

RefSeq: an update on mammalian reference sequences

Nucleic Acids Research

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Evolutionary conservation in genes underlying human psychiatric disorders. <i>Frontiers in Human Neuroscience</i> , 2014, 8, 283.	1.0	27
3	Control of Steroid Receptor Dynamics and Function by Genomic Actions of the Cochaperones p23 and Bag-1L. <i>Nuclear Receptor Signaling</i> , 2014, 12, nrs.12005.	1.0	16
4	In silico prediction of splice-altering single nucleotide variants in the human genome. <i>Nucleic Acids Research</i> , 2014, 42, 13534-13544.	6.5	396
5	The KDM5 family of histone demethylases as targets in oncology drug discovery. <i>Epigenomics</i> , 2014, 6, 277-286.	1.0	92
6	Non-coding RNA gene families in the genomes of anopheline mosquitoes. <i>BMC Genomics</i> , 2014, 15, 1038.	1.2	9
7	Alternative splicing at GYNNGY 5' splice sites: more noise, less regulation. <i>Nucleic Acids Research</i> , 2014, 42, 13969-13980.	6.5	22
8	MOPED 2.5"An Integrated Multi-Omics Resource: Multi-Omics Profiling Expression Database Now Includes Transcriptomics Data. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 335-343.	1.0	42
9	PeptideManager: a peptide selection tool for targeted proteomic studies involving mixed samples from different species. <i>Frontiers in Genetics</i> , 2014, 5, 305.	1.1	18
10	miRBase Tracker: keeping track of microRNA annotation changes. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	73
11	P2Y ₁₂ Receptor on the Verge of a Neuroinflammatory Breakdown. <i>Mediators of Inflammation</i> , 2014, 2014, 1-15.	1.4	65
12	Lynx web services for annotations and systems analysis of multi-gene disorders. <i>Nucleic Acids Research</i> , 2014, 42, W473-W477.	6.5	5
13	Medical genomics: The intricate path from genetic variant identification to clinical interpretation. <i>Applied & Translational Genomics</i> , 2014, 3, 60-67.	2.1	32
14	Construction and assessment of individualized proteogenomic databases for large-scale analysis of nonsynonymous single nucleotide variants. <i>Proteomics</i> , 2014, 14, 2699-2708.	1.3	17
15	TogoTable: cross-database annotation system using the Resource Description Framework (RDF) data model. <i>Nucleic Acids Research</i> , 2014, 42, W442-W448.	6.5	7
16	Potential non-B DNA regions in the human genome are associated with higher rates of nucleotide mutation and expression variation. <i>Nucleic Acids Research</i> , 2014, 42, 12367-12379.	6.5	45
17	FISH Oracle 2: a web server for integrative visualization of genomic data in cancer research. <i>Journal of Clinical Bioinformatics</i> , 2014, 4, 5.	1.2	5
18	Computational approaches to interpreting genomic sequence variation. <i>Genome Medicine</i> , 2014, 6, 87.	3.6	33
19	MORPHIN: a web tool for human disease research by projecting model organism biology onto a human integrated gene network. <i>Nucleic Acids Research</i> , 2014, 42, W147-W153.	6.5	16

#	ARTICLE	IF	CITATIONS
20	Expert curation in UniProtKB: a case study on dealing with conflicting and erroneous data. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau016-bau016.	1.4	56
21	ClinVar: public archive of relationships among sequence variation and human phenotype. Nucleic Acids Research, 2014, 42, D980-D985.	6.5	2,270
22	Genome-wide linkage and exome analyses identify variants of HMCN1 for splenic epidermoid cyst. BMC Medical Genetics, 2014, 15, 115.	2.1	3
23	What's that gene (or protein)? Online resources for exploring functions of genes, transcripts, and proteins. Molecular Biology of the Cell, 2014, 25, 1187-1201.	0.9	13
24	A draft map of the human proteome. Nature, 2014, 509, 575-581.	13.7	1,948
25	Distinct isoform of FABP7 revealed by screening for retroelement-activated genes in diffuse large B-cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3534-43.	3.3	62
26	Consideration of GREB1 as a potential therapeutic target for hormone-responsive or endocrine-resistant cancers. Expert Opinion on Therapeutic Targets, 2014, 18, 1065-1076.	1.5	19
27	Long-term tumor necrosis factor treatment induces NF κ B activation and proliferation, but not osteoblastic differentiation of adipose tissue-derived mesenchymal stem cells in vitro. International Journal of Biochemistry and Cell Biology, 2014, 54, 149-162.	1.2	7
28	Comparison of complexity measures for DNA sequence analysis. , 2014, , .		5
29	Folding Simulations for Proteins with Diverse Topologies Are Accessible in Days with a Physics-Based Force Field and Implicit Solvent. Journal of the American Chemical Society, 2014, 136, 13959-13962.	6.6	199
30	Transcriptome sequencing reveals altered long intergenic non-coding RNAs in lung cancer. Genome Biology, 2014, 15, 429.	3.8	179
31	Cytogenetic alterations and their molecular genetic correlates in head and neck squamous cell carcinoma: A next generation window to the biology of disease. Genes Chromosomes and Cancer, 2014, 53, 972-990.	1.5	53
32	Characterizing regions in the human genome unmappable by next-generation-sequencing at the read length of 1000 bases. Computational Biology and Chemistry, 2014, 53, 108-117.	1.1	16
33	Virus proteins similar to human proteins as possible disturbance on human pathways. Systems and Synthetic Biology, 2014, 8, 283-295.	1.0	2
34	Transcriptome assemblies for studying sex-biased gene expression in the guppy, Poecilia reticulata. BMC Genomics, 2014, 15, 400.	1.2	82
35	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	9.4	641
36	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. American Journal of Human Genetics, 2014, 94, 870-883.	2.6	116
37	Gene duplication followed by exon structure divergence substitutes for alternative splicing in zebrafish. Gene, 2014, 546, 271-276.	1.0	7

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38	BGMUT Database of Allelic Variants of Genes Encoding Human Blood Group Antigens. <i>Transfusion Medicine and Hemotherapy</i> , 2014, 41, 346-351.	0.7	36
39	A better sequence-read simulator program for metagenomics. <i>BMC Bioinformatics</i> , 2014, 15, S14.	1.2	43
40	Genome-wide p63-regulated gene expression in differentiating epidermal keratinocytes. <i>Genomics Data</i> , 2015, 5, 159-163.	1.3	16
41	A computational strategy for predicting lineage specifiers in stem cell subpopulations. <i>Stem Cell Research</i> , 2015, 15, 427-434.	0.3	10
42	Alterations in the NF2/LATS1/LATS2/YAP Pathway in Schwannomas. <i>Journal of Neuropathology and Experimental Neurology</i> , 2015, 74, 952-959.	0.9	52
43	Metagenome-assembled genomes uncover a global brackish microbiome. <i>Genome Biology</i> , 2015, 16, 279.	3.8	186
44	Comparison of Exome and Genome Sequencing Technologies for the Complete Capture of Protein-Coding Regions. <i>Human Mutation</i> , 2015, 36, 815-822.	1.1	156
45	Phenome-ing Microbes. <i>Springer Protocols</i> , 2015, , 83-96.	0.1	1
46	Genome-wide analysis of enhancer RNA in gene regulation across 12 mouse tissues. <i>Scientific Reports</i> , 2015, 5, 12648.	1.6	56
47	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. <i>EMBO Reports</i> , 2015, 16, 863-878.	2.0	134
48	Comprehensive assembly of novel transcripts from unmapped human RNA-seq data and their association with cancer. <i>Molecular Systems Biology</i> , 2015, 11, 826.	3.2	18
49	A differential network analysis approach for lineage specifier prediction in stem cell subpopulations. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15012.	1.4	20
50	A novel DNA sequence motif in human and mouse genomes. <i>Scientific Reports</i> , 2015, 5, 10444.	1.6	0
51	Analysis of nucleosome positioning landscapes enables gene discovery in the human malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2015, 16, 1005.	1.2	5
52	Bipartite structure of the inactive mouse X chromosome. <i>Genome Biology</i> , 2015, 16, 152.	3.8	211
53	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	80
54	Using mixtures of biological samples as process controls for RNA-sequencing experiments. <i>BMC Genomics</i> , 2015, 16, 708.	1.2	15
55	Generation of a de novo transcriptome from equine lamellar tissue. <i>BMC Genomics</i> , 2015, 16, 739.	1.2	14

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56	Functionally conserved enhancers with divergent sequences in distant vertebrates. <i>BMC Genomics</i> , 2015, 16, 882.	1.2	18
57	MisoMine: a genome-scale high-resolution data portal of expression, function and networks at the splice isoform level in the mouse. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav045.	1.4	15
58	Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 629-638.	0.8	10
59	The Confidence Information Ontology: a step towards a standard for asserting confidence in annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav043-bav043.	1.4	37
60	DENdb: database of integrated human enhancers. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav085.	1.4	51
61	The Role of MicroRNAs as Predictors of Response to Tamoxifen Treatment in Breast Cancer Patients. <i>International Journal of Molecular Sciences</i> , 2015, 16, 24243-24275.	1.8	51
62	De Novo Origin of VCY2 from Autosome to Y-Transposed Amplicon. <i>PLoS ONE</i> , 2015, 10, e0119651.	1.1	5
63	Discovery of Novel ncRNA Sequences in Multiple Genome Alignments on the Basis of Conserved and Stable Secondary Structures. <i>PLoS ONE</i> , 2015, 10, e0130200.	1.1	26
64	Uncovering Molecular Bases Underlying Bone Morphogenetic Protein Receptor Inhibitor Selectivity. <i>PLoS ONE</i> , 2015, 10, e0132221.	1.1	11
65	Improved Methods to Generate Spheroid Cultures from Tumor Cells, Tumor Cells & Fibroblasts or Tumor-Fragments: Microenvironment, Microvesicles and MiRNA. <i>PLoS ONE</i> , 2015, 10, e0133895.	1.1	28
66	Evolution of plant β -pyrroline-5-carboxylate reductases from phylogenetic and structural perspectives. <i>Frontiers in Plant Science</i> , 2015, 6, 567.	1.7	21
67	Trends in IT Innovation to Build a Next Generation Bioinformatics Solution to Manage and Analyse Biological Big Data Produced by NGS Technologies. <i>BioMed Research International</i> , 2015, 2015, 1-15.	0.9	26
68	Novel RNA variants in colorectal cancers. <i>Oncotarget</i> , 2015, 6, 36587-36602.	0.8	15
69	Topological Analysis of Hedgehog Acyltransferase, a Multipalmitoylated Transmembrane Protein. <i>Journal of Biological Chemistry</i> , 2015, 290, 3293-3307.	1.6	54
70	Gene: a gene-centered information resource at NCBI. <i>Nucleic Acids Research</i> , 2015, 43, D36-D42.	6.5	534
71	RNA structure generates natural cooperativity between single-stranded RNA binding proteins targeting 5' and 3' UTRs. <i>Nucleic Acids Research</i> , 2015, 43, 1160-1169.	6.5	10
72	GWIPSviz as a tool for exploring ribosome profiling evidence supporting the synthesis of alternative proteoforms. <i>Proteomics</i> , 2015, 15, 2410-2416.	1.3	19
73	mBISON: Finding miRNA target over-representation in gene lists from ChIP-sequencing data. <i>BMC Research Notes</i> , 2015, 8, 157.	0.6	3

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74	GeneTIER: prioritization of candidate disease genes using tissue-specific gene expression profiles. <i>Bioinformatics</i> , 2015, 31, 2728-2735.	1.8	25
75	Benchmark analysis of algorithms for determining and quantifying full-length mRNA splice forms from RNA-seq data. <i>Bioinformatics</i> , 2015, 31, 3938-3945.	1.8	90
76	Rapid Detection of Rare Deleterious Variants by Next Generation Sequencing with Optional Microarray SNP Genotype Data. <i>Human Mutation</i> , 2015, 36, 823-830.	1.1	15
77	RefSeq curation and annotation of antizyme and antizyme inhibitor genes in vertebrates. <i>Nucleic Acids Research</i> , 2015, 43, 7270-7279.	6.5	4
78	COXPRESdb in 2015: coexpression database for animal species by DNA-microarray and RNAseq-based expression data with multiple quality assessment systems. <i>Nucleic Acids Research</i> , 2015, 43, D82-D86.	6.5	137
79	Leveraging transcript quantification for fast computation of alternative splicing profiles. <i>Rna</i> , 2015, 21, 1521-1531.	1.6	213
80	The Ski2-family helicase Obelus regulates Crumbs alternative splicing and cell polarity. <i>Journal of Cell Biology</i> , 2015, 211, 1011-1024.	2.3	7
81	3USS: a web server for detecting alternative 3' UTRs from RNA-seq experiments. <i>Bioinformatics</i> , 2015, 31, 1845-1847.	1.8	40
82	Tissue-specific transcriptome sequencing analysis expands the non-human primate reference transcriptome resource (NHPRT). <i>Nucleic Acids Research</i> , 2015, 43, D737-D742.	6.5	61
83	MRPrimer: a MapReduce-based method for the thorough design of valid and ranked primers for PCR. <i>Nucleic Acids Research</i> , 2015, 43, e130-e130.	6.5	14
84	Discovery of an essential nucleotidylating activity associated with a newly delineated conserved domain in the RNA polymerase-containing protein of all nidoviruses. <i>Nucleic Acids Research</i> , 2015, 43, 8416-8434.	6.5	197
85	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	3.8	325
86	Nuclear Fractionation Reveals Thousands of Chromatin-Tethered Noncoding RNAs Adjacent to Active Genes. <i>Cell Reports</i> , 2015, 12, 1089-1098.	2.9	153
87	A novel signature for identification of upstream alternative translation initiation sites. , 2015, , .		0
88	Whole-exome sequencing identify a new mutation of MYH7 in a Chinese family with left ventricular noncompaction. <i>Gene</i> , 2015, 558, 138-142.	1.0	16
89	A Bayesian mixture model for chromatin interaction data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 53-64.	0.2	6
90	Nijmegen Breakage Syndrome Detected By Newborn Screening for T Cell Receptor Excision Circles (TRECs). <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, AB14.	1.5	1
91	Nijmegen Breakage Syndrome Detected by Newborn Screening for T Cell Receptor Excision Circles (TRECs). <i>Journal of Clinical Immunology</i> , 2015, 35, 227-233.	2.0	34

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92	Advances in <i>Setaria</i> genomics for genetic improvement of cereals and bioenergy grasses. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1-14.	1.8	190
93	Whole-exome characterization of pancreatic neuroendocrine tumor cell lines BON-1 and QGP-1. <i>Journal of Molecular Endocrinology</i> , 2015, 54, 137-147.	1.1	83
94	An internal ribosome entry site in the 5' untranslated region of epidermal growth factor receptor allows hypoxic expression. <i>Oncogenesis</i> , 2015, 4, e134-e134.	2.1	12
95	Global insights into the Chinese hamster and CHO cell transcriptomes. <i>Biotechnology and Bioengineering</i> , 2015, 112, 965-976.	1.7	32
96	Targeted Integration of RNA-Seq and Metabolite Data to Elucidate Curcuminoid Biosynthesis in Four Curcuma Species. <i>Plant and Cell Physiology</i> , 2015, 56, 843-851.	1.5	9
97	The landscape of long noncoding RNAs in the human transcriptome. <i>Nature Genetics</i> , 2015, 47, 199-208.	9.4	2,410
99	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015, 12, 339-342.	9.0	155
100	An update on LNCipedia: a database for annotated human lncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D174-D180.	6.5	298
101	Beyond protein expression, MOPED goes multi-omics. <i>Nucleic Acids Research</i> , 2015, 43, D1145-D1151.	6.5	17
102	Creating reference gene annotation for the mouse C57BL6/J genome assembly. <i>Mammalian Genome</i> , 2015, 26, 366-378.	1.0	182
103	Deep sequencing-generated modules demonstrate coherent expression patterns for various cardiac diseases. <i>Gene</i> , 2015, 574, 53-60.	1.0	1
104	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
105	Homo sapiens exhibit a distinct pattern of CNV genes regulation: an important role of miRNAs and SNPs in expression plasticity. <i>Scientific Reports</i> , 2015, 5, 12163.	1.6	9
106	microRNAs Regulate Cell-to-Cell Variability of Endogenous Target Gene Expression in Developing Mouse Thymocytes. <i>PLoS Genetics</i> , 2015, 11, e1005020.	1.5	22
107	Is the growth rate of Protein Data Bank sufficient to solve the protein structure prediction problem using template-based modeling?. <i>Bio-Algorithms and Med-Systems</i> , 2015, 11, 1-7.	1.0	10
108	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. <i>Journal of Proteome Research</i> , 2015, 14, 3555-3567.	1.8	36
109	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015, 16, 865-872.	3.2	6
110	Leveraging cross-link modification events in CLIP-seq for motif discovery. <i>Nucleic Acids Research</i> , 2015, 43, 95-103.	6.5	40

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111	ProCon – PROteomics CONversion tool. <i>Journal of Proteomics</i> , 2015, 129, 56-62.	1.2	14
112	Application of dual tree complex wavelet transform in tandem mass spectrometry. <i>Computers in Biology and Medicine</i> , 2015, 63, 36-41.	3.9	3
113	Improving Serodiagnosis of Human and Canine Leishmaniasis with Recombinant <i>Leishmania braziliensis</i> Cathepsin L-like Protein and a Synthetic Peptide Containing Its Linear B-cell Epitope. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3426.	1.3	21
114	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	1.8	53
115	PubAngioGen: a database and knowledge for angiogenesis and related diseases. <i>Nucleic Acids Research</i> , 2015, 43, D963-D967.	6.5	8
116	PhosphoSitePlus, 2014: mutations, PTMs and recalibrations. <i>Nucleic Acids Research</i> , 2015, 43, D512-D520.	6.5	2,488
117	Genetics of RA susceptibility, what comes next?. <i>RMD Open</i> , 2015, 1, e000028-e000028.	1.8	9
118	Necessary relations for nucleotide frequencies. <i>Journal of Theoretical Biology</i> , 2015, 374, 179-182.	0.8	3
119	An epigenetic regulatory element of the Nodal gene in the mouse and human genomes. <i>Mechanisms of Development</i> , 2015, 136, 143-154.	1.7	10
120	Pan-cancer transcriptome analysis reveals long noncoding RNAs with conserved function. <i>RNA Biology</i> , 2015, 12, 628-642.	1.5	85
121	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. <i>BMC Genomics</i> , 2015, 16, 1.	1.2	1,445
122	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	256
123	Functional analysis of <i>Girardia tigrina</i> transcriptome seeds pipeline for anthelmintic target discovery. <i>Parasites and Vectors</i> , 2015, 8, 34.	1.0	12
124	The Eukaryotic Promoter Database: expansion of EPDnew and new promoter analysis tools. <i>Nucleic Acids Research</i> , 2015, 43, D92-D96.	6.5	238
125	Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2015, 14, 3541-3554.	1.8	13
126	FlyBase: introduction of the <i>Drosophila melanogaster</i> Release 6 reference genome assembly and large-scale migration of genome annotations. <i>Nucleic Acids Research</i> , 2015, 43, D690-D697.	6.5	387
127	Dr.VIS v2.0: an updated database of human disease-related viral integration sites in the era of high-throughput deep sequencing. <i>Nucleic Acids Research</i> , 2015, 43, D887-D892.	6.5	15
128	Biological Databases for Human Research. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 55-63.	3.0	84

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129	Novel Observations From Next-Generation RNA Sequencing of Highly Purified Human Adult and Fetal Islet Cell Subsets. <i>Diabetes</i> , 2015, 64, 3172-3181.	0.3	268
130	RNA Exosome-Regulated Long Non-Coding RNA Transcription Controls Super-Enhancer Activity. <i>Cell</i> , 2015, 161, 774-789.	13.5	370
131	The terminal enzymes of cholesterol synthesis, DHCR24 and DHCR7, interact physically and functionally. <i>Journal of Lipid Research</i> , 2015, 56, 888-897.	2.0	63
132	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	1.5	13
133	CMPD: cancer mutant proteome database. <i>Nucleic Acids Research</i> , 2015, 43, D849-D855.	6.5	13
134	The SUPERFAMILY 1.75 database in 2014: a doubling of data. <i>Nucleic Acids Research</i> , 2015, 43, D227-D233.	6.5	74
135	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	6.5	103
136	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
137	Reproducible Analysis of Sequencing-Based RNA Structure Probing Data with User-Friendly Tools. <i>Methods in Enzymology</i> , 2015, 558, 153-180.	0.4	9
138	VaDE: a manually curated database of reproducible associations between various traits and human genomic polymorphisms. <i>Nucleic Acids Research</i> , 2015, 43, D868-D872.	6.5	3
139	Expanded GAA repeats impede transcription elongation through the <i>FXN</i> gene and induce transcriptional silencing that is restricted to the <i>FXN</i> locus. <i>Human Molecular Genetics</i> , 2015, 24, ddv397.	1.4	54
140	Intron retention is a widespread mechanism of tumor-suppressor inactivation. <i>Nature Genetics</i> , 2015, 47, 1242-1248.	9.4	322
141	Enhanced virome sequencing using targeted sequence capture. <i>Genome Research</i> , 2015, 25, 1910-1920.	2.4	209
142	Functional classification of memory CD8+ T cells by CX3CR1 expression. <i>Nature Communications</i> , 2015, 6, 8306.	5.8	231
143	The potential clinical impact of the release of two drafts of the human proteome. <i>Expert Review of Proteomics</i> , 2015, 12, 579-593.	1.3	26
144	Mouse genome annotation by the RefSeq project. <i>Mammalian Genome</i> , 2015, 26, 379-390.	1.0	17
145	GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. <i>Conservation Genetics Resources</i> , 2015, 7, 851-857.	0.4	5
146	Combining CRISPR/Cas9 and rAAV Templates for Efficient Gene Editing. <i>Nucleic Acid Therapeutics</i> , 2015, 25, 287-296.	2.0	26

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147	A unified gene catalog for the laboratory mouse reference genome. <i>Mammalian Genome</i> , 2015, 26, 295-304.	1.0	16
148	A pipeline for the systematic identification of non-redundant full-ORF cDNAs for polymorphic and evolutionary divergent genomes: Application to the ascidian <i>Ciona intestinalis</i> . <i>Developmental Biology</i> , 2015, 404, 149-163.	0.9	20
149	Systematic review and meta-analysis of Japanese familial Alzheimer's disease and FTDP-17. <i>Journal of Human Genetics</i> , 2015, 60, 281-283.	1.1	11
150	Translational control by lysine-encoding A-rich sequences. <i>Science Advances</i> , 2015, 1, .	4.7	94
151	Tissue alkaline phosphatase is involved in lipid metabolism and gene expression and secretion of adipokines in adipocytes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2015, 1850, 2485-2496.	1.1	30
152	Redox regulation of FoxO transcription factors. <i>Redox Biology</i> , 2015, 6, 51-72.	3.9	566
153	Genetic Variants That Predispose to DNA Double-Strand Breaks in Lymphocytes From a Subset of Patients With Familial Colorectal Carcinomas. <i>Gastroenterology</i> , 2015, 149, 1872-1883.e9.	0.6	31
154	Complex and multi-allelic copy number variation in human disease. <i>Briefings in Functional Genomics</i> , 2015, 14, 329-338.	1.3	50
155	A Genome-Wide Landscape of Retrocopies in Primate Genomes. <i>Genome Biology and Evolution</i> , 2015, 7, 2265-2275.	1.1	46
156	Influenza A virus preferentially snatches noncoding RNA caps. <i>Rna</i> , 2015, 21, 2067-2075.	1.6	60
157	A Combined Omics Approach to Generate the Surface Atlas of Human Naive CD4+ T Cells during Early T-Cell Receptor Activation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2085-2102.	2.5	40
158	Characterisation of hepcidin response to holotransferrin treatment in CHO TRVb-1 cells. <i>Blood Cells, Molecules, and Diseases</i> , 2015, 55, 110-118.	0.6	3
159	Bioinformatics Annotation of Human Y Chromosome-Encoded Protein Pathways and Interactions. <i>Journal of Proteome Research</i> , 2015, 14, 3503-3518.	1.8	9
160	A widespread role of the motif environment in transcription factor binding across diverse protein families. <i>Genome Research</i> , 2015, 25, 1268-1280.	2.4	134
161	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 2207-2217.	1.1	101
162	A modular open platform for systematic functional studies under physiological conditions. <i>Nucleic Acids Research</i> , 2015, 43, e112-e112.	6.5	39
163	Aberrant sperm DNA methylation predicts male fertility status and embryo quality. <i>Fertility and Sterility</i> , 2015, 104, 1388-1397.e5.	0.5	153
165	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114

#	ARTICLE	IF	CITATIONS
166	Under-detection of endospore-forming Firmicutes in metagenomic data. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 299-306.	1.9	88
167	Structural Bioinformatics Inspection of neXtProt PE5 Proteins in the Human Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 3750-3761.	1.8	13
168	<i>TOLLIP</i> , <i>MUC5B</i> , and the Response to <i>N</i> -Acetylcysteine among Individuals with Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 1475-1482.	2.5	257
169	The long noncoding RNA landscape in hypoxic and inflammatory renal epithelial injury. <i>American Journal of Physiology - Renal Physiology</i> , 2015, 309, F901-F913.	1.3	70
170	Genomic insights into the distribution, genetic diversity and evolution of polyketide synthases and nonribosomal peptide synthetases. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 79-85.	1.5	33
171	Current strategies for mutation detection in phenotype-driven screens utilising next generation sequencing. <i>Mammalian Genome</i> , 2015, 26, 486-500.	1.0	28
172	Genome-wide analysis of the ATP-binding cassette (ABC) transporter gene family in sea lamprey and Japanese lamprey. <i>BMC Genomics</i> , 2015, 16, 436.	1.2	22
173	Bioinformatics approaches for the functional interpretation of protein lists: From ontology term enrichment to network analysis. <i>Proteomics</i> , 2015, 15, 981-996.	1.3	27
174	Epithelial ovarian cancer stem cells: underlying complexity of a simple paradigm. <i>Reproduction</i> , 2015, 149, R59-R70.	1.1	63
175	Fine mapping of eight psoriasis susceptibility loci. <i>European Journal of Human Genetics</i> , 2015, 23, 844-853.	1.4	25
176	Predicting the human epigenome from DNA motifs. <i>Nature Methods</i> , 2015, 12, 265-272.	9.0	121
177	Selective forces and mutational biases drive stop codon usage in the human genome: a comparison with sense codon usage. <i>BMC Genomics</i> , 2016, 17, 366.	1.2	25
178	Design and application of a target capture sequencing of exons and conserved non-coding sequences for the rat. <i>BMC Genomics</i> , 2016, 17, 593.	1.2	12
179	Computational Analysis of Single Nucleotide Polymorphisms Associated with Altered Drug Responsiveness in Type 2 Diabetes. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1008.	1.8	8
180	Patterns of database citation in articles and patents indicate long-term scientific and industry value of biological data resources. <i>F1000Research</i> , 2016, 5, 160.	0.8	16
181	The somatic <i>POLE</i> P286R mutation defines a unique subclass of colorectal cancer featuring hypermutation, representing a potential genomic biomarker for immunotherapy. <i>Oncotarget</i> , 2016, 7, 68638-68649.	0.8	59
182	Optimizing an ion semiconductor sequencing data analysis method to identify somatic mutations in the genomes of cancer cells in clinical tissue samples. <i>Biomedical Research</i> , 2016, 37, 359-366.	0.3	23
183	ErythroGene: a database for in-depth analysis of the extensive variation in 36 blood group systems in the 1000 Genomes Project. <i>Blood Advances</i> , 2016, 1, 240-249.	2.5	122

#	ARTICLE	IF	CITATIONS
184	Potential Role of Activating Transcription Factor 5 during Osteogenesis. <i>Stem Cells International</i> , 2016, 2016, 1-8.	1.2	17
185	Structural characterization of single nucleotide variants at ligand binding sites and enzyme active sites of human proteins. <i>Biophysics and Physicobiology</i> , 2016, 13, 157-163.	0.5	7
186	Long Noncoding RNA and mRNA Expression Profiles in the Thyroid Gland of Two Phenotypically Extreme Pig Breeds Using Ribo-Zero RNA Sequencing. <i>Genes</i> , 2016, 7, 34.	1.0	36
187	A Multi-scale Computational Platform to Mechanistically Assess the Effect of Genetic Variation on Drug Responses in Human Erythrocyte Metabolism. <i>PLoS Computational Biology</i> , 2016, 12, e1005039.	1.5	12
188	Integrated Analysis of Dysregulated ncRNA and mRNA Expression Profiles in Humans Exposed to Carbon Nanotubes. <i>PLoS ONE</i> , 2016, 11, e0150628.	1.1	70
189	Downstream Antisense Transcription Predicts Genomic Features That Define the Specific Chromatin Environment at Mammalian Promoters. <i>PLoS Genetics</i> , 2016, 12, e1006224.	1.5	15
190	Linking Core Promoter Classes to Circadian Transcription. <i>PLoS Genetics</i> , 2016, 12, e1006231.	1.5	7
191	The Impact of Endurance Training on Human Skeletal Muscle Memory, Global Isoform Expression and Novel Transcripts. <i>PLoS Genetics</i> , 2016, 12, e1006294.	1.5	46
192	Transient Shifts of Incubation Temperature Reveal Immediate and Long-Term Transcriptional Response in Chicken Breast Muscle Underpinning Resilience and Phenotypic Plasticity. <i>PLoS ONE</i> , 2016, 11, e0162485.	1.1	8
193	Targeted Sequencing of FKBP5 in Suicide Attempters with Bipolar Disorder. <i>PLoS ONE</i> , 2016, 11, e0169158.	1.1	9
194	<scp>CRISPR</scp> guide <scp>RNA</scp> design for research applications. <i>FEBS Journal</i> , 2016, 283, 3232-3238.	2.2	74
195	deBGA: read alignment with de Bruijn graph-based seed and extension. <i>Bioinformatics</i> , 2016, 32, 3224-3232.	1.8	74
196	HistoneDB 2.0: a histone database with variantsâ€”an integrated resource to explore histones and their variants. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw014.	1.4	99
197	High-performance integrated virtual environment (HIVE): a robust infrastructure for next-generation sequence data analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw022.	1.4	80
198	Sister chromatid telomere fusions, but not NHEJ-mediated inter-chromosomal telomere fusions, occur independently of DNA ligases 3 and 4. <i>Genome Research</i> , 2016, 26, 588-600.	2.4	38
199	Common errors in mass spectrometryâ€”based analysis of postâ€”translational modifications. <i>Proteomics</i> , 2016, 16, 700-714.	1.3	106
200	Long-range regulators of the lncRNA<i>HOTAIR</i> enhance its prognostic potential in breast cancer. <i>Human Molecular Genetics</i> , 2016, 25, 3269-3283.	1.4	58
201	NPInter v3.0: an upgraded database of noncoding RNA-associated interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw057.	1.4	130

#	ARTICLE	IF	CITATIONS
202	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	1.4	912
203	Propagation on Molecular Interaction Networks: Prediction of Effective Drug Combinations and Biomarkers in Cancer Treatment. Current Pharmaceutical Design, 2016, 22, 1-1.	0.9	2
204	Alterations in the human proteome following administration of valproic acid. Journal of Trauma and Acute Care Surgery, 2016, 81, 1020-1027.	1.1	28
205	Large-scale gene co-expression network as a source of functional annotation for cattle genes. BMC Genomics, 2016, 17, 846.	1.2	18
206	Identifying transcription start sites and active enhancer elements using BruUV-seq. Scientific Reports, 2016, 5, 17978.	1.6	27
207	Constructing 3D interaction maps from 1D epigenomes. Nature Communications, 2016, 7, 10812.	5.8	135
208	VARPRISM: incorporating variant prioritization in tests of de novo mutation association. Genome Medicine, 2016, 8, 91.	3.6	7
209	Databases and bioinformatics tools for rice research. Current Plant Biology, 2016, 7-8, 39-52.	2.3	18
210	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. Nucleic Acids Research, 2017, 45, gkw973.	6.5	30
211	Network analysis of psoriasis reveals biological pathways and roles for coding and long non-coding RNAs. BMC Genomics, 2016, 17, 841.	1.2	74
212	High-throughput interpretation of gene structure changes in human and nonhuman resequencing data, using ACE. Bioinformatics, 2017, 33, 1437-1446.	1.8	2
213	CRISPR-Cas type I-A Cascade complex couples viral infection surveillance to host transcriptional regulation in the dependence of Csa3b. Nucleic Acids Research, 2017, 45, gkw1265.	6.5	48
214	CHO Cells Can Make More Protein. Cell Systems, 2016, 3, 412-413.	2.9	14
215	Finding approximate gene clusters with Gecko 3. Nucleic Acids Research, 2016, 44, gkw843.	6.5	23
216	Pharmacogenetics and interstitial lung disease. Current Opinion in Pulmonary Medicine, 2016, 22, 456-465.	1.2	8
217	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. Genome Biology, 2016, 17, 266.	3.8	94
218	Evaluation of the Tobacco Heating System 2.2 (THS2.2). Part 5: microRNA expression from a 90-day rat inhalation study indicates that exposure to THS2.2 aerosol causes reduced effects on lung tissue compared with cigarette smoke. Regulatory Toxicology and Pharmacology, 2016, 81, S82-S92.	1.3	37
219	Panel-based NGS Reveals Novel Pathogenic Mutations in Autosomal Recessive Retinitis Pigmentosa. Scientific Reports, 2016, 6, 19531.	1.6	48

#	ARTICLE	IF	CITATIONS
220	Distribution of single nucleotide variants on protein-protein interaction sites and its relationship with minor allele frequency. <i>Protein Science</i> , 2016, 25, 316-321.	3.1	14
221	Metagenomes provide valuable comparative information on soil microeukaryotes. <i>Research in Microbiology</i> , 2016, 167, 436-450.	1.0	38
222	<scp>HD</scp>5 and <scp>HBD</scp>1 variants'™ solvation potential energy correlates with their antibacterial activity against <i>Escherichia coli</i>. <i>Biopolymers</i> , 2016, 106, 43-50.	1.2	8
223	Proteogenomics: Integrating Next-Generation Sequencing and Mass Spectrometry to Characterize Human Proteomic Variation. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 521-545.	2.8	91
224	An evolutionary roadmap to the microtubule-associated protein MAP Tau. <i>BMC Genomics</i> , 2016, 17, 264.	1.2	48
225	The antitumor toxin CD437 is a direct inhibitor of DNA polymerase β . <i>Nature Chemical Biology</i> , 2016, 12, 511-515.	3.9	83
226	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
227	Extensive Hidden Genomic Mosaicism Revealed in Normal Tissue. <i>American Journal of Human Genetics</i> , 2016, 98, 571-578.	2.6	59
228	SOLiD SAGE sequencing shows differential gene expression in jejunal lymph node samples of resistant and susceptible red deer (<i>Cervus elaphus</i>) challenged with <i>Mycobacterium avium</i> subsp. paratuberculosis. <i>Veterinary Immunology and Immunopathology</i> , 2016, 169, 102-110.	0.5	4
229	Analysis of functional germline variants in APOBEC3 and driver genes on breast cancer risk in Moroccan study population. <i>BMC Cancer</i> , 2016, 16, 165.	1.1	20
230	Long non-coding RNA Databases in Cardiovascular Research. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 191-199.	3.0	38
231	T-Cell Epitope Discovery for Therapeutic Cancer Vaccines. <i>Methods in Molecular Biology</i> , 2016, 1403, 779-796.	0.4	11
232	Bisulfite oligonucleotide-capture sequencing for targeted base- and strand-specific absolute 5-methylcytosine quantitation. <i>Age</i> , 2016, 38, 49.	3.0	14
233	The Properties of Long Noncoding RNAs That Regulate Chromatin. <i>Annual Review of Genomics and Human Genetics</i> , 2016, 17, 69-94.	2.5	75
234	Update on Genomic Databases and Resources at the National Center for Biotechnology Information. <i>Methods in Molecular Biology</i> , 2016, 1415, 3-30.	0.4	14
235	Multivariate eQTL mapping uncovers functional variation on the X-chromosome associated with complex disease traits. <i>Human Genetics</i> , 2016, 135, 827-839.	1.8	14
236	Gene transcripts associated with muscle strength: a CHARGE meta-analysis of 7,781 persons. <i>Physiological Genomics</i> , 2016, 48, 1-11.	1.0	11
237	Long non-coding RNA ADNCR suppresses adipogenic differentiation by targeting miR-204. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 871-882.	0.9	148

#	ARTICLE	IF	CITATIONS
238	SoFIA: a data integration framework for annotating high-throughput datasets. <i>Bioinformatics</i> , 2016, 32, 2590-2597.	1.8	10
239	Macrophage Polarization by Titanium Dioxide (TiO ₂) Particles: Size Matters. <i>ACS Biomaterials Science and Engineering</i> , 2016, 2, 908-919.	2.6	26
240	Setdb1 maintains hematopoietic stem and progenitor cells by restricting the ectopic activation of nonhematopoietic genes. <i>Blood</i> , 2016, 128, 638-649.	0.6	61
241	A targeted sequencing study of glutamatergic candidate genes in suicide attempters with bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 1080-1087.	1.1	13
242	A Novel Associative Memory Based Architecture for Sequence Alignment. , 2016, , .		1
243	ZMYND8 Co-localizes with NuRD on Target Genes and Regulates Poly(ADP-Ribose)-Dependent Recruitment of GATAD2A/NuRD to Sites of DNA Damage. <i>Cell Reports</i> , 2016, 17, 783-798.	2.9	100
244	Mitochondrial heteroplasmy in vertebrates using ChIP-sequencing data. <i>Genome Biology</i> , 2016, 17, 139.	3.8	17
245	The Ensembl Variant Effect Predictor. <i>Genome Biology</i> , 2016, 17, 122.	3.8	5,181
246	Common genetic variants of GPC1 gene reduce risk of biliary atresia in a Chinese population. <i>Journal of Pediatric Surgery</i> , 2016, 51, 1661-1664.	0.8	15
247	A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease. <i>American Journal of Human Genetics</i> , 2016, 99, 595-606.	2.6	223
248	In silico studies of the interaction between BRN2 protein and MORE DNA. <i>Journal of Molecular Modeling</i> , 2016, 22, 228.	0.8	3
249	Covalent targeting of remote cysteine residues to develop CDK12 and CDK13 inhibitors. <i>Nature Chemical Biology</i> , 2016, 12, 876-884.	3.9	249
250	Transcriptome analysis reveals rod/cone photoreceptor specific signatures across mammalian retinas. <i>Human Molecular Genetics</i> , 2016, 25, ddw268.	1.4	36
251	Carboxylic ester hydrolases: Classification and database derived from their primary, secondary, and tertiary structures. <i>Protein Science</i> , 2016, 25, 1942-1953.	3.1	65
252	NOTCH1 mediates a switch between two distinct secretomes during senescence. <i>Nature Cell Biology</i> , 2016, 18, 979-992.	4.6	365
253	Family-based exome-wide assessment of maternal genetic effects on susceptibility to childhood B-cell acute lymphoblastic leukemia in hispanics. <i>Cancer</i> , 2016, 122, 3697-3704.	2.0	15
254	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
255	Association Between <i>RET</i> (rs1800860) and <i>GFR1</i> (rs45568534, rs8192663, rs181595401), Tj ETQq1 1 0.784314 rgBT Molecular Biomarkers, 2016, 20, 624-628.	0.3	4

#	ARTICLE	IF	CITATIONS
256	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33.	1.8	73
257	Centrifuge: rapid and sensitive classification of metagenomic sequences. <i>Genome Research</i> , 2016, 26, 1721-1729.	2.4	1,025
258	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. <i>Nature Communications</i> , 2016, 7, 13637.	5.8	58
259	Association of kidney structure-related gene variants with type 2 diabetes-attributed end-stage kidney disease in African Americans. <i>Human Genetics</i> , 2016, 135, 1251-1262.	1.8	43
260	Characterization of Greater Middle Eastern genetic variation for enhanced disease gene discovery. <i>Nature Genetics</i> , 2016, 48, 1071-1076.	9.4	314
261	Up-regulation of glutathione-related genes, enzyme activities and transport proteins in human cervical cancer cells treated with doxorubicin. <i>Biomedicine and Pharmacotherapy</i> , 2016, 83, 397-406.	2.5	26
262	Pathogenic variants in <i>KCTD7</i> perturb neuronal K ⁺ fluxes and glutamine transport. <i>Brain</i> , 2016, 139, 3109-3120.	3.7	31
263	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. <i>Nature Communications</i> , 2016, 7, 11778.	5.8	68
264	Flexible Data Analysis Pipeline for High-Confidence Proteogenomics. <i>Journal of Proteome Research</i> , 2016, 15, 4686-4695.	1.8	11
265	ImmunoChip analysis identifies novel susceptibility loci in the human leukocyte antigen region for acquired thrombotic thrombocytopenic purpura. <i>Journal of Thrombosis and Haemostasis</i> , 2016, 14, 2356-2367.	1.9	10
266	Microgravity induces proteomics changes involved in endoplasmic reticulum stress and mitochondrial protection. <i>Scientific Reports</i> , 2016, 6, 34091.	1.6	43
267	Comparative survey of the relative impact of mRNA features on local ribosome profiling read density. <i>Nature Communications</i> , 2016, 7, 12915.	5.8	96
268	What parameters characterize ϵ ? <i>Biophysics and Physicobiology</i> , 2016, 13, 305-310.	0.5	5
269	Sequence features accurately predict genome-wide MeCP2 binding in vivo. <i>Nature Communications</i> , 2016, 7, 11025.	5.8	46
270	Functional transcription factor target discovery via compendia of binding and expression profiles. <i>Scientific Reports</i> , 2016, 6, 20649.	1.6	16
271	Histone Modifications in a Mouse Model of Early Adversities and Panic Disorder: Role for <i>Asic1</i> and Neurodevelopmental Genes. <i>Scientific Reports</i> , 2016, 6, 25131.	1.6	33
272	Resurrecting ancestral structural dynamics of an antiviral immune receptor: adaptive binding pocket reorganization repeatedly shifts RNA preference. <i>BMC Evolutionary Biology</i> , 2016, 16, 241.	3.2	6
273	Pax6 associates with H3K4-specific histone methyltransferases Mll1, Mll2, and Set1a and regulates H3K4 methylation at promoters and enhancers. <i>Epigenetics and Chromatin</i> , 2016, 9, 37.	1.8	25

#	ARTICLE	IF	CITATIONS
274	Rare coding TTN variants are associated with electrocardiographic QT interval in the general population. <i>Scientific Reports</i> , 2016, 6, 28356.	1.6	6
275	Identifying the missing proteins in human proteome by biological language model. <i>BMC Systems Biology</i> , 2016, 10, 113.	3.0	2
276	Discrepancies between human DNA, mRNA and protein reference sequences and their relation to single nucleotide variants in the human population. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw124.	1.4	4
277	DNA methylation dynamics in plants and mammals: overview of regulation and dysregulation. <i>Cell Biochemistry and Function</i> , 2016, 34, 289-298.	1.4	55
278	Using ClinVar as a Resource to Support Variant Interpretation. <i>Current Protocols in Human Genetics</i> , 2016, 89, 8.16.1-8.16.23.	3.5	89
279	Long noncoding RNAs expressed in human hepatic stellate cells form networks with extracellular matrix proteins. <i>Genome Medicine</i> , 2016, 8, 31.	3.6	59
280	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing. , 2016, , .		6
281	Analysis of Long Noncoding RNAs in RNA-Seq Data. , 2016, , 143-174.		0
282	Characterisation of non-coding genetic variation in histamine receptors using AnNCR-SNP. <i>Amino Acids</i> , 2016, 48, 2433-2442.	1.2	10
283	PHASTER: a better, faster version of the PHAST phage search tool. <i>Nucleic Acids Research</i> , 2016, 44, W16-W21.	6.5	3,133
284	Analysis of the structure, evolution, and expression of CD24, an important regulator of cell fate. <i>Gene</i> , 2016, 590, 324-337.	1.0	21
285	Pairwise comparison of mammalian transcriptomes associated with the effect of polyploidy on the expression activity of developmental gene modules. <i>Cell and Tissue Biology</i> , 2016, 10, 122-132.	0.2	2
287	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. <i>Epigenetics</i> , 2016, 11, 501-516.	1.3	65
288	Immediate and long-term transcriptional response of hind muscle tissue to transient variation of incubation temperature in broilers. <i>BMC Genomics</i> , 2016, 17, 323.	1.2	7
289	Long non-coding RNAs display higher natural expression variation than protein-coding genes in healthy humans. <i>Genome Biology</i> , 2016, 17, 14.	3.8	129
290	Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. <i>Genome Biology</i> , 2016, 17, 19.	3.8	141
291	Integrative genomic deconvolution of rheumatoid arthritis GWAS loci into gene and cell type associations. <i>Genome Biology</i> , 2016, 17, 79.	3.8	70
292	High-performance web services for querying gene and variant annotation. <i>Genome Biology</i> , 2016, 17, 91.	3.8	166

#	ARTICLE	IF	CITATIONS
293	Identification of mutations in the <i>MYO9A</i> gene in patients with congenital myasthenic syndrome. <i>Brain</i> , 2016, 139, 2143-2153.	3.7	45
294	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. <i>Progress in Retinal and Eye Research</i> , 2016, 55, 1-31.	7.3	58
295	The UniProtKB guide to the human proteome. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav120.	1.4	130
296	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. <i>Science</i> , 2016, 353, 78-82.	6.0	1,983
297	Recurrent candidiasis and early-onset gastric cancer in a patient with a genetically defined partial MYD88 defect. <i>Familial Cancer</i> , 2016, 15, 289-296.	0.9	13
298	Genome-wide nucleosome specificity and function of chromatin remodellers in ES cells. <i>Nature</i> , 2016, 530, 113-116.	13.7	211
299	Arabidopsis Rab Geranylgeranyltransferases Demonstrate Redundancy and Broad Substrate Specificity in Vitro. <i>Journal of Biological Chemistry</i> , 2016, 291, 1398-1410.	1.6	10
300	NONCODE 2016: an informative and valuable data source of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2016, 44, D203-D208.	6.5	574
301	Differential gene expression levels might explain association of LAIR2 polymorphisms with pemphigus. <i>Human Genetics</i> , 2016, 135, 233-244.	1.8	18
302	Lynx: a knowledge base and an analytical workbench for integrative medicine. <i>Nucleic Acids Research</i> , 2016, 44, D882-D887.	6.5	8
303	A human haploid gene trap collection to study lncRNAs with unusual RNA biology. <i>RNA Biology</i> , 2016, 13, 196-220.	1.5	1
304	Cancer Gene Profiling. <i>Methods in Molecular Biology</i> , 2016, , .	0.4	2
305	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , 2016, 6, 166-175.	7.7	282
306	DASHR: database of small human noncoding RNAs. <i>Nucleic Acids Research</i> , 2016, 44, D216-D222.	6.5	74
307	PGx: Putting Peptides to BED. <i>Journal of Proteome Research</i> , 2016, 15, 795-799.	1.8	20
308	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. <i>Bioinformatics</i> , 2016, 32, 424-431.	1.8	62
309	dbSUPER: a database of super-enhancers in mouse and human genome. <i>Nucleic Acids Research</i> , 2016, 44, D164-D171.	6.5	347
310	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	6.5	376

#	ARTICLE	IF	CITATIONS
311	Canine Distemper Virus in Wild Felids of Costa Rica. <i>Journal of Wildlife Diseases</i> , 2016, 52, 373-377.	0.3	10
312	NCG 5.0: updates of a manually curated repository of cancer genes and associated properties from cancer mutational screenings. <i>Nucleic Acids Research</i> , 2016, 44, D992-D999.	6.5	95
313	Hymenoptera Genome Database: integrating genome annotations in HymenopteraMine. <i>Nucleic Acids Research</i> , 2016, 44, D793-D800.	6.5	105
314	BISQUE: locus- and variant-specific conversion of genomic, transcriptomic and proteomic database identifiers. <i>Bioinformatics</i> , 2016, 32, 1598-1600.	1.8	4
315	Transcription-associated processes cause DNA double-strand breaks and translocations in neural stem/progenitor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2258-2263.	3.3	88
316	Gene Expression Variation Resolves Species and Individual Strains among Coral-Associated Dinoflagellates within the Genus <i>Symbiodinium</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 665-680.	1.1	144
317	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. <i>Nucleic Acids Research</i> , 2016, 44, D471-D480.	6.5	1,788
318	Structural Insights into <i>Mycobacterium tuberculosis</i> Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to <i>para</i> -Aminosalicylic Acid Resistance. <i>Biochemistry</i> , 2016, 55, 1107-1119.	1.2	22
319	Social defeat leads to changes in the endocannabinoid system: An overexpression of calreticulin and motor impairment in mice. <i>Behavioural Brain Research</i> , 2016, 303, 34-43.	1.2	15
320	Mutational Landscape of Aggressive Prostate Tumors in African American Men. <i>Cancer Research</i> , 2016, 76, 1860-1868.	0.4	61
321	An interactive environment for agile analysis and visualization of ChIP-sequencing data. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 349-357.	3.6	223
322	Differences in codon bias and GC content contribute to the balanced expression of TLR7 and TLR9. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1362-71.	3.3	102
323	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016, 44, D710-D716.	6.5	1,372
324	Reproducible, Scalable Fusion Gene Detection from RNA-Seq. <i>Methods in Molecular Biology</i> , 2016, 1381, 223-237.	0.4	3
325	Clinically Linked Mutations in the Central Domains of Cardiac Myosin-Binding Protein C with Distinct Phenotypes Show Differential Structural Effects. <i>Structure</i> , 2016, 24, 105-115.	1.6	13
326	The promise and peril of genomic screening in the general population. <i>Genetics in Medicine</i> , 2016, 18, 593-599.	1.1	53
327	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. <i>Nature Genetics</i> , 2016, 48, 134-143.	9.4	1,167
328	Advances in clinical next-generation sequencing: target enrichment and sequencing technologies. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 357-372.	1.5	63

#	ARTICLE	IF	CITATIONS
329	Integrating 400 million variants from 80,000 human samples with extensive annotations: towards a knowledge base to analyze disease cohorts. <i>BMC Bioinformatics</i> , 2016, 17, 24.	1.2	13
330	RDDpred: a condition-specific RNA-editing prediction model from RNA-seq data. <i>BMC Genomics</i> , 2016, 17, 5.	1.2	35
331	Systematic study of <i>cis</i> -antisense miRNAs in animal species reveals miR-3661 to target <i>PPP2CA</i> in human cells. <i>Rna</i> , 2016, 22, 87-95.	1.6	14
332	A Loss-of-Function Variant in a Minor Isoform of ANK3 Protects Against Bipolar Disorder and Schizophrenia. <i>Biological Psychiatry</i> , 2016, 80, 323-330.	0.7	31
333	Comprehensive genotyping reveals RPE65 as the most frequently mutated gene in Leber congenital amaurosis in Denmark. <i>European Journal of Human Genetics</i> , 2016, 24, 1071-1079.	1.4	69
334	Comprehensive translational control of tyrosine kinase expression by upstream open reading frames. <i>Oncogene</i> , 2016, 35, 1736-1742.	2.6	28
335	DIANA-LncBase v2: indexing microRNA targets on non-coding transcripts. <i>Nucleic Acids Research</i> , 2016, 44, D231-D238.	6.5	628
336	PlanMine – a mineable resource of planarian biology and biodiversity. <i>Nucleic Acids Research</i> , 2016, 44, D764-D773.	6.5	130
337	TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice. <i>Plant and Cell Physiology</i> , 2016, 57, e7-e7.	1.5	84
338	Death of a dogma: eukaryotic mRNAs can code for more than one protein. <i>Nucleic Acids Research</i> , 2016, 44, 14-23.	6.5	98
339	Genomic variability and protein species – Improving sequence coverage for proteogenomics. <i>Journal of Proteomics</i> , 2016, 134, 25-36.	1.2	10
340	Utility of whole-genome sequencing for detection of newborn screening disorders in a population cohort of 1,696 neonates. <i>Genetics in Medicine</i> , 2016, 18, 221-230.	1.1	101
341	Bovine Genome Database: new tools for gleaning function from the <i>Bos taurus</i> genome. <i>Nucleic Acids Research</i> , 2016, 44, D834-D839.	6.5	87
342	Proteomic Tools for the Analysis of Cytoskeleton Proteins. <i>Methods in Molecular Biology</i> , 2016, 1365, 385-413.	0.4	1
343	Cytoskeleton Methods and Protocols. <i>Methods in Molecular Biology</i> , 2016, 1365, v-vi.	0.4	5
344	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. <i>Nucleic Acids Research</i> , 2016, 44, D515-D522.	6.5	746
345	WGSA: an annotation pipeline for human genome sequencing studies. <i>Journal of Medical Genetics</i> , 2016, 53, 111-112.	1.5	96
346	A comprehensive comparative review of sequence-based predictors of DNA- and RNA-binding residues. <i>Briefings in Bioinformatics</i> , 2016, 17, 88-105.	3.2	88

#	ARTICLE	IF	CITATIONS
347	An Annotation Agnostic Algorithm for Detecting Nascent RNA Transcripts in GRO-Seq. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1070-1081.	1.9	19
348	Characterizing and annotating the genome using RNA-seq data. <i>Science China Life Sciences</i> , 2017, 60, 116-125.	2.3	35
349	The regulation of <i>FGF21</i> gene expression by metabolic factors and nutrients. <i>Hormone Molecular Biology and Clinical Investigation</i> , 2017, 30, .	0.3	29
350	Unveiling alternative splice diversity from human oligodendrocyte proteome data. <i>Journal of Proteomics</i> , 2017, 151, 293-301.	1.2	12
351	Proteogenomics from a bioinformatics angle: A growing field. <i>Mass Spectrometry Reviews</i> , 2017, 36, 584-599.	2.8	65
352	Hidden Markov Models for Protein Domain Homology Identification and Analysis. <i>Methods in Molecular Biology</i> , 2017, 1555, 47-58.	0.4	3
353	MRPrimerV: a database of PCR primers for RNA virus detection. <i>Nucleic Acids Research</i> , 2017, 45, D475-D481.	6.5	15
354	Lineage-specific mutational clustering in protein structures predicts evolutionary shifts in function. <i>Bioinformatics</i> , 2017, 33, 1338-1345.	1.8	11
355	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017, 18, 16.	3.8	151
356	Missing something? Codon aversion as a new character system in phylogenetics. <i>Cladistics</i> , 2017, 33, 545-556.	1.5	14
357	miR-92a enhances recombinant protein productivity in CHO cells by increasing intracellular cholesterol levels. <i>Biotechnology Journal</i> , 2017, 12, 1600488.	1.8	26
358	miRDis: a Web tool for endogenous and exogenous microRNA discovery based on deep-sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw140.	3.2	15
359	Immunodominance of Antibody Recognition of the HIV Envelope V2 Region in Ig-Humanized Mice. <i>Journal of Immunology</i> , 2017, 198, 1047-1055.	0.4	7
360	Building and Improving Reference Genome Assemblies. <i>Proceedings of the IEEE</i> , 2017, , 1-14.	16.4	6
361	HIVE-heptagon: A sensible variant-calling algorithm with post-alignment quality controls. <i>Genomics</i> , 2017, 109, 131-140.	1.3	12
362	Short-Term Subclinical Zinc Deficiency in Weaned Piglets Affects Cardiac Redox Metabolism and Zinc Concentration. <i>Journal of Nutrition</i> , 2017, 147, 521-527.	1.3	13
363	Comprehensive genetic exploration of selective tooth agenesis of mandibular incisors by exome sequencing. <i>Human Genome Variation</i> , 2017, 4, 17005.	0.4	20
364	Identification of a functional polymorphism affecting microRNA binding in the susceptibility locus 1q25.3 for colorectal cancer. <i>Molecular Carcinogenesis</i> , 2017, 56, 2014-2021.	1.3	10

#	ARTICLE	IF	CITATIONS
365	Genomic variants in mouse model induced by azoxymethane and dextran sodium sulfate improperly mimic human colorectal cancer. <i>Scientific Reports</i> , 2017, 7, 25.	1.6	37
366	Whole-exome sequencing analysis of supernumerary teeth occurrence in Japanese individuals. <i>Human Genome Variation</i> , 2017, 4, 16046.	0.4	11
367	Molecular phenotype and bleeding risks of an inherited platelet disorder in a family with a <i>RUNX1</i> frameshift mutation. <i>Haemophilia</i> , 2017, 23, e204-e213.	1.0	14
368	SITEX 2.0: Projections of protein functional sites on eukaryotic genes. Extension with orthologous genes. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650044.	0.3	1
369	Molecular Modeling Applied to Nanobiosystems. , 2017, , 179-220.		1
370	Recurrently deregulated lncRNAs in hepatocellular carcinoma. <i>Nature Communications</i> , 2017, 8, 14421.	5.8	279
371	Fructose-driven glycolysis supports anoxia resistance in the naked mole-rat. <i>Science</i> , 2017, 356, 307-311.	6.0	503
372	SmProt: a database of small proteins encoded by annotated coding and non-coding RNA loci. <i>Briefings in Bioinformatics</i> , 2018, 19, bbx005.	3.2	85
373	ORIO (Online Resource for Integrative Omics): a web-based platform for rapid integration of next generation sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, 5678-5690.	6.5	11
374	Determination of disease phenotypes and pathogenic variants from exome sequence data in the CAGI 4 gene panel challenge. <i>Human Mutation</i> , 2017, 38, 1201-1216.	1.1	5
375	Regulation of mitochondrial biogenesis in erythropoiesis by mTORC1-mediated protein translation. <i>Nature Cell Biology</i> , 2017, 19, 626-638.	4.6	126
376	SVPV: a structural variant prediction viewer for paired-end sequencing datasets. <i>Bioinformatics</i> , 2017, 33, 2032-2033.	1.8	9
377	Expression proteomics study to determine metallodrug targets and optimal drug combinations. <i>Scientific Reports</i> , 2017, 7, 1590.	1.6	19
378	ChIP-seq analysis of genomic binding regions of five major transcription factors in mouse epiblast stem cells that highlights a central role for ZIC2. <i>Development (Cambridge)</i> , 2017, 144, 1948-1958.	1.2	31
379	Trinucleotide-repeat expanded and normal DMPK transcripts contain unusually long poly(A) tails despite differential nuclear residence. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 740-749.	0.9	7
380	Structural variants caused by <i>Alu</i> insertions are associated with risks for many human diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3984-E3992.	3.3	113
381	Comprehensive strategy for the design of precision drugs and identification of genetic signature behind proneness of the disease—a pharmacogenomic approach. <i>Functional and Integrative Genomics</i> , 2017, 17, 375-385.	1.4	9
382	ChimerScope: a novel alignment-free algorithm for fusion transcript prediction using paired-end RNA-Seq data. <i>Nucleic Acids Research</i> , 2017, 45, e120-e120.	6.5	29

#	ARTICLE	IF	CITATIONS
383	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. <i>Journal of Physiology</i> , 2017, 595, 4611-4630.	1.3	11
384	Neandertal and Denisovan DNA from Pleistocene sediments. <i>Science</i> , 2017, 356, 605-608.	6.0	329
385	Genomic Database Searching. <i>Methods in Molecular Biology</i> , 2017, 1525, 225-269.	0.4	2
386	Utilization of genomic sequencing for population screening of immunodeficiencies in the newborn. <i>Genetics in Medicine</i> , 2017, 19, 1367-1375.	1.1	23
387	Identification of a novel <i>RASD1</i> somatic mutation in a <i>USP8</i> -mutated corticotroph adenoma. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a001602.	0.5	8
388	CAGI4 SickKids clinical genomes challenge: A pipeline for identifying pathogenic variants. <i>Human Mutation</i> , 2017, 38, 1169-1181.	1.1	11
389	Mining for Micropeptides. <i>Trends in Cell Biology</i> , 2017, 27, 685-696.	3.6	191
390	CAGI4 Crohn's exome challenge: Marker SNP versus exome variant models for assigning risk of Crohn disease. <i>Human Mutation</i> , 2017, 38, 1225-1234.	1.1	15
391	Bioinformatic analysis of bacteria and host cell dual RNA-sequencing experiments. <i>Briefings in Bioinformatics</i> , 2018, 19, 1115-1129.	3.2	16
392	lncRNA-screen: an interactive platform for computationally screening long non-coding RNAs in large genomics datasets. <i>BMC Genomics</i> , 2017, 18, 434.	1.2	22
393	Radiation induced pulmonary fibrosis as a model of progressive fibrosis: Contributions of DNA damage, inflammatory response and cellular senescence genes. <i>Experimental Lung Research</i> , 2017, 43, 134-149.	0.5	32
394	Social well-being is associated with less pro-inflammatory and pro-metastatic leukocyte gene expression in women after surgery for breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017, 165, 169-180.	1.1	23
395	A compilation of Web-based research tools for miRNA analysis. <i>Briefings in Functional Genomics</i> , 2017, 16, 249-273.	1.3	32
396	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
397	Badger macrophages fail to produce nitric oxide, a key anti-mycobacterial effector molecule. <i>Scientific Reports</i> , 2017, 7, 45470.	1.6	11
398	The Human Gene Mutation Database: towards a comprehensive repository of inherited mutation data for medical research, genetic diagnosis and next-generation sequencing studies. <i>Human Genetics</i> , 2017, 136, 665-677.	1.8	1,106
399	Computational predictors fail to identify amino acid substitution effects at rheostat positions. <i>Scientific Reports</i> , 2017, 7, 41329.	1.6	47
400	Modeling the Mutational and Phenotypic Landscapes of Pelizaeus-Merzbacher Disease with Human iPSC-Derived Oligodendrocytes. <i>American Journal of Human Genetics</i> , 2017, 100, 617-634.	2.6	52

#	ARTICLE	IF	CITATIONS
401	Atypical Protein Phosphatase 2A Gene Families Do Not Expand via Paleopolyploidization. <i>Plant Physiology</i> , 2017, 173, 1283-1300.	2.3	46
402	Using Baseline Transcriptional Connectomes in Rat to Identify Genetic Pathways Associated with Predisposition to Complex Traits. <i>Methods in Molecular Biology</i> , 2017, 1488, 299-317.	0.4	2
403	Binding Sites for Amyloid- β^2 Oligomers and Synaptic Toxicity. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a024075.	2.9	76
404	The novel homozygous KCNJ10 c.986T>C (p.(Leu329Pro)) variant is pathogenic for the SeSAME/EAST homologue in Malinois dogs. <i>European Journal of Human Genetics</i> , 2017, 25, 222-226.	1.4	16
405	Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 4-23.	1.2	1,267
406	Prediction of genome-wide DNA methylation in repetitive elements. <i>Nucleic Acids Research</i> , 2017, 45, 8697-8711.	6.5	106
407	Molecular basis of CENP-C association with the CENP-A nucleosome at yeast centromeres. <i>Genes and Development</i> , 2017, 31, 1958-1972.	2.7	45
408	Preprocessing and Quality Control for Whole-Genome Sequences from the Illumina HiSeq X Platform. <i>Methods in Molecular Biology</i> , 2017, 1666, 629-647.	0.4	10
409	Understanding Sequence Conservation With Deep Learning. , 2017, , .		4
410	A Resource of Genome-Wide Single Nucleotide Polymorphisms (Snps) for the Conservation and Management of Golden Eagles. <i>Journal of Raptor Research</i> , 2017, 51, 368-377.	0.2	8
411	Integrating evolutionary and regulatory information with a multispecies approach implicates genes and pathways in obsessive-compulsive disorder. <i>Nature Communications</i> , 2017, 8, 774.	5.8	52
412	Framework and resource for more than 11,000 gene-transcript-protein-reaction associations in human metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9740-E9749.	3.3	29
413	Discovery of Variants Underlying Host Susceptibility to Virus Infection Using Whole-Exome Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1656, 209-227.	0.4	0
414	Finding Homologs in Amino Acid Sequences Using Network BLAST Searches. <i>Current Protocols in Bioinformatics</i> , 2017, 59, 3.4.1-3.4.24.	25.8	10
415	RAIN: RNA-protein Association and Interaction Networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw167.	1.4	53
416	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.2	9
417	Identification of new TSGA10 transcript variants in human testis with conserved regulatory RNA elements in 5'untranslated region and distinct expression in breast cancer. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 973-982.	0.9	6
419	Comprehensive analysis of gene expression patterns in Friedreich's ataxia fibroblasts by RNA sequencing reveals altered levels of protein synthesis factors and solute carriers. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 1353-1369.	1.2	38

#	ARTICLE	IF	CITATIONS
420	The rises and falls of opsin genes in 59 ray-finned fish genomes and their implications for environmental adaptation. <i>Scientific Reports</i> , 2017, 7, 15568.	1.6	76
421	Genome-wide discovery of long intergenic noncoding RNAs and their epigenetic signatures in the rat. <i>Scientific Reports</i> , 2017, 7, 14817.	1.6	3
422	Using the NONCODE Database Resource. <i>Current Protocols in Bioinformatics</i> , 2017, 58, 12.16.1-12.16.19.	25.8	14
423	Transcriptional consequences of XPA disruption in human cell lines. <i>DNA Repair</i> , 2017, 57, 76-90.	1.3	19
424	Increasing evidence for the presence of alternative proteins in human tissues and cell lines. <i>Applied Cancer Research</i> , 2017, 37, .	1.0	1
425	Genome-wide DNA methylation measurements in prostate tissues uncovers novel prostate cancer diagnostic biomarkers and transcription factor binding patterns. <i>BMC Cancer</i> , 2017, 17, 273.	1.1	48
426	A variant by any name: quantifying annotation discordance across tools and clinical databases. <i>Genome Medicine</i> , 2017, 9, 7.	3.6	58
427	Genome annotation for clinical genomic diagnostics: strengths and weaknesses. <i>Genome Medicine</i> , 2017, 9, 49.	3.6	51
428	FCGR Polymorphisms Influence Response to IL2 in Metastatic Renal Cell Carcinoma. <i>Clinical Cancer Research</i> , 2017, 23, 2159-2168.	3.2	12
429	Metazoan evolution of the armadillo repeat superfamily. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 525-541.	2.4	37
430	Hereditary Dopamine Transporter Deficiency Syndrome: Challenges in Diagnosis and Treatment. <i>Neuropediatrics</i> , 2017, 48, 049-052.	0.3	28
431	Alternative Splicing May Not Be the Key to Proteome Complexity. <i>Trends in Biochemical Sciences</i> , 2017, 42, 98-110.	3.7	277
432	TACO produces robust multisample transcriptome assemblies from RNA-seq. <i>Nature Methods</i> , 2017, 14, 68-70.	9.0	157
433	Novel algorithms for finding the closest l-mers in biological data. , 2017, , .		2
434	Evolution of the Human Genome I. <i>Evolutionary Studies</i> , 2017, , .	0.2	1
435	Protein-Coding and Noncoding RNA Genes. <i>Evolutionary Studies</i> , 2017, , 93-116.	0.2	2
436	Large-scale determination and characterization of cell type-specific regulatory elements in the human genome. <i>Journal of Molecular Cell Biology</i> , 2017, 9, 463-476.	1.5	6
437	Putative enhancer sites in the bovine genome are enriched with variants affecting complex traits. <i>Genetics Selection Evolution</i> , 2017, 49, 56.	1.2	41

#	ARTICLE	IF	CITATIONS
438	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). <i>Nucleic Acids Research</i> , 2017, 45, D896-D901.	6.5	1,932
439	Explorative visual analytics on interval-based genomic data and their metadata. <i>BMC Bioinformatics</i> , 2017, 18, 536.	1.2	4
440	Present Scenario of Long Non-Coding RNAs in Plants. <i>Non-coding RNA</i> , 2017, 3, 16.	1.3	51
441	Toward a Metagenomic Understanding on the Bacterial Composition and Resistome in Hong Kong Banknotes. <i>Frontiers in Microbiology</i> , 2017, 8, 632.	1.5	21
442	Mapping the mouse Allelome reveals tissue-specific regulation of allelic expression. <i>ELife</i> , 2017, 6, .	2.8	120
443	Nanoparticles for death-induced gene therapy in cancer (Review). <i>Molecular Medicine Reports</i> , 2018, 17, 1413-1420.	1.1	17
444	HMCAN-diff: a method to detect changes in histone modifications in cells with different genetic characteristics. <i>Nucleic Acids Research</i> , 2017, 45, gkw1319.	6.5	8
445	Genetic alterations in seborrhic keratoses. <i>Oncotarget</i> , 2017, 8, 36639-36649.	0.8	34
446	RNA sequencing analyses reveal novel differentially expressed genes and pathways in pancreatic cancer. <i>Oncotarget</i> , 2017, 8, 42537-42547.	0.8	46
448	Bioinformatics for Prohormone and Neuropeptide Discovery. <i>Methods in Molecular Biology</i> , 2018, 1719, 71-96.	0.4	6
449	Developing reduced SNP assays from whole-genome sequence data to estimate introgression in an organism with complex genetic patterns, the Iberian honeybee (<i>Apis mellifera</i>) Tj ETQq0 0 0 ngBT /Overlock 10 Tf	0.5	20
450	Germline Genetic IKZF1 Variation and Predisposition to Childhood Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2018, 33, 937-948.e8.	7.7	142
451	RNA-Seq-mediated transcriptomic analysis of heat stress response in a polar <i>Chlorella</i> sp. (Trebouxiophyceae, Chlorophyta). <i>Journal of Applied Phycology</i> , 2018, 30, 3103-3119.	1.5	16
452	Intramembranal disulfide cross-linking elucidates the super-quaternary structure of mammalian CatSpers. <i>Reproductive Biology</i> , 2018, 18, 76-82.	0.9	11
453	Effects of repeated long-term psychosocial stress and acute cannabinoid exposure on mouse corticostriatal circuitries: Implications for neuropsychiatric disorders. <i>CNS Neuroscience and Therapeutics</i> , 2018, 24, 528-538.	1.9	11
454	Genomic dissection of enhancers uncovers principles of combinatorial regulation and cell type-specific wiring of enhancer-promoter contacts. <i>Nucleic Acids Research</i> , 2018, 46, 2868-2882.	6.5	30
455	Methods for Mapping the Extracellular and Membrane Proteome in the Avian Embryo, and Identification of Putative Vascular Targets or Endothelial Genes. <i>Methods in Molecular Biology</i> , 2018, 1722, 31-56.	0.4	1
456	Respiratory Syncytial Virus Infection Changes Cargo Composition of Exosome Released from Airway Epithelial Cells. <i>Scientific Reports</i> , 2018, 8, 387.	1.6	93

#	ARTICLE	IF	CITATIONS
457	Complete motif analysis of sequence requirements for translation initiation at non-AUG start codons. <i>Nucleic Acids Research</i> , 2018, 46, 985-994.	6.5	68
458	A survey of localized sequence rearrangements in human DNA. <i>Nucleic Acids Research</i> , 2018, 46, 1661-1673.	6.5	21
459	Proteomic analysis of micro-scale bioreactors as scale-down model for a mAb producing CHO industrial fed-batch platform. <i>Journal of Biotechnology</i> , 2018, 279, 27-36.	1.9	18
460	A common polymorphic variant of <sc>UGT</sc>1A5 displays increased activity due to optimized cofactor binding. <i>FEBS Letters</i> , 2018, 592, 1837-1846.	1.3	10
461	Genome-wide linkage analysis in Spanish melanoma-prone families identifies a new familial melanoma susceptibility locus at 11q. <i>European Journal of Human Genetics</i> , 2018, 26, 1188-1193.	1.4	4
462	MSIQ: Joint modeling of multiple RNA-seq samples for accurate isoform quantification. <i>Annals of Applied Statistics</i> , 2018, 12, 510-539.	0.5	5
463	Loss and gain of N-linked glycosylation sequons due to single-nucleotide variation in cancer. <i>Scientific Reports</i> , 2018, 8, 4322.	1.6	15
464	Transcriptome sequencing of an Antarctic microalga, <i>Chlorella</i> sp. (Trebouxiophyceae, Chlorophyta) subjected to short-term ultraviolet radiation stress. <i>Journal of Applied Phycology</i> , 2018, 30, 87-99.	1.5	27
465	Sparselso: a novel Bayesian approach to identify alternatively spliced isoforms from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 56-63.	1.8	7
466	A heart-enriched antisense long non-coding RNA regulates the balance between cardiac and skeletal muscle triadin. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 247-258.	1.9	15
467	Polymorphism of the <i>STAT5A</i>, <i>MTNR1A</i> and <i>TNF α </i> genes and their effect on dairy production in <i>Bubalus bubalis</i>. <i>Italian Journal of Animal Science</i> , 2018, 17, 31-37.	0.8	6
468	<i>TP53</i> Germline Variations Influence the Predisposition and Prognosis of B-Cell Acute Lymphoblastic Leukemia in Children. <i>Journal of Clinical Oncology</i> , 2018, 36, 591-599.	0.8	121
469	Reveal cell type-specific regulatory elements and their characterized histone code classes via a hidden Markov model. <i>BMC Genomics</i> , 2018, 19, 903.	1.2	0
470	OBSOLETE: Transcriptome and Epigenome Applications for Coronary Heart Disease Research. , 2018, , .		0
471	Overlapping genes and the proteins they encode differ significantly in their sequence composition from non-overlapping genes. <i>PLoS ONE</i> , 2018, 13, e0202513.	1.1	45
472	Identification of deleterious and regulatory genomic variations in known asthma loci. <i>Respiratory Research</i> , 2018, 19, 248.	1.4	5
473	New antigens for the serological diagnosis of human visceral leishmaniasis identified by immunogenomic screening. <i>PLoS ONE</i> , 2018, 13, e0209599.	1.1	16
474	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , 2018, 9, 598.	1.0	34

#	ARTICLE	IF	CITATIONS
475	Transcription Factor Co-expression Networks of Adipose RNA-Seq Data Reveal Regulatory Mechanisms of Obesity. <i>Current Genomics</i> , 2018, 19, 289-299.	0.7	9
476	Elevated expression of a minor isoform of ANK3 is a risk factor for bipolar disorder. <i>Translational Psychiatry</i> , 2018, 8, 210.	2.4	24
477	Gene synthesis allows biologists to source genes from farther away in the tree of life. <i>Nature Communications</i> , 2018, 9, 4425.	5.8	20
478	A Whole Methylome Study of Ethanol Exposure in Brain and Blood: An Exploration of the Utility of Peripheral Blood as Proxy Tissue for Brain in Alcohol Methylation Studies. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2360-2368.	1.4	12
479	Alternative splicing links histone modifications to stem cell fate decision. <i>Genome Biology</i> , 2018, 19, 133.	3.8	53
480	Umap and Bimap: quantifying genome and methylome mappability. <i>Nucleic Acids Research</i> , 2018, 46, e120.	6.5	94
481	Disease-Associated Short Tandem Repeats Co-localize with Chromatin Domain Boundaries. <i>Cell</i> , 2018, 175, 224-238.e15.	13.5	169
482	A family of long intergenic non-coding RNA genes in human chromosomal region 22q11.2 carry a DNA translocation breakpoint/AT-rich sequence. <i>PLoS ONE</i> , 2018, 13, e0195702.	1.1	16
483	Multiple large inversions and breakpoint rewiring of gene expression in the evolution of the fire ant social supergene. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180221.	1.2	30
484	Towards a complete map of the human long non-coding RNA transcriptome. <i>Nature Reviews Genetics</i> , 2018, 19, 535-548.	7.7	451
485	An automated method for detecting alternatively spliced protein domains. <i>Bioinformatics</i> , 2018, 34, 3809-3816.	1.8	0
486	One for all and all for One: Improving replication of genetic studies through network diffusion. <i>PLoS Genetics</i> , 2018, 14, e1007306.	1.5	22
487	A comprehensive inventory of TLX1 controlled long non-coding RNAs in T-cell acute lymphoblastic leukemia through polyA+ and total RNA sequencing. <i>Haematologica</i> , 2018, 103, e585-e589.	1.7	20
488	High sample throughput genotyping for estimating C-lineage introgression in the dark honeybee: an accurate and cost-effective SNP-based tool. <i>Scientific Reports</i> , 2018, 8, 8552.	1.6	27
489	The Environmental Exposures and Inner- and Intercity Traffic Flows of the Metro System May Contribute to the Skin Microbiome and Resistome. <i>Cell Reports</i> , 2018, 24, 1190-1202.e5.	2.9	56
490	An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. <i>BMC Genomics</i> , 2018, 19, 476.	1.2	35
491	Association of the Polygenic Scores for Personality Traits and Response to Selective Serotonin Reuptake Inhibitors in Patients with Major Depressive Disorder. <i>Frontiers in Psychiatry</i> , 2018, 9, 65.	1.3	38
492	Clinical Genetics in Interstitial Lung Disease. <i>Frontiers in Medicine</i> , 2018, 5, 116.	1.2	19

#	ARTICLE	IF	CITATIONS
493	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. <i>Nature Communications</i> , 2018, 9, 2601.	5.8	47
494	VARReporter: variant reporter for cancer research of massive parallel sequencing. <i>BMC Genomics</i> , 2018, 19, 86.	1.2	2
495	Cattle infection response network and its functional modules. <i>BMC Immunology</i> , 2018, 19, 2.	0.9	7
496	Don't go in circles: confounding factors in gene expression profiling. <i>EMBO Journal</i> , 2018, 37, .	3.5	8
497	Immunogenomic screening approach to identify new antigens for the serological diagnosis of chronic Chagasâ€™ disease. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 6069-6080.	1.7	16
498	Beta-hydroxybutyrate infusion identifies acutely differentially expressed genes related to metabolism and reproduction in the hypothalamus and pituitary of castrated male sheep. <i>Physiological Genomics</i> , 2018, 50, 468-477.	1.0	2
499	JustOrthologs: a fast, accurate and user-friendly ortholog identification algorithm. <i>Bioinformatics</i> , 2019, 35, 546-552.	1.8	19
500	Exploring the functional impact of alternative splicing on human protein isoforms using available annotation sources. <i>Briefings in Bioinformatics</i> , 2019, 20, 1754-1768.	3.2	23
501	Bioinformatics Data Models, Representation and Storage. , 2019, , 110-116.		4
502	Efficient Algorithms for Finding the Closest l-mers in Biological Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, , 1-1.	1.9	0
503	DASHR 2.0: integrated database of human small non-coding RNA genes and mature products. <i>Bioinformatics</i> , 2019, 35, 1033-1039.	1.8	46
504	Hotspot DAXX, PTCH2 and CYFIP2 mutations in pancreatic neuroendocrine neoplasms. <i>Endocrine-Related Cancer</i> , 2019, 26, 1-12.	1.6	24
505	A practical guide for DNase-seq data analysis: from data management to common applications. <i>Briefings in Bioinformatics</i> , 2019, 20, 1865-1877.	3.2	7
506	Depletion of Hemoglobin Transcripts and Long-Read Sequencing Improves the Transcriptome Annotation of the Polar Bear (<i>Ursus maritimus</i>). <i>Frontiers in Genetics</i> , 2019, 10, 643.	1.1	23
507	MicroPro: using metagenomic unmapped reads to provide insights into human microbiota and disease associations. <i>Genome Biology</i> , 2019, 20, 154.	3.8	29
508	Transketolase and vitamin B1 influence on ROS-dependent neutrophil extracellular traps (NETs) formation. <i>PLoS ONE</i> , 2019, 14, e0221016.	1.1	16
509	Genome-wide investigation of intragenic DNA methylation identifies <i>ZMIZ1</i> gene as a prognostic marker in glioblastoma and multiple cancer types. <i>International Journal of Cancer</i> , 2019, 145, 3425-3435.	2.3	16
510	The Genome of the Steller Sea Lion (<i>Eumetopias jubatus</i>). <i>Genes</i> , 2019, 10, 486.	1.0	4

#	ARTICLE	IF	CITATIONS
511	Patient-specific cancer genes contribute to recurrently perturbed pathways and establish therapeutic vulnerabilities in esophageal adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 3101.	5.8	34
512	Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. <i>BMC Medical Genomics</i> , 2019, 12, 104.	0.7	10
513	Genome-wide mapping and profiling of γ H2AX binding hotspots in response to different replication stress inducers. <i>BMC Genomics</i> , 2019, 20, 579.	1.2	20
514	Chromosome-Level Alpaca Reference Genome VicPac3.1 Improves Genomic Insight Into the Biology of New World Camelids. <i>Frontiers in Genetics</i> , 2019, 10, 586.	1.1	19
515	RNA profiling of human testicular cells identifies syntenic lncRNAs associated with spermatogenesis. <i>Human Reproduction</i> , 2019, 34, 1278-1290.	0.4	35
516	Heterogeneous Loop Model to Infer 3D Chromosome Structures from Hi-C. <i>Biophysical Journal</i> , 2019, 117, 613-625.	0.2	20
517	Rare DEGS1 variant significantly alters de novo ceramide synthesis pathway. <i>Journal of Lipid Research</i> , 2019, 60, 1630-1639.	2.0	16
518	Paternal impacts on development: identification of genomic regions vulnerable to oxidative DNA damage in human spermatozoa. <i>Human Reproduction</i> , 2019, 34, 1876-1890.	0.4	43
519	The CLN3 gene and protein: What we know. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e859.	0.6	52
520	Identification of novel TGF- β 2 regulated genes with pro-migratory roles. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 165537.	1.8	7
521	Genome-wide quantification of ADAR adenosine-to-inosine RNA editing activity. <i>Nature Methods</i> , 2019, 16, 1131-1138.	9.0	126
522	BC200 overexpression contributes to luminal and triple negative breast cancer pathogenesis. <i>BMC Cancer</i> , 2019, 19, 994.	1.1	14
523	An expanded landscape of human long noncoding RNA. <i>Nucleic Acids Research</i> , 2019, 47, 7842-7856.	6.5	92
524	ATG5 cancer mutations and alternative mRNA splicing reveal a conjugation switch that regulates ATG12-ATG5-ATG16L1 complex assembly and autophagy. <i>Cell Discovery</i> , 2019, 5, 42.	3.1	44
525	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4267.	5.8	139
526	Translating Science to Medicine: When Will the Rubber Meet the Road?. <i>European Urology</i> , 2019, 76, 560-561.	0.9	0
527	Realizing the potential of full-length transcriptome sequencing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190097.	1.8	92
528	COXPRESdb v7: a gene coexpression database for 11 animal species supported by 23 coexpression platforms for technical evaluation and evolutionary inference. <i>Nucleic Acids Research</i> , 2019, 47, D55-D62.	6.5	125

#	ARTICLE	IF	CITATIONS
529	Bridging the gap between reference and real transcriptomes. <i>Genome Biology</i> , 2019, 20, 112.	3.8	38
530	Assessing concordance among human, in silico predictions and functional assays on genetic variant classification. <i>Bioinformatics</i> , 2019, 35, 5163-5170.	1.8	4
531	Rapid molecular evolution of pain insensitivity in multiple African rodents. <i>Science</i> , 2019, 364, 852-859.	6.0	57
532	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	1.1	27
533	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGI intellectual disability challenge. <i>Human Mutation</i> , 2019, 40, 1330-1345.	1.1	11
534	Altered microRNA expression profiles in large offspring syndrome and Beckwith-Wiedemann syndrome. <i>Epigenetics</i> , 2019, 14, 850-876.	1.3	32
535	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	1.0	25
536	AutoMLST: an automated web server for generating multi-locus species trees highlighting natural product potential. <i>Nucleic Acids Research</i> , 2019, 47, W276-W282.	6.5	286
538	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	1.3	147
539	Evolution of biosequence search algorithms: a brief survey. <i>Bioinformatics</i> , 2019, 35, 3547-3552.	1.8	27
540	Antibiotic Treatment Drives the Diversification of the Human Gut Resistome. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 39-51.	3.0	51
541	Fine-Scale Characterization of Genomic Structural Variation in the Human Genome Reveals Adaptive and Biomedically Relevant Hotspots. <i>Genome Biology and Evolution</i> , 2019, 11, 1136-1151.	1.1	41
542	A comprehensive overview of common polymorphic variants that cause missense mutations in human CYPs and UGTs. <i>Biomedicine and Pharmacotherapy</i> , 2019, 111, 983-992.	2.5	9
543	Comparison of different functional prediction scores using a gene-based permutation model for identifying cancer driver genes. <i>BMC Medical Genomics</i> , 2019, 12, 22.	0.7	12
544	A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. <i>Molecular Ecology Resources</i> , 2019, 19, 997-1014.	2.2	24
545	A gene regulatory architecture that controls region-independent dynamics of oligodendrocyte differentiation. <i>Glia</i> , 2019, 67, 825-843.	2.5	36
546	Genetic Association of Olanzapine Treatment Response in Han Chinese Schizophrenia Patients. <i>Frontiers in Pharmacology</i> , 2019, 10, 177.	1.6	13
547	A combined computational strategy of sequence and structural analysis predicts the existence of a functional eicosanoid pathway in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2019, 14, e0211897.	1.1	25

#	ARTICLE	IF	CITATIONS
549	Advances in Plant Transgenics: Methods and Applications. , 2019, , .		2
550	An Overview of the Intrinsic Role of Citrullination in Autoimmune Disorders. Journal of Immunology Research, 2019, 2019, 1-39.	0.9	65
551	eIF4A2 drives repression of translation at initiation by Ccr4-Not through purine-rich motifs in the 5'UTR. Genome Biology, 2019, 20, 262.	3.8	39
552	Immunosignature Screening for Multiple Cancer Subtypes Based on Expression Rule. Frontiers in Bioengineering and Biotechnology, 2019, 7, 370.	2.0	9
553	Splice-Junction-Based Mapping of Alternative Isoforms in the Human Proteome. Cell Reports, 2019, 29, 3751-3765.e5.	2.9	64
554	Comprehensive Identification and Characterization of Human Secretome Based on Integrative Proteomic and Transcriptomic Data. Frontiers in Cell and Developmental Biology, 2019, 7, 299.	1.8	25
555	SQulRE reveals locus-specific regulation of interspersed repeat expression. Nucleic Acids Research, 2019, 47, e27-e27.	6.5	115
556	ExtRamp: a novel algorithm for extracting the ramp sequence based on the tRNA adaptation index or relative codon adaptiveness. Nucleic Acids Research, 2019, 47, 1123-1131.	6.5	13
557	Genome-wide association study of an unusual dolphin mortality event reveals candidate genes for susceptibility and resistance to cetacean morbillivirus. Evolutionary Applications, 2019, 12, 718-732.	1.5	13
558	Integrated omics profiling reveals novel patterns of epigenetic programming in cancer-associated myofibroblasts. Carcinogenesis, 2019, 40, 500-512.	1.3	10
559	SEdb: a comprehensive human super-enhancer database. Nucleic Acids Research, 2019, 47, D235-D243.	6.5	166
560	DNMT3L facilitates DNA methylation partly by maintaining DNMT3A stability in mouse embryonic stem cells. Nucleic Acids Research, 2019, 47, 152-167.	6.5	99
561	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
562	Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bigheaded carps in the Mississippi River Basin. Evolutionary Applications, 2020, 13, 263-277.	1.5	20
563	The Clinical Genome and Ancestry Report: An interactive web application for prioritizing clinically implicated variants from genome sequencing data with ancestry composition. Human Mutation, 2020, 41, 387-396.	1.1	0
564	Matching whole genomes to rare genetic disorders: Identification of potential causative variants using phenotype-weighted knowledge in the CAGI SickKids5 clinical genomes challenge. Human Mutation, 2020, 41, 347-362.	1.1	4
565	Exome-chip association analysis of intracranial aneurysms. Neurology, 2020, 94, e481-e488.	1.5	5
566	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120

#	ARTICLE	IF	CITATIONS
567	Twin enzymes, divergent control: The cholesterologenic enzymes DHCR14 and LBR are differentially regulated transcriptionally and post-translationally. <i>Journal of Biological Chemistry</i> , 2020, 295, 2850-2865.	1.6	23
568	Targeted sequencing of the LRRTM gene family in suicide attempters with bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 128-139.	1.1	6
569	Codon use and aversion is largely phylogenetically conserved across the tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106697.	1.2	10
570	Evaluation of polymorphisms in microRNA-binding sites and pancreatic cancer risk in Chinese population. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 2252-2259.	1.6	6
571	Non-invasive epigenomic molecular phenotyping of the human brain via liquid biopsy of cerebrospinal fluid and next generation sequencing. <i>European Journal of Neuroscience</i> , 2020, 52, 4536-4545.	1.2	5
572	Frameshift Variant in Novel Adenosine-A1-Receptor Homolog Associated With Bovine Spastic Syndrome/Late-Onset Bovine Spastic Paresis in Holstein Sires. <i>Frontiers in Genetics</i> , 2020, 11, 591794.	1.1	3
573	Diversification of CpG-Island Promoters Revealed by Comparative Analysis Between Human and Rhesus Monkey Genomes. <i>Mammalian Genome</i> , 2020, 31, 240-251.	1.0	4
574	Newly established gastrointestinal cancer cell lines retain the genomic and immunophenotypic landscape of their parental cancers. <i>Scientific Reports</i> , 2020, 10, 17895.	1.6	5
575	Prediction of Exons using Normalized Probability Parameters derived from Statistical Analysis of Coding Sequences. , 2020, , .		0
576	Protein Databases Related to Liquid-Liquid Phase Separation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6796.	1.8	27
577	Genome-Wide Transcriptional Analysis Reveals Alternative Splicing Event Profiles in Hepatocellular Carcinoma and Their Prognostic Significance. <i>Frontiers in Genetics</i> , 2020, 11, 879.	1.1	12
578	PCOSKBR2: a database of genes, diseases, pathways, and networks associated with polycystic ovary syndrome. <i>Scientific Reports</i> , 2020, 10, 14738.	1.6	16
579	Predicting the Disease Risk of Protein Mutation Sequences With Pre-training Model. <i>Frontiers in Genetics</i> , 2020, 11, 605620.	1.1	4
580	Codon Pairs are Phylogenetically Conserved: A comprehensive analysis of codon pairing conservation across the Tree of Life. <i>PLoS ONE</i> , 2020, 15, e0232260.	1.1	8
581	Dynamics of the transcriptional landscape during human fetal testis and ovary development. <i>Human Reproduction</i> , 2020, 35, 1099-1119.	0.4	22
582	An Independent Locus Upstream of ASIP Controls Variation in the Shade of the Bay Coat Colour in Horses. <i>Genes</i> , 2020, 11, 606.	1.0	17
583	MeCP2 regulates gene expression through recognition of H3K27me3. <i>Nature Communications</i> , 2020, 11, 3140.	5.8	26
584	Type II Alexander disease caused by splicing errors and aberrant overexpression of an uncharacterized GFAP isoform. <i>Human Mutation</i> , 2020, 41, 1131-1137.	1.1	14

#	ARTICLE	IF	CITATIONS
585	Identification of QTL and loci for egg production traits to tropical climate conditions in chickens. <i>Livestock Science</i> , 2020, 234, 103980.	0.6	2
586	Formation of human long intergenic non-coding RNA genes, pseudogenes, and protein genes: Ancestral sequences are key players. <i>PLoS ONE</i> , 2020, 15, e0230236.	1.1	6
587	Nursing Genetic Research: New Insights Linking Breast Cancer Genetics and Bone Density. <i>Healthcare (Switzerland)</i> , 2020, 8, 172.	1.0	2
588	Variation of Human Neural Stem Cells Generating Organizer States In Vitro before Committing to Cortical Excitatory or Inhibitory Neuronal Fates. <i>Cell Reports</i> , 2020, 31, 107599.	2.9	20
589	FilTar: using RNA-Seq data to improve microRNA target prediction accuracy in animals. <i>Bioinformatics</i> , 2020, 36, 2410-2416.	1.8	3
590	Beyond mass spectrometry, the next step in proteomics. <i>Science Advances</i> , 2020, 6, eaax8978.	4.7	208
591	ORSO (Online Resource for Social Omics): A data-driven social network connecting scientists to genomics datasets. <i>PLoS Computational Biology</i> , 2020, 16, e1007571.	1.5	2
592	The genome-wide landscape of C:G > T:A polymorphism at the CpG contexts in the human population. <i>BMC Genomics</i> , 2020, 21, 270.	1.2	20
593	Transient vitamin B5 starving improves mammalian cell homeostasis and protein production. <i>Metabolic Engineering</i> , 2020, 60, 77-86.	3.6	13
594	HIPPIE2: a method for fine-scale identification of physically interacting chromatin regions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa022.	1.5	2
595	REV-ERB β activates the mTOR signalling pathway and promotes myotubes differentiation. <i>Biology of the Cell</i> , 2020, 112, 213-221.	0.7	6
596	DolphinNext: a distributed data processing platform for high throughput genomics. <i>BMC Genomics</i> , 2020, 21, 310.	1.2	66
597	Clinical trait-connected network analysis reveals transcriptional markers of active psoriasis treatment with Liangxue-Jiedu decoction. <i>Journal of Ethnopharmacology</i> , 2021, 268, 113551.	2.0	14
598	IntAPT: integrated assembly of phenotype-specific transcripts from multiple RNA-seq profiles. <i>Bioinformatics</i> , 2021, 37, 650-658.	1.8	1
599	A long-term study of AAV gene therapy in dogs with hemophilia A identifies clonal expansions of transduced liver cells. <i>Nature Biotechnology</i> , 2021, 39, 47-55.	9.4	238
600	REV-ERB β alters circadian rhythms by modulating mTOR signaling. <i>Molecular and Cellular Endocrinology</i> , 2021, 521, 111108.	1.6	10
601	OMA orthology in 2021: website overhaul, conserved isoforms, ancestral gene order and more. <i>Nucleic Acids Research</i> , 2021, 49, D373-D379.	6.5	137
602	Molecular characterization of ulcerative colitis-associated colorectal carcinomas. <i>Modern Pathology</i> , 2021, 34, 1153-1166.	2.9	7

#	ARTICLE	IF	CITATIONS
604	HGFDB: a collective database of helmeted guinea fowl genomics. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	2
607	Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. Gut Microbes, 2021, 13, 1-19.	4.3	24
608	MicroExonator enables systematic discovery and quantification of microexons across mouse embryonic development. Genome Biology, 2021, 22, 43.	3.8	17
609	Databases and tools for long noncoding RNAs. , 2021, , 35-47.		0
610	Software Options for the Analysis of MS-Proteomic Data. Methods in Molecular Biology, 2021, 2361, 35-59.	0.4	3
611	Role of Bioinformatics in Biological Sciences. , 2021, , 37-57.		5
612	A comprehensive analysis of the phylogenetic signal in ramp sequences in 211 vertebrates. Scientific Reports, 2021, 11, 622.	1.6	2
615	A chromosome-level genome of <i>Astyanax mexicanus</i> surface fish for comparing population-specific genetic differences contributing to trait evolution. Nature Communications, 2021, 12, 1447.	5.8	60
616	CRISPRi screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer. Nature Communications, 2021, 12, 1781.	5.8	32
620	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. BMC Bioinformatics, 2021, 22, 205.	1.2	17
621	Fast and Accurate Classification of Meta-Genomics Long Reads With deSAMBA. Frontiers in Cell and Developmental Biology, 2021, 9, 643645.	1.8	1
622	Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments. Science, 2021, 372, .	6.0	86
623	Identification of X-chromosomal genes that drive sex differences in embryonic stem cells through a hierarchical CRISPR screening approach. Genome Biology, 2021, 22, 110.	3.8	28
624	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. Nature Communications, 2021, 12, 2444.	5.8	58
626	Chromosome-Level Reference Genome Assembly for the American Pika (<i>Ochotona princeps</i>). Journal of Heredity, 2021, 112, 549-557.	1.0	10
628	Identification of sequence changes in myosin II that adjust muscle contraction velocity. PLoS Biology, 2021, 19, e3001248.	2.6	9
629	The Interpretation of Sequence Variants in Myeloid Neoplasms. American Journal of Clinical Pathology, 2021, 156, 728-748.	0.4	1
630	Selection and thermostability suggest G-quadruplexes are novel functional elements of the human genome. Genome Research, 2021, 31, 1136-1149.	2.4	20

#	ARTICLE	IF	CITATIONS
631	Probiotics: their action against pathogens can be turned around. <i>Scientific Reports</i> , 2021, 11, 13247.	1.6	4
632	The DEAD-box RNA helicase RhIE2 is a global regulator of <i>Pseudomonas aeruginosa</i> lifestyle and pathogenesis. <i>Nucleic Acids Research</i> , 2021, 49, 6925-6940.	6.5	12
633	BRLF1-dependent viral and cellular transcriptomes and transcriptional regulation during EBV primary infection in B lymphoma cells. <i>Genomics</i> , 2021, 113, 2591-2604.	1.3	5
634	RyÅ«tÅ† improved multi-sample transcript assembly for differential transcript expression analysis and more. <i>Bioinformatics</i> , 2021, 37, 4307-4313.	1.8	3
635	Analysis of gene expression and mutation data points on contribution of transcription to the mutagenesis by APOBEC enzymes. <i>NAR Cancer</i> , 2021, 3, zcab025.	1.6	11
636	Transcriptomic, proteomic and phosphoproteomic underpinnings of daily exercise performance and zeitgeber activity of training in mouse muscle. <i>Journal of Physiology</i> , 2022, 600, 769-796.	1.3	27
637	Epigenetic Regulation of the Vascular Endothelium by Angiogenic LncRNAs. <i>Frontiers in Genetics</i> , 2021, 12, 668313.	1.1	4
638	Biomarker Identification in Membranous Nephropathy Using a Long Non-coding RNA-Mediated Competitive Endogenous RNA Network. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 615-623.	2.2	7
639	Population genomics of the critically endangered kÄrÄpÅ. <i>Cell Genomics</i> , 2021, 1, 100002.	3.0	106
640	A Bayesian approach for accurate de novo transcriptome assembly. <i>Scientific Reports</i> , 2021, 11, 17663.	1.6	1
641	Discovery of a small protein-encoding cis-regulatory overlapping gene of the tumor suppressor gene Scribble in humans. <i>Communications Biology</i> , 2021, 4, 1098.	2.0	4
642	Germline RUNX1 variation and predisposition to childhood acute lymphoblastic leukemia. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	20
643	MUNDO: protein function prediction embedded in a multispecies world. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	2
644	Computational and functional annotation at genomic scale. , 2021, , 361-387.		0
645	Non-B DNA: a major contributor to small- and large-scale variation in nucleotide substitution frequencies across the genome. <i>Nucleic Acids Research</i> , 2021, 49, 1497-1516.	6.5	70
646	InsectORâ€”Webserver for sensitive identification of insect olfactory receptor genes from non-model genomes. <i>PLoS ONE</i> , 2021, 16, e0245324.	1.1	14
647	Cancerâ€”A Story on Fault Propagation in Gene-Cellular Networks. <i>Intelligent Systems Reference Library</i> , 2015, , 225-256.	1.0	1
648	Integrating the Bioinformatics and Omics Tools for Systems Analysis of Abiotic Stress Tolerance in <i>Oryza sativa</i> (L.). , 2019, , 59-77.		3

#	ARTICLE	IF	CITATIONS
649	CHARGE and Kabuki Syndromes: Gene-Specific DNA Methylation Signatures Identify Epigenetic Mechanisms Linking These Clinically Overlapping Conditions. <i>American Journal of Human Genetics</i> , 2017, 100, 773-788.	2.6	166
650	RNA-seq analysis in equine papillomavirus type 2-positive carcinomas identifies affected pathways and potential cancer markers as well as viral gene expression and splicing events. <i>Journal of General Virology</i> , 2019, 100, 985-998.	1.3	6
651	Arterivirus nsp12 versus the coronavirus nsp16 2â€²-O-methyltransferase: comparison of the C-terminal cleavage products of two nidovirus pp1ab polyproteins. <i>Journal of General Virology</i> , 2015, 96, 2643-2655.	1.3	14
672	Usp22 controls multiple signaling pathways that are essential for vasculature formation in the mouse placenta. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	30
673	Influenza A virus utilizes noncanonical cap-snatching to diversify its mRNA/ncRNA. <i>Rna</i> , 2020, 26, 1170-1183.	1.6	8
674	Abundance of ADAM9 transcripts increases in the blood in response to tissue damage. <i>F1000Research</i> , 2015, 4, 89.	0.8	15
675	Increased abundance of ADAM9 transcripts in the blood is associated with tissue damage. <i>F1000Research</i> , 2015, 4, 89.	0.8	19
676	The Diguanylate Cyclase HsbD Intersects with the HptB Regulatory Cascade to Control <i>Pseudomonas aeruginosa</i> Biofilm and Motility. <i>PLoS Genetics</i> , 2016, 12, e1006354.	1.5	57
677	Evolutionary history of Tibetans inferred from whole-genome sequencing. <i>PLoS Genetics</i> , 2017, 13, e1006675.	1.5	89
678	Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004440.	1.3	9
679	Bioinformatic Analysis Reveals Genome Size Reduction and the Emergence of Tyrosine Phosphorylation Site in the Movement Protein of New World Bipartite Begomoviruses. <i>PLoS ONE</i> , 2014, 9, e111957.	1.1	22
680	Methylation-Associated Partial Down-Regulation of Mesothelin Causes Resistance to Anti-Mesothelin Immunotoxins in a Pancreatic Cancer Cell Line. <i>PLoS ONE</i> , 2015, 10, e0122462.	1.1	12
681	The Shepherdsâ€™ Tale: A Genome-Wide Study across 9 Dog Breeds Implicates Two Loci in the Regulation of Fructosamine Serum Concentration in Belgian Shepherds. <i>PLoS ONE</i> , 2015, 10, e0123173.	1.1	8
682	Ratios of Four STAT3 Splice Variants in Human Eosinophils and Diffuse Large B Cell Lymphoma Cells. <i>PLoS ONE</i> , 2015, 10, e0127243.	1.1	13
683	Decreased Expression of CoREST1 and CoREST2 Together with LSD1 and HDAC1/2 during Neuronal Differentiation. <i>PLoS ONE</i> , 2015, 10, e0131760.	1.1	22
684	Genome-Wide Copy Number Variations Using SNP Genotyping in a Mixed Breed Swine Population. <i>PLoS ONE</i> , 2015, 10, e0133529.	1.1	18
685	Distilling a Visual Network of Retinitis Pigmentosa Gene-Protein Interactions to Uncover New Disease Candidates. <i>PLoS ONE</i> , 2015, 10, e0135307.	1.1	3
686	Novel Role of 3â€™UTR-Embedded Alu Elements as Facilitators of Processed Pseudogene Genesis and Host Gene Capture by Viral Genomes. <i>PLoS ONE</i> , 2016, 11, e0169196.	1.1	13

#	ARTICLE	IF	CITATIONS
687	Copy number gains at chr3p25 and chr11p11 are associated with lymph node involvement and survival in muscle-invasive bladder tumors. PLoS ONE, 2017, 12, e0187975.	1.1	4
688	In Vivo Molecular Dissection of the Effects of HIV-1 in Active Tuberculosis. PLoS Pathogens, 2016, 12, e1005469.	2.1	46
689	Human viruses have codon usage biases that match highly expressed proteins in the tissues they infect. Biomedical Genetics and Genomics, 2017, 2, .	0.1	12
690	LRH-1 expression patterns in breast cancer tissues are associated with tumour aggressiveness. Oncotarget, 2017, 8, 83626-83636.	0.8	13
691	Protein Arginine Deiminases and Associated Citrullination: Physiological Functions and Diseases Associated with Dysregulation. Current Drug Targets, 2015, 16, 700-710.	1.0	238
692	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. Journal of Medical Internet Research, 2017, 19, e212.	2.1	5
693	Genome-Wide Association Meta-Analysis of Single-Nucleotide Polymorphisms and Symptomatic Venous Thromboembolism during Therapy for Acute Lymphoblastic Leukemia and Lymphoma in Caucasian Children. Cancers, 2020, 12, 1285.	1.7	5
694	Type I Interferon Receptor Variants in Gene Regulatory Regions are Associated with Susceptibility to Cerebral Malaria in Malawi. American Journal of Tropical Medicine and Hygiene, 2018, 98, 1692-1698.	0.6	18
695	Clinical Interpretation of Genomic Variations. Turkish Journal of Haematology, 2016, 33, 172-179.	0.2	8
696	The Role of Artificial Intelligence and Machine Learning Techniques: Race for COVID-19 Vaccine. Archives of Clinical Infectious Diseases, 2020, 15, .	0.1	34
697	Long non-coding RNAs as a source of new peptides. ELife, 2014, 3, e03523.	2.8	451
698	Translation of 5' leaders is pervasive in genes resistant to eIF2 repression. ELife, 2015, 4, e03971.	2.8	294
699	Secretagogin expression delineates functionally-specialized populations of striatal parvalbumin-containing interneurons. ELife, 2016, 5, .	2.8	43
700	Co-option of an endogenous retrovirus envelope for host defense in hominid ancestors. ELife, 2017, 6, .	2.8	75
701	Mapping the transcriptional diversity of genetically and anatomically defined cell populations in the mouse brain. ELife, 2019, 8, .	2.8	59
702	PATACSBDB—the database of polyA translational attenuators in coding sequences. PeerJ Computer Science, 0, 2, e45.	2.7	10
703	Transcriptional similarity in couples reveals the impact of shared environment and lifestyle on gene regulation through modified cytosines. PeerJ, 2016, 4, e2123.	0.9	4
704	Identification of rare alternative splicing events in MS/MS data reveals a significant fraction of alternative translation initiation sites. PeerJ, 2014, 2, e673.	0.9	5

#	ARTICLE	IF	CITATIONS
705	CAM: an alignment-free method to recover phylogenies using codon aversion motifs. PeerJ, 2019, 7, e6984.	0.9	9
706	Comprehensive, structurally-informed alignment and phylogeny of vertebrate biogenic amine receptors. PeerJ, 2015, 3, e773.	0.9	20
707	Annotation of Full-Length Long Noncoding RNAs with Capture Long-Read Sequencing (CLS). Methods in Molecular Biology, 2021, 2254, 133-159.	0.4	3
708	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	6.5	1,103
709	The genome sequence of the common frog, <i>Rana temporaria</i> Linnaeus 1758. Wellcome Open Research, 2021, 6, 286.	0.9	11
710	Blood Transcriptomes of Anti-SARS-CoV-2 Antibody-Positive Healthy Individuals Who Experienced Asymptomatic Versus Clinical Infection. Frontiers in Immunology, 2021, 12, 746203.	2.2	10
711	The genome sequence of the common toad, <i>Bufo bufo</i> (Linnaeus, 1758). Wellcome Open Research, 2021, 6, 281.	0.9	10
712	MODELAGEM MOLECULAR APLICADA A NANOBIOSSISTEMAS. , 2015, , 219-267.		0
716	Identifying the missing protein in human proteome by structure and function prediction. , 2015, , 19-26.		0
734	Germline Genetic IKZF1 Variation and Predisposition to Childhood Acute Lymphoblastic Leukemia. SSRN Electronic Journal, 0, , .	0.4	0
735	Polyploidy activates biological pathways related to morphogenesis in mammalian tissues. MOJ Immunology, 2018, 6, .	11.0	2
736	Transcriptome and Epigenome Applications for Coronary Heart Disease Research. , 2018, , 572-581.		0
753	Decoding the Equine Genome: Lessons from ENCODE. Genes, 2021, 12, 1707.	1.0	5
754	Mitochondria Autoimmunity and MNRR1 in Breast Carcinogenesis: A Review. , 2020, 2, 138-158.		2
755	Phenotypic differences of mutation-negative cases in Gitelman syndrome clinically diagnosed in adulthood. Human Mutation, 2021, 42, 300-309.	1.1	4
760	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
761	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
762	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0

#	ARTICLE	IF	CITATIONS
763	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
764	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
765	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
766	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
767	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
768	Introducing, OncoTarget. Oncotarget, 2010, 1, 2-2.	0.8	0
770	On the privacy risks of sharing clinical proteomics data. AMIA Summits on Translational Science Proceedings, 2016, 2016, 122-31.	0.4	3
771	Transcriptome diversity and differential expression in supporting limb laminitis. Veterinary Immunology and Immunopathology, 2022, 243, 110353.	0.5	1
772	Emerging role of long non-coding RNAs in endothelial dysfunction and their molecular mechanisms. Biomedicine and Pharmacotherapy, 2022, 145, 112421.	2.5	25
773	Ion Channel and Ubiquitin Differential Expression during Erythromycin-Induced Anhidrosis in Foals. Animals, 2021, 11, 3379.	1.0	1
774	Pseudoexon activation in disease by nonâ€splice site deep intronic sequence variation â€” wild type pseudoexons constitute highâ€risk sites in the human genome. Human Mutation, 2022, 43, 103-127.	1.1	17
776	Comparison of RNA content from hydrophobic interaction chromatographyâ€isolated seminal plasma exosomes from intrauterine insemination (IUI) pregnancies. Andrologia, 2022, 54, e14325.	1.0	4
777	Database resources of the national center for biotechnology information. Nucleic Acids Research, 2022, 50, D20-D26.	6.5	887
779	Incidental germline findings during molecular profiling of tumor tissues for precision oncology: molecular survey and methodological obstacles. Journal of Translational Medicine, 2022, 20, 29.	1.8	2
780	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
781	Limb development genes underlie variation in human fingerprint patterns. Cell, 2022, 185, 95-112.e18.	13.5	30
782	Neurodevelopmental Syndrome with Intellectual Disability, Speech Impairment, and Quadrapedia Is Associated with Glutamate Receptor Delta 2 Gene Defect. Cells, 2022, 11, 400.	1.8	5
783	RefSeq Functional Elements as experimentally assayed nongenic reference standards and functional interactions in human and mouse. Genome Research, 2022, 32, 175-188.	2.4	7

#	ARTICLE	IF	CITATIONS
784	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
785	Clinical exome sequencing—Mistakes and caveats. <i>Human Mutation</i> , 2022, 43, 1041-1055.	1.1	20
786	Paleozoic Protein Fossils Illuminate the Evolution of Vertebrate Genomes and Transposable Elements. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
787	Impact of gene annotation choice on the quantification of RNA-seq data. <i>BMC Bioinformatics</i> , 2022, 23, 107.	1.2	8
789	Impact of Vimentin on Regulation of Cell Signaling and Matrix Remodeling. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 869069.	1.8	23
790	Middle Eastern Genetic Variation Improves Clinical Annotation of the Human Genome. <i>Journal of Personalized Medicine</i> , 2022, 12, 423.	1.1	7
791	Establishment and characterization of the third non-functional human pancreatic neuroendocrine tumor cell line. <i>Human Cell</i> , 2022, 35, 1248-1261.	1.2	5
792	Human disease prediction from microbiome data by multiple feature fusion and deep learning. <i>IScience</i> , 2022, 25, 104081.	1.9	10
793	Identification of model systems expressing circFAT3. <i>Journal of the Pennsylvania Academy of Science</i> , 2021, 95, 59-75.	0.1	0
794	The genome sequence of the common green lacewing, <i>Chrysoperla carnea</i> (Stephens, 1836). <i>Wellcome Open Research</i> , 0, 6, 334.	0.9	4
795	In-silico analysis reveals druggable single nucleotide polymorphisms in angiotensin 1 converting enzyme involved in the onset of blood pressure. <i>BMC Research Notes</i> , 2021, 14, 457.	0.6	2
796	Role of lncRNA LIPE-AS1 in adipogenesis. <i>Adipocyte</i> , 2022, 11, 11-27.	1.3	11
797	The genome sequence of the red deer, <i>Cervus elaphus</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 336.	0.9	7
826	APOBEC3A regulates transcription from interferon-stimulated response elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2011665119.	3.3	7
827	Downregulation of CRTCL1 Is Involved in CUMS-Induced Depression-Like Behavior in the Hippocampus and Its RNA Sequencing Analysis. <i>Molecular Neurobiology</i> , 2022, 59, 4405-4418.	1.9	8
828	Mutations in <i>RPS19</i> may affect ribosome function and biogenesis in Diamond Blackfan anemia. <i>FEBS Open Bio</i> , 2022, 12, 1419-1434.	1.0	2
829	Current status and future perspectives of the evaluation of missense variants by using three-dimensional structures of proteins. <i>Biophysics and Physicobiology</i> , 2022, , .	0.5	0
830	Drug-Induced Epigenomic Plasticity Reprograms Circadian Rhythm Regulation to Drive Prostate Cancer toward Androgen Independence. <i>Cancer Discovery</i> , 2022, 12, 2074-2097.	7.7	22

#	ARTICLE	IF	CITATIONS
831	Genome-wide association meta-analysis of 88,250 individuals highlights pleiotropic mechanisms of five ocular diseases in UK Biobank. <i>EBioMedicine</i> , 2022, 82, 104161.	2.7	21
832	Increased Soil Fertility in Tea Gardens Leads to Declines in Fungal Diversity and Complexity in Subsoils. <i>Agronomy</i> , 2022, 12, 1751.	1.3	6
833	Web-Based Protein Interactions Calculator Identifies Likely Proteome Coevolution with Alzheimer's Disease-Associated Proteins. <i>Genes</i> , 2022, 13, 1346.	1.0	0
834	Genetics, mechanism, and pathophysiology of 22q11.2 deletion syndrome. , 2022, , 34-52.		0
835	EfGD: the <i>Erianthus fulvus</i> genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	3
837	csORF-finder: an effective ensemble learning framework for accurate identification of multi-species coding short open reading frames. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	9
838	Cytotoxic T Cell Expression of Leukocyte-Associated Immunoglobulin-Like Receptor-1 (LAIR-1) in Viral Hepatitis C-Mediated Hepatocellular Carcinoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12541.	1.8	7
839	Transcriptomic analysis reveals distinct mechanisms of adaptation of a polar picophytoplankter under ocean acidification conditions. <i>Marine Environmental Research</i> , 2022, 182, 105782.	1.1	0
840	A chromosome-level genome assembly reveals genomic characteristics of the American mink (<i>Neogale) Tj ETQq0 0.0 rgBT /Overlock 10</i>	2.0	6
841	Genome-wide analysis of copy-number variation in humans with cleft lip and/or cleft palate identifies COBLL1, RIC1, and ARHGEF38 as clefting genes. <i>American Journal of Human Genetics</i> , 2023, 110, 71-91.	2.6	4
842	Clustered variants in the 5' coding region of TRA2B cause a distinctive neurodevelopmental syndrome. <i>Genetics in Medicine</i> , 2023, 25, 100003.	1.1	1
847	Response of the Soil Fungal Community and Its Function during the Conversion of Forestland to Tea Plantations: A Case Study in Southeast China. <i>Forests</i> , 2023, 14, 209.	0.9	2
848	A chromosome-level reference genome and pangenome for barn swallow population genomics. <i>Cell Reports</i> , 2023, 42, 111992.	2.9	4
849	Fourth Report on Chicken Genes and Chromosomes 2022. <i>Cytogenetic and Genome Research</i> , 2022, 162, 405-528.	0.6	12
850	Discovery of natural non-circular permutations in non-coding RNAs. <i>Nucleic Acids Research</i> , 2023, 51, 2850-2861.	6.5	1
851	Potential role of a maize metallothionein gene in pest resistance. <i>Plant Gene</i> , 2023, 34, 100409.	1.4	1
854	Divergent sensory and immune gene evolution in sea turtles with contrasting demographic and life histories. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	11
856	Resequencing of a Pekin duck breeding population provides insights into the genomic response to short-term artificial selection. <i>GigaScience</i> , 2023, 12, .	3.3	1

#	ARTICLE	IF	CITATIONS
857	First Reported Case of Gabriele-de Vries Syndrome with Spinal Dysraphism. <i>Children</i> , 2023, 10, 623.	0.6	1
858	RIP-PEN-seq identifies a class of kink-turn RNAs as splicing regulators. <i>Nature Biotechnology</i> , 2024, 42, 119-131.	9.4	5