct4, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	28
395	High-quality genome assembly of <i>Capsella bursa-pastoris</i> reveals asymmetry of regulatory elements at early stages of polyploid genome evolution. <i>Plant Journal</i> , 2017, 91, 278-291.	2.8	40
396	Deep Cap Analysis of Gene Expression (CAGE): Genome-Wide Identification of Promoters, Quantification of Their Activity, and Transcriptional Network Inference. <i>Methods in Molecular Biology</i> , 2017, 1543, 111-126.	0.4	4
397	Enlightening discriminative network functional modules behind Principal Component Analysis separation in differential-omic science studies. <i>Scientific Reports</i> , 2017, 7, 43946.	1.6	45
398	High expression of insulin receptor on tumour-associated blood vessels in invasive bladder cancer predicts poor overall and progression-free survival. <i>Journal of Pathology</i> , 2017, 242, 193-205.	2.1	24
399	Genome-wide mapping of autonomous promoter activity in human cells. <i>Nature Biotechnology</i> , 2017, 35, 145-153.	9.4	97
400	Reversible methylation of m6Am in the 5' cap controls mRNA stability. <i>Nature</i> , 2017, 541, 371-375.	13.7	797
401	Transcriptional response to mitochondrial protease IMMP2L knockdown in human primary astrocytes. <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 1252-1258.	1.0	11
402	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. <i>Science</i> , 2017, 355, .	6.0	566
403	Distinct global binding patterns of the Wilms tumor gene 1 (WT1) $\hat{\sim}$ KTS and +KTS isoforms in leukemic cells. <i>Haematologica</i> , 2017, 102, 336-345.	1.7	12

#	ARTICLE	IF	CITATIONS
404	Timing and localization of human dystrophin isoform expression provide insights into the cognitive phenotype of Duchenne muscular dystrophy. <i>Scientific Reports</i> , 2017, 7, 12575.	1.6	123
405	Isoform-specific localization of DNMT3A regulates DNA methylation fidelity at bivalent CpG islands. <i>EMBO Journal</i> , 2017, 36, 3421-3434.	3.5	99
406	Mammalian APE1 controls miRNA processing and its interactome is linked to cancer RNA metabolism. <i>Nature Communications</i> , 2017, 8, 797.	5.8	107
407	Constructing Strong Cell Type-Specific Promoters Through Informed Design. <i>Methods in Molecular Biology</i> , 2017, 1651, 131-145.	0.4	4
408	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147.	2.4	29
409	HTLV-1 bZIP factor suppresses TDP1 expression through inhibition of NRF-1 in adult T-cell leukemia. <i>Scientific Reports</i> , 2017, 7, 12849.	1.6	13
410	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	2.7	24
411	DNA methylation and transcriptional trajectories during human development and reprogramming of isogenic pluripotent stem cells. <i>Nature Communications</i> , 2017, 8, 908.	5.8	53
412	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , 2017, 4, 170113.	2.4	55
413	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
414	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
415	Application of a CAGE Method to an Avian Development Study. <i>Methods in Molecular Biology</i> , 2017, 1650, 101-109.	0.4	4
416	Apoptotic resistance of human skin mast cells is mediated by Mcl-1. <i>Cell Death Discovery</i> , 2017, 3, 17048.	2.0	16
417	RefEx, a reference gene expression dataset as a web tool for the functional analysis of genes. <i>Scientific Data</i> , 2017, 4, 170105.	2.4	55
418	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	2.4	195
419	Acute doses of caffeine shift nervous system cell expression profiles toward promotion of neuronal projection growth. <i>Scientific Reports</i> , 2017, 7, 11458.	1.6	14
420	Regulation of Inflammatory Signaling in Health and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2017, , .	0.8	7
421	Emerging Roles for Epigenetic Programming in the Control of Inflammatory Signaling Integration in Health and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1024, 63-90.	0.8	7

#	ARTICLE	IF	CITATIONS
422	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , 2017, 4, 170107.	2.4	68
423	Nanopore long-read RNAseq reveals widespread transcriptional variation among the surface receptors of individual B cells. <i>Nature Communications</i> , 2017, 8, 16027.	5.8	329
424	Pan-urolologic cancer genomic subtypes that transcend tissue of origin. <i>Nature Communications</i> , 2017, 8, 199.	5.8	49
425	Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. <i>Scientific Reports</i> , 2017, 7, 5557.	1.6	19
426	Genome-wide screen for differentially methylated long noncoding RNAs identifies <i>Esrp2</i> and lncRNA <i>Esrp2-as</i> regulated by enhancer DNA methylation with prognostic relevance for human breast cancer. <i>Oncogene</i> , 2017, 36, 6446-6461.	2.6	77
427	Transcriptional mechanisms that control expression of the macrophage colony-stimulating factor receptor locus. <i>Clinical Science</i> , 2017, 131, 2161-2182.	1.8	66
428	Identification of the macrophage-specific promoter signature in FANTOM5 mouse embryo developmental time course data. <i>Journal of Leukocyte Biology</i> , 2017, 102, 1081-1092.	1.5	35
429	Gene Expression Networks in the Murine Pulmonary Myocardium Provide Insight into the Pathobiology of Atrial Fibrillation. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2999-3017.	0.8	8
430	Network analysis identifies chromosome intermingling regions as regulatory hotspots for transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13714-13719.	3.3	45
431	Promoter-level transcriptome in primary lesions of endometrial cancer identified biomarkers associated with lymph node metastasis. <i>Scientific Reports</i> , 2017, 7, 14160.	1.6	11
432	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , 2017, 4, 170173.	2.4	6
433	CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. <i>Cell Systems</i> , 2017, 5, 628-637.e6.	2.9	80
434	Deep RNA Sequencing Uncovers a Repertoire of Human Macrophage Long Intergenic Noncoding RNAs Modulated by Macrophage Activation and Associated With Cardiometabolic Diseases. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	36
435	Restricted Presence of POU6F2 in Human Corneal Endothelial Cells Uncovered by Extension of the Promoter-level Expression Atlas. <i>EBioMedicine</i> , 2017, 25, 175-186.	2.7	7
436	IL-11 is a crucial determinant of cardiovascular fibrosis. <i>Nature</i> , 2017, 552, 110-115.	13.7	451
437	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. <i>Nature Genetics</i> , 2017, 49, 1731-1740.	9.4	227
438	The effect of genetic variation on promoter usage and enhancer activity. <i>Nature Communications</i> , 2017, 8, 1358.	5.8	50
439	A Comprehensive Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. <i>Scientific Reports</i> , 2017, 7, 4200.	1.6	139

#	ARTICLE	IF	CITATIONS
440	Context-specific effects of genetic variants associated with autoimmune disease. <i>Human Molecular Genetics</i> , 2017, 26, R185-R192.	1.4	38
441	Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. <i>Human Molecular Genetics</i> , 2017, 26, 3442-3450.	1.4	25
442	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017, 15, 1354-1365.	1.5	25
443	Expression of a SOX1 overlapping transcript in neural differentiation and cancer models. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 4245-4258.	2.4	24
444	A Pentanucleotide ATTTC Repeat Insertion in the Non-coding Region of DAB1, Mapping to SCA37, Causes Spinocerebellar Ataxia. <i>American Journal of Human Genetics</i> , 2017, 101, 87-103.	2.6	112
445	Both maintenance and avoidance of RNA-binding protein interactions constrain coding sequence evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, msx061.	3.5	22
446	Gene expression profiling of puberty-associated genes reveals abundant tissue and sex-specific changes across postnatal development. <i>Human Molecular Genetics</i> , 2017, 26, 3585-3599.	1.4	33
447	NEArender: an R package for functional interpretation of omics data via network enrichment analysis. <i>BMC Bioinformatics</i> , 2017, 18, 118.	1.2	16
448	Zipper plot: visualizing transcriptional activity of genomic regions. <i>BMC Bioinformatics</i> , 2017, 18, 231.	1.2	5
449	Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. <i>BMC Bioinformatics</i> , 2017, 18, 301.	1.2	40
450	Uncovering the transcriptomic and epigenomic landscape of nicotinic receptor genes in non-neuronal tissues. <i>BMC Genomics</i> , 2017, 18, 439.	1.2	15
451	A high-quality annotated transcriptome of swine peripheral blood. <i>BMC Genomics</i> , 2017, 18, 479.	1.2	7
452	CARMIL family proteins as multidomain regulators of actin-based motility. <i>Molecular Biology of the Cell</i> , 2017, 28, 1713-1723.	0.9	40
453	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	6.5	116
454	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230.	0.3	27
455	The Gene Ontology Handbook. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	63
456	A systematic comparison reveals substantial differences in chromosomal versus episomal encoding of enhancer activity. <i>Genome Research</i> , 2017, 27, 38-52.	2.4	244
457	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , 2017, 26, 314-327.	1.1	4

#	ARTICLE	IF	CITATIONS
458	Multiplatform-based molecular subtypes of non-small-cell lung cancer. <i>Oncogene</i> , 2017, 36, 1384-1393.	2.6	118
459	The Vision and Challenges of the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 291-302.	0.4	11
460	New era in genetics of early-onset muscle disease: Breakthroughs and challenges. <i>Seminars in Cell and Developmental Biology</i> , 2017, 64, 160-170.	2.3	24
461	c-Rel is dispensable for the differentiation and functional maturation of M cells in the follicle-associated epithelium. <i>Immunobiology</i> , 2017, 222, 316-326.	0.8	8
462	Evolutionary clues in <scp>lncRNAs</scp>. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1376.	3.2	60
463	The Yin and Yang of nucleic acid-based therapy in the brain. <i>Progress in Neurobiology</i> , 2017, 155, 194-211.	2.8	22
464	Titin-truncating variants affect heart function in disease cohorts and the general population. <i>Nature Genetics</i> , 2017, 49, 46-53.	9.4	255
465	Co-regulation of paralog genes in the three-dimensional chromatin architecture. <i>Nucleic Acids Research</i> , 2017, 45, 81-91.	6.5	88
466	Transcription start site profiling of 15 anatomical regions of the <i>Macaca mulatta</i> central nervous system. <i>Scientific Data</i> , 2017, 4, 170163.	2.4	4
467	Glucocorticoid Receptor Binding Induces Rapid and Prolonged Large-Scale Chromatin Decompaction at Multiple Target Loci. <i>Cell Reports</i> , 2017, 21, 3022-3031.	2.9	43
468	Genomic and molecular control of cell type and cell type conversions. <i>Cell Regeneration</i> , 2017, 6, 1-7.	1.1	12
469	Sex differences in microRNA-mRNA networks: examination of novel epigenetic programming mechanisms in the sexually dimorphic neonatal hypothalamus. <i>Biology of Sex Differences</i> , 2017, 8, 27.	1.8	27
470	Models of global gene expression define major domains of cell type and tissue identity. <i>Nucleic Acids Research</i> , 2017, 45, 2354-2367.	6.5	50
471	Expitope 2.0: a tool to assess immunotherapeutic antigens for their potential cross-reactivity against naturally expressed proteins in human tissues. <i>BMC Cancer</i> , 2017, 17, 892.	1.1	22
473	KLF1 directly activates expression of the novel fetal globin repressor ZBTB7A/LRF in erythroid cells. <i>Blood Advances</i> , 2017, 1, 685-692.	2.5	42
474	RUNX1 regulates site specificity of DNA demethylation by recruitment of DNA demethylation machineries in hematopoietic cells. <i>Blood Advances</i> , 2017, 1, 1699-1711.	2.5	64
475	Transcriptional Regulation and Macrophage Differentiation. , 2017, , 117-139.		1
476	Developmental Control of NRAMP1 (SLC11A1) Expression in Professional Phagocytes. <i>Biology</i> , 2017, 6, 28.	1.3	11

#	ARTICLE	IF	CITATIONS
477	Retinoic Acid Negatively Impacts Proliferation and MCTC Specific Attributes of Human Skin Derived Mast Cells, but Reinforces Allergic Stimulability. <i>International Journal of Molecular Sciences</i> , 2017, 18, 525.	1.8	30
478	Jmjd6, a JmjC Dioxygenase with Many Interaction Partners and Pleiotropic Functions. <i>Frontiers in Genetics</i> , 2017, 8, 32.	1.1	49
479	Regulatory Roles of Long Non-Coding RNAs in the Central Nervous System and Associated Neurodegenerative Diseases. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 175.	1.8	117
480	Genes uniquely expressed in human growth plate chondrocytes uncover a distinct regulatory network. <i>BMC Genomics</i> , 2017, 18, 983.	1.2	17
481	Body-hypomethylated human genes harbor extensive intragenic transcriptional activity and are prone to cancer-associated dysregulation. <i>Nucleic Acids Research</i> , 2017, 45, gkx020.	6.5	34
482	Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN. <i>PLoS ONE</i> , 2017, 12, e0169249.	1.1	73
483	EINCR1 is an EGF inducible lincRNA overexpressed in lung adenocarcinomas. <i>PLoS ONE</i> , 2017, 12, e0181902.	1.1	5
484	A high resolution atlas of gene expression in the domestic sheep (<i>Ovis aries</i>). <i>PLoS Genetics</i> , 2017, 13, e1006997.	1.5	210
485	Correlation of EGFR or KRAS mutation status with 18F-FDG uptake on PET-CT scan in lung adenocarcinoma. <i>PLoS ONE</i> , 2017, 12, e0175622.	1.1	20
486	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017, 15, e2002887.	2.6	68
487	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. <i>PLoS Genetics</i> , 2017, 13, e1006641.	1.5	161
488	Rare coding variants pinpoint genes that control human hematological traits. <i>PLoS Genetics</i> , 2017, 13, e1006925.	1.5	39
489	Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimer's disease. <i>PLoS Genetics</i> , 2017, 13, e1006933.	1.5	96
490	Maize network analysis revealed gene modules involved in development, nutrients utilization, metabolism, and stress response. <i>BMC Plant Biology</i> , 2017, 17, 131.	1.6	24
491	A subset of conserved mammalian long non-coding RNAs are fossils of ancestral protein-coding genes. <i>Genome Biology</i> , 2017, 18, 162.	3.8	57
492	Intergenic disease-associated regions are abundant in novel transcripts. <i>Genome Biology</i> , 2017, 18, 241.	3.8	45
493	Bidirectional transcription initiation marks accessible chromatin and is not specific to enhancers. <i>Genome Biology</i> , 2017, 18, 242.	3.8	52
494	Genome-wide profiling of transcribed enhancers during macrophage activation. <i>Epigenetics and Chromatin</i> , 2017, 10, 50.	1.8	41

#	ARTICLE	IF	CITATIONS
495	A screening system to identify transcription factors that induce binding site-directed DNA demethylation. <i>Epigenetics and Chromatin</i> , 2017, 10, 60.	1.8	48
496	Novel promoters and coding first exons in <i>DLG2</i> linked to developmental disorders and intellectual disability. <i>Genome Medicine</i> , 2017, 9, 67.	3.6	29
497	Biological function integrated prediction of severe radiographic progression in rheumatoid arthritis: a nested case control study. <i>Arthritis Research and Therapy</i> , 2017, 19, 244.	1.6	11
498	AODTH-008â€¦Proximity extension assay based proteins show immune cell specificity and can diagnose and predict outcomes in inflammatory bowel diseases: ibd character study. , 2017, , .		0
499	Genome build information is an essential part of genomic track files. <i>Genome Biology</i> , 2017, 18, 175.	3.8	6
500	Predicting enhancers with deep convolutional neural networks. <i>BMC Bioinformatics</i> , 2017, 18, 478.	1.2	76
501	Big knowledge from big data in functional genomics. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 245-248.	1.1	4
502	Effects of Type 1 Diabetes Risk Alleles on Immune Cell Gene Expression. <i>Genes</i> , 2017, 8, 167.	1.0	17
503	The genomic architecture of mastitis resistance in dairy sheep. <i>BMC Genomics</i> , 2017, 18, 624.	1.2	59
504	The eukaryotic promoter database in its 30th year: focus on non-vertebrate organisms. <i>Nucleic Acids Research</i> , 2017, 45, D51-D55.	6.5	218
505	Disruption of the aortic wall by coelomic lining-derived mesenchymal cells accompanies the onset of aortic hematopoiesis. <i>International Journal of Developmental Biology</i> , 2017, 61, 329-335.	0.3	6
506	TcoF-DB v2: update of the database of human and mouse transcription co-factors and transcription factor interactions. <i>Nucleic Acids Research</i> , 2017, 45, D145-D150.	6.5	63
507	Higher-Level Pathway Objectives of Epigenetic Therapy: A Solution to the p53 Problem in Cancer. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2017, 37, 812-824.	1.8	12
508	Whole Genome Sequencing in the Molecular Pathology Laboratory. , 2017, , 531-540.		0
509	A <i>RAB27A</i> 5â€² untranslated region structural variant associated with late-onset hemophagocytic lymphohistiocytosis and normal pigmentation. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 317-321.e8.	1.5	22
510	A Gain-of-Function Mutation in <i>EPO</i> in Familial Erythrocytosis. <i>New England Journal of Medicine</i> , 2018, 378, 924-930.	13.9	42
511	Alternative transcription of a shorter, non-anti-angiogenic thrombospondin-2 variant in cancer-associated blood vessels. <i>Oncogene</i> , 2018, 37, 2573-2585.	2.6	22
512	The Human Cell Atlas: Technical approaches and challenges. <i>Briefings in Functional Genomics</i> , 2018, 17, 283-294.	1.3	34

#	ARTICLE	IF	CITATIONS
513	Whole genome sequencing analysis for cancer genomics and precision medicine. <i>Cancer Science</i> , 2018, 109, 513-522.	1.7	235
514	TERIUS: accurate prediction of lncRNA via high-throughput sequencing data representing RNA-binding protein association. <i>BMC Bioinformatics</i> , 2018, 19, 41.	1.2	8
515	PARP14 Controls the Nuclear Accumulation of a Subset of Type I IFN-Inducible Proteins. <i>Journal of Immunology</i> , 2018, 200, 2439-2454.	0.4	70
516	Unravelling the molecular basis for regulatory T cell plasticity and loss of function in disease. <i>Clinical and Translational Immunology</i> , 2018, 7, e1011.	1.7	23
517	Discovery of coding regions in the human genome by integrated proteogenomics analysis workflow. <i>Nature Communications</i> , 2018, 9, 903.	5.8	108
518	DNA-mediated dimerization on a compact sequence signature controls enhancer engagement and regulation by FOXA1. <i>Nucleic Acids Research</i> , 2018, 46, 5470-5486.	6.5	18
519	Informational limits of biological organisms. <i>EMBO Journal</i> , 2018, 37, .	3.5	4
520	In Pursuit of Precision Medicine in the Critically Ill. <i>Annual Update in Intensive Care and Emergency Medicine</i> , 2018, , 649-658.	0.1	5
521	Intron retention induced by microsatellite expansions as a disease biomarker. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4234-4239.	3.3	96
522	Integrated analysis sheds light on evolutionary trajectories of young transcription start sites in the human genome. <i>Genome Research</i> , 2018, 28, 676-688.	2.4	22
523	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
524	Intragenic transcriptional interference regulates the human immune ligand <sc>MICA</sc>. <i>EMBO Journal</i> , 2018, 37, .	3.5	13
525	Antisense transcription-dependent chromatin signature modulates sense transcript dynamics. <i>Molecular Systems Biology</i> , 2018, 14, e8007.	3.2	42
526	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. <i>GigaScience</i> , 2018, 7, 1-17.	3.3	27
527	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. <i>Journal of Hepatology</i> , 2018, 68, 959-969.	1.8	254
528	CRISPR interference-based specific and efficient gene inactivation in the brain. <i>Nature Neuroscience</i> , 2018, 21, 447-454.	7.1	133
529	Methods and Applications of Epigenomics. , 2018, , 19-38.		0
530	A molecular atlas of cell types and zonation in the brain vasculature. <i>Nature</i> , 2018, 554, 475-480.	13.7	1,310

#	ARTICLE	IF	CITATIONS
531	Pan-Cancer Molecular Classes Transcending Tumor Lineage Across 32 Cancer Types, Multiple Data Platforms, and over 10,000 Cases. <i>Clinical Cancer Research</i> , 2018, 24, 2182-2193.	3.2	68
532	Transcriptional decomposition reveals active chromatin architectures and cell specific regulatory interactions. <i>Nature Communications</i> , 2018, 9, 487.	5.8	50
533	Lysyl Oxidases: Functions and Disorders. <i>Journal of Glaucoma</i> , 2018, 27, S15-S19.	0.8	27
534	ASSA: Fast identification of statistically significant interactions between long RNAs. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840001.	0.3	10
535	IW-Scoring: an Integrative Weighted Scoring framework for annotating and prioritizing genetic variations in the noncoding genome. <i>Nucleic Acids Research</i> , 2018, 46, e47-e47.	6.5	30
536	Making Use of Cancer Genomic Databases. <i>Current Protocols in Molecular Biology</i> , 2018, 121, 19.14.1-19.14.13.	2.9	13
537	Reduced <i>CDHR3</i> expression in children wheezing with rhinovirus. <i>Pediatric Allergy and Immunology</i> , 2018, 29, 200-206.	1.1	20
538	The complex genetics of human insulin-like growth factor 2 are not reflected in public databases. <i>Journal of Biological Chemistry</i> , 2018, 293, 4324-4333.	1.6	21
539	1700108J01Rik and 1700101O22Rik are mouse testis-specific long non-coding RNAs. <i>Histochemistry and Cell Biology</i> , 2018, 149, 517-527.	0.8	12
540	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. <i>Nucleic Acids Research</i> , 2018, 46, D260-D266.	6.5	1,232
541	Genome-wide association study of self-reported food reactions in Japanese identifies shrimp and peach specific loci in the HLA-DR/DQ gene region. <i>Scientific Reports</i> , 2018, 8, 1069.	1.6	29
542	Cancer transcriptome profiling at the juncture of clinical translation. <i>Nature Reviews Genetics</i> , 2018, 19, 93-109.	7.7	202
543	HOCOMOCO: towards a complete collection of transcription factor binding models for human and mouse via large-scale ChIP-Seq analysis. <i>Nucleic Acids Research</i> , 2018, 46, D252-D259.	6.5	660
544	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , 2018, 17, 308-325.	1.4	6
545	Palladin Is a Neuron-Specific Translational Target of mTOR Signaling That Regulates Axon Morphogenesis. <i>Journal of Neuroscience</i> , 2018, 38, 4985-4995.	1.7	13
546	Inferring a nonlinear biochemical network model from a heterogeneous single-cell time course data. <i>Scientific Reports</i> , 2018, 8, 6790.	1.6	13
547	Regressed but Not Gone: Patterns of Vision Gene Loss and Retention in Subterranean Mammals. <i>Integrative and Comparative Biology</i> , 2018, 58, 441-451.	0.9	22
548	Characterization of the enhancer and promoter landscape of inflammatory bowel disease from human colon biopsies. <i>Nature Communications</i> , 2018, 9, 1661.	5.8	78

#	ARTICLE	IF	CITATIONS
549	Characterization of the human RFX transcription factor family by regulatory and target gene analysis. <i>BMC Genomics</i> , 2018, 19, 181.	1.2	73
550	Towards a map of cis-regulatory sequences in the human genome. <i>Nucleic Acids Research</i> , 2018, 46, 5395-5409.	6.5	20
551	Functional domain analysis of SOX18 transcription factor using a single-chain variable fragment-based approach. <i>MAbs</i> , 2018, 10, 596-606.	2.6	7
552	Divergence of Noncoding Regulatory Elements Explains Geneâ€™Phenotype Differences between Human and Mouse Orthologous Genes. <i>Molecular Biology and Evolution</i> , 2018, 35, 1653-1667.	3.5	12
553	Transcriptional landscape of <i>Mycobacterium tuberculosis</i> infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758.	1.6	92
554	Sequential regulatory activity prediction across chromosomes with convolutional neural networks. <i>Genome Research</i> , 2018, 28, 739-750.	2.4	324
555	The role of CSF1R-dependent macrophages in control of the intestinal stem-cell niche. <i>Nature Communications</i> , 2018, 9, 1272.	5.8	155
556	GWIPS-viz: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D823-D830.	6.5	45
557	An analysis of anterior segment development in the chicken eye. <i>Mechanisms of Development</i> , 2018, 150, 42-49.	1.7	12
558	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. <i>Nucleic Acids Research</i> , 2018, 46, 582-592.	6.5	209
559	ZFR coordinates crosstalk between RNA decay and transcription in innate immunity. <i>Nature Communications</i> , 2018, 9, 1145.	5.8	36
560	Looking for Broken TAD Boundaries and Changes on DNA Interactions: Clinical Guide to 3D Chromatin Change Analysis in Complex Chromosomal Rearrangements and Chromothripsis. <i>Methods in Molecular Biology</i> , 2018, 1769, 353-361.	0.4	7
561	Evaluation of the Glypican 3 promoter for transcriptional targeting of hepatocellular carcinoma. <i>Gene Therapy</i> , 2018, 25, 115-128.	2.3	13
563	Complexities of post-transcriptional regulation and the modeling of ceRNA crosstalk. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2018, 53, 231-245.	2.3	175
564	SEASTAR: systematic evaluation of alternative transcription start sites in RNA. <i>Nucleic Acids Research</i> , 2018, 46, e45-e45.	6.5	17
565	The discovery potential of RNA processing profiles. <i>Nucleic Acids Research</i> , 2018, 46, e15-e15.	6.5	9
566	Evolution of Brain Active Gene Promoters in Human Lineage Towards the Increased Plasticity of Gene Regulation. <i>Molecular Neurobiology</i> , 2018, 55, 1871-1904.	1.9	12
567	HEDD: Human Enhancer Disease Database. <i>Nucleic Acids Research</i> , 2018, 46, D113-D120.	6.5	47

#	ARTICLE	IF	CITATIONS
568	Combinatorial genetics in liver repopulation and carcinogenesis with a in vivo CRISPR activation platform. <i>Hepatology</i> , 2018, 68, 663-676.	3.6	63
569	Furin deficiency in myeloid cells leads to attenuated revascularization in a mouse-model of oxygen-induced retinopathy. <i>Experimental Eye Research</i> , 2018, 166, 160-167.	1.2	14
570	TBX4 is involved in the super-enhancer-driven transcriptional programs underlying features specific to lung fibroblasts. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 314, L177-L191.	1.3	42
571	Allergic FcγRI and pseudoallergic MRGPRX2-triggered mast cell activation routes are independent and inversely regulated by SCF. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2018, 73, 256-260.	2.7	68
572	Protein kinase C-delta (PKCδ), a marker of inflammation and tuberculosis disease progression in humans, is important for optimal macrophage killing effector functions and survival in mice. <i>Mucosal Immunology</i> , 2018, 11, 496-511.	2.7	28
573	A review of structural brain abnormalities in Pallister-Killian syndrome. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 92-98.	0.6	14
574	Genomic structural variations lead to dysregulation of important coding and non-coding RNA species in dilated cardiomyopathy. <i>EMBO Molecular Medicine</i> , 2018, 10, 107-120.	3.3	43
575	Birth, coming of age and death: The intriguing life of long noncoding RNAs. <i>Seminars in Cell and Developmental Biology</i> , 2018, 79, 143-152.	2.3	15
576	RIKEN MetaDatabase. <i>International Journal on Semantic Web and Information Systems</i> , 2018, 14, 140-164.	2.2	10
577	Recent advances in functional genome analysis. <i>F1000Research</i> , 2018, 7, 1968.	0.8	16
578	SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , 2018, 28, 1943-1956.	2.4	33
579	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. <i>Nature Communications</i> , 2018, 9, 4568.	5.8	44
580	ChIP-Atlas: a data-mining suite powered by full integration of public ChIP-seq data. <i>EMBO Reports</i> , 2018, 19, .	2.0	544
581	Causal Transcription Regulatory Network Inference Using Enhancer Activity as a Causal Anchor. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3609.	1.8	5
582	Classifying human promoters by occupancy patterns identifies recurring sequence elements, combinatorial binding, and spatial interactions. <i>BMC Biology</i> , 2018, 16, 138.	1.7	9
583	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	13.7	224
584	Expression of murine muscle-enriched A-type lamin-interacting protein (MLIP) is regulated by tissue-specific alternative transcription start sites. <i>Journal of Biological Chemistry</i> , 2018, 293, 19761-19770.	1.6	9
585	An integrative approach for building personalized gene regulatory networks for precision medicine. <i>Genome Medicine</i> , 2018, 10, 96.	3.6	49

#	ARTICLE	IF	CITATIONS
586	Modelling of the breadth of expression from promoter architectures identifies pro-housekeeping transcription factors. <i>PLoS ONE</i> , 2018, 13, e0198961.	1.1	4
587	Optimized libraries for CRISPR-Cas9 genetic screens with multiple modalities. <i>Nature Communications</i> , 2018, 9, 5416.	5.8	535
588	The codon sequences predict protein lifetimes and other parameters of the protein life cycle in the mouse brain. <i>Scientific Reports</i> , 2018, 8, 16913.	1.6	17
589	The conservation landscape of the human ribosomal RNA gene repeats. <i>PLoS ONE</i> , 2018, 13, e0207531.	1.1	55
590	Predicting Enhancers from Multiple Cell Lines and Tissues across Different Developmental Stages Based On SVM Method. <i>Current Bioinformatics</i> , 2018, 13, 655-660.	0.7	30
591	Enhancer and super-enhancer: Positive regulators in gene transcription. <i>Animal Models and Experimental Medicine</i> , 2018, 1, 169-179.	1.3	49
592	Immune Cell Gene Signatures for Profiling the Microenvironment of Solid Tumors. <i>Cancer Immunology Research</i> , 2018, 6, 1388-1400.	1.6	169
593	Vimentin Diversity in Health and Disease. <i>Cells</i> , 2018, 7, 147.	1.8	192
594	DNA Motif Recognition Modeling from Protein Sequences. <i>IScience</i> , 2018, 7, 198-211.	1.9	7
595	Towards a Quantitative Understanding of Cell Identity. <i>Trends in Cell Biology</i> , 2018, 28, 1030-1048.	3.6	26
596	Carbonic anhydrase related protein expression in astrocytomas and oligodendroglial tumors. <i>BMC Cancer</i> , 2018, 18, 584.	1.1	13
597	Lipoteichoic acid anchor triggers Mincle to drive protective immunity against invasive group A <i>Streptococcus</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10662-E10671.	3.3	37
598	ADGRE1 (EMR1, F4/80) Is a Rapidly-Evolving Gene Expressed in Mammalian Monocyte-Macrophages. <i>Frontiers in Immunology</i> , 2018, 9, 2246.	2.2	149
599	Pan-Cancer Landscape of Aberrant DNA Methylation across Human Tumors. <i>Cell Reports</i> , 2018, 25, 1066-1080.e8.	2.9	239
600	Bioinformatics: Sequences, Structures, Phylogeny. , 2018, , .		0
601	Maximizing the Utility of Cancer Transcriptomic Data. <i>Trends in Cancer</i> , 2018, 4, 823-837.	3.8	32
602	Understanding Genomic Variations in the Context of Health and Disease: Annotation, Interpretation, and Challenges. , 2018, , 71-95.		0
603	Computational Epigenomics and Its Application in Regulatory Genomics. , 2018, , 115-139.		0

#	ARTICLE	IF	CITATIONS
604	Regulation of DNA Double-Strand Break Repair by Non-Coding RNAs. <i>Molecules</i> , 2018, 23, 2789.	1.7	64
605	Chromatin accessibility landscape of articular knee cartilage reveals aberrant enhancer regulation in osteoarthritis. <i>Scientific Reports</i> , 2018, 8, 15499.	1.6	37
606	Bi-allelic mutations in MYL1 cause a severe congenital myopathy. <i>Human Molecular Genetics</i> , 2018, 27, 4263-4272.	1.4	31
607	Inorganic Polyphosphate and Cancer. <i>Biochemistry (Moscow)</i> , 2018, 83, 961-968.	0.7	9
608	Overexpression of CLC-3 is regulated by XRCC5 and is a poor prognostic biomarker for gastric cancer. <i>Journal of Hematology and Oncology</i> , 2018, 11, 115.	6.9	29
609	Paired-cell sequencing enables spatial gene expression mapping of liver endothelial cells. <i>Nature Biotechnology</i> , 2018, 36, 962-970.	9.4	262
610	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1 β . <i>Scientific Reports</i> , 2018, 8, 13164.	1.6	10
611	Decoding the non-coding genome: Opportunities and challenges of genomic and epigenomic consortium data. <i>Current Opinion in Systems Biology</i> , 2018, 11, 82-90.	1.3	4
612	Selective Activation of Alternative MYC Core Promoters by Wnt-Responsive Enhancers. <i>Genes</i> , 2018, 9, 270.	1.0	1
613	The new world of RNA biomarkers and explorersâ€™ prudence rules. <i>International Journal of Biological Markers</i> , 2018, 33, 239-243.	0.7	0
614	Cap-Independent Translation: Whatâ€™s in a Name?. <i>Trends in Biochemical Sciences</i> , 2018, 43, 882-895.	3.7	77
615	The functions and unique features of long intergenic non-coding RNA. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 143-157.	16.1	968
616	An Evaluation of Function of Multicopy Noncoding RNAs in Mammals Using ENCODE/FANTOM Data and Comparative Genomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 1451-1462.	3.5	5
617	The Ensembl Genome Browser: Strategies for Accessing Eukaryotic Genome Data. <i>Methods in Molecular Biology</i> , 2018, 1757, 115-139.	0.4	13
618	SNPnexus: assessing the functional relevance of genetic variation to facilitate the promise of precision medicine. <i>Nucleic Acids Research</i> , 2018, 46, W109-W113.	6.5	163
619	Leveraging epigenomics and contactomics data to investigate SNP pairs in GWAS. <i>Human Genetics</i> , 2018, 137, 413-425.	1.8	8
620	Eukaryotic core promoters and the functional basis of transcription initiation. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 621-637.	16.1	480
621	Toward predictive R-loop computational biology: genome-scale prediction of R-loops reveals their association with complex promoter structures, G-quadruplexes and transcriptionally active enhancers. <i>Nucleic Acids Research</i> , 2018, 46, 7566-7585.	6.5	37

#	ARTICLE	IF	CITATIONS
622	Platforms for Investigating LncRNA Functions. <i>SLAS Technology</i> , 2018, 23, 493-506.	1.0	136
623	Emerging roles of long non-coding RNA in cancer. <i>Cancer Science</i> , 2018, 109, 2093-2100.	1.7	489
624	N-lysine acetyltransferase 10 (NAA10) in development: the role of NAA10. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-11.	3.2	15
625	CpG island composition differences are a source of gene expression noise indicative of promoter responsiveness. <i>Genome Biology</i> , 2018, 19, 81.	3.8	25
626	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. <i>Epigenetics</i> , 2018, 13, 410-431.	1.3	32
627	Combination of novel and public RNA-seq datasets to generate an mRNA expression atlas for the domestic chicken. <i>BMC Genomics</i> , 2018, 19, 594.	1.2	86
628	Human Enhancers Harboring Specific Sequence Composition, Activity, and Genome Organization Are Linked to the Immune Response. <i>Genetics</i> , 2018, 209, 1055-1071.	1.2	16
629	Genome-wide prediction of cis-regulatory regions using supervised deep learning methods. <i>BMC Bioinformatics</i> , 2018, 19, 202.	1.2	88
630	Genome-wide association study of developmental dysplasia of the hip identifies an association with GDF5. <i>Communications Biology</i> , 2018, 1, 56.	2.0	45
631	Intrachromosomal colocalization strengthens co-expression, co-modification and evolutionary conservation of neighboring genes. <i>BMC Genomics</i> , 2018, 19, 455.	1.2	18
632	Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. <i>Nature Genetics</i> , 2018, 50, 1171-1179.	9.4	375
633	Application of High-Throughput Technologies in Personal Genomics: How Is the Progress in Personal Genome Service?. <i>Respiratory Disease Series</i> , 2018, , 319-331.	0.1	0
634	Strategies to Annotate and Characterize Long Noncoding RNAs: Advantages and Pitfalls. <i>Trends in Genetics</i> , 2018, 34, 704-721.	2.9	86
635	Conflicts of CpG density and DNA methylation are proximally and distally involved in gene regulation in human and mouse tissues. <i>Epigenetics</i> , 2018, 13, 721-741.	1.3	8
636	Oral Prion Neuroinvasion Occurs Independently of PrP ^C Expression in the Gut Epithelium. <i>Journal of Virology</i> , 2018, 92, .	1.5	7
637	Deciphering the roles of lncRNAs in breast development and disease. <i>Oncotarget</i> , 2018, 9, 20179-20212.	0.8	42
638	Distinct core promoter codes drive transcription initiation at key developmental transitions in a marine chordate. <i>BMC Genomics</i> , 2018, 19, 164.	1.2	14
639	Weak sharing of genetic association signals in three lung cancer subtypes: evidence at the SNP, gene, regulation, and pathway levels. <i>Genome Medicine</i> , 2018, 10, 16.	3.6	32

#	ARTICLE	IF	CITATIONS
640	Whole-transcriptome splicing profiling of E7.5 mouse primary germ layers reveals frequent alternative promoter usage during mouse early embryogenesis. <i>Biology Open</i> , 2018, 7, .	0.6	6
641	An integrative functional genomics framework for effective identification of novel regulatory variants in genome-wide phenome studies. <i>Genome Medicine</i> , 2018, 10, 7.	3.6	29
642	TrawlerWeb: an online de novo motif discovery tool for next-generation sequencing datasets. <i>BMC Genomics</i> , 2018, 19, 238.	1.2	12
643	Automated transition analysis of activated gene regulation during diauxic nutrient shift in <i>Escherichia coli</i> and adipocyte differentiation in mouse cells. <i>BMC Bioinformatics</i> , 2018, 19, 89.	1.2	0
644	Creating Transparent and Reproducible Pipelines: Best Practices for Tools, Data, and Workflow Management Systems. , 2018, , 15-43.		1
645	Early hematopoietic and vascular development in the chick. <i>International Journal of Developmental Biology</i> , 2018, 62, 137-144.	0.3	10
646	A comprehensive analysis of <i>SNCA</i> -related genetic risk in sporadic parkinson disease. <i>Annals of Neurology</i> , 2018, 84, 117-129.	2.8	50
647	Identification of novel <i>GLI1</i> target genes and regulatory circuits in human cancer cells. <i>Molecular Oncology</i> , 2018, 12, 1718-1734.	2.1	30
648	Patterns and mechanisms of structural variations in human cancer. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-11.	3.2	73
649	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	5.8	85
650	<i>MRGPR2</i> is negatively targeted by <i>SCF</i> and <i>IL4</i> to diminish pseudo-allergic stimulation of skin mast cells in culture. <i>Experimental Dermatology</i> , 2018, 27, 1298-1303.	1.4	29
651	Evolutionary stability of topologically associating domains is associated with conserved gene regulation. <i>BMC Biology</i> , 2018, 16, 87.	1.7	119
652	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. <i>Scientific Reports</i> , 2018, 8, 11635.	1.6	30
653	Comprehensive comparative analysis of 5'-end RNA-sequencing methods. <i>Nature Methods</i> , 2018, 15, 505-511.	9.0	90
654	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , 2018, 46, 5950-5966.	6.5	101
655	Cas9-mediated excision of proximal DNaseI/H3K4me3 signatures confers robust silencing of microRNA and long non-coding RNA genes. <i>PLoS ONE</i> , 2018, 13, e0193066.	1.1	20
656	Whole Exome Sequencing of Patients from Multicase Families with Systemic Lupus Erythematosus Identifies Multiple Rare Variants. <i>Scientific Reports</i> , 2018, 8, 8775.	1.6	32
657	Genome-wide association study in Japanese females identifies fifteen novel skin-related trait associations. <i>Scientific Reports</i> , 2018, 8, 8974.	1.6	59

#	ARTICLE	IF	CITATIONS
658	Long Noncoding RNAs in the Immune Response. , 2018, , 107-131.		0
659	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
660	Integrative Analysis of Multi-Omics Data. , 2019, , 194-199.		1
661	Genome-Wide Scanning of Gene Expression. , 2019, , 452-462.		0
662	Regulatory variants: from detection to predicting impact. Briefings in Bioinformatics, 2019, 20, 1639-1654.	3.2	82
663	Multiparametric slice culture platform for the investigation of human cardiac tissue physiology. Progress in Biophysics and Molecular Biology, 2019, 144, 139-150.	1.4	28
664	Genome Informatics. , 2019, , 178-194.		0
665	New MiniPromoter Ple345 (<i>NEFL</i>) Drives Strong and Specific Expression in Retinal Ganglion Cells of Mouse and Primate Retina. Human Gene Therapy, 2019, 30, 257-272.	1.4	21
666	Thymic Stromal Lymphopoietin Interferes with the Apoptosis of Human Skin Mast Cells by a Dual Strategy Involving STAT5/Mcl-1 and JNK/Bcl-xL. Cells, 2019, 8, 829.	1.8	24
667	Whole genome and transcriptome sequencing of post-mortem cardiac tissues from sudden cardiac death victims identifies a gene regulatory variant in NEXN. International Journal of Legal Medicine, 2019, 133, 1699-1709.	1.2	23
668	Genetic Variation in Long-Range Enhancers. Current Topics in Behavioral Neurosciences, 2019, 42, 35-50.	0.8	2
669	Transcriptional Profiling of Stem Cells: Moving from Descriptive to Predictive Paradigms. Stem Cell Reports, 2019, 13, 237-246.	2.3	9
670	RNA sequencing: the teenage years. Nature Reviews Genetics, 2019, 20, 631-656.	7.7	1,192
671	Combinatorial perturbation analysis reveals divergent regulations of mesenchymal genes during epithelial-to-mesenchymal transition. Npj Systems Biology and Applications, 2019, 5, 21.	1.4	65
672	Getting the Entire Message: Progress in Isoform Sequencing. Frontiers in Genetics, 2019, 10, 709.	1.1	39
673	Computational Biology Solutions to Identify Enhancers-target Gene Pairs. Computational and Structural Biotechnology Journal, 2019, 17, 821-831.	1.9	29
674	Estimating dispensable content in the human interactome. Nature Communications, 2019, 10, 3205.	5.8	9
675	Open chromatin landscape of rat microglia upon proinvasive or inflammatory polarization. Glia, 2019, 67, 2312-2328.	2.5	8

#	ARTICLE	IF	CITATIONS
676	Networks of mRNA Processing and Alternative Splicing Regulation in Health and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1157, 1-27.	0.8	9
677	An integrative genomic analysis of the Longshanks selection experiment for longer limbs in mice. <i>ELife</i> , 2019, 8, .	2.8	58
678	The Magnitude of IFN- β Responses Is Fine-Tuned by DNA Architecture and the Non-coding Transcript of <i>lfn3-as1</i> . <i>Molecular Cell</i> , 2019, 75, 1229-1242.e5.	4.5	58
679	Single-Cell Transcriptomics Reveals Spatial and Temporal Turnover of Keratinocyte Differentiation Regulators. <i>Frontiers in Genetics</i> , 2019, 10, 775.	1.1	45
680	<i>PTBP1</i> mRNA isoforms and regulation of their translation. <i>Rna</i> , 2019, 25, 1324-1336.	1.6	24
681	LINE-1 Evasion of Epigenetic Repression in Humans. <i>Molecular Cell</i> , 2019, 75, 590-604.e12.	4.5	106
682	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. <i>Scientific Reports</i> , 2019, 9, 9511.	1.6	24
683	Transcription Start Site Mapping Using Super-low Input Carrier-CAGE. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	5
684	RegulationSpotter: annotation and interpretation of extratranscriptic DNA variants. <i>Nucleic Acids Research</i> , 2019, 47, W106-W113.	6.5	17
685	mountainClimber Identifies Alternative Transcription Start and Polyadenylation Sites in RNA-Seq. <i>Cell Systems</i> , 2019, 9, 393-400.e6.	2.9	15
686	CAGEfightR: analysis of 5'-end data using R/Bioconductor. <i>BMC Bioinformatics</i> , 2019, 20, 487.	1.2	59
687	Interconnection of Biological Knowledge Using NIKKajiRDF and Interlinking Ontology for Biological Concepts. <i>New Generation Computing</i> , 2019, 37, 525-549.	2.5	5
688	Sufu- and Spop-mediated downregulation of Hedgehog signaling promotes beta cell differentiation through organ-specific niche signals. <i>Nature Communications</i> , 2019, 10, 4647.	5.8	35
689	A nucleotide resolution map of Top2-linked DNA breaks in the yeast and human genome. <i>Nature Communications</i> , 2019, 10, 4846.	5.8	64
690	Signatures of Recent Positive Selection in Enhancers Across 41 Human Tissues. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2761-2774.	0.8	18
691	Generation of a Nebulizable CDR-Modified MERS-CoV Neutralizing Human Antibody. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5073.	1.8	8
692	The Many Faces of Emerging and Reemerging Infectious Disease. <i>Epidemiologic Reviews</i> , 2019, 41, 1-5.	1.3	5
693	EPD in 2020: enhanced data visualization and extension to ncRNA promoters. <i>Nucleic Acids Research</i> , 2020, 48, D65-D69.	6.5	26

#	ARTICLE	IF	CITATIONS
694	CASPR, an analysis pipeline for single and paired guide RNA CRISPR screens, reveals optimal target selection for long non-coding RNAs. <i>Bioinformatics</i> , 2020, 36, 1673-1680.	1.8	12
695	Regulation of CHD2 expression by the Chaserr long noncoding RNA gene is essential for viability. <i>Nature Communications</i> , 2019, 10, 5092.	5.8	71
696	Use of circulating nucleic acids, metabolites, and proteins as clinical biomarkers for earlier prognosis and diagnosis of disease. , 2019, , 85-116.		2
697	Direct prediction of regulatory elements from partial data without imputation. <i>PLoS Computational Biology</i> , 2019, 15, e1007399.	1.5	13
698	CAUSALdb: a database for disease/trait causal variants identified using summary statistics of genome-wide association studies. <i>Nucleic Acids Research</i> , 2019, 48, D807-D816.	6.5	34
699	Long Read Single-Molecule Real-Time Sequencing Elucidates Transcriptome-Wide Heterogeneity and Complexity in Esophageal Squamous Cells. <i>Frontiers in Genetics</i> , 2019, 10, 915.	1.1	12
700	Inference of genetic networks using random forests: Assigning different weights for gene expression data. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1950015.	0.3	12
701	Molecular Portraits of Early Rheumatoid Arthritis Identify Clinical and Treatment Response Phenotypes. <i>Cell Reports</i> , 2019, 28, 2455-2470.e5.	2.9	241
702	Functional Genomics and CRISPR Applied to Cardiovascular Research and Medicine. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, e188-e194.	1.1	7
703	Non-coding RNAs in cardiovascular cell biology and atherosclerosis. <i>Cardiovascular Research</i> , 2019, 115, 1732-1756.	1.8	138
704	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019, 178, 1465-1477.e17.	13.5	144
705	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379.	9.4	72
706	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. <i>Developmental Cell</i> , 2019, 51, 21-34.e5.	3.1	26
707	The Cancer-Associated Genetic Variant Rs3903072 Modulates Immune Cells in the Tumor Microenvironment. <i>Frontiers in Genetics</i> , 2019, 10, 754.	1.1	21
708	An integrated genome-wide multi-omics analysis of gene expression dynamics in the preimplantation mouse embryo. <i>Scientific Reports</i> , 2019, 9, 13356.	1.6	39
709	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019, 20, 718.	1.2	11
710	Druggable Transcriptional Networks in the Human Neurogenic Epigenome. <i>Pharmacological Reviews</i> , 2019, 71, 520-538.	7.1	11
711	Inferring the Molecular Mechanisms of Noncoding Alzheimer's Disease-Associated Genetic Variants. <i>Journal of Alzheimer's Disease</i> , 2019, 72, 301-318.	1.2	19

#	ARTICLE	IF	CITATIONS
712	SINEUP non-coding RNAs rescue defective frataxin expression and activity in a cellular model of Friedreich's Ataxia. <i>Nucleic Acids Research</i> , 2019, 47, 10728-10743.	6.5	30
713	The RNA-binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs. <i>FASEB Journal</i> , 2019, 33, 13572-13589.	0.2	20
714	LTR retroelement expansion of the human cancer transcriptome and immunopeptidome revealed by de novo transcript assembly. <i>Genome Research</i> , 2019, 29, 1578-1590.	2.4	66
715	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019, 10, 360.	5.8	102
716	High-throughput functional analysis of lncRNA core promoters elucidates rules governing tissue specificity. <i>Genome Research</i> , 2019, 29, 344-355.	2.4	100
717	Stems cells, big data and compendium-based analyses for identifying cell types, signalling pathways and gene regulatory networks. <i>Biophysical Reviews</i> , 2019, 11, 41-50.	1.5	7
718	Arginine to Glutamine Variant in Olfactomedin Like 3 (<i>OLFML3</i>) Is a Candidate for Severe Goniodysgenesis and Glaucoma in the Border Collie Dog Breed. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 943-954.	0.8	11
719	Characterization of Glucose Transporter 6 in Lipopolysaccharide-Induced Bone Marrow-Derived Macrophage Function. <i>Journal of Immunology</i> , 2019, 202, 1826-1832.	0.4	30
720	Translation of Human β -Actin mRNA is Regulated by mTOR Pathway. <i>Genes</i> , 2019, 10, 96.	1.0	15
721	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. <i>Nucleic Acids Research</i> , 2019, 47, 1671-1691.	6.5	34
722	CG dinucleotides enhance promoter activity independent of DNA methylation. <i>Genome Research</i> , 2019, 29, 554-563.	2.4	49
723	Sequence Characteristics Distinguish Transcribed Enhancers from Promoters and Predict Their Breadth of Activity. <i>Genetics</i> , 2019, 211, 1205-1217.	1.2	10
724	CpG traffic lights are markers of regulatory regions in human genome. <i>BMC Genomics</i> , 2019, 20, 102.	1.2	43
725	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. <i>Nature Genetics</i> , 2019, 51, 973-980.	9.4	216
726	The immune cell landscape in kidneys of patients with lupus nephritis. <i>Nature Immunology</i> , 2019, 20, 902-914.	7.0	501
727	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. <i>Journal of Molecular Biology</i> , 2019, 431, 2407-2422.	2.0	72
728	Functional genomics in cancer immunotherapy: computational approaches for biomarker and drug discovery. <i>Molecular Systems Design and Engineering</i> , 2019, 4, 689-700.	1.7	3
729	lncRRlsearch: A Web Server for lncRNA-RNA Interaction Prediction Integrated With Tissue-Specific Expression and Subcellular Localization Data. <i>Frontiers in Genetics</i> , 2019, 10, 462.	1.1	86

#	ARTICLE	IF	CITATIONS
730	Dynamic UTR Usage Regulates Alternative Translation to Modulate Gap Junction Formation during Stress and Aging. <i>Cell Reports</i> , 2019, 27, 2737-2747.e5.	2.9	22
731	A comparison of two workflows for regulome and transcriptome-based prioritization of genetic variants associated with myocardial mass. <i>Genetic Epidemiology</i> , 2019, 43, 717-726.	0.6	1
732	YeastTSS: an integrative web database of yeast transcription start sites. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	34
733	Multi-Color Single-Molecule Imaging Uncovers Extensive Heterogeneity in mRNA Decoding. <i>Cell</i> , 2019, 178, 458-472.e19.	13.5	120
734	Pan-Cancer analysis of the expression and regulation of matrisome genes across 32 tumor types. <i>Matrix Biology Plus</i> , 2019, 1, 100004.	1.9	38
735	IRF2 transcriptionally induces <i>GSDMD</i> expression for pyroptosis. <i>Science Signaling</i> , 2019, 12, .	1.6	120
736	HOT or not: examining the basis of high-occupancy target regions. <i>Nucleic Acids Research</i> , 2019, 47, 5735-5745.	6.5	41
737	Characterising the genetic basis of immune response variation to identify causal mechanisms underlying disease susceptibility. <i>Hla</i> , 2019, 94, 275-284.	0.4	5
738	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. <i>Frontiers in Genetics</i> , 2019, 10, 309.	1.1	28
739	Molecular Interaction Networks to Select Factors for Cell Conversion. <i>Methods in Molecular Biology</i> , 2019, 1975, 333-361.	0.4	2
740	Expression of endogenous retroviruses reflects increased usage of atypical enhancers in T cells. <i>EMBO Journal</i> , 2019, 38, .	3.5	15
741	Retrospective analysis of model-based predictivity of human pharmacokinetics for anti-IL-36R monoclonal antibody MAB92 using a rat anti-mouse IL-36R monoclonal antibody and RNA expression data (FANTOM5). <i>MAbs</i> , 2019, 11, 956-964.	2.6	7
742	Associations between Maternal Tobacco Smoke Exposure and the Cord Blood CD4+ DNA Methylome. <i>Environmental Health Perspectives</i> , 2019, 127, 47009.	2.8	13
743	Computational Methods for Mapping, Assembly and Quantification for Coding and Non-coding Transcripts. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 628-637.	1.9	25
744	Lysine demethylases KDM6A and UTY: The X and Y of histone demethylation. <i>Molecular Genetics and Metabolism</i> , 2019, 127, 31-44.	0.5	44
745	Transcriptional cofactors display specificity for distinct types of core promoters. <i>Nature</i> , 2019, 570, 122-126.	13.7	112
746	Pervasive and dynamic transcription initiation in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2019, 29, 1198-1210.	2.4	53
747	Endogenous APOBEC3B Overexpression Constitutively Generates DNA Substitutions and Deletions in Myeloma Cells. <i>Scientific Reports</i> , 2019, 9, 7122.	1.6	28

#	ARTICLE	IF	CITATIONS
748	LINC01420 RNA structure and influence on cell physiology. <i>BMC Genomics</i> , 2019, 20, 298.	1.2	9
749	Accurate differential analysis of transcription factor activity from gene expression. <i>Bioinformatics</i> , 2019, 35, 5018-5029.	1.8	3
750	Improved Prediction of Regulatory Element Using Hybrid Abelian Complexity Features with DNA Sequences. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1704.	1.8	5
751	Yin-Yang of IL-33 in Human Skin Mast Cells: Reduced Degranulation, but Augmented Histamine Synthesis through p38 Activation. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1516-1525.e3.	0.3	39
752	Evidence that alternative transcriptional initiation is largely nonadaptive. <i>PLoS Biology</i> , 2019, 17, e3000197.	2.6	46
753	IsoformSwitchAnalyzeR: analysis of changes in genome-wide patterns of alternative splicing and its functional consequences. <i>Bioinformatics</i> , 2019, 35, 4469-4471.	1.8	189
754	Development of a high efficient promoter finding method based on transient transfection. <i>Gene: X</i> , 2019, 2, 100008.	2.3	3
755	Selective translational usage of TSS and core promoters revealed by translome sequencing. <i>BMC Genomics</i> , 2019, 20, 282.	1.2	10
756	Subtype classification and functional annotation of L1Md retrotransposon promoters. <i>Mobile DNA</i> , 2019, 10, 14.	1.3	18
757	OVOL2 induces mesenchymal-to-epithelial transition in fibroblasts and enhances cell-state reprogramming towards epithelial lineages. <i>Scientific Reports</i> , 2019, 9, 6490.	1.6	38
758	scMatch: a single-cell gene expression profile annotation tool using reference datasets. <i>Bioinformatics</i> , 2019, 35, 4688-4695.	1.8	108
759	Optimized protocol for the hepatic differentiation of induced pluripotent stem cells in a fluidic microenvironment. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1762-1776.	1.7	27
760	Functional characterization of the C7ORF76 genomic region, a prominent GWAS signal for osteoporosis in 7q21.3. <i>Bone</i> , 2019, 123, 39-47.	1.4	12
761	Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. <i>EBioMedicine</i> , 2019, 41, 427-442.	2.7	26
762	CellSim: a novel software to calculate cell similarity and identify their co-regulation networks. <i>BMC Bioinformatics</i> , 2019, 20, 111.	1.2	3
763	Myoglobinopathy is an adult-onset autosomal dominant myopathy with characteristic sarcoplasmic inclusions. <i>Nature Communications</i> , 2019, 10, 1396.	5.8	11
764	Exomic and transcriptomic alterations of hereditary gingival fibromatosis. <i>Oral Diseases</i> , 2019, 25, 1374-1383.	1.5	6
765	Magic roundabout is an endothelial-specific ohnolog of ROBO1 which neo-functionalized to an essential new role in angiogenesis. <i>PLoS ONE</i> , 2019, 14, e0208952.	1.1	7

#	ARTICLE	IF	CITATIONS
766	Hypoxia induces rapid changes to histone methylation and reprograms chromatin. <i>Science</i> , 2019, 363, 1222-1226.	6.0	266
767	Platelet Genomics. , 2019, , 99-126.		0
768	Breast cancer quantitative proteome and proteogenomic landscape. <i>Nature Communications</i> , 2019, 10, 1600.	5.8	152
769	Multi-year whole-blood transcriptome data for the study of onset and progression of Parkinson's Disease. <i>Scientific Data</i> , 2019, 6, 20.	2.4	8
770	FVIII expression by its native promoter sustains long-term correction avoiding immune response in hemophilic mice. <i>Blood Advances</i> , 2019, 3, 825-838.	2.5	24
771	Promoter-Intrinsic and Local Chromatin Features Determine Gene Repression in LADs. <i>Cell</i> , 2019, 177, 852-864.e14.	13.5	108
772	Transposable elements drive widespread expression of oncogenes in human cancers. <i>Nature Genetics</i> , 2019, 51, 611-617.	9.4	253
773	SSS-test: a novel test for detecting positive selection on RNA secondary structure. <i>BMC Bioinformatics</i> , 2019, 20, 151.	1.2	12
774	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. <i>Scientific Reports</i> , 2019, 9, 5685.	1.6	14
775	Using mouse genetics to understand human skeletal disease. <i>Bone</i> , 2019, 126, 27-36.	1.4	5
776	Probing transcription factor combinatorics in different promoter classes and in enhancers. <i>BMC Genomics</i> , 2019, 20, 103.	1.2	27
777	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. <i>Translational Psychiatry</i> , 2019, 9, 77.	2.4	82
778	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells. <i>ELife</i> , 2019, 8, .	2.8	32
779	Hacking the Cancer Genome: Profiling Therapeutically Actionable Long Non-coding RNAs Using CRISPR-Cas9 Screening. <i>Cancer Cell</i> , 2019, 35, 545-557.	7.7	163
780	Revealing the alternative promoter usage of SAF/MAZ gene by bichromatic fluorescent reporter construct. <i>Bioscience Reports</i> , 2019, 39, .	1.1	2
781	Integrated Functional Genomic Analysis Enables Annotation of Kidney Genome-Wide Association Study Loci. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 421-441.	3.0	27
782	HERES, a lincRNA that regulates canonical and noncanonical Wnt signaling pathways via interaction with EZH2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24620-24629.	3.3	45
783	Draft genome assembly of <i>Tenualosa ilisha</i> , Hilsa shad, provides resource for osmoregulation studies. <i>Scientific Reports</i> , 2019, 9, 16511.	1.6	23

#	ARTICLE	IF	CITATIONS
784	Testicular expression of long non-coding RNAs is affected by curative GnRHa treatment of cryptorchidism. <i>Basic and Clinical Andrology</i> , 2019, 29, 18.	0.8	12
785	Insights into malaria susceptibility using genome-wide data on 17,000 individuals from Africa, Asia and Oceania. <i>Nature Communications</i> , 2019, 10, 5732.	5.8	126
786	A framework for identification of on- and off-target transcriptional responses to drug treatment. <i>Scientific Reports</i> , 2019, 9, 17603.	1.6	29
787	Personalised analytics for rare disease diagnostics. <i>Nature Communications</i> , 2019, 10, 5274.	5.8	15
788	Dynamic Assembly of Human Salivary Stem/Progenitor Microstructures Requires Coordinated β 1 Integrin-Mediated Motility. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 224.	1.8	14
789	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	2.4	52
790	Multivariable regulation of gene expression plasticity in metazoans. <i>Open Biology</i> , 2019, 9, 190150.	1.5	11
791	Gene expression models based on transcription factor binding events confer insight into functional cis-regulatory variants. <i>Bioinformatics</i> , 2019, 35, 2610-2617.	1.8	19
792	CNOT3 targets negative cell cycle regulators in non-small cell lung cancer development. <i>Oncogene</i> , 2019, 38, 2580-2594.	2.6	19
793	Temporal enhancer profiling of parallel lineages identifies AHR and GLIS1 as regulators of mesenchymal multipotency. <i>Nucleic Acids Research</i> , 2019, 47, 1141-1163.	6.5	16
794	Ras regulates vascular permeability, but not overall healing in skin wounds. <i>Experimental Dermatology</i> , 2019, 28, 202-206.	1.4	8
795	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758.	6.5	172
796	A neuronal enhancer network upstream of MEF2C is compromised in patients with Rett-like characteristics. <i>Human Molecular Genetics</i> , 2019, 28, 818-827.	1.4	14
797	Assembly of a parts list of the human mitotic cell cycle machinery. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 703-718.	1.5	80
798	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019, 56, 5392-5415.	1.9	29
799	Hybrid sequencing-based personal full-length transcriptomic analysis implicates proteostatic stress in metastatic ovarian cancer. <i>Oncogene</i> , 2019, 38, 3047-3060.	2.6	6
800	Atypical nested 22q11.2 duplications between LCR22B and LCR22D are associated with neurodevelopmental phenotypes including autism spectrum disorder with incomplete penetrance. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00507.	0.6	26
801	TransmiR v2.0: an updated transcription factor-microRNA regulation database. <i>Nucleic Acids Research</i> , 2019, 47, D253-D258.	6.5	243

#	ARTICLE	IF	CITATIONS
802	SEdb: a comprehensive human super-enhancer database. <i>Nucleic Acids Research</i> , 2019, 47, D235-D243.	6.5	166
803	Mouse Genome Database (MGD) 2019. <i>Nucleic Acids Research</i> , 2019, 47, D801-D806.	6.5	625
804	How many cadherins do human endothelial cells express?. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 1299-1317.	2.4	24
805	Understanding Specialized Ribosomal Protein Functions and Associated Ribosomopathies by Navigating Across Sequence, Literature, and Phenotype Information Resources. , 2019, , 35-51.		6
806	<i>De novo</i> pattern discovery enables robust assessment of functional consequences of non-coding variants. <i>Bioinformatics</i> , 2019, 35, 1453-1460.	1.8	15
807	A Fast Exact Functional Test for Directional Association and Cancer Biology Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 818-826.	1.9	20
808	Prediction of lncRNAs and their interactions with nucleic acids: benchmarking bioinformatics tools. <i>Briefings in Bioinformatics</i> , 2019, 20, 551-564.	3.2	47
809	An integrative analysis of non-coding regulatory DNA variations associated with autism spectrum disorder. <i>Molecular Psychiatry</i> , 2019, 24, 1707-1719.	4.1	59
810	Translational bioinformatics in mental health: open access data sources and computational biomarker discovery. <i>Briefings in Bioinformatics</i> , 2019, 20, 842-856.	3.2	16
811	Shaping the nebulous enhancer in the era of high-throughput assays and genome editing. <i>Briefings in Bioinformatics</i> , 2020, 21, 836-850.	3.2	4
812	Determinants of enhancer and promoter activities of regulatory elements. <i>Nature Reviews Genetics</i> , 2020, 21, 71-87.	7.7	464
813	QTLbase: an integrative resource for quantitative trait loci across multiple human molecular phenotypes. <i>Nucleic Acids Research</i> , 2020, 48, D983-D991.	6.5	82
814	The Landscape of Circular RNA Expression in the Human Brain. <i>Biological Psychiatry</i> , 2020, 87, 294-304.	0.7	57
815	Phenotypic impacts of CSF1R deficiencies in humans and model organisms. <i>Journal of Leukocyte Biology</i> , 2020, 107, 205-219.	1.5	97
816	Synaptic Dysfunction in Human Neurons With Autism-Associated Deletions in PTCHD1-AS. <i>Biological Psychiatry</i> , 2020, 87, 139-149.	0.7	57
817	SINEUP Non-coding RNA Targeting GDNF Rescues Motor Deficits and Neurodegeneration in a Mouse Model of Parkinson's Disease. <i>Molecular Therapy</i> , 2020, 28, 642-652.	3.7	41
818	The how and why of lncRNA function: An innate immune perspective. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194419.	0.9	196
819	Epithelial Expression of YAP and TAZ Is Sequentially Required in Lung Development. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020, 62, 256-266.	1.4	40

#	ARTICLE	IF	CITATIONS
820	Hypoxia drives glucose transporter 3 expression through hypoxia-inducible transcription factor (HIF)-mediated induction of the long noncoding RNA NIC1. <i>Journal of Biological Chemistry</i> , 2020, 295, 4065-4078.	1.6	34
821	Erythema migrans: the cutaneous manifestation of Lyme disease. <i>QJM - Monthly Journal of the Association of Physicians</i> , 2020, 113, 580-580.	0.2	0
822	Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. <i>Nature Communications</i> , 2020, 11, 168.	5.8	37
823	A human minisatellite hosts an alternative transcription start site for NPRL3 driving its expression in a repeat number-dependent manner. <i>Human Mutation</i> , 2020, 41, 807-824.	1.1	6
824	From genome-wide association studies to rational drug target prioritisation in inflammatory arthritis. <i>Lancet Rheumatology</i> , The, 2020, 2, e50-e62.	2.2	17
825	Regulation and function of macrophage colony-stimulating factor (CSF1) in the chicken immune system. <i>Developmental and Comparative Immunology</i> , 2020, 105, 103586.	1.0	25
826	Tyrosine kinase inhibitor imatinib augments tumor immunity by depleting effector regulatory T cells. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	58
827	A regulatory role for CHD2 in myelopoiesis. <i>Epigenetics</i> , 2020, 15, 702-714.	1.3	6
828	B Cell Synovitis and Clinical Phenotypes in Rheumatoid Arthritis: Relationship to Disease Stages and Drug Exposure. <i>Arthritis and Rheumatology</i> , 2020, 72, 714-725.	2.9	33
829	Minor C allele of the SNP rs7873784 associated with rheumatoid arthritis and type-2 diabetes mellitus binds PU.1 and enhances TLR4 expression.. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165626.	1.8	15
830	Network Inference Analysis Identifies SETDB1 as a Key Regulator for Reverting Colorectal Cancer Cells into Differentiated Normal-Like Cells. <i>Molecular Cancer Research</i> , 2020, 18, 118-129.	1.5	23
831	Stable gene expression for normalisation and single-sample scoring. <i>Nucleic Acids Research</i> , 2020, 48, e113-e113.	6.5	34
832	Altered Enhancer and Promoter Usage Leads to Differential Gene Expression in the Normal and Failed Human Heart. <i>Circulation: Heart Failure</i> , 2020, 13, e006926.	1.6	10
833	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. <i>Scientific Data</i> , 2020, 7, 326.	2.4	40
834	Interleukin-11 is important for vascular smooth muscle phenotypic switching and aortic inflammation, fibrosis and remodeling in mouse models. <i>Scientific Reports</i> , 2020, 10, 17853.	1.6	43
835	Disease-Specific Autoantibodies Induce Trained Immunity in RA Synovial Tissues and Its Gene Signature Correlates with the Response to Clinical Therapy. <i>Mediators of Inflammation</i> , 2020, 2020, 1-14.	1.4	3
836	Network analysis of transcriptomic diversity amongst resident tissue macrophages and dendritic cells in the mouse mononuclear phagocyte system. <i>PLoS Biology</i> , 2020, 18, e3000859.	2.6	94
837	Expression and Clinicopathological Significances of lncRNAs: Could ARA and ZEB2NAT be the Potential Breast Cancer-Related Biomarkers?. <i>Archives of Medical Research</i> , 2020, 51, 851-859.	1.5	2

#	ARTICLE	IF	CITATIONS
838	EpiMogrify Models H3K4me3 Data to Identify Signaling Molecules that Improve Cell Fate Control and Maintenance. <i>Cell Systems</i> , 2020, 11, 509-522.e10.	2.9	10
839	An era of single-cell genomics consortia. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1409-1418.	3.2	12
840	Identification of ribavirin-responsive cis-elements for GPAM suppression in the GPAM genome. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 148-154.	1.0	0
841	Cross-species regulatory sequence activity prediction. <i>PLoS Computational Biology</i> , 2020, 16, e1008050.	1.5	116
842	Ancestrally Duplicated Conserved Noncoding Element Suggests Dual Regulatory Roles of HOTAIR in cis and trans. <i>IScience</i> , 2020, 23, 101008.	1.9	9
843	Gene expression and <i>in situ</i> protein profiling of candidate SARS-CoV-2 receptors in human airway epithelial cells and lung tissue. <i>European Respiratory Journal</i> , 2020, 56, 2001123.	3.1	138
844	TALC: Transcript-level Aware Long-read Correction. <i>Bioinformatics</i> , 2020, 36, 5000-5006.	1.8	14
845	A holistic view of mouse enhancer architectures reveals analogous pleiotropic effects and correlation with human disease. <i>BMC Genomics</i> , 2020, 21, 754.	1.2	3
846	Global Analysis of Transcription Start Sites in the New Ovine Reference Genome (Oar rambouillet) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	21
847	Highly diversified core promoters in the human genome and their effects on gene expression and disease predisposition. <i>BMC Genomics</i> , 2020, 21, 842.	1.2	3
848	Robustness and lethality in multilayer biological molecular networks. <i>Nature Communications</i> , 2020, 11, 6043.	5.8	61
849	Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. <i>Cell Systems</i> , 2020, 11, 625-639.e13.	2.9	31
850	Epigenome engineering: new technologies for precision medicine. <i>Nucleic Acids Research</i> , 2020, 48, 12453-12482.	6.5	34
851	Mitochondrial stress and GDF15 in the pathophysiology of sepsis. <i>Archives of Biochemistry and Biophysics</i> , 2020, 696, 108668.	1.4	22
852	Single-cell analysis uncovers fibroblast heterogeneity and criteria for fibroblast and mural cell identification and discrimination. <i>Nature Communications</i> , 2020, 11, 3953.	5.8	316
853	A Contemporary Message from Mendel's Logical Empiricism. <i>BioEssays</i> , 2020, 42, e2000120.	1.2	5
854	Fetal HLA-G mediated immune tolerance and interferon response in preeclampsia. <i>EBioMedicine</i> , 2020, 59, 102872.	2.7	25
855	The intersectional genetics landscape for humans. <i>GigaScience</i> , 2020, 9, .	3.3	1

#	ARTICLE	IF	CITATIONS
856	Exploring the possibility of predicting human head hair greying from DNA using whole-exome and targeted NGS data. <i>BMC Genomics</i> , 2020, 21, 538.	1.2	20
857	The RNA-binding protein SERBP1 functions as a novel oncogenic factor in glioblastoma by bridging cancer metabolism and epigenetic regulation. <i>Genome Biology</i> , 2020, 21, 195.	3.8	55
858	Fractional diffusion on the human proteome as an alternative to the multi-organ damage of SARS-CoV-2. <i>Chaos</i> , 2020, 30, 081104.	1.0	14
859	Expression of Calcification and Extracellular Matrix Genes in the Cardiovascular System of the Healthy Domestic Sheep (<i>Ovis aries</i>). <i>Frontiers in Genetics</i> , 2020, 11, 919.	1.1	9
860	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , 2020, 583, 737-743.	13.7	134
861	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	13.7	131
862	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020, 30, 1047-1059.	2.4	32
863	Investigation of genetically regulated gene expression and response to treatment in rheumatoid arthritis highlights an association between <i>IL18RAP</i> expression and treatment response. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1446-1452.	0.5	13
864	Trimester-Specific Associations of Prenatal Lead Exposure With Infant Cord Blood DNA Methylation at Birth. <i>Epigenetics Insights</i> , 2020, 13, 251686572093866.	0.6	18
865	Inducers of the endothelial cell barrier identified through chemogenomic screening in genome-edited hPSC-endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19854-19865.	3.3	35
866	The RNA exosome shapes the expression of key protein-coding genes. <i>Nucleic Acids Research</i> , 2020, 48, 8509-8528.	6.5	12
867	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	2.4	29
868	SOX10-regulated promoter use defines isoform-specific gene expression in Schwann cells. <i>BMC Genomics</i> , 2020, 21, 549.	1.2	13
869	Computational Methods for Predicting Functions at the mRNA Isoform Level. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5686.	1.8	4
870	Feedback enrichment analysis for transcription factor-target genes in signaling pathways. <i>BioSystems</i> , 2020, 198, 104262.	0.9	3
871	Distinctive regulatory architectures of germline-active and somatic genes in <i>C. elegans</i> . <i>Genome Research</i> , 2020, 30, 1752-1765.	2.4	32
872	Brain-Enriched Coding and Long Non-coding RNA Genes Are Overrepresented in Recurrent Neurodevelopmental Disorder CNVs. <i>Cell Reports</i> , 2020, 33, 108307.	2.9	20
873	CAGE-seq analysis of osteoblast derived from cleidocranial dysplasia human induced pluripotent stem cells. <i>Bone</i> , 2020, 141, 115582.	1.4	2

#	ARTICLE	IF	CITATIONS
874	Expression profiling of WD40 family genes including DDB1- and CUL4- associated factor (DCAF) genes in mice and human suggests important regulatory roles in testicular development and spermatogenesis. <i>BMC Genomics</i> , 2020, 21, 602.	1.2	12
875	Models of the Gene Must Inform Data-Mining Strategies in Genomics. <i>Entropy</i> , 2020, 22, 942.	1.1	5
876	Sources of variation in cell-type RNA-Seq profiles. <i>PLoS ONE</i> , 2020, 15, e0239495.	1.1	20
877	FOXL1 Regulates Lung Fibroblast Function via Multiple Mechanisms. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020, 63, 831-842.	1.4	18
878	Regulation of cellular sterol homeostasis by the oxygen responsive noncoding RNA lincNORS. <i>Nature Communications</i> , 2020, 11, 4755.	5.8	12
879	Molecular Insights Into Regulatory T-Cell Adaptation to Self, Environment, and Host Tissues: Plasticity or Loss of Function in Autoimmune Disease. <i>Frontiers in Immunology</i> , 2020, 11, 1269.	2.2	14
880	Low Baseline Pulmonary Levels of Cytotoxic Lymphocytes as a Predisposing Risk Factor for Severe COVID-19. <i>MSystems</i> , 2020, 5, .	1.7	9
881	STARR-seq identifies active, chromatin-masked, and dormant enhancers in pluripotent mouse embryonic stem cells. <i>Genome Biology</i> , 2020, 21, 243.	3.8	48
882	Identification of Potential Prognostic Biomarkers for Breast Cancer Based on lncRNA-TF-Associated ceRNA Network and Functional Module. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	0
883	Cis and trans effects differentially contribute to the evolution of promoters and enhancers. <i>Genome Biology</i> , 2020, 21, 210.	3.8	35
884	TIF-Seq2 disentangles overlapping isoforms in complex human transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, e104-e104.	6.5	10
885	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	9.4	146
886	A flexible computational pipeline for research analyses of unsolved clinical exome cases. <i>Npj Genomic Medicine</i> , 2020, 5, 54.	1.7	4
887	Development of a sequencing system for spatial decoding of DNA barcode molecules at single-molecule resolution. <i>Communications Biology</i> , 2020, 3, 788.	2.0	3
888	The lncRNA Toolkit: Databases and In Silico Tools for lncRNA Analysis. <i>Non-coding RNA</i> , 2020, 6, 49.	1.3	32
889	State of the Field in Multi-Omics Research: From Computational Needs to Data Mining and Sharing. <i>Frontiers in Genetics</i> , 2020, 11, 610798.	1.1	180
890	In Vivo Validation of Alternative FXR Transcripts in Human Blood in Response to Ionizing Radiation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7851.	1.8	24
891	CRELD1 modulates homeostasis of the immune system in mice and humans. <i>Nature Immunology</i> , 2020, 21, 1517-1527.	7.0	13

#	ARTICLE	IF	CITATIONS
892	ZNF354C is a transcriptional repressor that inhibits endothelial angiogenic sprouting. <i>Scientific Reports</i> , 2020, 10, 19079.	1.6	8
893	Microbial Stimulation Reverses the Age-Related Decline in M Cells in Aged Mice. <i>IScience</i> , 2020, 23, 101147.	1.9	24
894	Predicting mRNA Abundance Directly from Genomic Sequence Using Deep Convolutional Neural Networks. <i>Cell Reports</i> , 2020, 31, 107663.	2.9	144
895	Modeling neuronal consequences of autism-associated gene regulatory variants with human induced pluripotent stem cells. <i>Molecular Autism</i> , 2020, 11, 33.	2.6	6
896	Myocardial micro-biopsy procedure for molecular characterization with increased precision and reduced trauma. <i>Scientific Reports</i> , 2020, 10, 8029.	1.6	11
897	Molecular design of hypothalamus development. <i>Nature</i> , 2020, 582, 246-252.	13.7	105
898	Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. <i>Genome Biology</i> , 2020, 21, 114.	3.8	39
899	Genetic algorithm-based personalized models of human cardiac action potential. <i>PLoS ONE</i> , 2020, 15, e0231695.	1.1	19
900	HOXB13 controls cell state through super-enhancers. <i>Experimental Cell Research</i> , 2020, 393, 112039.	1.2	9
901	ORF Capture-Seq as a versatile method for targeted identification of full-length isoforms. <i>Nature Communications</i> , 2020, 11, 2326.	5.8	19
902	TASL is the SLC15A4-associated adaptor for IRF5 activation by TLR7–9. <i>Nature</i> , 2020, 581, 316-322.	13.7	117
903	PGE2 deficiency predisposes to anaphylaxis by causing mast cell hyperresponsiveness. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 1387-1396.e13.	1.5	31
904	Biophysical mechanisms of chromatin patterning. <i>Current Opinion in Genetics and Development</i> , 2020, 61, 62-68.	1.5	23
905	A practical view of fine-mapping and gene prioritization in the post-genome-wide association era. <i>Open Biology</i> , 2020, 10, 190221.	1.5	88
906	Clinical, molecular, and epidemiological characterization of the SARS-CoV-2 virus and the Coronavirus Disease 2019 (COVID-19), a comprehensive literature review. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 98, 115094.	0.8	293
907	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene HELB. <i>Genetics Selection Evolution</i> , 2020, 52, 27.	1.2	17
908	Duplication and divergence of the retrovirus restriction gene Fv1 in <i>Mus caroli</i> allows protection from multiple retroviruses. <i>PLoS Genetics</i> , 2020, 16, e1008471.	1.5	10
909	In The Blood: Connecting Variant to Function In Human Hematopoiesis. <i>Trends in Genetics</i> , 2020, 36, 563-576.	2.9	12

#	ARTICLE	IF	CITATIONS
910	Different roles of interleukin 6 and interleukin 11 in the liver: implications for therapy. <i>Human Vaccines and Immunotherapeutics</i> , 2020, 16, 2357-2362.	1.4	33
911	Analysis of hiPSCs differentiation toward hepatocyte-like cells upon extended exposition to oncostatin. <i>Differentiation</i> , 2020, 114, 36-48.	1.0	11
912	Distinct subtypes of polycystic ovary syndrome with novel genetic associations: An unsupervised, phenotypic clustering analysis. <i>PLoS Medicine</i> , 2020, 17, e1003132.	3.9	134
913	Rare variant association testing in the non-coding genome. <i>Human Genetics</i> , 2020, 139, 1345-1362.	1.8	21
914	Universal promoter scanning by Pol II during transcription initiation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2020, 21, 132.	3.8	35
915	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
916	MIPPIE: the mouse integrated proteinâ€“protein interaction reference. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	14
917	Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. <i>Cell</i> , 2020, 181, 1502-1517.e23.	13.5	33
918	Alternative UNC13D Promoter Encodes a Functional Munc13-4 Isoform Predominantly Expressed in Lymphocytes and Platelets. <i>Frontiers in Immunology</i> , 2020, 11, 1154.	2.2	2
919	microRNA-875-5p plays critical role for mesenchymal condensation in epithelial-mesenchymal interaction during tooth development. <i>Scientific Reports</i> , 2020, 10, 4918.	1.6	11
920	A putative silencer variant in a spontaneous canine model of retinitis pigmentosa. <i>PLoS Genetics</i> , 2020, 16, e1008659.	1.5	9
921	Enhancer occlusion transcripts regulate the activity of human enhancer domains via transcriptional interference: a computational perspective. <i>Nucleic Acids Research</i> , 2020, 48, 3435-3454.	6.5	5
922	CDK1 dependent phosphorylation of hTERT contributes to cancer progression. <i>Nature Communications</i> , 2020, 11, 1557.	5.8	38
923	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. <i>EMBO Journal</i> , 2020, 39, e103949.	3.5	37
924	Functional Annotation of the Transcriptome of the Pig, <i>Sus scrofa</i> , Based Upon Network Analysis of an RNAseq Transcriptional Atlas. <i>Frontiers in Genetics</i> , 2019, 10, 1355.	1.1	42
925	The Transcriptional Network That Controls Growth Arrest and Macrophage Differentiation in the Human Myeloid Leukemia Cell Line THP-1. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 498.	1.8	25
926	Age-Induced Reduction in Human Lipolysis: A Potential Role for Adipocyte Noradrenaline Degradation. <i>Cell Metabolism</i> , 2020, 32, 1-3.	7.2	42
927	A Long Non-coding RNA, LOC157273, Is an Effector Transcript at the Chromosome 8p23.1-PPP1R3B Metabolic Traits and Type 2 Diabetes Risk Locus. <i>Frontiers in Genetics</i> , 2020, 11, 615.	1.1	14

#	ARTICLE	IF	CITATIONS
928	Simple and efficient profiling of transcription initiation and transcript levels with STRIPE-seq. <i>Genome Research</i> , 2020, 30, 910-923.	2.4	23
929	Editorial: Non-Coding RNAs and Human Diseases. <i>Frontiers in Genetics</i> , 2020, 11, 523.	1.1	11
930	IL-11 in cardiac and renal fibrosis: Late to the party but a central player. <i>British Journal of Pharmacology</i> , 2020, 177, 1695-1708.	2.7	59
931	Alternative transcription start sites of the enolase-encoding gene <i>enoA</i> are stringently used in glycolytic/gluconeogenic conditions in <i>Aspergillus oryzae</i> . <i>Current Genetics</i> , 2020, 66, 729-747.	0.8	7
932	High expression of ACE2 receptor of 2019-nCoV on the epithelial cells of oral mucosa. <i>International Journal of Oral Science</i> , 2020, 12, 8.	3.6	2,019
933	Bioinformatics for Cancer Immunotherapy. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	1
934	Mechanisms governing the pioneering and redistribution capabilities of the non-classical pioneer PU.1. <i>Nature Communications</i> , 2020, 11, 402.	5.8	76
935	β4GALT1 controls β1 integrin function to govern thrombopoiesis and hematopoietic stem cell homeostasis. <i>Nature Communications</i> , 2020, 11, 356.	5.8	34
936	The identity and methylation status of the first transcribed nucleotide in eukaryotic mRNA 5' cap modulates protein expression in living cells. <i>Nucleic Acids Research</i> , 2020, 48, 1607-1626.	6.5	76
937	Independent Transposon Exaptation Is a Widespread Mechanism of Redundant Enhancer Evolution in the Mammalian Genome. <i>Genome Biology and Evolution</i> , 2020, 12, 1-17.	1.1	14
938	Novel eye genes systematically discovered through an integrated analysis of mouse transcriptomes and phenome. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 73-82.	1.9	9
939	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. <i>Nature Communications</i> , 2020, 11, 393.	5.8	59
940	Solving the transcription start site identification problem with ADAPT-CAGE: a Machine Learning algorithm for the analysis of CAGE data. <i>Scientific Reports</i> , 2020, 10, 877.	1.6	17
941	DNA hypermethylation associated with upregulated gene expression in prostate cancer demonstrates the diversity of epigenetic regulation. <i>BMC Medical Genomics</i> , 2020, 13, 6.	0.7	81
942	HMGA2 Antisense Long Non-coding RNAs as New Players in the Regulation of HMGA2 Expression and Pancreatic Cancer Promotion. <i>Frontiers in Oncology</i> , 2019, 9, 1526.	1.3	19
943	Liver gene regulatory networks: Contributing factors to nonalcoholic fatty liver disease. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1480.	6.6	1
944	The pseudo-allergic/neurogenic route of mast cell activation via MRGPRX2: discovery, functional programs, regulation, relevance to disease, and relation with allergic stimulation. <i>Itch (Philadelphia, Pa.)</i> 2020, 10, 10.	0.0	0
945	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	13.7	724

#	ARTICLE	IF	CITATIONS
946	Emerging Roles and Potential Applications of Non-Coding RNAs in Glioblastoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2611.	1.8	17
947	Reverse-genetics studies of lncRNAs—what we have learnt and paths forward. <i>Genome Biology</i> , 2020, 21, 93.	3.8	55
948	Long Noncoding RNAs in Gastrointestinal Cancer: Tumor Suppression Versus Tumor Promotion. <i>Digestive Diseases and Sciences</i> , 2021, 66, 381-397.	1.1	16
949	Computational annotation of miRNA transcription start sites. <i>Briefings in Bioinformatics</i> , 2021, 22, 380-392.	3.2	23
950	The methyltransferase SETD3-mediated histidine methylation: Biological functions and potential implications in cancers. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1875, 188465.	3.3	11
951	Massively Parallel Reporter Assays: Defining Functional Psychiatric Genetic Variants Across Biological Contexts. <i>Biological Psychiatry</i> , 2021, 89, 76-89.	0.7	34
952	Serum proteomic profiling at diagnosis predicts clinical course, and need for intensification of treatment in inflammatory bowel disease. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 699-708.	0.6	36
953	Therapeutic potential of miRNAs targeting SARS-CoV-2 host cell receptor ACE2. <i>Meta Gene</i> , 2021, 27, 100831.	0.3	27
954	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D892-D898.	6.5	57
955	GTRD: an integrated view of transcription regulation. <i>Nucleic Acids Research</i> , 2021, 49, D104-D111.	6.5	137
956	H1 histones control the epigenetic landscape by local chromatin compaction. <i>Nature</i> , 2021, 589, 293-298.	13.7	101
957	Epigenomic differences in the human and chimpanzee genomes are associated with structural variation. <i>Genome Research</i> , 2021, 31, 279-290.	2.4	7
958	Large-scale meta-analysis across East Asian and European populations updated genetic architecture and variant-driven biology of rheumatoid arthritis, identifying 11 novel susceptibility loci. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 558-565.	0.5	93
959	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	6.5	354
960	VARAdb: a comprehensive variation annotation database for human. <i>Nucleic Acids Research</i> , 2021, 49, D1431-D1444.	6.5	26
961	A systematic review of long non-coding RNAs with a potential role in breast cancer. <i>Mutation Research - Reviews in Mutation Research</i> , 2021, 787, 108375.	2.4	17
963	Thymic Stromal Lymphopoietin Promotes MRGPRX2-Triggered Degranulation of Skin Mast Cells in a STAT5-Dependent Manner with Further Support from JNK. <i>Cells</i> , 2021, 10, 102.	1.8	24
964	Challenges for Computational Stem Cell Biology: A Discussion for the Field. <i>Stem Cell Reports</i> , 2021, 16, 3-9.	2.3	4

#	ARTICLE	IF	CITATIONS
965	CRISPRi enables isoform-specific loss-of-function screens and identification of gastric cancer-specific isoform dependencies. <i>Genome Biology</i> , 2021, 22, 47.	3.8	12
966	Using TIF-Seq2 to investigate association between 5' and 3' mRNA ends. <i>Methods in Enzymology</i> , 2021, 655, 85-118.	0.4	2
967	Deconvolution of expression for nascent RNA-sequencing data (DENR) highlights pre-RNA isoform diversity in human cells. <i>Bioinformatics</i> , 2021, 37, 4727-4736.	1.8	4
968	Genetic Epidemiology of Complex Phenotypes. <i>Methods in Molecular Biology</i> , 2021, 2249, 335-367.	0.4	3
969	Identification and Characterisation of Putative Enhancer Elements in Mouse Embryonic Stem Cells. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222097462.	1.0	3
970	High-Resolution Mapping of Transcription Initiation in the Asexual Stages of <i>Toxoplasma gondii</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 617998.	1.8	11
971	High-resolution analysis of cell-state transitions in yeast suggests widespread transcriptional tuning by alternative starts. <i>Genome Biology</i> , 2021, 22, 34.	3.8	30
972	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. <i>Nature Communications</i> , 2021, 12, 463.	5.8	109
973	Rituximab versus tocilizumab in anti-TNF inadequate responder patients with rheumatoid arthritis (R4RA): 16-week outcomes of a stratified, biopsy-driven, multicentre, open-label, phase 4 randomised controlled trial. <i>Lancet, The</i> , 2021, 397, 305-317.	6.3	145
974	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. <i>Genome Biology</i> , 2021, 22, 62.	3.8	38
975	Nongenetic Evolution Drives Lung Adenocarcinoma Spatial Heterogeneity and Progression. <i>Cancer Discovery</i> , 2021, 11, 1490-1507.	7.7	67
976	Human MiniPromoters for ocular-rAAV expression in ON bipolar, cone, corneal, endothelial, Müller glial, and PAX6 cells. <i>Gene Therapy</i> , 2021, 28, 351-372.	2.3	18
977	DeepCAPE: A Deep Convolutional Neural Network for the Accurate Prediction of Enhancers. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 565-577.	3.0	17
978	TATA and paused promoters active in differentiated tissues have distinct expression characteristics. <i>Molecular Systems Biology</i> , 2021, 17, e9866.	3.2	20
979	HiC-ACT: improved detection of chromatin interactions from Hi-C data via aggregated Cauchy test. <i>American Journal of Human Genetics</i> , 2021, 108, 257-268.	2.6	17
980	Elucidation of disease etiology by trans-layer omics analysis. <i>Inflammation and Regeneration</i> , 2021, 41, 6.	1.5	2
981	Autocrine Signaling in Cardiac Remodeling: A Rich Source of Therapeutic Targets. <i>Journal of the American Heart Association</i> , 2021, 10, e019169.	1.6	28
983	A missense variant in IFT122 associated with a canine model of retinitis pigmentosa. <i>Human Genetics</i> , 2021, 140, 1569-1579.	1.8	4

#	ARTICLE	IF	CITATIONS
984	Transmissibility: To be or not to be. , 0, 2, 12.		0
985	Transcription initiation mapping in 31 bovine tissues reveals complex promoter activity, pervasive transcription, and tissue-specific promoter usage. <i>Genome Research</i> , 2021, 31, 732-744.	2.4	11
986	Cruciform Formable Sequences within Pou5f1 Enhancer Are Indispensable for Mouse ES Cell Integrity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3399.	1.8	4
988	Cytokines Stimulated by IL-33 in Human Skin Mast Cells: Involvement of NF- κ B and p38 at Distinct Levels and Potent Co-Operation with Fc γ RI and MRGPRX2. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3580.	1.8	33
989	Remus: A Web Application for Prioritization of Regulatory Regions and Variants in Monogenic Diseases. <i>Frontiers in Genetics</i> , 2021, 12, 638960.	1.1	1
991	Molecular mechanisms of transcription factor mediated cell reprogramming: conversion of liver to pancreas. <i>Biochemical Society Transactions</i> , 2021, 49, 579-590.	1.6	5
992	Long Non-Coding RNAs: Role in Testicular Cancers. <i>Frontiers in Oncology</i> , 2021, 11, 605606.	1.3	12
993	CAGE-Seq Reveals that HIV-1 Latent Infection Does Not Trigger Unique Cellular Responses in a Jurkat T Cell Model. <i>Journal of Virology</i> , 2021, 95, .	1.5	1
994	Cancer-associated fibroblast migration in non-small cell lung cancers is modulated by increased integrin α 11 expression. <i>Molecular Oncology</i> , 2021, 15, 1507-1527.	2.1	24
995	DeltaNeTS+: elucidating the mechanism of drugs and diseases using gene expression and transcriptional regulatory networks. <i>BMC Bioinformatics</i> , 2021, 22, 108.	1.2	0
996	Functional annotation of lncRNA in high-throughput screening. <i>Essays in Biochemistry</i> , 2021, 65, 761-773.	2.1	14
997	Investigation of the Wilson gene ATP7B transcriptional start site and the effect of core promoter alterations. <i>Scientific Reports</i> , 2021, 11, 7674.	1.6	2
1000	The landscape of molecular chaperones across human tissues reveals a layered architecture of core and variable chaperones. <i>Nature Communications</i> , 2021, 12, 2180.	5.8	62
1001	Promoter switching in response to changing environment and elevated expression of protein-coding genes overlapping at their 5'UTR ends. <i>Scientific Reports</i> , 2021, 11, 8984.	1.6	4
1002	Understanding transcription across scales: From base pairs to chromosomes. <i>Molecular Cell</i> , 2021, 81, 1601-1616.	4.5	10
1003	Analysis of homozygous and heterozygous Csf1r knockout in the rat as a model for understanding microglial function in brain development and the impacts of human CSF1R mutations. <i>Neurobiology of Disease</i> , 2021, 151, 105268.	2.1	29
1004	Fish-Ing for Enhancers in the Heart. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3914.	1.8	5
1006	Deletion of a non-canonical regulatory sequence causes loss of Scn1a expression and epileptic phenotypes in mice. <i>Genome Medicine</i> , 2021, 13, 69.	3.6	15

#	ARTICLE	IF	CITATIONS
1007	Assessment of the role of non-coding RNAs in the pathophysiology of Parkinson's disease. <i>European Journal of Pharmacology</i> , 2021, 896, 173914.	1.7	20
1008	Accurate prediction of <i>cis</i> -regulatory modules reveals a prevalent regulatory genome of humans. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab052.	1.5	21
1009	Identification of candidate PAX2-regulated genes implicated in human kidney development. <i>Scientific Reports</i> , 2021, 11, 9123.	1.6	7
1010	Modeling transcriptional regulation using gene regulatory networks based on multi-omics data sources. <i>BMC Bioinformatics</i> , 2021, 22, 200.	1.2	7
1011	Nanopore sequencing reveals TACC2 locus complexity and diversity of isoforms transcribed from an intronic promoter. <i>Scientific Reports</i> , 2021, 11, 9355.	1.6	2
1012	Unlocking the Non-IgE-Mediated Pseudo-Allergic Reaction Puzzle with Mas-Related G-Protein Coupled Receptor Member X2 (MRGPRX2). <i>Cells</i> , 2021, 10, 1033.	1.8	49
1013	A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures. <i>Diabetes</i> , 2021, 70, 1581-1591.	0.3	7
1015	Automatic identification of small molecules that promote cell conversion and reprogramming. <i>Stem Cell Reports</i> , 2021, 16, 1381-1390.	2.3	14
1016	Intergenic RNA mainly derives from nascent transcripts of known genes. <i>Genome Biology</i> , 2021, 22, 136.	3.8	13
1017	Long noncoding RNAs in cancer metastasis. <i>Nature Reviews Cancer</i> , 2021, 21, 446-460.	12.8	342
1018	Transcription start site- κ level expression of thyroid transcription factor 1 isoforms in lung adenocarcinoma and its clinicopathological significance. <i>Journal of Pathology: Clinical Research</i> , 2021, 7, 361-374.	1.3	1
1019	Regulation and functional roles of chemokines in liver diseases. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2021, 18, 630-647.	8.2	46
1020	Modeling regulatory network topology improves genome-wide analyses of complex human traits. <i>Nature Communications</i> , 2021, 12, 2851.	5.8	17
1021	Genetic and Epigenetic Alterations of CDH1 Regulatory Regions in Hereditary and Sporadic Gastric Cancer. <i>Pharmaceutics</i> , 2021, 14, 457.	1.7	12
1022	Microdeletion of 9q22.3: A patient with minimal deletion size associated with a severe phenotype. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 2070-2083.	0.7	2
1024	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. <i>Nature Communications</i> , 2021, 12, 2444.	5.8	58
1025	The IDIP framework for assessing protein function and its application to the prion protein. <i>Biological Reviews</i> , 2021, 96, 1907-1932.	4.7	5
1026	Long-read cDNA sequencing identifies functional pseudogenes in the human transcriptome. <i>Genome Biology</i> , 2021, 22, 146.	3.8	26

#	ARTICLE	IF	CITATIONS
1027	Implications of Enhancer Transcription and eRNAs in Cancer. <i>Cancer Research</i> , 2021, 81, 4174-4182.	0.4	38
1028	Two repeated motifs enriched within some enhancers and origins of replication are bound by SETMAR isoforms in human colon cells. <i>Genomics</i> , 2021, 113, 1589-1604.	1.3	5
1029	Development of p53 knockout U87MG cell line for unbiased drug delivery testing system using CRISPR-Cas9 and transcriptomic analysis. <i>Journal of Biotechnology</i> , 2021, 332, 72-82.	1.9	0
1030	CRISPR-Cas9 Editing of Human Histone Deubiquitinase Gene USP16 in Human Monocytic Leukemia Cell Line THP-1. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 679544.	1.8	2
1031	LanCLs add glutathione to dehydroamino acids generated at phosphorylated sites in the proteome. <i>Cell</i> , 2021, 184, 2680-2695.e26.	13.5	34
1032	Very long intergenic non-coding (vlinc) RNAs directly regulate multiple genes in cis and trans. <i>BMC Biology</i> , 2021, 19, 108.	1.7	14
1034	The Mononuclear Phagocyte System of the Rat. <i>Journal of Immunology</i> , 2021, 206, 2251-2263.	0.4	15
1035	Fundamental gene network rewiring at the second order within and across mammalian systems. <i>Bioinformatics</i> , 2021, , .	1.8	2
1036	Clump sequencing exposes the spatial expression programs of intestinal secretory cells. <i>Nature Communications</i> , 2021, 12, 3074.	5.8	43
1037	Inflammation drives alternative first exon usage to regulate immune genes including a novel iron-regulated isoform of Aim2. <i>ELife</i> , 2021, 10, .	2.8	23
1038	Non-coding RNA crosstalk with nuclear receptors in liver disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166083.	1.8	12
1040	Endogenous retroviruses in the origins and treatment of cancer. <i>Genome Biology</i> , 2021, 22, 147.	3.8	73
1042	Targeting hepatocyte growth factor in epithelialâ€‘stromal interactions in an in vitro experimental model of human periodontitis. <i>Odontology / the Society of the Nippon Dental University</i> , 2021, 109, 912-920.	0.9	3
1043	Selection and thermostability suggest G-quadruplexes are novel functional elements of the human genome. <i>Genome Research</i> , 2021, 31, 1136-1149.	2.4	20
1044	Upregulation of RNA cap methyltransferase RNMT drives ribosome biogenesis during T cell activation. <i>Nucleic Acids Research</i> , 2021, 49, 6722-6738.	6.5	29
1045	Non-coding region variants upstream of MEF2C cause severe developmental disorder through three distinct loss-of-function mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 1083-1094.	2.6	42
1046	Conserved pan-cancer microenvironment subtypes predict response to immunotherapy. <i>Cancer Cell</i> , 2021, 39, 845-865.e7.	7.7	503
1048	Methods of massive parallel reporter assays for investigation of enhancers. <i>Vavilovskii Zhurnal Genetiki I Selektcii</i> , 2021, 25, 344-355.	0.4	2

#	ARTICLE	IF	CITATIONS
1049	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
1051	Transcription factor enrichment analysis (TFEA) quantifies the activity of multiple transcription factors from a single experiment. <i>Communications Biology</i> , 2021, 4, 661.	2.0	21
1052	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	9.4	75
1053	Functional annotation of noncoding mutations in cancer. <i>Life Science Alliance</i> , 2021, 4, e201900523.	1.3	3
1054	Airway basal stem cells reutilize the embryonic proliferation regulator, Tgfi ² -Id2 axis, for tissue regeneration. <i>Developmental Cell</i> , 2021, 56, 1917-1929.e9.	3.1	29
1055	dCas9 techniques for transcriptional repression in mammalian cells: Progress, applications and challenges. <i>BioEssays</i> , 2021, 43, 2100086.	1.2	3
1056	Highly conserved and cis-acting lncRNAs produced from paralogous regions in the center of HOXA and HOXB clusters in the endoderm lineage. <i>PLoS Genetics</i> , 2021, 17, e1009681.	1.5	12
1057	Machine learning methods to model multicellular complexity and tissue specificity. <i>Nature Reviews Materials</i> , 2021, 6, 717-729.	23.3	13
1059	Filtering of Data-Driven Gene Regulatory Networks Using <i>Drosophila melanogaster</i> as a Case Study. <i>Frontiers in Genetics</i> , 2021, 12, 649764.	1.1	2
1060	Evolution of tissue and developmental specificity of transcription start sites in <i>Bos taurus indicus</i> . <i>Communications Biology</i> , 2021, 4, 829.	2.0	2
1061	Mammalian circular RNAs result largely from splicing errors. <i>Cell Reports</i> , 2021, 36, 109439.	2.9	48
1062	A hypothetical model of trans-acting R-loops-mediated promoter-enhancer interactions by Alu elements. <i>Journal of Genetics and Genomics</i> , 2021, 48, 1007-1019.	1.7	14
1063	Global patterns of enhancer activity during sea urchin embryogenesis assessed by eRNA profiling. <i>Genome Research</i> , 2021, 31, 1680-1692.	2.4	9
1065	Systematic dissection of transcriptional regulatory networks by genome-scale and single-cell CRISPR screens. <i>Science Advances</i> , 2021, 7, .	4.7	19
1066	Cytokine Stimulation via MRGPRX2 Occurs with Lower Potency than by Fc̳RI-aggregation but with Similar Dependence on the ERK1/2 Module in Human Skin Mast Cells. <i>Journal of Investigative Dermatology</i> , 2021, , .	0.3	8
1067	Searching for improvements in predicting human eye colour from DNA. <i>International Journal of Legal Medicine</i> , 2021, 135, 2175-2187.	1.2	5
1068	Cell-autonomous inflammation of BRCA1-deficient ovarian cancers drives both tumor-intrinsic immunoreactivity and immune resistance via STING. <i>Cell Reports</i> , 2021, 36, 109412.	2.9	60
1069	Analysis of a Set of KDM5C Regulatory Genes Mutated in Neurodevelopmental Disorders Identifies Temporal Coexpression Brain Signatures. <i>Genes</i> , 2021, 12, 1088.	1.0	18

#	ARTICLE	IF	CITATIONS
1072	Risks and Function of Breast Cancer Susceptibility Alleles. <i>Cancers</i> , 2021, 13, 3953.	1.7	8
1073	In silico comparative analysis of LRRK2 interactomes from brain, kidney and lung. <i>Brain Research</i> , 2021, 1765, 147503.	1.1	6
1074	Transposable element sequence fragments incorporated into coding and noncoding transcripts modulate the transcriptome of human pluripotent stem cells. <i>Nucleic Acids Research</i> , 2021, 49, 9132-9153.	6.5	19
1075	Targeted regulation of transcription in primary cells using CRISPRa and CRISPRi. <i>Genome Research</i> , 2021, 31, 2120-2130.	2.4	29
1076	Computational identification and experimental characterization of preferred downstream positions in human core promoters. <i>PLoS Computational Biology</i> , 2021, 17, e1009256.	1.5	2
1077	Computational resources to define alleles and altered regulatory motifs at genomically edited candidate response elements. <i>Nucleic Acids Research</i> , 2021, 49, 9117-9131.	6.5	1
1078	Non-Coding RNA in Systemic Sclerosis: A Valuable Tool for Translational and Personalized Medicine. <i>Genes</i> , 2021, 12, 1296.	1.0	6
1079	Transposable elements and their KZFP controllers are drivers of transcriptional innovation in the developing human brain. <i>Genome Research</i> , 2021, 31, 1531-1545.	2.4	27
1080	TERA-Seq: true end-to-end sequencing of native RNA molecules for transcriptome characterization. <i>Nucleic Acids Research</i> , 2021, 49, e115-e115.	6.5	18
1081	Investigation of LINC00493/SMIM26 Gene Suggests Its Dual Functioning at mRNA and Protein Level. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8477.	1.8	2
1084	Systematic functional interrogation of human pseudogenes using CRISPRi. <i>Genome Biology</i> , 2021, 22, 240.	3.8	13
1086	Protein phosphatase 2A holoenzymes regulate leucine-rich repeat kinase 2 phosphorylation and accumulation. <i>Neurobiology of Disease</i> , 2021, 157, 105426.	2.1	7
1087	Systems Analysis Reveals Ageing-Related Perturbations in Retinoids and Sex Hormones in Alzheimer's and Parkinson's Diseases. <i>Biomedicines</i> , 2021, 9, 1310.	1.4	8
1089	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. <i>Nature Genetics</i> , 2021, 53, 1456-1468.	9.4	111
1090	Evidence in disease and non-disease contexts that nonsense mutations cause altered splicing via motif disruption. <i>Nucleic Acids Research</i> , 2021, 49, 9665-9685.	6.5	7
1091	P2X Receptor-Dependent Modulation of Mast Cell and Glial Cell Activities in Neuroinflammation. <i>Cells</i> , 2021, 10, 2282.	1.8	4
1092	Spatial mapping reveals human adipocyte subpopulations with distinct sensitivities to insulin. <i>Cell Metabolism</i> , 2021, 33, 1869-1882.e6.	7.2	92
1094	Cap analysis of gene expression (CAGE) and noncoding regulatory elements. <i>Seminars in Immunopathology</i> , 2022, 44, 127-136.	2.8	3

#	ARTICLE	IF	CITATIONS
1095	From GWAS to Gene: Transcriptome-Wide Association Studies and Other Methods to Functionally Understand GWAS Discoveries. <i>Frontiers in Genetics</i> , 2021, 12, 713230.	1.1	55
1097	Global approaches for profiling transcription initiation. <i>Cell Reports Methods</i> , 2021, 1, 100081.	1.4	11
1098	Evolutionary cell type mapping with single-cell genomics. <i>Trends in Genetics</i> , 2021, 37, 919-932.	2.9	43
1099	A putative long noncoding RNA-encoded micropeptide maintains cellular homeostasis in pancreatic β^2 cells. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 307-320.	2.3	19
1101	Computational cancer genomics. , 2021, , 329-359.		0
1102	Western Blot Analysis of Protein-DNA Complexes Formed during Gel Shift Experiments. <i>Techniques in Life Science and Biomedicine for the Non-expert</i> , 2021, , 311-330.	0.1	0
1103	Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. <i>Methods in Molecular Biology</i> , 2021, 2351, 67-90.	0.4	6
1105	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. <i>Methods in Molecular Biology</i> , 2020, 2120, 277-301.	0.4	22
1106	Shift-Western Blotting: Separate Analysis of Protein and DNA from Protein-DNA Complexes. <i>Methods in Molecular Biology</i> , 2015, 1312, 355-373.	0.4	7
1107	Stem Cells for the Replacement of Auditory Neurons. <i>Springer Handbook of Auditory Research</i> , 2016, , 263-286.	0.3	3
1108	Deep Feature Selection: Theory and Application to Identify Enhancers and Promoters. <i>Lecture Notes in Computer Science</i> , 2015, , 205-217.	1.0	32
1109	RIKEN MetaDatabase: A Database Platform as a Microcosm of Linked Open Data Cloud in the Life Sciences. <i>Lecture Notes in Computer Science</i> , 2016, , 99-115.	1.0	3
1111	Dyslexia Candidate Gene and Ciliary Gene Expression Dynamics During Human Neuronal Differentiation. <i>Molecular Neurobiology</i> , 2020, 57, 2944-2958.	1.9	11
1112	The Circular RNA circHUWE1 Sponges the miR-29b-AKT3 Axis to Regulate Myoblast Development. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 1086-1097.	2.3	44
1113	Expanded ENCODE delivers invaluable genomic encyclopedia. <i>Nature</i> , 2020, 583, 685-686.	13.7	7
1114	Activity-based probes for functional interrogation of retaining β^2 -glucuronidases. <i>Nature Chemical Biology</i> , 2017, 13, 867-873.	3.9	76
1115	A conserved abundant cytoplasmic long noncoding RNA modulates repression by Pumilio proteins in human cells. <i>Nature Communications</i> , 2016, 7, 12209.	5.8	192
1116	An integrated multi-omics approach identifies the landscape of interferon- β -mediated responses of human pancreatic beta cells. <i>Nature Communications</i> , 2020, 11, 2584.	5.8	87

#	ARTICLE	IF	CITATIONS
1117	Direct cell reprogramming: approaches, mechanisms and progress. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 410-424.	16.1	178
1118	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	13.7	1,014
1119	DIANA-miRGen v4: indexing promoters and regulators for more than 1500 microRNAs. <i>Nucleic Acids Research</i> , 2021, 49, D151-D159.	6.5	18
1200	Transcript assembly improves expression quantification of transposable elements in single-cell RNA-seq data. <i>Genome Research</i> , 2021, 31, 88-100.	2.4	34
1201	The Importance of Controlling Transcription Elongation at Coding and Noncoding RNA Loci. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 33-44.	2.0	6
1202	Regulatory T Cells and Human Disease. <i>Annual Review of Immunology</i> , 2020, 38, 541-566.	9.5	552
1203	Secretome profiling identifies neuron-derived neurotrophic factor as a tumor-suppressive factor in lung cancer. <i>JCI Insight</i> , 2019, 4, .	2.3	15
1204	Intronic locus determines SHROOM3 expression and potentiates renal allograft fibrosis. <i>Journal of Clinical Investigation</i> , 2015, 125, 208-221.	3.9	62
1205	Discovering Genes Essential to the Hypothalamic Regulation of Human Reproduction Using a Human Disease Model: Adjusting to Life in the "Omics" Era. <i>Endocrine Reviews</i> , 2016, 2016, 4-22.	8.9	41
1206	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. <i>F1000Research</i> , 2018, 7, 121.	0.8	4
1207	A step-by-step guide to analyzing CAGE data using R/Bioconductor. <i>F1000Research</i> , 2019, 8, 886.	0.8	23
1208	Probing instructions for expression regulation in gene nucleotide compositions. <i>PLoS Computational Biology</i> , 2018, 14, e1005921.	1.5	11
1209	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1005934.	1.5	17
1210	A simple, scalable approach to building a cross-platform transcriptome atlas. <i>PLoS Computational Biology</i> , 2020, 16, e1008219.	1.5	12
1211	Origins of De Novo Genes in Human and Chimpanzee. <i>PLoS Genetics</i> , 2015, 11, e1005721.	1.5	123
1212	Cis-regulatory differences in isoform expression associate with life history strategy variation in Atlantic salmon. <i>PLoS Genetics</i> , 2020, 16, e1009055.	1.5	29
1213	In-Silico Analysis of Inflammatory Bowel Disease (IBD) GWAS Loci to Novel Connections. <i>PLoS ONE</i> , 2015, 10, e0119420.	1.1	23
1214	Relevance of Vitamin D Receptor Target Genes for Monitoring the Vitamin D Responsiveness of Primary Human Cells. <i>PLoS ONE</i> , 2015, 10, e0124339.	1.1	64

#	ARTICLE	IF	CITATIONS
1215	Predisposition to Childhood Otitis Media and Genetic Polymorphisms within the Toll-Like Receptor 4 (TLR4) Locus. PLoS ONE, 2015, 10, e0132551.	1.1	35
1216	Embryonic Stem Cells Exhibit mRNA Isoform Specific Translational Regulation. PLoS ONE, 2016, 11, e0143235.	1.1	12
1217	Intragenic Locus in Human PIWIL2 Gene Shares Promoter and Enhancer Functions. PLoS ONE, 2016, 11, e0156454.	1.1	4
1218	Identification and prediction of alternative transcription start sites that generate rod photoreceptor-specific transcripts from ubiquitously expressed genes. PLoS ONE, 2017, 12, e0179230.	1.1	6
1219	Genome-wide association analysis identifies genetic correlates of immune infiltrates in solid tumors. PLoS ONE, 2017, 12, e0179726.	1.1	216
1220	Bioinformatic characterization of angiotensin-converting enzyme 2, the entry receptor for SARS-CoV-2. PLoS ONE, 2020, 15, e0240647.	1.1	24
1221	Adult Conditional Knockout of PGC-1 β Leads to Loss of Dopamine Neurons. ENeuro, 2016, 3, ENEURO.0183-16.2016.	0.9	87
1222	So close, no matter how far: multiple paths connecting transcription to mRNA translation in eukaryotes. EMBO Reports, 2020, 21, e50799.	2.0	24
1223	Predictive features of gene expression variation reveal mechanistic link with differential expression. Molecular Systems Biology, 2020, 16, e9539.	3.2	42
1224	Genomics of chromophobe renal cell carcinoma: implications from a rare tumor for pan-cancer studies. Oncoscience, 2015, 2, 81-90.	0.9	27
1225	The ETS factor ESE3/EHF represses IL-6 preventing STAT3 activation and expansion of the prostate cancer stem-like compartment. Oncotarget, 2016, 7, 76756-76768.	0.8	35
1226	The transcriptional coregulator <i>NAB2</i> is a target gene for the Wilms' tumor gene 1 protein (WT1) in leukemic cells. Oncotarget, 2017, 8, 87136-87150.	0.8	3
1227	PTEN regulates spindle assembly checkpoint timing through MAD1 in interphase. Oncotarget, 2017, 8, 98040-98050.	0.8	7
1228	Targeting Batf2 for infectious diseases and cancer. Oncotarget, 2015, 6, 26575-26582.	0.8	31
1229	Long Non-Coding RNAs As Epigenetic Regulators in Cancer. Current Pharmaceutical Design, 2019, 25, 3563-3577.	0.9	98
1230	Allele-specific expression and alternative splicing in horse \times donkey and cattle \times yak hybrids. Zoological Research, 2019, 40, 293-304.	0.9	18
1231	Inference of Genetic Networks From Time-Series and Static Gene Expression Data: Combining a Random-Forest-Based Inference Method With Feature Selection Methods. Frontiers in Genetics, 2020, 11, 595912.	1.1	7
1232	Practical Guidance in Genome-Wide RNA:DNA Triple Helix Prediction. International Journal of Molecular Sciences, 2020, 21, 830.	1.8	16

#	ARTICLE	IF	CITATIONS
1233	Neuropilinâ€1 as a new potential SARSâ€CoVâ€2 infection mediator implicated in the neurologic features and central nervous system involvement of COVIDâ€19. <i>Molecular Medicine Reports</i> , 2020, 22, 4221-4226.	1.1	102
1234	Species-Specific Transcriptional Regulation of Genes Involved in Nitric Oxide Production and Arginine Metabolism in Macrophages. <i>ImmunoHorizons</i> , 2018, 2, 27-37.	0.8	124
1235	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. <i>ELife</i> , 2016, 5, .	2.8	349
1236	Cap-proximal nucleotides via differential eIF4E binding and alternative promoter usage mediate translational response to energy stress. <i>ELife</i> , 2017, 6, .	2.8	75
1237	Genetic effects on promoter usage are highly context-specific and contribute to complex traits. <i>ELife</i> , 2019, 8, .	2.8	53
1238	The long non-coding RNA Cerx1 is a post transcriptional regulator of mitochondrial complex I catalytic activity. <i>ELife</i> , 2019, 8, .	2.8	42
1239	Embryo polarity in moth flies and mosquitoes relies on distinct old genes with localized transcript isoforms. <i>ELife</i> , 2019, 8, .	2.8	25
1240	Combined transient ablation and single-cell RNA-sequencing reveals the development of medullary thymic epithelial cells. <i>ELife</i> , 2020, 9, .	2.8	53
1241	Detection of condition-specific marker genes from RNA-seq data with MGFR. <i>PeerJ</i> , 2019, 7, e6970.	0.9	8
1242	TcoFBase: a comprehensive database for decoding the regulatory transcription co-factors in human and mouse. <i>Nucleic Acids Research</i> , 2022, 50, D391-D401.	6.5	16
1244	<i>HAR1</i>: an insight into lncRNA genetic evolution. <i>Epigenomics</i> , 2021, 13, 1831-1843.	1.0	12
1245	Effective gene expression prediction from sequence by integrating long-range interactions. <i>Nature Methods</i> , 2021, 18, 1196-1203.	9.0	385
1246	Organ Specificity and Heterogeneity of Cancer-Associated Fibroblasts in Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10973.	1.8	12
1248	SINEUIPs: a novel toolbox for RNA therapeutics. <i>Essays in Biochemistry</i> , 2021, 65, 775-789.	2.1	13
1249	Ssl2/TFIIH function in transcription start site scanning by RNA polymerase II in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2021, 10, .	2.8	5
1250	Interactions between long non-coding RNAs and RNA-binding proteins in cancer (Review). <i>Oncology Reports</i> , 2021, 46, .	1.2	16
1252	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , 2021, 31, 1983-1993.	2.4	7
1253	Targeting the Non-Coding Genome for the Diagnosis of Disorders of Sex Development. <i>Sexual Development</i> , 2021, 15, 392-410.	1.1	9

#	ARTICLE	IF	CITATIONS
1254	Direct reprogramming based on transcriptional regulatory network analysis. <i>Inflammation and Regeneration</i> , 2014, 34, 224-232.	1.5	0
1255	Kinesin-8 Members and Their Potential as Biomarker or Therapeutic Target. , 2015, , 171-191.		1
1258	Long Noncoding RNAs in Heart Disease. <i>Cardiac and Vascular Biology</i> , 2016, , 297-316.	0.2	1
1272	Pathogenetics of Chronic Pancreatitis. , 2017, , 63-77.		0
1273	Epigenetic Regulation of Myeloid Cells. , 0, , 571-590.		1
1274	Cis -Acting Locus â†. , 2017, , .		0
1294	Cellular Reprogramming. <i>Computational Biology</i> , 2018, , 41-55.	0.1	1
1297	FANTOM History Paving the Way to Understand â€œWhat Is Written in Genomeâ€- Application of Omics Science to Healthcare -. <i>Juntendo Medical Journal</i> , 2018, 64, 183-190.	0.1	0
1298	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. <i>F1000Research</i> , 2018, 7, 121.	0.8	3
1325	Genes and Cell Type Specification in Cerebellar Development. , 2019, , 1-19.		2
1341	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 0, 8, 1677.	0.8	0
1349	DiS-TSS: An Annotation Agnostic Algorithm for TSS Identification. <i>Lecture Notes in Computer Science</i> , 2020, , 613-623.	1.0	1
1366	Deep Learning to Identify Transcription Start Sites from CAGE Data. , 2020, , .		2
1367	Tissue-selective alternate promoters guide NLRP6 expression. <i>Life Science Alliance</i> , 2021, 4, e202000897.	1.3	1
1368	Assessment of transcriptional importance of cell line-specific features based on GTRD and FANTOM5 data. <i>PLoS ONE</i> , 2020, 15, e0243332.	1.1	0
1372	Promoter Repression and 3D-Restructuring Resolves Divergent Developmental Gene Expression in TADs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
1375	The Positive and Negative Psychological Impact on Adolescents During COVID-19 Epidemic: A Large Sample Study in China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1376	In Silico Cell-Type Deconvolution Methods in Cancer Immunotherapy. <i>Methods in Molecular Biology</i> , 2020, 2120, 213-222.	0.4	3

#	ARTICLE	IF	CITATIONS
1382	Identification of cell states using super-enhancer RNA. BMC Genomics, 2021, 22, 787.	1.2	0
1389	Besca, a single-cell transcriptomics analysis toolkit to accelerate translational research. NAR Genomics and Bioinformatics, 2021, 3, lqab102.	1.5	13
1391	Genome-wide CRISPR interference screen identifies long non-coding RNA loci required for differentiation and pluripotency. PLoS ONE, 2021, 16, e0252848.	1.1	12
1394	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. Rna, 2022, 28, 162-176.	1.6	12
1395	Expression profile of SARS-CoV-2 cellular entry proteins in normal oral mucosa and oral squamous cell carcinoma. Clinical and Experimental Dental Research, 2021, , .	0.8	6
1409	Genetic Complexity of Mitral Valve Prolapse Revealed by Clinical and Genetic Evaluation of a Large Family. Journal of Heart Valve Disease, 2017, 26, 569-580.	0.5	1
1412	Integrative transcription start site analysis and physiological phenotyping reveal torpor-specific expression program in mouse skeletal muscle. Communications Biology, 2021, 4, 1290.	2.0	2
1413	Gene Regulation Analysis Reveals Perturbations of Autism Spectrum Disorder during Neural System Development. Genes, 2021, 12, 1901.	1.0	4
1414	Comprehensive characterization of single-cell full-length isoforms in human and mouse with long-read sequencing. Genome Biology, 2021, 22, 310.	3.8	83
1415	Enhancer RNA Profiling in Smoking and HPV Associated HNSCC Reveals Associations to Key Oncogenes. International Journal of Molecular Sciences, 2021, 22, 12546.	1.8	1
1416	Relating multivariate shapes to genescapes using phenotype-biological process associations for craniofacial shape. ELife, 2021, 10, .	2.8	7
1417	Gestational Age Dependence of the Maternal Circulating Long Non-Coding RNA Transcriptome During Normal Pregnancy Highlights Antisense and Pseudogene Transcripts. Frontiers in Genetics, 2021, 12, 760849.	1.1	7
1418	Profiling of immune features to predict immunotherapy efficacy. Innovation(China), 2021, 3, 100194.	5.2	13
1421	Computational Methods and Approaches in Pharmacogenomic Research. , 2022, , 53-83.		1
1423	Cap analysis of gene expression reveals alternative promoter usage in a rat model of hypertension. Life Science Alliance, 2022, 5, e202101234.	1.3	0
1424	Targeting GPCRs and Their Signaling as a Therapeutic Option in Melanoma. Cancers, 2022, 14, 706.	1.7	8
1426	Genomic studies controvert the existence of the CUX1 p75 isoform. Scientific Reports, 2022, 12, 151.	1.6	1
1428	Molecular mechanisms governing circulating immune cell heterogeneity across different species revealed by single-cell sequencing. Clinical and Translational Medicine, 2022, 12, e689.	1.7	6

#	ARTICLE	IF	CITATIONS
1429	Prediction of New Risk Genes and Potential Drugs for Rheumatoid Arthritis from Multiomics Data. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-11.	0.7	2
1430	Diverse Regulation of YB-1 and YB-3 Abundance in Mammals. <i>Biochemistry (Moscow)</i> , 2022, 87, S48-S70.	0.7	1
1431	Identification of an IDO1-based immune classifier for survival prediction of upper tract urothelial carcinoma. <i>Cancer Science</i> , 2021, , .	1.7	1
1432	Deconstructing a Syndrome: Genomic Insights Into PCOS Causal Mechanisms and Classification. <i>Endocrine Reviews</i> , 2022, 43, 927-965.	8.9	75
1434	Distribution of alternative untranslated regions within the mRNA of the CELF1 splicing factor affects its expression. <i>Scientific Reports</i> , 2022, 12, 190.	1.6	6
1435	Towards unveiling the nature of short SERPINA1 transcripts: Avoiding the main ORF control to translate alpha1-antitrypsin C-terminal peptides. <i>International Journal of Biological Macromolecules</i> , 2022, 203, 703-717.	3.6	1
1436	Evolutionary rewiring of regulatory networks contributes to phenotypic differences between human and mouse orthologous genes. <i>Nucleic Acids Research</i> , 2022, 50, 1849-1863.	6.5	6
1437	The volume-regulated anion channel LRRC8C suppresses T cell function by regulating cyclic dinucleotide transport and STING-p53 signaling. <i>Nature Immunology</i> , 2022, 23, 287-302.	7.0	40
1438	Comparison of confound adjustment methods in the construction of gene co-expression networks. <i>Genome Biology</i> , 2022, 23, 44.	3.8	4
1439	RNAi-based therapeutics and tumor targeted delivery in cancer. <i>Advanced Drug Delivery Reviews</i> , 2022, 182, 114113.	6.6	123
1440	Inhibition of BCL2A1 by STAT5 inactivation overcomes resistance to targeted therapies of FLT3-ITD/D835 mutant AML. <i>Translational Oncology</i> , 2022, 18, 101354.	1.7	9
1441	CCR8-targeted specific depletion of clonally expanded Treg cells in tumor tissues evokes potent tumor immunity with long-lasting memory. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	68
1442	TRmir: A Comprehensive Resource for Human Transcriptional Regulatory Information of MiRNAs. <i>Frontiers in Genetics</i> , 2022, 13, 808950.	1.1	1
1443	Prediction of transcription factors associated with DNA demethylation during human cellular development. <i>Chromosome Research</i> , 2022, 30, 109-121.	1.0	4
1444	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. <i>Nature</i> , 2022, 602, 623-631.	13.7	38
1445	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.	2.7	5
1446	Generation and network analysis of an RNA-seq transcriptional atlas for the rat. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac017.	1.5	4
1447	Multi-tissue DNA methylation microarray signature is predictive of gene function. <i>Epigenetics</i> , 2022, , 1-15.	1.3	0

#	ARTICLE	IF	CITATIONS
1451	A versatile 5â€² RACE-Seq methodology for the accurate identification of the 5â€² termini of mRNAs. <i>BMC Genomics</i> , 2022, 23, 163.	1.2	8
1453	Carbonic anhydrases in metazoan model organisms: molecules, mechanisms, and physiology. <i>Physiological Reviews</i> , 2022, 102, 1327-1383.	13.1	44
1454	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. <i>BMC Biology</i> , 2022, 20, 79.	1.7	12
1455	Comprehensive evaluation of deconvolution methods for human brain gene expression. <i>Nature Communications</i> , 2022, 13, 1358.	5.8	32
1456	GREEN-DB: a framework for the annotation and prioritization of non-coding regulatory variants from whole-genome sequencing data. <i>Nucleic Acids Research</i> , 2022, 50, 2522-2535.	6.5	13
1457	Promoter/enhancer-based controllability of regulatory networks. <i>Scientific Reports</i> , 2022, 12, 3528.	1.6	2
1458	Fragments of rDNA Genes Scattered over the Human Genome Are Targets of Small RNAs. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3014.	1.8	1
1459	Vitamin D and Its Target Genes. <i>Nutrients</i> , 2022, 14, 1354.	1.7	52
1460	Circular RNA ACTA1 Acts as a Sponge for miR-199a-5p and miR-433 to Regulate Bovine Myoblast Development through the MAP3K11/MAP2K7/JNK Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 3357-3373.	2.4	6
1461	A multi-dimensional integrative scoring framework for predicting functional variants in the human genome. <i>American Journal of Human Genetics</i> , 2022, 109, 446-456.	2.6	18
1462	PTCHD1: Identification and Neurodevelopmental Contributions of an Autism Spectrum Disorder and Intellectual Disability Susceptibility Gene. <i>Genes</i> , 2022, 13, 527.	1.0	7
1463	Supervised promoter recognition: a benchmark framework. <i>BMC Bioinformatics</i> , 2022, 23, 118.	1.2	2
1464	The contribution of evolutionarily volatile promoters to molecular phenotypes and human trait variation. <i>Genome Biology</i> , 2022, 23, 89.	3.8	4
1465	DUX4 is a multifunctional factor priming human embryonic genome activation. <i>IScience</i> , 2022, 25, 104137.	1.9	20
1466	Duplications disrupt chromatin architecture and rewire GPR101-enhancer communication in X-linked acrogigantism. <i>American Journal of Human Genetics</i> , 2022, 109, 553-570.	2.6	18
1467	Serological profiling reveals hsa-miR-451a as a possible biomarker of anaphylaxis. <i>JCI Insight</i> , 2022, 7, .	2.3	9
1469	A Bibliometric Analysis of Deafness Gene Literature From 2009 to 2018 based on Web of Science. , 2021, 17, 541-550.		0
1470	A network-based method for predicting disease-associated enhancers. <i>PLoS ONE</i> , 2021, 16, e0260432.	1.1	1

#	ARTICLE	IF	CITATIONS
1471	A cis-regulatory-directed pipeline for the identification of genes involved in cardiac development and disease. <i>Genome Biology</i> , 2021, 22, 335.	3.8	4
1472	Integration of high-resolution promoter profiling assays reveals novel, cell type-specific transcription start sites across 115 human cell and tissue types. <i>Genome Research</i> , 2022, 32, 389-402.	2.4	8
1473	Aging-Related Impairments to M Cells in Peyer's Patches Coincide With Disturbances to Paneth Cells. <i>Frontiers in Immunology</i> , 2021, 12, 761949.	2.2	8
1474	Virtual Gene Concept and a Corresponding Pragmatic Research Program in Genetical Data Science. <i>Entropy</i> , 2022, 24, 17.	1.1	0
1475	Genes and Cell Type Specification in Cerebellar Development. , 2022, , 333-351.		0
1478	Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. <i>Methods in Molecular Biology</i> , 2022, 2403, 147-186.	0.4	20
1479	Are transient protein-protein interactions more dispensable?. <i>PLoS Computational Biology</i> , 2022, 18, e1010013.	1.5	10
1480	Investigation of Cross-Reactivity of Anti-Ephrin-B2 Antibody to Other Ephrin-B Members in an Immunohistochemical Study in a Cohort of Oral Squamous Cell Carcinoma. <i>Oral</i> , 2022, 2, 148-162.	0.6	0
1481	Cav ² 1 regulates T cell expansion and apoptosis independently of voltage-gated Ca ²⁺ channel function. <i>Nature Communications</i> , 2022, 13, 2033.	5.8	18
1566	Meiotic cDNA libraries reveal gene truncations and mitochondrial proteins important for competitive fitness in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2022, , .	1.2	0
1567	Comprehensive enhancer-target gene assignments improve gene set level interpretation of genome-wide regulatory data. <i>Genome Biology</i> , 2022, 23, 105.	3.8	6
1568	Epigenetic Regulation of Endothelial Cell Lineages During Zebrafish Development—New Insights From Technical Advances. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	1
1569	GATA6 is predicted to regulate DNA methylation in an in vitro model of human hepatocyte differentiation. <i>Communications Biology</i> , 2022, 5, 414.	2.0	7
1570	The Alu-ome™ shapes the epigenetic environment of regulatory elements controlling cellular defense. <i>Nucleic Acids Research</i> , 2022, 50, 5095-5110.	6.5	2
1571	SCN1A overexpression, associated with a genomic region marked by a risk variant for a common epilepsy, raises seizure susceptibility. <i>Acta Neuropathologica</i> , 2022, 144, 107-127.	3.9	3
1572	A new liver regeneration molecular mechanism involving hepatic stellate cells, Kupffer cells, and glucose-regulated protein 78 as a new hepatotrophic factor. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2022, , .	1.4	0
1575	Gene product diversity: adaptive or not?. <i>Trends in Genetics</i> , 2022, 38, 1112-1122.	2.9	9
1577	Brown Adipose Tissue—A Translational Perspective. <i>Endocrine Reviews</i> , 2023, 44, 143-192.	8.9	49

#	ARTICLE	IF	CITATIONS
1580	The <scp>SCF</scp>/<scp>KIT</scp> axis in human mast cells: Capicua acts as potent <scp>KIT</scp> repressor and <scp>ERK</scp> predominates <scp>PI3K</scp>. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 3337-3349.	2.7	8
1581	Differential cofactor dependencies define distinct types of human enhancers. Nature, 2022, 606, 406-413.	13.7	49
1582	Compatibility rules of human enhancer and promoter sequences. Nature, 2022, 607, 176-184.	13.7	67
1583	MaxHiC: A robust background correction model to identify biologically relevant chromatin interactions in Hi-C and capture Hi-C experiments. PLoS Computational Biology, 2022, 18, e1010241.	1.5	7
1584	Systematic Analysis of Actively Transcribed Core Matrisome Genes Across Tissues and Cell Phenotypes. Matrix Biology, 2022, 111, 95-107.	1.5	6
1585	Somatic point mutations are enriched in non-coding RNAs with possible regulatory function in breast cancer. Communications Biology, 2022, 5, .	2.0	5
1586	Detection of ovarian cancer using plasma cell-free DNA methylomes. Clinical Epigenetics, 2022, 14, .	1.8	10
1587	In-Depth Temporal Transcriptome Profiling of an Alphaherpesvirus Using Nanopore Sequencing. Viruses, 2022, 14, 1289.	1.5	6
1588	Endogenous spacing enables co-processing of microRNAs and efficient combinatorial RNAi. Cell Reports Methods, 2022, , 100239.	1.4	3
1589	<scp>GGC</scp> Repeat Expansion of <scp><i>RILPL1</i></scp> is Associated with Oculopharyngodistal Myopathy. Annals of Neurology, 2022, 92, 512-526.	2.8	16
1590	Genes Possessing the Most Frequent DNA DSBs Are Highly Associated with Development and Cancers, and Essentially Overlap with the rDNA-Contacting Genes. International Journal of Molecular Sciences, 2022, 23, 7201.	1.8	2
1591	Hypomethylation of miR-17-92 cluster in lupus T cells and no significant role for genetic factors in the lupus-associated DNA methylation signature. Annals of the Rheumatic Diseases, 2022, 81, 1428-1437.	0.5	5
1592	Bookend: precise transcript reconstruction with end-guided assembly. Genome Biology, 2022, 23, .	3.8	5
1593	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	9.4	26
1594	A high-resolution map of human RNA translation. Molecular Cell, 2022, 82, 2885-2899.e8.	4.5	37
1595	Precision Anti-Cancer Medicines by Oligonucleotide Therapeutics in Clinical Research Targeting Undruggable Proteins and Non-Coding RNAs. Pharmaceutics, 2022, 14, 1453.	2.0	6
1597	Deciphering the regulatory syntax of genomic DNA with deep learning. Journal of Biosciences, 2022, 47, .	0.5	0
1598	Postmitotic differentiation of human monocytes requires cohesin-structured chromatin. Nature Communications, 2022, 13, .	5.8	5

#	ARTICLE	IF	CITATIONS
1599	Alternative transcription start sites contribute to acute-stress-induced transcriptome response in human skeletal muscle. <i>Human Genomics</i> , 2022, 16, .	1.4	11
1600	Pathogenic Roles of RNA-Binding Proteins in Sarcomas. <i>Cancers</i> , 2022, 14, 3812.	1.7	2
1601	Polysome-CAGE of TCL1-driven chronic lymphocytic leukemia revealed multiple N-terminally altered epigenetic regulators and a translation stress signature. <i>ELife</i> , 0, 11, .	2.8	0
1602	Deep sequencing of short capped RNAs reveals novel families of noncoding RNAs. <i>Genome Research</i> , 2022, 32, 1727-1735.	2.4	1
1603	Temporally divergent regulatory mechanisms govern neuronal diversification and maturation in the mouse and marmoset neocortex. <i>Nature Neuroscience</i> , 2022, 25, 1049-1058.	7.1	16
1604	Temporal analysis of enhancers during mouse cerebellar development reveals dynamic and novel regulatory functions. <i>ELife</i> , 0, 11, .	2.8	7
1607	Transcriptomic diversity in human medullary thymic epithelial cells. <i>Nature Communications</i> , 2022, 13, .	5.8	11
1609	In silico gene expression and pathway analysis of <i>DEK</i> in the human brain across the lifespan. <i>European Journal of Neuroscience</i> , 2022, 56, 4720-4743.	1.2	1
1610	Rituximab versus tocilizumab and B-cell status in TNF-alpha inadequate-responder rheumatoid arthritis patients: the R4-RA RCT. <i>Efficacy and Mechanism Evaluation</i> , 2022, 9, 1-58.	0.9	0
1611	Hotspots of single-strand DNA "breakome" are enriched at transcriptional start sites of genes. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	6
1613	Lyl1-deficiency promotes inflammatory responses and increases mycobacterial burden in response to <i>Mycobacterium tuberculosis</i> infection in mice. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
1614	Analyses of rare predisposing variants of lung cancer in 6,004 whole genomes in Chinese. <i>Cancer Cell</i> , 2022, 40, 1223-1239.e6.	7.7	23
1615	A CRISPR/Cas9-Based Toolkit to Test Gain- and Loss-of-Gene Function in Brain Organoids. <i>Neuromethods</i> , 2022, , 75-92.	0.2	1
1618	Updated review of advances in microRNAs and complex diseases: experimental results, databases, web servers and data fusion. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	27
1619	Repression and 3D-restructuring resolves regulatory conflicts in evolutionarily rearranged genomes. <i>Cell</i> , 2022, 185, 3689-3704.e21.	13.5	25
1621	Building integrative functional maps of gene regulation. <i>Human Molecular Genetics</i> , 0, , .	1.4	2
1623	Multiplexed functional genomic assays to decipher the noncoding genome. <i>Human Molecular Genetics</i> , 2022, 31, R84-R96.	1.4	4
1624	Scalable Functional Assays for the Interpretation of Human Genetic Variation. <i>Annual Review of Genetics</i> , 2022, 56, 441-465.	3.2	18

#	ARTICLE	IF	CITATIONS
1625	SCAFE: a software suite for analysis of transcribed cis-regulatory elements in single cells. <i>Bioinformatics</i> , 2022, 38, 5126-5128.	1.8	6
1626	Pathway-Specific Polygenic Risk Scores Identify Obstructive Sleep Apnea-Related Pathways Differentially Moderating Genetic Susceptibility to Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, .	1.6	10
1627	Regulatory variants in a novel distal enhancer regulate the expression of CYP3A4 and CYP3A5. <i>Clinical and Translational Science</i> , 2022, 15, 2720-2731.	1.5	5
1628	How "Neuronal" Are Human Skin Mast Cells?. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10871.	1.8	8
1629	Stroke genetics informs drug discovery and risk prediction across ancestries. <i>Nature</i> , 2022, 611, 115-123.	13.7	143
1631	Tracing the evolutionary history of blood cells to the unicellular ancestor of animals. <i>Blood</i> , 2022, 140, 2611-2625.	0.6	7
1632	Isoform-resolved mRNA profiling of ribosome load defines interplay of HIF and mTOR dysregulation in kidney cancer. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 871-880.	3.6	6
1634	Accurate prediction of functional states of cis-regulatory modules reveals common epigenetic rules in humans and mice. <i>BMC Biology</i> , 2022, 20, .	1.7	5
1635	CSF1R as a Therapeutic Target in Bone Diseases: Obvious but Not so Simple. <i>Current Osteoporosis Reports</i> , 2022, 20, 516-531.	1.5	6
1637	HNRNPK/CLCN3 axis facilitates the progression of LUAD through CAF-tumor interaction. <i>International Journal of Biological Sciences</i> , 2022, 18, 6084-6101.	2.6	2
1638	Structure-based screening for functional non-coding RNAs in fission yeast identifies a factor repressing untimely initiation of sexual differentiation. <i>Nucleic Acids Research</i> , 0, , .	6.5	0
1639	The Comparative Anatomy of Nanopublications and FAIR Digital Objects. <i>Research Ideas and Outcomes</i> , 0, 8, .	1.0	3
1641	Perturbation of Gene Regulation by Genome Editing. <i>Methods in Molecular Biology</i> , 2023, , 59-68.	0.4	0
1643	Whole genome sequence analysis of blood lipid levels in >66,000 individuals. <i>Nature Communications</i> , 2022, 13, .	5.8	26
1644	A map of cis-regulatory modules and constituent transcription factor binding sites in 80% of the mouse genome. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
1645	A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies. <i>Nature Methods</i> , 2022, 19, 1599-1611.	9.0	36
1646	CRdb: a comprehensive resource for deciphering chromatin regulators in human. <i>Nucleic Acids Research</i> , 2023, 51, D88-D100.	6.5	1
1647	HIF1-AS1 is a DNA:DNA:RNA triplex-forming lncRNA interacting with the HUSH complex. <i>Nature Communications</i> , 2022, 13, .	5.8	13

#	ARTICLE	IF	CITATIONS
1648	Deconvolution of bulk tumors into distinct immune cell states predicts colorectal cancer recurrence. <i>IScience</i> , 2022, 25, 105392.	1.9	2
1649	SEdb 2.0: a comprehensive super-enhancer database of human and mouse. <i>Nucleic Acids Research</i> , 2023, 51, D280-D290.	6.5	31
1650	Integrating Multimorbidity into a Whole-Body Understanding of Disease Using Spatial Genomics. <i>Results and Problems in Cell Differentiation</i> , 2022, , 157-187.	0.2	0
1653	Machine Learning Applications for Transcription Level and Phenotype Predictions. <i>IUBMB Life</i> , 0, , .	1.5	2
1654	Genome-wide screening of genes involved in programming diapause in the next generation in silkworm, <i>Bombyx mori</i> (Lepidoptera: Bombycidae). <i>European Journal of Entomology</i> , 0, 119, 405-412.	1.2	2
1655	FAVOR: functional annotation of variants online resource and annotator for variation across the human genome. <i>Nucleic Acids Research</i> , 2023, 51, D1300-D1311.	6.5	39
1656	Implications of differential transcription start site selection on chronic myeloid leukemia and prostate cancer cell protein expression. <i>IScience</i> , 2022, 25, 105519.	1.9	1
1657	Retrotransposon insertions associated with risk of neurologic and psychiatric diseases. <i>EMBO Reports</i> , 2023, 24, .	2.0	3
1658	Promoter sequence and architecture determine expression variability and confer robustness to genetic variants. <i>ELife</i> , 0, 11, .	2.8	12
1659	Multi-Layered Regulations on the Chromatin Architectures: Establishing the Tight and Specific Responses of Fission Yeast <i>fbp1</i> Gene Transcription. <i>Biomolecules</i> , 2022, 12, 1642.	1.8	3
1660	Systematic characterization of cancer transcriptome at transcript resolution. <i>Nature Communications</i> , 2022, 13, .	5.8	7
1661	Long non-coding RNA PCAT19 safeguards DNA in quiescent endothelial cells by preventing uncontrolled phosphorylation of RPA2. <i>Cell Reports</i> , 2022, 41, 111670.	2.9	7
1662	DNA replication initiation shapes the mutational landscape and expression of the human genome. <i>Science Advances</i> , 2022, 8, .	4.7	4
1663	EpiCas-DL: Predicting sgRNA activity for CRISPR-mediated epigenome editing by deep learning. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 202-211.	1.9	5
1664	Regulation of non-coding RNA promoters. , 2023, , 53-76.		0
1665	Computational Methods for Identifying MicroRNA-Gene Regulatory Modules. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 187-208.	0.2	0
1666	Efficient Selection of Enhancers and Promoters from MIA PaCa-2 Pancreatic Cancer Cells by ChIP-lentiMPRA. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15011.	1.8	0
1667	Prediction of the cell-type-specific transcription of non-coding RNAs from genome sequences via machine learning. <i>Nature Biomedical Engineering</i> , 2023, 7, 830-844.	11.6	8

#	ARTICLE	IF	CITATIONS
1668	Annotating TSSs in Multiple Cell Types Based on DNA Sequence and RNA-seq Data via DeeReCT-TSS. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 959-973.	3.0	2
1669	Classification and characterization of alternative promoters in 26 lung adenocarcinoma cell lines. <i>Japanese Journal of Clinical Oncology</i> , 0, , .	0.6	1
1670	Fibrillin-1 and asprosin, novel players in metabolic syndrome. <i>Molecular Genetics and Metabolism</i> , 2023, 138, 106979.	0.5	5
1672	The cap epitranscriptome: Early directions to a complex life as mRNA. <i>BioEssays</i> , 2023, 45, .	1.2	8
1673	Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole genome sequencing studies. <i>Nature Genetics</i> , 2023, 55, 154-164.	9.4	12
1675	Pan-cancer surveys indicate cell cycle-related roles of primate-specific genes in tumors and embryonic cerebrum. <i>Genome Biology</i> , 2022, 23, .	3.8	6
1676	DeepTSS: multi-branch convolutional neural network for transcription start site identification from CAGE data. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
1678	The sound of silence: Transgene silencing in mammalian cell engineering. <i>Cell Systems</i> , 2022, 13, 950-973.	2.9	26
1679	Expression of Paired box 9 defines an aggressive subset of lung adenocarcinoma preferentially occurring in smokers. <i>Histopathology</i> , 0, , .	1.6	0
1681	Machine learning in the development of targeting microRNAs in human disease. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
1682	Endogenous IL-1 receptor antagonist restricts healthy and malignant myeloproliferation. <i>Nature Communications</i> , 2023, 14, .	5.8	9
1683	ATM suppresses c-Myc overexpression in the mammary epithelium in response to estrogen. <i>Cell Reports</i> , 2023, 42, 111909.	2.9	2
1684	Practical application of massively parallel reporter assay in biotechnology and medicine. <i>Journal of Clinical Practice</i> , 2023, 13, 74-87.	0.2	0
1685	The HAPSTR2 retrogene buffers stress signaling and resilience in mammals. <i>Nature Communications</i> , 2023, 14, .	5.8	4
1686	A KO mouse model for the lncRNA Lhx1os produces motor neuron alterations and locomotor impairment. <i>IScience</i> , 2023, 26, 105891.	1.9	0
1687	An atlas of transcribed human cardiac promoters and enhancers reveals an important role of regulatory elements in heart failure. , 2023, 2, 58-75.		7
1688	Quality assessment and refinement of chromatin accessibility data using a sequence-based predictive model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
1689	Inducible lncRNA transgenic mice reveal continual role of HOTAIR in promoting breast cancer metastasis. <i>ELife</i> , 0, 11, .	2.8	15

#	ARTICLE	IF	CITATIONS
1690	New insights into genome annotation in <i>Podospora anserina</i> through re-exploiting multiple RNA-seq data. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
1691	What Has Genomics Taught An Evolutionary Biologist?. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 1-12.	3.0	1
1693	SCN1A: bioinformatically informed revised boundaries for promoter and enhancer regions. <i>Human Molecular Genetics</i> , 2023, 32, 1753-1763.	1.4	1
1695	The landscape of cryptic antisense transcription in human cancers reveals an oncogenic noncoding RNA in lung cancer. <i>Science Advances</i> , 2023, 9, .	4.7	0
1696	HTLV-1 bZIP factor impairs DNA mismatch repair system. <i>Biochemical and Biophysical Research Communications</i> , 2023, 657, 43-49.	1.0	1
1697	Comprehensive characterization of the embryonic factor LEUTX. <i>IScience</i> , 2023, 26, 106172.	1.9	1
1698	The endothelial-enriched lncRNA LINC00607 mediates angiogenic function. <i>Basic Research in Cardiology</i> , 2023, 118, .	2.5	6
1699	mRNA ageing shapes the Cap2 methylome in mammalian mRNA. <i>Nature</i> , 2023, 614, 358-366.	13.7	14
1700	RNA m6A methylation across the transcriptome. <i>Molecular Cell</i> , 2023, 83, 428-441.	4.5	60
1701	Pan-cancer molecular subtypes of metastasis reveal distinct and evolving transcriptional programs. <i>Cell Reports Medicine</i> , 2023, 4, 100932.	3.3	5
1703	CREB Is Activated by the SCF/KIT Axis in a Partially ERK-Dependent Manner and Orchestrates Survival and the Induction of Immediate Early Genes in Human Skin Mast Cells. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4135.	1.8	5
1704	Combining an Ensemble Clustering Method and a New Similarity Criterion for Modeling the Hereditary Behavior of Diseases. <i>Signal and Data Processing</i> , 2021, 18, 97-114.	0.0	1
1705	The Role of Non-coding RNAs in Cerebellar Development. <i>Contemporary Clinical Neuroscience</i> , 2023, , 111-128.	0.3	0
1707	Rare coding variants as risk modifiers of the 22q11.2 deletion implicate postnatal cortical development in syndromic schizophrenia. <i>Molecular Psychiatry</i> , 2023, 28, 2071-2080.	4.1	2
1709	<scp>CALML5</scp> is a novel diagnostic marker for differentiating thymic squamous cell carcinoma from type <scp>B3</scp> thymoma. <i>Thoracic Cancer</i> , 2023, 14, 1089-1097.	0.8	1
1710	Distinct HOX Gene Family DNA Methylation Profiles in Histologically Normal Skin Dependent on Dermoscopic Pattern of Adjacent Nevi. <i>Journal of Investigative Dermatology</i> , 2023, 143, 1830-1834.e6.	0.3	2
1712	An integrated single cell and spatial transcriptomic map of human white adipose tissue. <i>Nature Communications</i> , 2023, 14, .	5.8	35
1713	Cell typeâ€‘specific interpretation of noncoding variants using deep learningâ€‘based methods. <i>GigaScience</i> , 2023, 12, .	3.3	3

#	ARTICLE	IF	CITATIONS
1714	Epi-Impute: Single-Cell RNA-seq Imputation via Integration with Single-Cell ATAC-seq. International Journal of Molecular Sciences, 2023, 24, 6229.	1.8	5
1715	A novel CCDC91 isoform associated with ossification of the posterior longitudinal ligament of the spine works as a non-coding RNA to regulate osteogenic genes. American Journal of Human Genetics, 2023, 110, 638-647.	2.6	2
1717	In silico prioritisation of microRNA-associated common variants in multiple sclerosis. Human Genomics, 2023, 17, .	1.4	0
1718	Transfer learning identifies sequence determinants of cell-type specific regulatory element accessibility. NAR Genomics and Bioinformatics, 2023, 5, .	1.5	2
1719	Functionally distinct promoter classes initiate transcription via different mechanisms reflected in focused versus dispersed initiation patterns. EMBO Journal, 2023, 42, .	3.5	6
1720	SINEUP non-coding RNA activity depends on specific N6-methyladenosine nucleotides. Molecular Therapy - Nucleic Acids, 2023, 32, 402-414.	2.3	2
1721	Multi-trait genome-wide association study identifies a novel endometrial cancer risk locus that associates with testosterone levels. IScience, 2023, 26, 106590.	1.9	1
1725	The ENCODE Imputation Challenge: a critical assessment of methods for cross-cell type imputation of epigenomic profiles. Genome Biology, 2023, 24, .	3.8	6
1726	Genome-Wide Principles of Gene Regulation. , 2023, , 145-159.		0
1727	Information about immune cell proportions and tumor stage improves the prediction of recurrence in patients with colorectal cancer. Patterns, 2023, , 100736.	3.1	0
1786	Prediction and Analysis of Transcription Factor Binding Sites: Practical Examples and Case Studies Using R Programming. Methods in Molecular Biology, 2024, , 199-225.	0.4	0
1791	Whole-exome and whole-genome sequencing in the molecular diagnostic laboratory. , 2024, , 27-38.		0
1825	Review of gene expression using microarray and RNA-seq. , 2024, , 159-187.		0