

`BLAT` – The `BLAST`-Like Alignment Tool

Genome Research

12, 656-664

DOI: [10.1101/gr.229202](https://doi.org/10.1101/gr.229202)

Citation Report

#	ARTICLE	IF	CITATIONS
3	A computational/functional genomics approach for the enrichment of the retinal transcriptome and the identification of positional candidate retinopathy genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14326-14331.	3.3	31
4	Identification of Candidate Genes Regulating HDL Cholesterol Using a Chromosomal Region Expression Array. Genome Research, 2002, 12, 1693-1702.	2.4	24
5	POTE, a highly homologous gene family located on numerous chromosomes and expressed in prostate, ovary, testis, placenta, and prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16975-16980.	3.3	75
6	Comparison of whole genome assemblies of the human genome. Nucleic Acids Research, 2002, 30, 5004-5014.	6.5	10
7	Accessing the Human Genome. Current Protocols in Human Genetics, 2002, 34, Unit 6.9.	3.5	0
8	Fast and sensitive algorithm for aligning ESTs to human genome. , 0, , .		10
9	The Human Genome Browser at UCSC. Genome Research, 2002, 12, 996-1006.	2.4	8,776
10	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. Science, 2002, 298, 2157-2167.	6.0	1,539
11	Computational comparison of two mouse draft genomes and the human golden path. Genome Biology, 2002, 4, R1.	13.9	34
12	Apollo: a sequence annotation editor. Genome Biology, 2002, 3, research0082.1.	13.9	369
13	Assessing the impact of comparative genomic sequence data on the functional annotation of the <i>Drosophila</i> genome. Genome Biology, 2002, 3, research0086.1.	13.9	120
14	Visualization techniques for genomic data. , 0, , .		1
16	Genomic Rearrangements Resulting in PLP1 Deletion Occur by Nonhomologous End Joining and Cause Different Dysmyelinating Phenotypes in Males and Females. American Journal of Human Genetics, 2002, 71, 838-853.	2.6	144
17	Visualizing the genome: techniques for presenting human genome data and annotations. BMC Bioinformatics, 2002, 3, 19.	1.2	30
18	Development and production of an oligonucleotide MuscleChip: use for validation of ambiguous ESTs. BMC Bioinformatics, 2002, 3, 33.	1.2	8
19	Genetics of the immune response: identifying immune variation within the MHC and throughout the genome. Immunological Reviews, 2002, 190, 69-85.	2.8	49
20	A physical map of the mouse genome. Nature, 2002, 418, 743-750.	13.7	316
21	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	13.7	1,548

#	ARTICLE	IF	CITATIONS
35	Commentary: keeping biology in mind. <i>Nature Genetics</i> , 2002, 32, 74-75.	9.4	32
36	Genome-wide association study and mouse model identify interaction between RET and EDNRB pathways in Hirschsprung disease. <i>Nature Genetics</i> , 2002, 32, 237-244.	9.4	255
37	The UCSC Genome Browser Database. <i>Nucleic Acids Research</i> , 2003, 31, 51-54.	6.5	1,460
38	Comparative fine maps of bovine toll-like receptor 4 and toll-like receptor 2 regions. <i>Mammalian Genome</i> , 2003, 14, 149-155.	1.0	23
39	The mouse salivary androgen-binding protein (ABP) gene cluster on Chromosomes 7: characterization and evolutionary relationships. <i>Mammalian Genome</i> , 2003, 14, 679-691.	1.0	22
40	Identification of a novel liver-specific expressed gene, TCP10L, encoding a human leucine zipper protein with transcription inhibition activity. <i>Journal of Human Genetics</i> , 2003, 48, 556-563.	1.1	5
41	Bioinformatics: not just for sequences anymore. <i>Biosilico</i> , 2003, 1, 103-111.	0.5	2
42	AGRIS: Arabidopsis gene regulatory information server, an information resource of Arabidopsis cis-regulatory elements and transcription factors. <i>BMC Bioinformatics</i> , 2003, 4, 25.	1.2	349
43	High-resolution mapping of amplifications and deletions in pediatric osteosarcoma by use of CGH analysis of cDNA microarrays. <i>Genes Chromosomes and Cancer</i> , 2003, 38, 215-225.	1.5	149
44	Sequence-Based, in situ detection of chromosomal abnormalities at high resolution. <i>American Journal of Medical Genetics Part A</i> , 2003, 121A, 245-257.	2.4	25
45	11th Intelligent Systems for Molecular Biology 2003 (ISMB 2003). <i>Comparative and Functional Genomics</i> , 2003, 4, 654-659.	2.0	1
46	Identification of conserved regulatory elements by comparative genome analysis. <i>Journal of Biology</i> , 2003, 2, 13.	2.7	222
47	The DNA sequence and analysis of human chromosome 14. <i>Nature</i> , 2003, 421, 601-607.	13.7	108
48	Introduction: putting it together. <i>Nature Genetics</i> , 2003, 35, 5-8.	9.4	1
49	Question 1—How does one find a gene of interest and determine that gene's structure? Once the gene has been located on the map, how does one easily examine other genes in that same region?. <i>Nature Genetics</i> , 2003, 35, 9-17.	9.4	32
51	Question 3—During a positional cloning project aimed at finding a human disease gene, linkage data have been obtained suggesting that the gene of interest lies between two sequence-tagged site markers. How can all the known and predicted candidate genes in this interval be identified? What BAC clones cover that particular region?. <i>Nature Genetics</i> , 2003, 35, 21-28.	9.4	2
55	Question 10—For a given protein, how can one determine whether it contains any functional domains of interest? What other proteins contain the same functional domains as this protein? How can one determine whether there is a similarity to other proteins, not only at the sequence level, but also at the structural level?. <i>Nature Genetics</i> , 2003, 35, 57-62.	9.4	2
58	Commentary: keeping biology in mind. <i>Nature Genetics</i> , 2003, 35, 74-74.	9.4	1

#	ARTICLE	IF	CITATIONS
59	Clonality analysis after retroviral-mediated gene transfer to CD34+ cells from the cord blood of ADA-deficient SCID neonates. <i>Nature Medicine</i> , 2003, 9, 463-468.	15.2	134
60	Comparative genomics: genome-wide analysis in metazoan eukaryotes. <i>Nature Reviews Genetics</i> , 2003, 4, 251-262.	7.7	203
61	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2003, 00, 1.4.1.	25.8	6
62	SPAM1 (PH-20) protein and mRNA expression in the epididymides of humans and macaques: utilizing laser microdissection/RT-PCR. <i>Reproductive Biology and Endocrinology</i> , 2003, 1, 54.	1.4	33
63	Structural Context of Exons in Protein Domains: Implications for Protein Modelling and Design. <i>Journal of Molecular Biology</i> , 2003, 333, 1045-1059.	2.0	9
64	Genome Rearrangements in Mammalian Evolution: Lessons From Human and Mouse Genomes. <i>Genome Research</i> , 2003, 13, 37-45.	2.4	302
65	Dissecting the transcription networks of a cell using computational genomics. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 611-616.	1.5	27
66	Vertebrate gene predictions and the problem of large genes. <i>Nature Reviews Genetics</i> , 2003, 4, 741-749.	7.7	56
67	Is there an evolutionary relationship between WARP (von Willebrand factor A-domain-related protein) and the FACIT and FACIT-like collagens?. <i>FEBS Letters</i> , 2003, 552, 91-94.	1.3	6
68	Identification of a Novel Bardet-Biedl Syndrome Protein, BBS7, That Shares Structural Features with BBS1 and BBS2. <i>American Journal of Human Genetics</i> , 2003, 72, 650-658.	2.6	207
69	Large Differences between LINE-1 Amplification Rates in the Human and Chimpanzee Lineages. <i>American Journal of Human Genetics</i> , 2003, 72, 739-748.	2.6	30
70	ATLAS: A System to Selectively Identify Human-Specific L1 Insertions. <i>American Journal of Human Genetics</i> , 2003, 72, 823-838.	2.6	105
71	Mutations in the Fumarate Hydratase Gene Cause Hereditary Leiomyomatosis and Renal Cell Cancer in Families in North America. <i>American Journal of Human Genetics</i> , 2003, 73, 95-106.	2.6	563
72	Identification, characterization and expression analysis of a new fibrillar collagen gene, COL27A1. <i>Matrix Biology</i> , 2003, 22, 3-14.	1.5	112
73	In silico searching of human and mouse genome data identifies known and unknown HNF1 binding sites upstream of $\beta^2$ -cell genes. <i>Molecular Genetics and Metabolism</i> , 2003, 78, 145-151.	0.5	15
74	Two promoters within the human LMO4 gene contribute to its overexpression in breast cancer cells. <i>Genomics</i> , 2003, 82, 280-287.	1.3	13
75	Farnesoid X Receptor Activates Transcription of the Phospholipid Pump MDR3. <i>Journal of Biological Chemistry</i> , 2003, 278, 51085-51090.	1.6	195
76	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. <i>Genome Research</i> , 2003, 13, 13-26.	2.4	263

#	ARTICLE	IF	CITATIONS
77	Enrichment of Gene-Coding Sequences in Maize by Genome Filtration. <i>Science</i> , 2003, 302, 2118-2120.	6.0	207
78	Expressed sequence tag profiling identifies developmental and anatomic partitioning of gene expression in the mouse prostate. <i>Genome Biology</i> , 2003, 4, R79.	13.9	21
79	Whole-genome screening indicates a possible burst of formation of processed pseudogenes and Alu repeats by particular L1 subfamilies in ancestral primates. <i>Genome Biology</i> , 2003, 4, R74.	13.9	172
80	ProSplicer: a database of putative alternative splicing information derived from protein, mRNA and expressed sequence tag sequence data. <i>Genome Biology</i> , 2003, 4, R29.	13.9	33
81	The GeneCards/spl trade/ family of databases: GeneCards, GeneLoc, GeneNote and GeneAnnot. , 0, , .		2
82	An assessment of a metric space database index to support sequence homology. , 0, , .		2
83	MoBloS: a metric-space DBMS to support biological discovery. , 0, , .		7
84	Impact of Alternative Initiation, Splicing, and Termination on the Diversity of the mRNA Transcripts Encoded by the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1290-1300.	2.4	168
85	Aligning ESTs to genome using multilayer unique makers. , 0, , .		1
86	A coming of age for bioinformatics. <i>Journal of Cell Science</i> , 2003, 116, 6-7.	1.2	1
87	Mastering seeds for genomic size nucleotide BLAST searches. <i>Nucleic Acids Research</i> , 2003, 31, 6935-6941.	6.5	25
88	Strategies and Tools for Whole-Genome Alignments. <i>Genome Research</i> , 2003, 13, 73-80.	2.4	190
89	Assessing the <i>Drosophila melanogaster</i> and <i>Anopheles gambiae</i> Genome Annotations Using Genome-Wide Sequence Comparisons. <i>Genome Research</i> , 2003, 13, 1595-1599.	2.4	7
90	A Complexity Reduction Algorithm for Analysis and Annotation of Large Genomic Sequences. <i>Genome Research</i> , 2003, 13, 313-322.	2.4	15
91	Glocal alignment: finding rearrangements during alignment. <i>Bioinformatics</i> , 2003, 19, i54-i62.	1.8	333
92	Matrix attachment region (MAR) properties and abnormal expansion of AT island minisatellites in FRA16B fragile sites in leukemic CEM cells. <i>Nucleic Acids Research</i> , 2003, 31, 6354-6364.	6.5	15
93	Locating Sequence on FPC Maps and Selecting a Minimal Tiling Path. <i>Genome Research</i> , 2003, 13, 2152-2163.	2.4	37
94	GeneLynx Mouse: Integrated Portal to the Mouse Genome. <i>Genome Research</i> , 2003, 13, 1501-1504.	2.4	13

#	ARTICLE	IF	CITATIONS
95	A comparative analysis of HGSC and Celera human genome assemblies and gene sets. <i>Bioinformatics</i> , 2003, 19, 1597-1605.	1.8	8
96	Genome-wide single-nucleotide polymorphism analysis defines haplotype patterns in mouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3380-3385.	3.3	222
97	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. <i>Genome Research</i> , 2003, 13, 1-12.	2.4	210
98	GeneAnnot: Interfacing GeneCards with high-throughput gene expression compendia. <i>Briefings in Bioinformatics</i> , 2003, 4, 349-360.	3.2	17
99	Computational Discovery of Internal Micro-Exons. <i>Genome Research</i> , 2003, 13, 1216-1221.	2.4	62
100	PromoSer: a large-scale mammalian promoter and transcription start site identification service. <i>Nucleic Acids Research</i> , 2003, 31, 3554-3559.	6.5	75
101	Exon Structure Analysis, Ortholog Identification, and SNP Candidate Screening by Mapping Mouse RIKEN Sequences to Multiple Genome Assemblies. <i>Genome Research</i> , 2003, 13, 1552-1553.	2.4	0
102	Elevated Rates of Protein Secretion, Evolution, and Disease Among Tissue-Specific Genes. <i>Genome Research</i> , 2003, 14, 54-61.	2.4	160
103	Global disruption of the cerebellar transcriptome in a Down syndrome mouse model. <i>Human Molecular Genetics</i> , 2003, 12, 2013-2019.	1.4	143
104	Multiple, dispersed human U6 small nuclear RNA genes with varied transcriptional efficiencies. <i>Nucleic Acids Research</i> , 2003, 31, 2344-2352.	6.5	66
105	Human Gene-Centric Databases at the Weizmann Institute of Science: GeneCards, UDB, CroW 21 and HORDE. <i>Nucleic Acids Research</i> , 2003, 31, 142-146.	6.5	199
106	Annotating Large Genomes With Exact Word Matches. <i>Genome Research</i> , 2003, 13, 2306-2315.	2.4	62
107	Multiple Variable First Exons: A Mechanism for Cell- and Tissue-Specific Gene Regulation. <i>Genome Research</i> , 2003, 14, 79-89.	2.4	123
108	A General Approach for Identifying Distant Regulatory Elements Applied to the Gdf6 Gene. <i>Genome Research</i> , 2003, 13, 2069-2081.	2.4	85
109	1-Mb Resolution Array-Based Comparative Genomic Hybridization Using a BAC Clone Set Optimized for Cancer Gene Analysis. <i>Genome Research</i> , 2003, 14, 179-187.	2.4	100
110	Physical evidence of Mcs5, a QTL controlling mammary carcinoma susceptibility, in congenic rats. <i>Carcinogenesis</i> , 2003, 24, 1455-1460.	1.3	21
111	gff2aplot: Plotting sequence comparisons. <i>Bioinformatics</i> , 2003, 19, 2477-2479.	1.8	9
112	Identification of Promoter Regions in the Human Genome by Using a Retroviral Plasmid Library-Based Functional Reporter Gene Assay. <i>Genome Research</i> , 2003, 13, 1765-1774.	2.4	21

#	ARTICLE	IF	CITATIONS
113	G Protein-Coupled Receptor Genes in the FANTOM2 Database. <i>Genome Research</i> , 2003, 13, 1466-1477.	2.4	32
114	Continued Discovery of Transcriptional Units Expressed in Cells of the Mouse Mononuclear Phagocyte Lineage. <i>Genome Research</i> , 2003, 13, 1360-1365.	2.4	41
115	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , 2003, 31, 5654-5666.	6.5	1,597
116	Molecular classification of familial non-BRCA1/BRCA2 breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2532-2537.	3.3	182
117	A Fast and Sensitive Algorithm for Aligning ESTs to the Human Genome. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 363-386.	0.3	7
118	Reevaluating Human Gene Annotation: A Second-Generation Analysis of Chromosome 22. <i>Genome Research</i> , 2003, 13, 27-36.	2.4	73
119	WormBase: a cross-species database for comparative genomics. <i>Nucleic Acids Research</i> , 2003, 31, 133-137.	6.5	107
120	Shuffling of Genes Within Low-Copy Repeats on 22q11 (LCR22) by Alu-Mediated Recombination Events During Evolution. <i>Genome Research</i> , 2003, 13, 2519-2532.	2.4	115
121	DNannotator: annotation software tool kit for regional genomic sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3729-3735.	6.5	4
122	Assessment of SAGE in Transcript Identification. <i>Genome Research</i> , 2003, 13, 1203-1215.	2.4	61
123	An Interactive Tool for Extracting Exons and SNP from Genomic Sequence: Isolation of HCN1 and HCN3 Ion Channel Genes. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 433-446.	0.3	0
124	NONSYNDROMICSEIZUREDISORDERS: Epilepsy and the Use of the Internet to Advance Research. <i>Annual Review of Genomics and Human Genetics</i> , 2003, 4, 437-457.	2.5	1
125	Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 605-610.	3.3	526
126	The Role of Declarative Querying in Bioinformatics. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 89-91.	1.0	12
127	The Histone Deacetylase 9 Gene Encodes Multiple Protein Isoforms. <i>Journal of Biological Chemistry</i> , 2003, 278, 16059-16072.	1.6	128
128	LAGAN and Multi-LAGAN: Efficient Tools for Large-Scale Multiple Alignment of Genomic DNA. <i>Genome Research</i> , 2003, 13, 721-731.	2.4	960
129	A 1-Mb resolution radiation hybrid map of the canine genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5296-5301.	3.3	219
130	Discovery of the breast cancer gene BASE using a molecular approach to enrich for genes encoding membrane and secreted proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1099-1104.	3.3	55

#	ARTICLE	IF	CITATIONS
131	Human-Mouse Alignments with BLASTZ. <i>Genome Research</i> , 2003, 13, 103-107.	2.4	1,071
132	PRIMEX: rapid identification of oligonucleotide matches in whole genomes. <i>Bioinformatics</i> , 2003, 19, 2486-2488.	1.8	31
133	Alignment of BLAST high-scoring segment pairs based on the longest increasing subsequence algorithm. <i>Bioinformatics</i> , 2003, 19, 1391-1396.	1.8	31
134	Genome Sequencing, Assembly and Gene Prediction in Fungi. <i>Applied Mycology and Biotechnology</i> , 2003, 3, 65-81.	0.3	1
135	Detecting protein sequence conservation via metric embeddings. <i>Bioinformatics</i> , 2003, 19, i122-i129.	1.8	25
136	GS-Aligner: A Novel Tool for Aligning Genomic Sequences Using Bit-Level Operations. <i>Molecular Biology and Evolution</i> , 2003, 20, 1299-1309.	3.5	9
137	Match Chaining Algorithms for cDNA Mapping. <i>Lecture Notes in Computer Science</i> , 2003, , 462-475.	1.0	23
138	Vector Seeds: An Extension to Spaced Seeds Allows Substantial Improvements in Sensitivity and Specificity. <i>Lecture Notes in Computer Science</i> , 2003, , 39-54.	1.0	22
139	Transcriptome Analysis of Mouse Stem Cells and Early Embryos. <i>PLoS Biology</i> , 2003, 1, e74.	2.6	156
140	The ND-Tree. , 2003, , 620-631.		14
141	Large-scale RT-PCR recovery of full-length cDNA clones. <i>BioTechniques</i> , 2004, 36, 690-700.	0.8	11
142	Bioinformatic Approaches to Assigning Protein Function From Novel Sequence Data. , 2005, 104, 313-332.		0
143	A Neutral Model of Transcriptome Evolution. <i>PLoS Biology</i> , 2004, 2, e132.	2.6	294
144	DoOP: Databases of Orthologous Promoters, collections of clusters of orthologous upstream sequences from chordates and plants. <i>Nucleic Acids Research</i> , 2004, 33, D86-D90.	6.5	26
145	Efficient combination of multiple word models for improved sequence comparison. <i>Bioinformatics</i> , 2004, 20, 2529-2533.	1.8	12
146	SPD--a web-based secreted protein database. <i>Nucleic Acids Research</i> , 2004, 33, D169-D173.	6.5	172
147	Identification of a commonly amplified 4.3 Mb region with overexpression of C8FW, but not MYC in MYC-containing double minutes in myeloid malignancies. <i>Human Molecular Genetics</i> , 2004, 13, 1479-1485.	1.4	56
148	Designing multiple simultaneous seeds for DNA similarity search. , 2004, , .		26

#	ARTICLE	IF	CITATIONS
149	The UniMarker (UM) method for synteny mapping of large genomes. <i>Bioinformatics</i> , 2004, 20, 3156-3165.	1.8	9
150	Multiple organism gene finding by collapsed gibbs sampling. , 2004, , .		4
151	T1DBase, a community web-based resource for type 1 diabetes research. <i>Nucleic Acids Research</i> , 2004, 33, D544-D549.	6.5	44
152	Pooled Genomic Indexing (PGI): Analysis and Design of Experiments. <i>Journal of Computational Biology</i> , 2004, 11, 1001-1021.	0.8	8
153	Computational Searches for Missing Orthologs: The Case of S100A12 in Mice. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 334-340.	1.0	22
154	Inferred Functions of "Novel" Genes Identified in Fibroblasts Chondroinduced by Demineralized Bone. <i>DNA and Cell Biology</i> , 2004, 23, 15-24.	0.9	1
155	HGVbase: a curated resource describing human DNA variation and phenotype relationships. <i>Nucleic Acids Research</i> , 2004, 32, 516D-519.	6.5	60
156	Natural Genetic Variation Caused by Transposable Elements in Humans. <i>Genetics</i> , 2004, 168, 933-951.	1.2	138
157	HemoPDB: Hematopoiesis Promoter Database, an information resource of transcriptional regulation in blood cell development. <i>Nucleic Acids Research</i> , 2004, 32, 86D-90.	6.5	14
158	Identifying gene regulatory elements by genome-wide recovery of DNase hypersensitive sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 992-997.	3.3	166
159	A novel TEAD1 mutation is the causative allele in Sveinsson's chorioretinal atrophy (helicoid) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 T	1.4	118
160	Comparative Recombination Rates in the Rat, Mouse, and Human Genomes. <i>Genome Research</i> , 2004, 14, 528-538.	2.4	452
161	Using MoBloS' scalable genome join to find conserved primer pair candidates between two genomes. <i>Bioinformatics</i> , 2004, 20, i355-i362.	1.8	15
162	1274 Full-Open Reading Frames of Transcripts Expressed in the Developing Mouse Nervous System. <i>Genome Research</i> , 2004, 14, 2053-2063.	2.4	17
163	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. <i>Nucleic Acids Research</i> , 2004, 32, 3977-3983.	6.5	77
164	Building Genomic Profiles for Uncovering Segmental Homology in the Twilight Zone. <i>Genome Research</i> , 2004, 14, 1095-1106.	2.4	62
165	Full-malaria 2004: an enlarged database for comparative studies of full-length cDNAs of malaria parasites, Plasmodium species. <i>Nucleic Acids Research</i> , 2004, 32, 334D-338.	6.5	26
166	ORFcurator: molecular curation of genes and gene clusters in prokaryotic organisms. <i>Bioinformatics</i> , 2004, 20, 3462-3465.	1.8	12

#	ARTICLE	IF	CITATIONS
167	Comparative Evolutionary Genomics of Androgen-Binding Protein Genes. <i>Genome Research</i> , 2004, 14, 1516-1529.	2.4	79
168	A comparative method for identification of gene structures and alternatively spliced variants. <i>Bioinformatics</i> , 2004, 20, 3064-3079.	1.8	14
169	The Ensembl Automatic Gene Annotation System. <i>Genome Research</i> , 2004, 14, 942-950.	2.4	352
170	Parallel Genotyping of Over 10,000 SNPs Using a One-Primer Assay on a High-Density Oligonucleotide Array. <i>Genome Research</i> , 2004, 14, 414-425.	2.4	281
171	Noncoding Sequences Conserved in a Limited Number of Mammals in the SIM2 Interval are Frequently Functional. <i>Genome Research</i> , 2004, 14, 367-372.	2.4	73
172	Genomic Analysis of the Nuclear Receptor Family: New Insights Into Structure, Regulation, and Evolution From the Rat Genome. <i>Genome Research</i> , 2004, 14, 580-590.	2.4	187
173	RTCGD: retroviral tagged cancer gene database. <i>Nucleic Acids Research</i> , 2004, 32, 523D-527.	6.5	289
174	Automated Whole-Genome Multiple Alignment of Rat, Mouse, and Human. <i>Genome Research</i> , 2004, 14, 685-692.	2.4	79
175	Gene trap as a tool for genome annotation and analysis of X chromosome inactivation in human embryonic stem cells. <i>Nucleic Acids Research</i> , 2004, 32, 3995-4002.	6.5	69
176	Molecular structure of double-minute chromosomes bearing amplified copies of the epidermal growth factor receptor gene in gliomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11368-11373.	3.3	145
177	Discovery of functional noncoding elements by digital analysis of chromatin structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16837-16842.	3.3	135
178	Novel Antigen Identification Method for Discovery of Protective Malaria Antigens by Rapid Testing of DNA Vaccines Encoding Exons from the Parasite Genome. <i>Infection and Immunity</i> , 2004, 72, 1594-1602.	1.0	28
179	Evolution and Comparative Genomics of Odorant- and Pheromone-Associated Genes in Rodents. <i>Genome Research</i> , 2004, 14, 591-602.	2.4	97
180	High-Density Rat Radiation Hybrid Maps Containing Over 24,000 SSLPs, Genes, and ESTs Provide a Direct Link to the Rat Genome Sequence. <i>Genome Research</i> , 2004, 14, 750-757.	2.4	36
181	WormBase: a comprehensive data resource for <i>Caenorhabditis</i> biology and genomics. <i>Nucleic Acids Research</i> , 2004, 33, D383-D389.	6.5	155
182	WormBase as an Integrated Platform for the <i>C. elegans</i> ORFeome. <i>Genome Research</i> , 2004, 14, 2155-2161.	2.4	19
183	Coamplification of DDX1 Correlates With an Improved Survival Probability in Children With MYCN-Amplified Human Neuroblastoma. <i>Journal of Clinical Oncology</i> , 2004, 22, 2681-2690.	0.8	45
184	Identification of MEF2-regulated genes during muscle differentiation. <i>Physiological Genomics</i> , 2004, 20, 143-151.	1.0	22

#	ARTICLE	IF	CITATIONS
185	OPTIMAL SPACED SEEDS FOR HOMOLOGOUS CODING REGIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 01, 595-610.	0.3	48
186	From masking repeats to identifying functional repeats in the mouse transcriptome. <i>Briefings in Bioinformatics</i> , 2004, 5, 107-117.	3.2	5
187	Integrated analysis of the genome and the transcriptome by FANTOM. <i>Briefings in Bioinformatics</i> , 2004, 5, 249-258.	3.2	12
188	Gene structure prediction from consensus spliced alignment of multiple ESTs matching the same genomic locus. <i>Bioinformatics</i> , 2004, 20, 1157-1169.	1.8	97
189	GeneAnnot: comprehensive two-way linking between oligonucleotide array probesets and GeneCards genes. <i>Bioinformatics</i> , 2004, 20, 1457-1458.	1.8	53
190	Eukaryotic Regulatory Element Conservation Analysis and Identification Using Comparative Genomics. <i>Genome Research</i> , 2004, 14, 451-458.	2.4	130
191	Differential Alu Mobilization and Polymorphism Among the Human and Chimpanzee Lineages. <i>Genome Research</i> , 2004, 14, 1068-1075.	2.4	108
192	HERVd: the Human Endogenous RetroViruses Database: update. <i>Nucleic Acids Research</i> , 2004, 32, 50D-50.	6.5	63
193	Hembase: browser and genome portal for hematology and erythroid biology. <i>Nucleic Acids Research</i> , 2004, 32, 572D-574.	6.5	21
194	The mouse genome: Experimental examination of gene predictions and transcriptional start sites. <i>Genome Research</i> , 2004, 14, 2424-2429.	2.4	11
195	Good spaced seeds for homology search. <i>Bioinformatics</i> , 2004, 20, 1053-1059.	1.8	69
196	Identifying estrogen receptor $\hat{A}$ target genes using integrated computational genomics and chromatin immunoprecipitation microarray. <i>Nucleic Acids Research</i> , 2004, 32, 6627-6635.	6.5	79
197	MAVID: Constrained Ancestral Alignment of Multiple Sequences. <i>Genome Research</i> , 2004, 14, 693-699.	2.4	232
198	me-PCR: a refined ultrafast algorithm for identifying sequence-defined genomic elements. <i>Bioinformatics</i> , 2004, 20, 588-590.	1.8	12
199	Gene expression changes associated with fibronectin-induced cardiac myocyte hypertrophy. <i>Physiological Genomics</i> , 2004, 18, 273-283.	1.0	50
200	Estimating seed sensitivity on homogeneous alignments. , 0, , .		14
201	GeneTide–Terra Incognita Discovery Endeavor: a new transcriptome focused member of the GeneCards/GeneNote suite of databases. <i>Nucleic Acids Research</i> , 2004, 33, D556-D561.	6.5	10
202	ECR Browser: a tool for visualizing and accessing data from comparisons of multiple vertebrate genomes. <i>Nucleic Acids Research</i> , 2004, 32, W280-W286.	6.5	462

#	ARTICLE	IF	CITATIONS
203	siRNA Selection Server: an automated siRNA oligonucleotide prediction server. <i>Nucleic Acids Research</i> , 2004, 32, W130-W134.	6.5	283
204	ASmodeler: gene modeling of alternative splicing from genomic alignment of mRNA, EST and protein sequences. <i>Nucleic Acids Research</i> , 2004, 32, W181-W186.	6.5	17
205	PromoSer: improvements to the algorithm, visualization and accessibility. <i>Nucleic Acids Research</i> , 2004, 32, W191-W194.	6.5	22
206	ProbeLynx: a tool for updating the association of microarray probes to genes. <i>Nucleic Acids Research</i> , 2004, 32, W471-W474.	6.5	14
207	e2g: an interactive web-based server for efficiently mapping large EST and cDNA sets to genomic sequences. <i>Nucleic Acids Research</i> , 2004, 32, W301-W304.	6.5	10
208	ChickVD: a sequence variation database for the chicken genome. <i>Nucleic Acids Research</i> , 2004, 33, D438-D441.	6.5	33
209	The UCSC Proteome Browser. <i>Nucleic Acids Research</i> , 2004, 33, D454-D458.	6.5	43
210	Systematic Recovery and Analysis of Full-ORF Human cDNA Clones. <i>Genome Research</i> , 2004, 14, 2083-2092.	2.4	28
211	Selective pressures on the olfactory receptor repertoire since the human-chimpanzee divergence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9019-9022.	3.3	66
212	Identification and Analysis of the Promoter Region of the Human Hyaluronan Synthase 2 Gene. <i>Journal of Biological Chemistry</i> , 2004, 279, 20576-20581.	1.6	34
213	Genome annotation by high-throughput 5' RNA end determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1650-1655.	3.3	26
214	Pash: Efficient Genome-Scale Sequence Anchoring by Positional Hashing. <i>Genome Research</i> , 2004, 14, 672-678.	2.4	33
215	Genetic Divergence of the Rhesus Macaque Major Histocompatibility Complex. <i>Genome Research</i> , 2004, 14, 1501-1515.	2.4	195
216	Analysis of Human mRNAs With the Reference Genome Sequence Reveals Potential Errors, Polymorphisms, and RNA Editing. <i>Genome Research</i> , 2004, 14, 2034-2040.	2.4	26
217	Packaging and reverse transcription of snRNAs by retroviruses may generate pseudogenes. <i>Rna</i> , 2004, 10, 299-307.	1.6	33
218	CHARACTERIZATION OF THE SPLICE SITES IN GT <sup>+</sup> AG AND GC <sup>+</sup> AG INTRONS IN HIGHER EUKARYOTES USING FULL-LENGTH cDNAs. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 309-331.	0.3	33
219	A TUTORIAL OF RECENT DEVELOPMENTS IN THE SEEDING OF LOCAL ALIGNMENT. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 819-842.	0.3	22
220	FREP: a database of functional repeats in mouse cDNAs. <i>Nucleic Acids Research</i> , 2004, 32, 471D-475.	6.5	6

#	ARTICLE	IF	CITATIONS
221	EXPRESSION OF TESTIS SPECIFIC ANKYRIN REPEAT AND SOCS BOX-CONTAINING 17 GENE. Archives of Andrology, 2004, 50, 155-161.	1.0	10
222	Predicting rules on organization of cis-regulatory elements, taking the order of elements into account. Bioinformatics, 2004, 20, 1119-1128.	1.8	17
223	Speeding up whole-genome alignment by indexing frequency vectors. Bioinformatics, 2004, 20, 2122-2134.	1.8	15
224	Distinct Genomic Integration of MLV and SIV Vectors in Primate Hematopoietic Stem and Progenitor Cells. PLoS Biology, 2004, 2, e423.	2.6	243
225	Site2genome: locating short DNA sequences in whole genomes. Bioinformatics, 2004, 20, 1468-1469.	1.8	3
226	Over 20% of human transcripts might form sense-antisense pairs. Nucleic Acids Research, 2004, 32, 4812-4820.	6.5	287
227	Integration of the Rat Recombination and EST Maps in the Rat Genomic Sequence and Comparative Mapping Analysis With the Mouse Genome. Genome Research, 2004, 14, 758-765.	2.4	22
228	Characterization of a human colonic cDNA encoding a structurally novel urea transporter, hUT-A6. American Journal of Physiology - Cell Physiology, 2004, 287, C1087-C1093.	2.1	60
229	An online database for the detection of novel archaeal sequences in human ESTs. Bioinformatics, 2004, 20, 2361-2362.	1.8	1
230	New human and mouse microRNA genes found by homology search. FEBS Journal, 2004, 272, 59-73.	2.2	268
231	Identification of putative homology between horse microsatellite flanking sequences and cross-species ESTs, mRNAs and genomic sequences. Animal Genetics, 2004, 35, 28-33.	0.6	17
232	High-throughput screening of genome fragments bound to differentially acetylated histones. Genes To Cells, 2004, 9, 1167-1174.	0.5	10
233	The DNA sequence and biology of human chromosome 19. Nature, 2004, 428, 529-535.	13.7	298
234	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
235	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	13.7	391
236	The sequence and analysis of duplication-rich human chromosome 16. Nature, 2004, 432, 988-994.	13.7	156
237	Retrotransposition of Alu elements: how many sources?. Trends in Genetics, 2004, 20, 464-467.	2.9	103
238	Mammalian phylogenomics comes of age. Trends in Genetics, 2004, 20, 631-639.	2.9	327

#	ARTICLE	IF	CITATIONS
239	Comprehensive analysis of keratin gene clusters in humans and rodents. <i>European Journal of Cell Biology</i> , 2004, 83, 19-26.	1.6	176
240	Improved hit criteria for DNA local alignment. <i>BMC Bioinformatics</i> , 2004, 5, 149.	1.2	49
241	Combining gene expression data from different generations of oligonucleotide arrays. <i>BMC Bioinformatics</i> , 2004, 5, 159.	1.2	52
242	Assessment of clusters of transcription factor binding sites in relationship to human promoter, CpG islands and gene expression. <i>BMC Genomics</i> , 2004, 5, 16.	1.2	25
243	A genome-wide screen identifies a single $\beta$ -defensin gene cluster in the chicken: implications for the origin and evolution of mammalian defensins. <i>BMC Genomics</i> , 2004, 5, 56.	1.2	258
244	Polymorphic segmental duplications at 8p23.1 challenge the determination of individual defensin gene repertoires and the assembly of a contiguous human reference sequence. <i>BMC Genomics</i> , 2004, 5, 92.	1.2	51
245	Arrays of ultraconserved non-coding regions span the loci of key developmental genes in vertebrate genomes. <i>BMC Genomics</i> , 2004, 5, 99.	1.2	267
246	Dipeptidyl peptidase 9 has two forms, a broad tissue distribution, cytoplasmic localization and DPIP-like peptidase activity. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1679, 18-28.	2.4	116
247	Fine mapping a gene for pediatric gastroesophageal reflux on human chromosome 13q14. <i>Human Genetics</i> , 2004, 114, 562-572.	1.8	19
248	Evolutionary implication of human endogenous retrovirus HERV-H family. <i>Journal of Human Genetics</i> , 2004, 49, 215-219.	1.1	8
249	Comprehensive association analysis of APOE regulatory region polymorphisms in Alzheimer disease. <i>Neurogenetics</i> , 2004, 5, 201-208.	0.7	22
250	An interactive bovine in silico SNP database (IBISS). <i>Mammalian Genome</i> , 2004, 15, 819-827.	1.0	60
251	Comparative genomics: methods and applications. <i>Die Naturwissenschaften</i> , 2004, 91, 405-21.	0.6	20
252	Open reading frame sequencing and structure-based alignment of polypeptides encoded by RT1-Bb, RT1-Ba, RT1-Db, and RT1-Da alleles. <i>Immunogenetics</i> , 2004, 56, 585-596.	1.2	15
253	A digenic cause of cleft lip in A-strain mice and definition of candidate genes for the two loci. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2004, 70, 509-518.	1.6	35
254	Recent developments in computational approaches for uncovering genomic homology. <i>BioEssays</i> , 2004, 26, 1225-1235.	1.2	22
255	Prognostic classification of relapsing favorable histology Wilms tumor using cDNA microarray expression profiling and support vector machines. <i>Genes Chromosomes and Cancer</i> , 2004, 41, 65-79.	1.5	48
256	PromoLign: A database for upstream region analysis and SNPs. <i>Human Mutation</i> , 2004, 23, 534-539.	1.1	33

#	ARTICLE	IF	CITATIONS
257	Two-color multiplex ligation-dependent probe amplification: Detecting genomic rearrangements in hereditary multiple exostoses. <i>Human Mutation</i> , 2004, 24, 86-92.	1.1	142
258	Characterization of a mutagenic B1 retrotransposon insertion in the jittery mouse. <i>Human Mutation</i> , 2004, 24, 9-13.	1.1	21
259	Gene expression analysis in the hippocampal formation of tree shrews chronically treated with cortisol. <i>Journal of Neuroscience Research</i> , 2004, 78, 702-710.	1.3	33
260	MAGIC Database and Interfaces: An Integrated Package for Gene Discovery and Expression. <i>Comparative and Functional Genomics</i> , 2004, 5, 268-275.	2.0	16
261	An IDC-based algorithm for efficient homology filtration with guaranteed seriate coverage. , 0, , .		0
262	Improved gapped alignment in BLAST. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 116-129.	1.9	88
263	Xpro: database of eukaryotic protein-encoding genes. <i>Nucleic Acids Research</i> , 2004, 32, 59D-63.	6.5	21
264	A metric model of amino acid substitution. <i>Bioinformatics</i> , 2004, 20, 1214-1221.	1.8	35
265	Evolution of the tumor suppressor BRCA1 locus in primates: implications for cancer predisposition. <i>Human Molecular Genetics</i> , 2004, 13, 2737-2751.	1.4	88
266	Creation of the whole human genome microarray. <i>Expert Review of Proteomics</i> , 2004, 1, 19-28.	1.3	33
267	Genome-wide mutagenesis of <i>Zea mays</i> L. using RescueMu transposons. <i>Genome Biology</i> , 2004, 5, R82.	13.9	66
268	Alternative splicing of mouse transcription factors affects their DNA-binding domain architecture and is tissue specific. <i>Genome Biology</i> , 2004, 5, R75.	13.9	67
269	Evolutionary conservation and selection of human disease gene orthologs in the rat and mouse genomes. <i>Genome Biology</i> , 2004, 5, R47.	13.9	116
270	ELXR: a resource for rapid exon-directed sequence analysis. <i>Genome Biology</i> , 2004, 5, R36.	13.9	14
271	Cloning, expression and subcellular localization of HN1 and HN1L genes, as well as characterization of their orthologs, defining an evolutionarily conserved gene family. <i>Gene</i> , 2004, 331, 115-123.	1.0	38
272	A novel mitochondrial C1-tetrahydrofolate synthetase is upregulated in human colon adenocarcinoma. <i>Biochemical and Biophysical Research Communications</i> , 2004, 315, 204-211.	1.0	33
273	Odorant and vomeronasal receptor genes in two mouse genome assemblies. <i>Genomics</i> , 2004, 83, 802-811.	1.3	149
274	Comparative sequence analysis of the <i>Gdf6</i> locus reveals a duplicon-mediated chromosomal rearrangement in rodents and rapidly diverging coding and regulatory sequences. <i>Genomics</i> , 2004, 84, 814-823.	1.3	8

#	ARTICLE	IF	CITATIONS
275	Interpreting mammalian evolution using Fugu genome comparisons. <i>Genomics</i> , 2004, 84, 890-895.	1.3	39
276	Construction of representative transcript and protein sets of human, mouse, and rat as a platform for their transcriptome and proteome analysis. <i>Genomics</i> , 2004, 84, 913-921.	1.3	23
277	Identification of a novel alternative splicing form of human netrin-4 and analyzing the expression patterns in adult rat brain. <i>Molecular Brain Research</i> , 2004, 130, 68-80.	2.5	19
278	Genes transcribed in the salivary glands of female <i>Rhipicephalus appendiculatus</i> ticks infected with <i>Theileria parva</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2004, 34, 1117-1128.	1.2	98
279	A transcriptional profile of human fetal cartilage. <i>Matrix Biology</i> , 2004, 23, 299-307.	1.5	19
280	Identification of New Human Cadherin Genes Using a Combination of Protein Motif Search and Gene Finding Methods. <i>Journal of Molecular Biology</i> , 2004, 337, 307-317.	2.0	36
281	Analysis of the Human Alu Ya-lineage. <i>Journal of Molecular Biology</i> , 2004, 342, 109-118.	2.0	49
282	A gene atlas of the mouse and human protein-encoding transcriptomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6062-6067.	3.3	3,290
283	Reconstructing the Genomic Architecture of Ancestral Mammals: Lessons From Human, Mouse, and Rat Genomes. <i>Genome Research</i> , 2004, 14, 507-516.	2.4	210
284	VISTA: computational tools for comparative genomics. <i>Nucleic Acids Research</i> , 2004, 32, W273-W279.	6.5	2,033
285	Building and managing production bioclusters. <i>Drug Discovery Today Biosilico</i> , 2004, 2, 208-213.	0.7	1
286	Regional Patterns of Gene Expression in Human and Chimpanzee Brains. <i>Genome Research</i> , 2004, 14, 1462-1473.	2.4	311
287	Bioinformatics and Management Science: Some Common Tools and Techniques. <i>Operations Research</i> , 2004, 52, 165-190.	1.2	15
288	Identification of the major promoter and non-coding exons of the human arylamine N-acetyltransferase 1 gene (NAT1). <i>Pharmacogenetics and Genomics</i> , 2004, 14, 397-406.	5.7	50
289	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2004, 33, D141-D146.	6.5	140
290	Detecting Copy Number Changes in Genomic DNA: MAPH and MLPA. <i>Methods in Cell Biology</i> , 2004, 75, 751-768.	0.5	25
291	Good spaced seeds for homology search. , 0, , .		0
292	Parkin and relatives: the RBR family of ubiquitin ligases. <i>Physiological Genomics</i> , 2004, 17, 253-263.	1.0	103

#	ARTICLE	IF	CITATIONS
293	Searching WormBase for Information About <i>Caenorhabditis elegans</i> . <i>Current Protocols in Bioinformatics</i> , 2004, 6, 1.8.1.	25.8	1
294	Rapid evolution and diversification of mammalian $\hat{\pm}$ -defensins as revealed by comparative analysis of rodent and primate genes. <i>Physiological Genomics</i> , 2004, 20, 1-11.	1.0	145
295	Large-scale gene discovery in human airway epithelia reveals novel transcripts. <i>Physiological Genomics</i> , 2004, 17, 69-77.	1.0	23
296	Gene structure prediction in plant genomes. , 2005, , .		1
297	Databases for Comparative Analysis of Human-Mouse Orthologous Alternative Splicing. <i>Lecture Notes in Computer Science</i> , 2005, , 123-131.	1.0	3
298	AN ASSESSMENT OF A METRIC SPACE DATABASE INDEX TO SUPPORT SEQUENCE HOMOMOLOGY. <i>International Journal on Artificial Intelligence Tools</i> , 2005, 14, 867-885.	0.7	12
299	Neighboring-Nucleotide Effects on the Mutation Patterns of the Rice Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 158-168.	3.0	3
300	Spliced alignment. , 2005, , .		0
301	Using ESTs for genome annotation - predicting the transcriptome. , 2005, , .		0
302	Dcode.org anthology of comparative genomic tools. <i>Nucleic Acids Research</i> , 2005, 33, W56-W64.	6.5	32
303	Efficient q-Gram Filters for Finding All $\hat{\mu}$ -Matches over a Given Length. <i>Lecture Notes in Computer Science</i> , 2005, , 189-203.	1.0	21
304	Genomic rearrangements by LINE-1 insertion-mediated deletion in the human and chimpanzee lineages. <i>Nucleic Acids Research</i> , 2005, 33, 4040-4052.	6.5	127
305	Preferential selection of human T-cell leukemia virus type I provirus integration sites in leukemic versus carrier states. <i>Blood</i> , 2005, 106, 1048-1053.	0.6	64
306	A newly discovered human $\hat{\pm}$ -globin gene. <i>Blood</i> , 2005, 106, 1466-1472.	0.6	59
307	Characterization of CA XV, a new GPI-anchored form of carbonic anhydrase. <i>Biochemical Journal</i> , 2005, 392, 83-92.	1.7	152
308	Comparisons of Long Genomic Sequences. <i>Chapman &amp; Hall/CRC Computer and Information Science Series</i> , 2005, , 14-1-14-23.	0.4	0
309	Comparative analysis for mapping and sequence assembly. , 2005, , .		0
310	Retroviral expression screening of oncogenes in natural killer cell leukemia. <i>Leukemia Research</i> , 2005, 29, 943-949.	0.4	13

#	ARTICLE	IF	CITATIONS
311	Designing seeds for similarity search in genomic DNA. <i>Journal of Computer and System Sciences</i> , 2005, 70, 342-363.	0.9	64
312	Vector seeds: An extension to spaced seeds. <i>Journal of Computer and System Sciences</i> , 2005, 70, 364-380.	0.9	42
313	A mobile element based phylogeny of Old World monkeys. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 872-880.	1.2	90
314	Tri-nucleotide repeats and their association with genes in rice genome. <i>BioSystems</i> , 2005, 82, 248-256.	0.9	5
315	Engineering a software tool for gene structure prediction in higher organisms. <i>Information and Software Technology</i> , 2005, 47, 965-978.	3.0	251
316	GAME: A simple and efficient whole genome alignment method using maximal exact match filtering. <i>Computational Biology and Chemistry</i> , 2005, 29, 244-253.	1.1	14
317	Complete reannotation of the Arabidopsis genome: methods, tools, protocols and the final release. <i>BMC Biology</i> , 2005, 3, 7.	1.7	149
318	“Beijing Region” (3pter-D3S3397) of the Human Genome: Complete sequence and analysis. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 311.	1.3	1
319	Genome-wide analysis of mouse transcripts using exon microarrays and factor graphs. <i>Nature Genetics</i> , 2005, 37, 991-996.	9.4	38
320	Computational screening of conserved genomic DNA in search of functional noncoding elements. <i>Nature Methods</i> , 2005, 2, 535-545.	9.0	52
321	Mutation analysis of the WFS1 gene in seven Danish Wolfram syndrome families; four new mutations identified. <i>European Journal of Human Genetics</i> , 2005, 13, 1275-1284.	1.4	75
322	Retroviral insertional mutagenesis: past, present and future. <i>Oncogene</i> , 2005, 24, 7656-7672.	2.6	250
323	Cerebellar Gene Expression Profiling and eQTL Analysis in Inbred Mouse Strains Selected for Ethanol Sensitivity. <i>Alcoholism: Clinical and Experimental Research</i> , 2005, 29, 1568-1579.	1.4	22
324	Downregulation of major histocompatibility complex antigens in invading glioma cells: stealth invasion of the brain. <i>Laboratory Investigation</i> , 2005, 85, 328-341.	1.7	149
325	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	13.7	85
326	Transcription of mammalian messenger RNAs by a nuclear RNA polymerase of mitochondrial origin. <i>Nature</i> , 2005, 436, 735-739.	13.7	61
327	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	13.7	53
328	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	13.7	2,222

#	ARTICLE	IF	CITATIONS
329	Natural selection on protein-coding genes in the human genome. <i>Nature</i> , 2005, 437, 1153-1157.	13.7	718
330	$\hat{I}^{3}N$ -crystallin and the evolution of the $\hat{I}^{2}\hat{I}^{3}$ -crystallin superfamily in vertebrates. <i>FEBS Journal</i> , 2005, 272, 2276-2291.	2.2	84
331	Comparative Study of Apoptosis-related Gene Loci in Human, Mouse and Rat Genomes. <i>Acta Biochimica Et Biophysica Sinica</i> , 2005, 37, 341-348.	0.9	0
332	Tissue distribution of a human Cav1.2 $\hat{I} \pm 1$ subunit splice variant with a 75bp insertion $\hat{I}^{\dagger}$ . <i>Cell Calcium</i> , 2005, 38, 11-21.	1.1	24
333	Isolation, sequencing, and functional analysis of the TATA-less human ATPase II promoter. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005, 1728, 186-198.	2.4	4
334	A computational view of microRNAs and their targets. <i>Drug Discovery Today</i> , 2005, 10, 595-601.	3.2	101
335	A limited role for balancing selection. <i>Trends in Genetics</i> , 2005, 21, 30-32.	2.9	103
336	Refined repetitive sequence searches utilizing a fast hash function and cross species information retrievals. <i>BMC Bioinformatics</i> , 2005, 6, 111.	1.2	10
337	A multistep bioinformatic approach detects putative regulatory elements in gene promoters. <i>BMC Bioinformatics</i> , 2005, 6, 121.	1.2	18
338	Satelloq: a database for the identification and prioritization of satellite repeats in disease association studies. <i>BMC Bioinformatics</i> , 2005, 6, 145.	1.2	16
339	A computational approach for identifying pathogenicity islands in prokaryotic genomes. <i>BMC Bioinformatics</i> , 2005, 6, 184.	1.2	55
340	A method for finding single-nucleotide polymorphisms with allele frequencies in sequences of deep coverage. <i>BMC Bioinformatics</i> , 2005, 6, 220.	1.2	10
341	ASPIC: a novel method to predict the exon-intron structure of a gene that is optimally compatible to a set of transcript sequences. <i>BMC Bioinformatics</i> , 2005, 6, 244.	1.2	32
342	A method of precise mRNA/DNA homology-based gene structure prediction. <i>BMC Bioinformatics</i> , 2005, 6, 261.	1.2	6
343	Statistical Viewer: a tool to upload and integrate linkage and association data as plots displayed within the Ensembl genome browser. <i>BMC Bioinformatics</i> , 2005, 6, 95.	1.2	11
344	Phylogenomic approaches to common problems encountered in the analysis of low copy repeats: the sulfotransferase 1A gene family example. <i>BMC Evolutionary Biology</i> , 2005, 5, 22.	3.2	21
345	A systematic search for new mammalian noncoding RNAs indicates little conserved intergenic transcription. <i>BMC Genomics</i> , 2005, 6, 104.	1.2	72
346	Construction and characterization of a genomic BAC library for the <i>Mus m. musculus</i> mouse subspecies (PWD/Ph inbred strain). <i>BMC Genomics</i> , 2005, 6, 161.	1.2	12

#	ARTICLE	IF	CITATIONS
347	Characterization of 954 bovine full-CDS cDNA sequences. <i>BMC Genomics</i> , 2005, 6, 166.	1.2	26
348	Efficient single nucleotide polymorphism discovery in laboratory rat strains using wild rat-derived SNP candidates. <i>BMC Genomics</i> , 2005, 6, 170.	1.2	17
349	Identification of functional SNPs in the 5-prime flanking sequences of human genes. <i>BMC Genomics</i> , 2005, 6, 18.	1.2	44
350	A method for accurate detection of genomic microdeletions using real-time quantitative PCR. <i>BMC Genomics</i> , 2005, 6, 180.	1.2	89
351	Genome-scale analysis of positional clustering of mouse testis-specific genes. <i>BMC Genomics</i> , 2005, 6, 7.	1.2	47
352	Linkage mapping bovine EST-based SNP. <i>BMC Genomics</i> , 2005, 6, 74.	1.2	58
353	Molecular profile of catabolic versus anabolic treatment regimens of parathyroid hormone (PTH) in rat bone: An analysis by DNA microarray. <i>Journal of Cellular Biochemistry</i> , 2005, 95, 403-418.	1.2	92
354	Identification and validation of novel ERBB2 (HER2, NEU) targets including genes involved in angiogenesis. <i>International Journal of Cancer</i> , 2005, 114, 590-597.	2.3	53
355	Investigations of the genomic region that contains the <i>clf1</i> mutation, a causal gene in multifactorial cleft lip and palate in mice. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2005, 73, 103-113.	1.6	54
356	Analysis of NF1 transcriptional regulatory elements. <i>American Journal of Medical Genetics, Part A</i> , 2005, 137A, 130-135.	0.7	10
357	The synthetic form of a novel chicken $\theta$ -defensin identified in silico is predominantly active against intestinal pathogens. <i>Immunogenetics</i> , 2005, 57, 90-98.	1.2	74
358	Validation of mRNA/EST-based gene predictions in human Xp11.4 revealed differences to the organization of the orthologous mouse locus. <i>Mammalian Genome</i> , 2005, 16, 934-941.	1.0	1
359	Random sheared fosmid library as a new genomic tool to accelerate complete finishing of rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf euchromatic portions of the genome. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1596-1607.	1.8	36
360	DING proteins are from <i>Pseudomonas</i> . <i>FEMS Microbiology Letters</i> , 2005, 252, 215-222.	0.7	20
361	Cataloging transcription factor and major signaling molecule genes for functional genomic studies in <i>Ciona intestinalis</i> . <i>Development Genes and Evolution</i> , 2005, 215, 580-596.	0.4	22
362	Analysis of porcine MHC expression profile. <i>Science Bulletin</i> , 2005, 50, 880-890.	1.7	2
363	Test Data Sets and Evaluation of Gene Prediction Programs on the Rice Genome. <i>Journal of Computer Science and Technology</i> , 2005, 20, 446-453.	0.9	14
364	Analysis of 70,000 EST sequences to study divergence between two closely related <i>Populus</i> species. <i>Tree Genetics and Genomes</i> , 2005, 1, 109-115.	0.6	11

#	ARTICLE	IF	CITATIONS
365	Characterisation and application of a bovine U6 promoter for expression of short hairpin RNAs. <i>BMC Biotechnology</i> , 2005, 5, 13.	1.7	26
366	Exploring hepatic hormone actions using a compilation of gene expression profiles. <i>BMC Physiology</i> , 2005, 5, 8.	3.6	39
367	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	2.6	808
369	Restriction fragment fingerprinting software. , 2005, , .		0
370	Tools and strategies for physiological genomics: the Rat Genome Database. <i>Physiological Genomics</i> , 2005, 23, 246-256.	1.0	25
371	Learning Interpretable SVMs for Biological Sequence Classification. <i>Lecture Notes in Computer Science</i> , 2005, , 389-407.	1.0	24
372	Mapping of genetic determinants of the sympathoneural response to stress. <i>Physiological Genomics</i> , 2005, 20, 183-187.	1.0	13
373	Genomic Resources for Cancer Biologists. , 2005, , 3-17.		1
374	A model-based scan statistic for identifying extreme chromosomal regions of gene expression in human tumors. <i>Bioinformatics</i> , 2005, 21, 2867-2874.	1.8	29
375	LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. <i>Bioinformatics</i> , 2005, 21, 2814-2820.	1.8	202
376	The Evolution of Transcription-Initiation Sites. <i>Molecular Biology and Evolution</i> , 2005, 22, 1137-1146.	3.5	60
377	Differential Effects of Estrogen and Raloxifene on Messenger RNA and Matrix Metalloproteinase 2 Activity in the Rat Uterus. <i>Biology of Reproduction</i> , 2005, 72, 830-841.	1.2	37
378	Autosomal dominant optic atrophy associated with hearing impairment and impaired glucose regulation caused by a missense mutation in the WFS1 gene. <i>Journal of Medical Genetics</i> , 2005, 43, 435-440.	1.5	114
379	Global analysis of IL-2 target genes: identification of chromosomal clusters of expressed genes. <i>International Immunology</i> , 2005, 17, 1009-1021.	1.8	50
380	Integration Targeting by Avian Sarcoma-Leukosis Virus and Human Immunodeficiency Virus in the Chicken Genome. <i>Journal of Virology</i> , 2005, 79, 12035-12044.	1.5	80
381	A retrocopy of a gene can functionally displace the source gene in evolution. <i>Nucleic Acids Research</i> , 2005, 33, 6654-6661.	6.5	41
382	Comparative EST Analyses in Plant Systems. <i>Methods in Enzymology</i> , 2005, 395, 400-418.	0.4	22
383	A Tiling Microarray Expression Analysis of Rice Chromosome 4 Suggests a Chromosome-Level Regulation of Transcription. <i>Plant Cell</i> , 2005, 17, 1641-1657.	3.1	56

#	ARTICLE	IF	CITATIONS
384	Genomic deletions and precise removal of transposable elements mediated by short identical DNA segments in primates. <i>Genome Research</i> , 2005, 15, 1243-1249.	2.4	110
385	Dynamic structure of the SPANX gene cluster mapped to the prostate cancer susceptibility locus HPCX at Xq27. <i>Genome Research</i> , 2005, 15, 1477-1486.	2.4	38
386	ΔC31 Integrase Confers Genomic Integration and Long-Term Transgene Expression in Rat Retina. , 2005, 46, 2140.		94
387	Multi-species microarrays reveal the effect of sequence divergence on gene expression profiles. <i>Genome Research</i> , 2005, 15, 674-680.	2.4	155
388	Traffic of genetic information between segmental duplications flanking the typical 22q11.2 deletion in velo-cardio-facial syndrome/DiGeorge syndrome. <i>Genome Research</i> , 2005, 15, 1487-1495.	2.4	30
389	A Genetic Linkage Map for the Tiger Pufferfish, <i>Takifugu rubripes</i> . <i>Genetics</i> , 2005, 171, 227-238.	1.2	93
390	Assembly of polymorphic genomes: Algorithms and application to <i>Ciona savignyi</i> . <i>Genome Research</i> , 2005, 15, 1127-1135.	2.4	170
391	Chromosomal copy number changes in patients with non-syndromic X linked mental retardation detected by array CGH. <i>Journal of Medical Genetics</i> , 2005, 43, 362-370.	1.5	85
392	The evolutionary fate of MULE-mediated duplications of host gene fragments in rice. <i>Genome Research</i> , 2005, 15, 1292-1297.	2.4	210
393	Multiple Fates of L1 Retrotransposition Intermediates in Cultured Human Cells. <i>Molecular and Cellular Biology</i> , 2005, 25, 7780-7795.	1.1	255
394	Identification and characterization of the peroxiredoxin gene family in chickens. <i>Poultry Science</i> , 2005, 84, 1432-1438.	1.5	19
395	Inferring gene transcriptional modulatory relations: a genetical genomics approach. <i>Human Molecular Genetics</i> , 2005, 14, 1119-1125.	1.4	76
396	Large-scale structure of genomic methylation patterns. <i>Genome Research</i> , 2005, 16, 157-163.	2.4	325
397	ECgene: Genome-based EST clustering and gene modeling for alternative splicing. <i>Genome Research</i> , 2005, 15, 566-576.	2.4	86
398	Direct crossregulation between retinoic acid receptor $\beta^2$ and Hox genes during hindbrain segmentation. <i>Development (Cambridge)</i> , 2005, 132, 503-513.	1.2	65
399	Interchromosomal Segmental Duplications Explain the Unusual Structure of PRSS3, the Gene for an Inhibitor-Resistant Trypsinogen. <i>Molecular Biology and Evolution</i> , 2005, 22, 1712-1720.	3.5	31
400	RASE: recognition of alternatively spliced exons in <i>C.elegans</i> . <i>Bioinformatics</i> , 2005, 21, i369-i377.	1.8	109
401	Pooled genomic indexing of rhesus macaque. <i>Genome Research</i> , 2005, 15, 292-301.	2.4	14

#	ARTICLE	IF	CITATIONS
402	Genome-wide transcriptional analysis of flagellar regeneration in <i>Chlamydomonas reinhardtii</i> identifies orthologs of ciliary disease genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3703-3707.	3.3	203
403	A large-scale analysis of mRNA polyadenylation of human and mouse genes. <i>Nucleic Acids Research</i> , 2005, 33, 201-212.	6.5	854
404	Identification of coexpressed gene clusters in a comparative analysis of transcriptome and proteome in mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8621-8626.	3.3	75
405	AnoEST: Toward <i>A. gambiae</i> functional genomics. <i>Genome Research</i> , 2005, 15, 893-899.	2.4	19
406	Genome-wide assembly and analysis of alternative transcripts in mouse. <i>Genome Research</i> , 2005, 15, 748-754.	2.4	49
407	Using multiple alignments to improve seeded local alignment algorithms. <i>Nucleic Acids Research</i> , 2005, 33, 4563-4577.	6.5	8
408	Experimental comparison and cross-validation of the Affymetrix and Illumina gene expression analysis platforms. <i>Nucleic Acids Research</i> , 2005, 33, 5914-5923.	6.5	222
409	Quick, Practical Selection of Effective Seeds for Homology Search. <i>Journal of Computational Biology</i> , 2005, 12, 1137-1152.	0.8	13
410	Key Features of the UCSC Genome Site. , 0, , .		1
411	Clusters of Adjacent and Similarly Expressed Genes across Normal Human Tissues Complicate Comparative Transcriptomic Discovery. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 351-363.	1.0	6
412	ESTmapper: Efficiently Aligning DNA Sequences to Genomes. , 0, , .		4
413	Cross-species analysis of the mammalian $\beta$ -defensin gene family: presence of syntenic gene clusters and preferential expression in the male reproductive tract. <i>Physiological Genomics</i> , 2005, 23, 5-17.	1.0	191
414	Symmetrical base preferences surrounding HIV-1, avian sarcoma/leukosis virus, and murine leukemia virus integration sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6103-6107.	3.3	158
415	Complex genomic rearrangements lead to novel primate gene function. <i>Genome Research</i> , 2005, 15, 343-351.	2.4	104
416	EVOPRINTER, a multigenomic comparative tool for rapid identification of functionally important DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14700-14705.	3.3	62
417	MAASE: An alternative splicing database designed for supporting splicing microarray applications. <i>Rna</i> , 2005, 11, 1767-1776.	1.6	23
418	Using shared genomic synteny and shared protein functions to enhance the identification of orthologous gene pairs. <i>Bioinformatics</i> , 2005, 21, 703-710.	1.8	85
419	Designing Multiple Simultaneous Seeds for DNA Similarity Search. <i>Journal of Computational Biology</i> , 2005, 12, 847-861.	0.8	46

#	ARTICLE	IF	CITATIONS
420	High-Performance Direct Pairwise Comparison of Large Genomic Sequences. , 0, , .		1
421	Genome-Wide Screening for Target Regions of Histone Deacetylases in Cardiomyocytes. <i>Circulation Research</i> , 2005, 97, 210-218.	2.0	26
423	Large-Scale Analysis of Adeno-Associated Virus Vector Integration Sites in Normal Human Cells. <i>Journal of Virology</i> , 2005, 79, 11434-11442.	1.5	148
424	Substitution Rate and Structural Divergence of 5â€™UTR Evolution: Comparative Analysis Between Human and Cynomolgus Monkey cDNAs. <i>Molecular Biology and Evolution</i> , 2005, 22, 1976-1982.	3.5	21
425	MuPlex: multi-objective multiplex PCR assay design. <i>Nucleic Acids Research</i> , 2005, 33, W544-W547.	6.5	76
426	Gene identification in novel eukaryotic genomes by self-training algorithm. <i>Nucleic Acids Research</i> , 2005, 33, 6494-6506.	6.5	746
427	Identification of transposable elements using multiple alignments of related genomes. <i>Genome Research</i> , 2005, 16, 260-270.	2.4	45
428	On the feasibility of using network processors for DNA queries. , 2005, , 197-218.		2
429	GMAP: a genomic mapping and alignment program for mRNA and EST sequences. <i>Bioinformatics</i> , 2005, 21, 1859-1875.	1.8	2,121
430	JIGSAW: integration of multiple sources of evidence for gene prediction. <i>Bioinformatics</i> , 2005, 21, 3596-3603.	1.8	147
431	Coupling of Metabotropic Glutamate Receptor 8 to N-Type Ca <sup>2+</sup> Channels in Rat Sympathetic Neurons. <i>Molecular Pharmacology</i> , 2005, 67, 1840-1851.	1.0	22
432	Comparing low coverage random shotgun sequence data from <i>Brassica oleracea</i> and <i>Oryza sativa</i> genome sequence for their ability to add to the annotation of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2005, 15, 496-504.	2.4	27
433	Under the genomic radar: The Stealth model of Alu amplification. <i>Genome Research</i> , 2005, 15, 655-664.	2.4	65
434	Survey of allelic expression using EST mining. <i>Genome Research</i> , 2005, 15, 1584-1591.	2.4	115
435	The Institute for Genomic Research Osa1 Rice Genome Annotation Database. <i>Plant Physiology</i> , 2005, 138, 18-26.	2.3	201
436	Comparison of Current BLAST Software on Nucleotide Sequences. , 2005, 19, 8.		8
437	MUSTANG Is a Novel Family of Domesticated Transposase Genes Found in Diverse Angiosperms. <i>Molecular Biology and Evolution</i> , 2005, 22, 2084-2089.	3.5	66
438	Incorporation of splice site probability models for non-canonical introns improves gene structure prediction in plants. <i>Bioinformatics</i> , 2005, 21, iii20-iii30.	1.8	31

#	ARTICLE	IF	CITATIONS
439	Multiple mechanisms are implicated in the generation of 5q35 microdeletions in Sotos syndrome. <i>Journal of Medical Genetics</i> , 2005, 42, 307-313.	1.5	60
440	ASePCR: alternative splicing electronic RT-PCR in multiple tissues and organs. <i>Nucleic Acids Research</i> , 2005, 33, W681-W685.	6.5	9
441	Retropseudogenes derived from the human Ro/SS-A autoantigen-associated hY RNAs. <i>Nucleic Acids Research</i> , 2005, 33, 2032-2041.	6.5	49
442	CpG Island microarray probe sequences derived from a physical library are representative of CpG Islands annotated on the human genome. <i>Nucleic Acids Research</i> , 2005, 33, 2952-2961.	6.5	89
443	miBLAST: scalable evaluation of a batch of nucleotide sequence queries with BLAST. <i>Nucleic Acids Research</i> , 2005, 33, 4335-4344.	6.5	30
444	Distortion of quantitative genomic and expression hybridization by Cot-1 DNA: mitigation of this effect. <i>Nucleic Acids Research</i> , 2005, 33, e191-e191.	6.5	11
445	Fast Pattern Detection in Stream Data. , 0, , .		2
446	Integrating probe-level expression changes across generations of Affymetrix arrays. <i>Nucleic Acids Research</i> , 2005, 33, e193-e193.	6.5	51
447	Cloning and Characterization of Mouse E2F8, a Novel Mammalian E2F Family Member Capable of Blocking Cellular Proliferation. <i>Journal of Biological Chemistry</i> , 2005, 280, 18211-18220.	1.6	153
448	EST Data Mining and Applications in Fungal Genomics. <i>Applied Mycology and Biotechnology</i> , 2005, 5, 33-70.	0.3	0
449	An organizational grid of federated MOSIX clusters. , 2005, , .		17
450	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
451	Evolution of the secretoglobins: a genomic and proteomic view. <i>Biological Journal of the Linnean Society</i> , 2005, 84, 493-501.	0.7	18
452	An Integrated Database of the Ascidian, <i>Ciona intestinalis</i> : Towards Functional Genomics. <i>Zoological Science</i> , 2005, 22, 837-843.	0.3	173
453	Nine unknown rearrangements in 16p13.3 and 11p15.4 causing $\hat{A}$ - and $\hat{A}$ -thalassaemia characterised by high resolution multiplex ligation-dependent probe amplification. <i>Journal of Medical Genetics</i> , 2005, 42, 922-931.	1.5	213
454	Composite genome map and recombination parameters derived from three archetypal lineages of <i>Toxoplasma gondii</i> . <i>Nucleic Acids Research</i> , 2005, 33, 2980-2992.	6.5	147
455	Computational prediction of miRNAs in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2005, 15, 78-91.	2.4	324
456	Finding Keywords for Intergenic and Gene Regions for Human Genome. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2005, 24, 191-198.	0.4	0

#	ARTICLE	IF	CITATIONS
457	Cloning and characterization a novel human 1-acyl-sn-glycerol-3-phosphate acyltransferase geneAGPAT7. DNA Sequence, 2005, 16, 386-390.	0.7	35
458	EST-Based Analysis of Gene Expression in the Human Cochea. , 2005, 2005, .		0
459	Alu Retrotransposition-mediated Deletion. Journal of Molecular Biology, 2005, 348, 791-800.	2.0	114
460	SVA Elements: A Hominid-specific Retroposon Family. Journal of Molecular Biology, 2005, 354, 994-1007.	2.0	319
461	Genome-wide localization of histone 4 arginine 3 methylation in a differentiation primed myeloid leukemia cell line. Immunobiology, 2005, 210, 141-152.	0.8	11
462	SVM classification of human intergenic and gene sequences. Mathematical Biosciences, 2005, 195, 168-178.	0.9	5
463	Optimised real-time quantitative PCR assays for RANKL regulated genes. Molecular and Cellular Probes, 2005, 19, 119-126.	0.9	22
464	Evaluation of EST-data using the genome assembly. Biochemical and Biophysical Research Communications, 2005, 331, 1566-1576.	1.0	14
465	Identification and analysis of the human neural polypyrimidine tract binding protein (nPTB) gene promoter region. Gene, 2005, 356, 11-18.	1.0	9
466	Endogenous retrovirus long terminal repeats as ready-to-use mobile promoters: The case of primate Î²3GAL-T5. Gene, 2005, 364, 2-12.	1.0	50
467	Chromosomal aberrations induced by double strand DNA breaks. DNA Repair, 2005, 4, 1038-1046.	1.3	69
468	Comparison of the current RefSeq, Ensembl and EST databases for counting genes and gene discovery. FEBS Letters, 2005, 579, 690-698.	1.3	31
469	Genome-wide prediction of human VNTRs. Genomics, 2005, 85, 24-35.	1.3	47
470	Application of functional genomic technologies in a mouse model of retinal degeneration. Genomics, 2005, 85, 309-321.	1.3	9
471	Detecting false expression signals in high-density oligonucleotide arrays by an in silico approach. Genomics, 2005, 85, 297-308.	1.3	50
472	Discovery of 342 putative new genes from the analysis of 5â€²-end-sequenced full-length-enriched cDNA human transcripts. Genomics, 2005, 85, 739-751.	1.3	5
473	Nested genes in the human genome. Genomics, 2005, 86, 414-422.	1.3	71
474	Comparative genomic analysis of human and chimpanzee proteases. Genomics, 2005, 86, 638-647.	1.3	78

#	ARTICLE	IF	CITATIONS
475	The HSP90 family of genes in the human genome: Insights into their divergence and evolution. <i>Genomics</i> , 2005, 86, 627-637.	1.3	317
476	Computational analysis of protein tyrosine phosphatases: practical guide to bioinformatics and data resources. <i>Methods</i> , 2005, 35, 90-114.	1.9	40
477	Computational searches for splicing signals. <i>Methods</i> , 2005, 37, 292-305.	1.9	50
478	Identification of Chicken Transmembrane Channel-like (TMC) genes: Expression analysis in the cochlea. <i>Neuroscience</i> , 2005, 132, 1115-1122.	1.1	15
479	A reappraisal of the genomic organization of human Nox1 and its splice variants. <i>Archives of Biochemistry and Biophysics</i> , 2005, 435, 323-330.	1.4	17
480	A genome-wide survey demonstrates widespread non-linear mRNA in expressed sequences from multiple species. <i>Nucleic Acids Research</i> , 2005, 33, 5904-5913.	6.5	45
481	Regulation of cancer cell growth and death: Evaluating new anticancer targets. <i>Drug Discovery Today Disease Mechanisms</i> , 2005, 2, 383-387.	0.8	2
482	Generating a Genome Assembly with PCAP. <i>Current Protocols in Bioinformatics</i> , 2005, 11, Unit11.3.	25.8	19
483	Computational Identification of Related Proteins. , 2005, , 555-570.		2
484	Genomic Sequencing of Pleistocene Cave Bears. <i>Science</i> , 2005, 309, 597-599.	6.0	221
485	Genetic Analysis and Attribution of Microbial Forensics Evidence. <i>Critical Reviews in Microbiology</i> , 2005, 31, 233-254.	2.7	66
486	A novel approach to identifying regulatory motifs in distantly related genomes. <i>Genome Biology</i> , 2005, 6, R113.	13.9	12
487	Genome-wide promoter extraction and analysis in human, mouse, and rat. <i>Genome Biology</i> , 2005, 6, R72.	13.9	60
488	Transcript copy number estimation using a mouse whole-genome oligonucleotide microarray. <i>Genome Biology</i> , 2005, 6, R61.	13.9	109
489	Tiling microarray analysis of rice chromosome 10 to identify the transcriptome and relate its expression to chromosomal architecture. <i>Genome Biology</i> , 2005, 6, R52.	13.9	41
490	Genome-wide prediction and identification of cis-natural antisense transcripts in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2005, 6, R30.	13.9	240
491	Identification of ciliated sensory neuron-expressed genes in <i>Caenorhabditis elegans</i> using targeted pull-down of poly(A) tails. <i>Genome Biology</i> , 2005, 6, R17.	13.9	81
492	Recurrent insertion and duplication generate networks of transposable element sequences in the <i>Drosophila melanogaster</i> genome. <i>Genome Biology</i> , 2006, 7, R112.	13.9	188

#	ARTICLE	IF	CITATIONS
493	Ancient genomic architecture for mammalian olfactory receptor clusters. <i>Genome Biology</i> , 2006, 7, R88.	13.9	47
494	Prediction of trans-antisense transcripts in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2006, 7, R92.	13.9	72
495	Sex-specific expression of alternative transcripts in <i>Drosophila</i> . <i>Genome Biology</i> , 2006, 7, R79.	13.9	93
496	The cnidarian-bilaterian ancestor possessed at least 56 homeoboxes: evidence from the starlet sea anemone, <i>Nematostella vectensis</i> . <i>Genome Biology</i> , 2006, 7, R64.	13.9	162
497	Reference based annotation with GeneMapper. <i>Genome Biology</i> , 2006, 7, R29.	13.9	66
498	<i>Anopheles gambiae</i> genome reannotation through synthesis of ab initio and comparative gene prediction algorithms. <i>Genome Biology</i> , 2006, 7, R24.	13.9	18
499	Comparison of dot chromosome sequences from <i>D. melanogaster</i> and <i>D. virilis</i> reveals an enrichment of DNA transposon sequences in heterochromatic domains. <i>Genome Biology</i> , 2006, 7, R15.	3.8	50
500	AUGUSTUS at EGASP: using EST, protein and genomic alignments for improved gene prediction in the human genome. <i>Genome Biology</i> , 2006, 7, S11.	13.9	263
501	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. <i>Genome Biology</i> , 2006, 7, S5.	13.9	15
502	Exogean: a framework for annotating protein-coding genes in eukaryotic genomic DNA. <i>Genome Biology</i> , 2006, 7, S7.	13.9	14
503	JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. <i>Genome Biology</i> , 2006, 7, S9.	13.9	61
504	Identifying repeat domains in large genomes. <i>Genome Biology</i> , 2006, 7, R7.	13.9	31
505	Comparisons of Annotation Predictions for Affymetrix GeneChips. <i>Applied Bioinformatics</i> , 2006, 5, 237-248.	1.7	4
506	Alternative mRNA Polyadenylation Can Potentially Affect Detection of Gene Expression by Affymetrix GeneChip. <i>Applied Bioinformatics</i> , 2006, 5, 249-253.	1.7	15
508	Exploring I/O Strategies for Parallel Sequence-Search Tools with S3aSim. , 0, , .		9
509	fjoin: Simple and Efficient Computation of Feature Overlaps. <i>Journal of Computational Biology</i> , 2006, 13, 1457-1464.	0.8	34
510	Efficient q-Gram Filters for Finding All $\hat{\mu}$ -Matches over a Given Length. <i>Journal of Computational Biology</i> , 2006, 13, 296-308.	0.8	90
511	Parallel Genomic Sequence-Searching on an Ad-Hoc Grid: Experiences, Lessons Learned, and Implications. , 2006, , .		7

#	ARTICLE	IF	CITATIONS
512	Ultra-high resolution array painting facilitates breakpoint sequencing. <i>Journal of Medical Genetics</i> , 2006, 44, 51-58.	1.5	26
513	A hitchhiker's guide to expressed sequence tag (EST) analysis. <i>Briefings in Bioinformatics</i> , 2006, 8, 6-21.	3.2	235
514	ClustDB: A High-Performance Tool for Large Scale Sequence Matching. , 0, , .		2
515	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. <i>Plant Cell</i> , 2006, 18, 1791-1802.	3.1	207
516	Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. <i>American Journal of Human Genetics</i> , 2006, 79, 500-513.	2.6	261
517	Comparative Analysis of Eubacterial DNA Polymerase III Alpha Subunits. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 203-211.	3.0	28
518	Characterization of Phagosome Trafficking and Identification of PhoP-Regulated Genes Important for Survival of <i>Yersinia pestis</i> in Macrophages. <i>Infection and Immunity</i> , 2006, 74, 3727-3741.	1.0	131
519	Whole Genome Alignment with BLAST on Grid Environment. , 2006, , .		1
520	<i>C. elegans</i> : an invaluable model organism for the proteomics studies of the cholesterol-mediated signaling pathway. <i>Expert Review of Proteomics</i> , 2006, 3, 439-453.	1.3	15
521	Asymptotic behaviour and optimal word size for exact and approximate word matches between random sequences. <i>BMC Bioinformatics</i> , 2006, 7, S21.	1.2	22
522	Positive selection on the nonhomologous end-joining factor Cernunnos-XLF in the human lineage. <i>Biology Direct</i> , 2006, 1, 15.	1.9	12
523	Bioinformatics Packages for Sequence Analysis. <i>Applied Mycology and Biotechnology</i> , 2006, 6, 143-160.	0.3	8
524	Searching WormBase for Information about <i>Caenorhabditis elegans</i> . , 2006, Chapter 1, Unit 1.8.		3
525	DNA microarray detection of antimicrobial resistance genes in diverse bacteria. <i>International Journal of Antimicrobial Agents</i> , 2006, 27, 138-151.	1.1	94
526	A Deterministic Finite Automaton for Faster Protein Hit Detection in BLAST. <i>Journal of Computational Biology</i> , 2006, 13, 965-978.	0.8	31
527	High-Performance Direct Pairwise Comparison of Large Genomic Sequences. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2006, 17, 764-772.	4.0	6
528	Identification and characterization of an interleukin-15 homologue from <i>Tetraodon nigroviridis</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2006, 143, 335-343.	0.7	36
529	Origin and diversification of minisatellites derived from human Alu sequences. <i>Gene</i> , 2006, 365, 21-26.	1.0	18

#	ARTICLE	IF	CITATIONS
530	Identification of highly specific localized sequence motifs in human ribosomal protein gene promoters. <i>Gene</i> , 2006, 365, 48-56.	1.0	20
531	mNSC1 shows no evidence of protein-coding capacity. <i>Gene</i> , 2006, 370, 83-85.	1.0	2
532	A novel primate specific gene, CEI, is located in the homeobox gene IRXA2 promoter in Homo sapiens. <i>Gene</i> , 2006, 371, 167-173.	1.0	8
533	Identification and analysis of putative regulatory sequences for the MYF5/MYF6 locus in different vertebrate species. <i>Gene</i> , 2006, 379, 141-147.	1.0	33
534	Integration Specificity of Phage $\lambda$ -C31 Integrase in the Human Genome. <i>Journal of Molecular Biology</i> , 2006, 357, 28-48.	2.0	228
535	Use of competitive DNA hybridization to identify differences in the genomes of bacteria. <i>Journal of Microbiological Methods</i> , 2006, 66, 321-330.	0.7	19
536	Characterization and expression sites of newly identified chicken collectins. <i>Molecular Immunology</i> , 2006, 43, 1604-1616.	1.0	49
537	Mutation analyses of genes on 6p12-p11 in patients with juvenile myoclonic epilepsy. <i>Neuroscience Letters</i> , 2006, 405, 126-131.	1.0	12
538	Thioredoxin1 Upregulates Mitochondrial Proteins Related to Oxidative Phosphorylation and TCA Cycle in the Heart. <i>Antioxidants and Redox Signaling</i> , 2006, 8, 1635-1650.	2.5	47
539	Genome conservation between the bovine and human interleukin-8 receptor complex: Improper annotation of bovine interleukin-8 receptor b identified. <i>Veterinary Immunology and Immunopathology</i> , 2006, 114, 335-340.	0.5	18
540	The echinoderm adhesome. <i>Developmental Biology</i> , 2006, 300, 252-266.	0.9	158
541	Analysis of cytoskeletal and motility proteins in the sea urchin genome assembly. <i>Developmental Biology</i> , 2006, 300, 219-237.	0.9	53
542	The presence of GC-AG introns in <i>Neurospora crassa</i> and other eukaryotes determined from analyses of complete genomes: implications for automated gene prediction. <i>Genomics</i> , 2006, 87, 338-347.	1.3	23
543	Applying genomics to the avian inner ear: Development of subtractive cDNA resources for exploring sensory function and hair cell regeneration. <i>Genomics</i> , 2006, 87, 801-808.	1.3	19
544	Conservation patterns in different functional sequence categories of divergent <i>Drosophila</i> species. <i>Genomics</i> , 2006, 88, 431-442.	1.3	18
545	ChickGCE: A novel germ cell EST database for studying the early developmental stage in chickens. <i>Genomics</i> , 2006, 88, 252-257.	1.3	10
546	Novel genes identified by manual annotation and microarray expression analysis in the pancreas. <i>Genomics</i> , 2006, 88, 752-761.	1.3	6
547	In silico identification and Bayesian phylogenetic analysis of multiple new mammalian kallikrein gene families. <i>Genomics</i> , 2006, 88, 591-599.	1.3	31

#	ARTICLE	IF	CITATIONS
548	Fourteen novel human members of mitochondrial solute carrier family 25 (SLC25) widely expressed in the central nervous system. <i>Genomics</i> , 2006, 88, 779-790.	1.3	145
549	Comparative analysis of the paired immunoglobulin-like receptor (PILR) locus in six mammalian genomes: duplication, conversion, and the birth of new genes. <i>Physiological Genomics</i> , 2006, 27, 201-218.	1.0	27
553	MGOS: A Resource for Studying Magnaporthe grisea and Oryza sativa Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1055-1061.	1.4	24
554	A Homeodomain-Zinc Finger Protein, ZFH4, Is Expressed in Neuronal Differentiation Manner and Suppressed in Muscle Differentiation Manner. <i>Biological and Pharmaceutical Bulletin</i> , 2006, 29, 1830-1835.	0.6	35
555	NF-Y, AP2, Nrf1 and Sp1 regulate the fragile X-related gene 2 (FXR2). <i>Biochemical Journal</i> , 2006, 400, 327-335.	1.7	9
557	Comparison of human (and other) genome browsers. <i>Human Genomics</i> , 2006, 2, 266.	1.4	18
558	A Hybrid, Recursive Algorithm for Clustering Expressed Sequence Tags in Chlamydomonas reinhardtii. , 2006, , .		0
559	LINE-1 RNA splicing and influences on mammalian gene expression. <i>Nucleic Acids Research</i> , 2006, 34, 1512-1521.	6.5	180
560	ChimerDB--a knowledgebase for fusion sequences. <i>Nucleic Acids Research</i> , 2006, 34, D21-D24.	6.5	34
561	Novel Tools for Plant Genome Annotation and Applications to Arabidopsis and Rice. , 2005, , 63-76.		2
562	Genomic overview of mRNA 5'-leader trans-splicing in the ascidian Ciona intestinalis. <i>Nucleic Acids Research</i> , 2006, 34, 3378-3388.	6.5	62
563	ARTS: accurate recognition of transcription starts in human. <i>Bioinformatics</i> , 2006, 22, e472-e480.	1.8	101
564	The PLAC1-homology region of the ZP domain is sufficient for protein polymerisation. <i>BMC Biochemistry</i> , 2006, 7, 11.	4.4	71
565	Genomic characterization of five deletions in the LDL receptor gene in Danish Familial Hypercholesterolemic subjects. <i>BMC Medical Genetics</i> , 2006, 7, 55.	2.1	12
566	Polymorphisms in the glucocerebrosidase gene and pseudogene urge caution in clinical analysis of Gaucher disease allele c.1448T>C (L444P). <i>BMC Medical Genetics</i> , 2006, 7, 69.	2.1	9
567	Composition-based statistics and translated nucleotide searches: Improving the TBLASTN module of BLAST. <i>BMC Biology</i> , 2006, 4, 41.	1.7	420
568	EMMA: An Efficient Massive Mapping Algorithm Using Improved Approximate Mapping Filtering. <i>Acta Biochimica Et Biophysica Sinica</i> , 2006, 38, 857-864.	0.9	0
569	Bioinformatic analysis of expressed sequence tags derived from a compatible Alternaria brassicicola-Brassica oleracea interaction. <i>Molecular Plant Pathology</i> , 2006, 7, 113-124.	2.0	30

#	ARTICLE	IF	CITATIONS
570	A sequence-oriented comparison of gene expression measurements across different hybridization-based technologies. <i>Nature Biotechnology</i> , 2006, 24, 832-840.	9.4	144
571	Genome-wide transcription analyses in rice using tiling microarrays. <i>Nature Genetics</i> , 2006, 38, 124-129.	9.4	154
572	Mutations in the gene encoding pejvakin, a newly identified protein of the afferent auditory pathway, cause DFNB59 auditory neuropathy. <i>Nature Genetics</i> , 2006, 38, 770-778.	9.4	262
573	Genome-wide analysis of estrogen receptor binding sites. <i>Nature Genetics</i> , 2006, 38, 1289-1297.	9.4	1,227
574	Genome assembly comparison identifies structural variants in the human genome. <i>Nature Genetics</i> , 2006, 38, 1413-1418.	9.4	150
575	Regional copy number-independent deregulation of transcription in cancer. <i>Nature Genetics</i> , 2006, 38, 1386-1396.	9.4	198
576	Segmental duplication density decrease with distance to human-mouse breaks of synteny. <i>European Journal of Human Genetics</i> , 2006, 14, 216-221.	1.4	4
577	Identification of cryptic imbalance in phenotypically normal and abnormal translocation carriers. <i>European Journal of Human Genetics</i> , 2006, 14, 1255-1262.	1.4	25
578	Two-dimensional electrophoretic mobility shift assay: Identification and mapping of transcription factor CTCF target sequences within an FXVD5- <i>COX7A1</i> region of human chromosome 19. <i>Analytical Biochemistry</i> , 2006, 354, 85-93.	1.1	16
579	Comparative genomics as a tool for gene discovery. <i>Current Opinion in Biotechnology</i> , 2006, 17, 161-167.	3.3	40
580	Evolution of glyoxylate cycle enzymes in Metazoa: evidence of multiple horizontal transfer events and pseudogene formation. <i>Biology Direct</i> , 2006, 1, 31.	1.9	135
581	Histone H3 acetylated at lysine 9 in promoter is associated with low nucleosome density in the vicinity of transcription start site in human cell. <i>Chromosome Research</i> , 2006, 14, 203-211.	1.0	84
582	Characterization of a complex rearrangement with interstitial deletions and inversion on human chromosome 1. <i>Chromosome Research</i> , 2006, 14, 277-282.	1.0	19
583	Tempo and mode of ERV-K evolution in human and chimpanzee genomes. <i>Archives of Virology</i> , 2006, 151, 2215-2228.	0.9	24
584	A founder mutation for ichthyosis prematurity syndrome restricted to 76 kb by haplotype association. <i>Journal of Human Genetics</i> , 2006, 51, 864-871.	1.1	18
585	Identification of alternatively spliced <i>dab1</i> isoforms in zebrafish. <i>Development Genes and Evolution</i> , 2006, 216, 291-299.	0.4	14
586	Grey, a novel mutation in the murine <i>Lyst</i> gene, causes the beige phenotype by skipping of exon 25. <i>Mammalian Genome</i> , 2006, 17, 203-210.	1.0	26
587	Expression profiling identifies novel candidate genes for ethanol sensitivity QTLs. <i>Mammalian Genome</i> , 2006, 17, 147-156.	1.0	21

#	ARTICLE	IF	CITATIONS
588	Identification, genome mapping, and CTCF binding of potential insulators within the FXVD5-COX7A1 locus of human Chromosome 19q13.12. <i>Mammalian Genome</i> , 2006, 17, 1042-1049.	1.0	14
589	Primate-Specific Endogenous Cis-Antisense Transcription in the Human 5q31 Protocadherin Gene Cluster. <i>Journal of Molecular Evolution</i> , 2006, 62, 73-88.	0.8	16
590	Nonrandom Representation of Sex-Biased Genes on Chicken Z Chromosome. <i>Journal of Molecular Evolution</i> , 2006, 63, 676-681.	0.8	70
591	The study of neighboring nucleotide composition and transition/transversion bias. <i>Science in China Series C: Life Sciences</i> , 2006, 49, 395-402.	1.3	35
592	A novel genome-wide full-length kinesin prediction analysis reveals additional mammalian kinesins. <i>Science Bulletin</i> , 2006, 51, 1836-1847.	1.7	3
593	A global genomic transcriptional code associated with CNS-expressed genes. <i>Experimental Cell Research</i> , 2006, 312, 3108-3119.	1.2	41
594	Identification and characterization of GSRP-56, a novel Golgi-localized spectrin repeat-containing protein. <i>Experimental Cell Research</i> , 2006, 312, 3152-3164.	1.2	23
595	Lengsin Is a Survivor of an Ancient Family of Class I Glutamine Synthetases Re-engineered by Evolution for a Role in the Vertebrate Lens. <i>Structure</i> , 2006, 14, 1823-1834.	1.6	33
596	A comprehensive survey of DNA-binding transcription factor gene expression in human fetal and adult organs. <i>Gene Expression Patterns</i> , 2006, 6, 678-686.	0.3	12
597	The NEIBank project for ocular genomics: Data-mining gene expression in human and rodent eye tissues. <i>Progress in Retinal and Eye Research</i> , 2006, 25, 43-77.	7.3	32
598	Differential expression of a new isoform of DLG2 in renal oncocytoma. <i>BMC Cancer</i> , 2006, 6, 106.	1.1	14
599	Fast-Find: a novel computational approach to analyzing combinatorial motifs. <i>BMC Bioinformatics</i> , 2006, 7, 1.	1.2	467
600	Choosing the best heuristic for seeded alignment of DNA sequences. <i>BMC Bioinformatics</i> , 2006, 7, 133.	1.2	21
601	GENOMEMASKER package for designing unique genomic PCR primers. <i>BMC Bioinformatics</i> , 2006, 7, 172.	1.2	37
602	Ebbie: automated analysis and storage of small RNA cloning data using a dynamic web server. <i>BMC Bioinformatics</i> , 2006, 7, 185.	1.2	3
603	Automatic generation of gene finders for eukaryotic species. <i>BMC Bioinformatics</i> , 2006, 7, 263.	1.2	25
604	Using ESTs to improve the accuracy of de novo gene prediction. <i>BMC Bioinformatics</i> , 2006, 7, 327.	1.2	47
605	G-InforBIO: integrated system for microbial genomics. <i>BMC Bioinformatics</i> , 2006, 7, 368.	1.2	11

#	ARTICLE	IF	CITATIONS
606	Detecting the limits of regulatory element conservation and divergence estimation using pairwise and multiple alignments. <i>BMC Bioinformatics</i> , 2006, 7, 376.	1.2	46
607	MICA: desktop software for comprehensive searching of DNA databases. <i>BMC Bioinformatics</i> , 2006, 7, 427.	1.2	4
608	CGAT: a comparative genome analysis tool for visualizing alignments in the analysis of complex evolutionary changes between closely related genomes. <i>BMC Bioinformatics</i> , 2006, 7, 472.	1.2	22
609	CAFTAN: a tool for fast mapping, and quality assessment of cDNAs. <i>BMC Bioinformatics</i> , 2006, 7, 473.	1.2	0
610	Quantitative comparison of EST libraries requires compensation for systematic biases in cDNA generation. <i>BMC Bioinformatics</i> , 2006, 7, 77.	1.2	31
611	Learning Interpretable SVMs for Biological Sequence Classification. <i>BMC Bioinformatics</i> , 2006, 7, S9.	1.2	58
612	Phylogenetic analysis of the tenascin gene family: evidence of origin early in the chordate lineage. <i>BMC Evolutionary Biology</i> , 2006, 6, 60.	3.2	92
613	Widespread ectopic expression of olfactory receptor genes. <i>BMC Genomics</i> , 2006, 7, 121.	1.2	216
614	Gene expression profiling in the striatum of inbred mouse strains with distinct opioid-related phenotypes. <i>BMC Genomics</i> , 2006, 7, 146.	1.2	48
615	Comparative analysis of cancer genes in the human and chimpanzee genomes. <i>BMC Genomics</i> , 2006, 7, 15.	1.2	94
616	Gene order data from a model amphibian ( <i>Ambystoma</i> ): new perspectives on vertebrate genome structure and evolution. <i>BMC Genomics</i> , 2006, 7, 219.	1.2	30
617	Gene expression profiling of chicken primordial germ cell ESTs. <i>BMC Genomics</i> , 2006, 7, 220.	1.2	26
618	Comparison of methods for genomic localization of gene trap sequences. <i>BMC Genomics</i> , 2006, 7, 236.	1.2	1
619	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , 2006, 7, 246.	1.2	173
620	Design factors that influence PCR amplification success of cross-species primers among 1147 mammalian primer pairs. <i>BMC Genomics</i> , 2006, 7, 253.	1.2	35
621	Evolution and comparative analysis of the MHC Class III inflammatory region. <i>BMC Genomics</i> , 2006, 7, 281.	1.2	54
622	SAGE detects microRNA precursors. <i>BMC Genomics</i> , 2006, 7, 285.	1.2	12
623	Simultaneous host and parasite expression profiling identifies tissue-specific transcriptional programs associated with susceptibility or resistance to experimental cerebral malaria. <i>BMC Genomics</i> , 2006, 7, 295.	1.2	62

#	ARTICLE	IF	CITATIONS
624	Comprehensive analysis of alternative splicing in rice and comparative analyses with Arabidopsis. <i>BMC Genomics</i> , 2006, 7, 327.	1.2	375
625	Duplication and relocation of the functional DPY19L2 gene within low copy repeats. <i>BMC Genomics</i> , 2006, 7, 45.	1.2	28
626	Periodicity of SNP distribution around transcription start sites. <i>BMC Genomics</i> , 2006, 7, 66.	1.2	19
627	Analysis of 10,000 ESTs from lymphocytes of the cynomolgus monkey to improve our understanding of its immune system. <i>BMC Genomics</i> , 2006, 7, 82.	1.2	13
628	Sex-dependent gene expression in early brain development of chicken embryos. <i>BMC Neuroscience</i> , 2006, 7, 12.	0.8	59
629	Piloting the zebrafish genome browser. <i>Developmental Dynamics</i> , 2006, 235, 747-753.	0.8	5
630	Identification of candidates for tumor-specific alternative splicing in the thyroid. <i>Genes Chromosomes and Cancer</i> , 2006, 45, 540-553.	1.5	15
631	Nonsynonymous SNPs: validation characteristics, derived allele frequency patterns, and suggestive evidence for natural selection. <i>Human Mutation</i> , 2006, 27, 173-186.	1.1	9
632	dbRIP: A highly integrated database of retrotransposon insertion polymorphisms in humans. <i>Human Mutation</i> , 2006, 27, 323-329.	1.1	177
633	Frequency of genomic rearrangements involving the SHFM3 locus at chromosome 10q24 in syndromic and non-syndromic split-hand/foot malformation. <i>American Journal of Medical Genetics, Part A</i> , 2006, 140A, 1375-1383.	0.7	22
634	Split-hand/split-foot malformation 3 (SHFM3) at 10q24, development of rapid diagnostic methods and gene expression from the region. <i>American Journal of Medical Genetics, Part A</i> , 2006, 140A, 1384-1395.	0.7	33
635	Tetrahymena Genome Database (TGD): a new genomic resource for Tetrahymena thermophila research. <i>Nucleic Acids Research</i> , 2006, 34, D500-D503.	6.5	107
636	Regions of extreme synonymous codon selection in mammalian genes. <i>Nucleic Acids Research</i> , 2006, 34, 1700-1710.	6.5	47
637	Indel seeds for homology search. <i>Bioinformatics</i> , 2006, 22, e341-e349.	1.8	28
638	Meisetz and the birth of the KRAB motif. <i>Bioinformatics</i> , 2006, 22, 2841-2845.	1.8	90
639	CisView: A Browser and Database of cis-regulatory Modules Predicted in the Mouse Genome. <i>DNA Research</i> , 2006, 13, 123-134.	1.5	28
640	TISA: Tissue-specific Alternative Splicing in Human and Mouse Genes. <i>DNA Research</i> , 2006, 13, 229-243.	1.5	29
641	snoRNA-LBME-db, a comprehensive database of human H/ACA and C/D box snoRNAs. <i>Nucleic Acids Research</i> , 2006, 34, D158-D162.	6.5	463

#	ARTICLE	IF	CITATIONS
642	VMD: a community annotation database for oomycetes and microbial genomes. <i>Nucleic Acids Research</i> , 2006, 34, D379-D381.	6.5	28
643	The TIGR Maize Database. <i>Nucleic Acids Research</i> , 2006, 34, D771-D776.	6.5	35
644	The Mouse Functional Genome Database (MfunGD): functional annotation of proteins in the light of their cellular context. <i>Nucleic Acids Research</i> , 2006, 34, D568-D571.	6.5	15
645	MPromDb: an integrated resource for annotation and visualization of mammalian gene promoters and ChIP-chip experimental data. <i>Nucleic Acids Research</i> , 2006, 34, D98-D103.	6.5	41
646	The UCSC Archaeal Genome Browser. <i>Nucleic Acids Research</i> , 2006, 34, D407-D410.	6.5	107
647	The UCSC Genome Browser Database: update 2006. <i>Nucleic Acids Research</i> , 2006, 34, D590-D598.	6.5	1,156
648	Application of a superword array in genome assembly. <i>Nucleic Acids Research</i> , 2006, 34, 201-205.	6.5	29
649	Dynamic use of multiple parameter sets in sequence alignment. <i>Nucleic Acids Research</i> , 2006, 35, 678-686.	6.5	26
650	MutScreener: primer design tool for PCR-direct sequencing. <i>Nucleic Acids Research</i> , 2006, 34, W660-W664.	6.5	7
651	An open-access long oligonucleotide microarray resource for analysis of the human and mouse transcriptomes. <i>Nucleic Acids Research</i> , 2006, 34, e87-e87.	6.5	89
652	Gene Evolution and Drug Discovery. , 2006, 316, 87-109.		1
653	Global Profiles of Gene Expression Induced by Adrenocorticotropin in Y1 Mouse Adrenal Cells. <i>Endocrinology</i> , 2006, 147, 2357-2367.	1.4	40
654	Identification and Mapping of Paralogous Genes on a Known Genomic DNA Sequence. , 2006, 338, 21-30.		2
655	Use of Genome Browsers to Locate Your Favorite Genes. , 2006, 338, 1-8.		1
656	Intron Size, Abundance, and Distribution within Untranslated Regions of Genes. <i>Molecular Biology and Evolution</i> , 2006, 23, 2392-2404.	3.5	154
657	Chromosome-wide identification of novel imprinted genes using microarrays and uniparental disomies. <i>Nucleic Acids Research</i> , 2006, 34, e88-e88.	6.5	61
658	Alternative isoform discrimination by the next generation of expression profiling microarrays. <i>Expert Opinion on Therapeutic Targets</i> , 2006, 10, 613-625.	1.5	9
659	Accurate anchoring alignment of divergent sequences. <i>Bioinformatics</i> , 2006, 22, 29-34.	1.8	36

#	ARTICLE	IF	CITATIONS
660	A space-partitioning-based indexing method for multidimensional non-ordered discrete data spaces. ACM Transactions on Information Systems, 2006, 24, 79-110.	3.8	17
661	Grid applications---Parallel genomic sequence-searching on an ad-hoc grid. , 2006, , .		28
662	Dynamic indexing for multidimensional non-ordered discrete data spaces using a data-partitioning approach. ACM Transactions on Database Systems, 2006, 31, 439-484.	1.5	20
663	Aligning DNA sequences using dynamic programming. Xrds, 2006, 13, 9-9.	0.2	2
664	A Map of Recent Positive Selection in the Human Genome. PLoS Biology, 2006, 4, e72.	2.6	2,329
665	Functionality of Intergenic Transcription: An Evolutionary Comparison. PLoS Genetics, 2006, 2, e171.	1.5	73
666	A large quantity of novel human antisense transcripts detected by LongSAGE. Bioinformatics, 2006, 22, 2475-2479.	1.8	49
667	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. PLoS Biology, 2006, 4, e46.	2.6	150
668	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33.	1.5	439
669	Unusual Intron Conservation near Tissue-Regulated Exons Found by Splicing Microarrays. PLoS Computational Biology, 2006, 2, e4.	1.5	175
670	Parametric Alignment of Drosophila Genomes. PLoS Computational Biology, 2006, 2, e73.	1.5	38
671	An Integrative Method for Accurate Comparative Genome Mapping. PLoS Computational Biology, 2006, 2, e75.	1.5	25
672	Identification and Analysis of Genes and Pseudogenes within Duplicated Regions in the Human and Mouse Genomes. PLoS Computational Biology, 2006, 2, e76.	1.5	22
673	A High-Resolution Map of Synteny Disruptions in Gibbon and Human Genomes. PLoS Genetics, 2006, 2, e223.	1.5	48
674	Gene Losses during Human Origins. PLoS Biology, 2006, 4, e52.	2.6	188
675	SPA: A Probabilistic Algorithm for Spliced Alignment. PLoS Genetics, 2006, 2, e24.	1.5	21
676	Mammalian Small Nucleolar RNAs Are Mobile Genetic Elements. PLoS Genetics, 2006, 2, e205.	1.5	131
677	Recent Assembly of an Imprinted Domain from Non-Imprinted Components. PLoS Genetics, 2006, 2, e182.	1.5	84

#	ARTICLE	IF	CITATIONS
678	The Rice Annotation Project Database (RAP-DB): hub for <i>Oryza sativa</i> ssp. <i>japonica</i> genome information. <i>Nucleic Acids Research</i> , 2006, 34, D741-D744.	6.5	219
679	Heterogeneous Genomic Molecular Clocks in Primates. <i>PLoS Genetics</i> , 2006, 2, e163.	1.5	89
680	The G Protein-coupled Receptor Subset of the Chicken Genome. <i>PLoS Computational Biology</i> , 2006, 2, e54.	1.5	104
681	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. <i>PLoS Genetics</i> , 2006, 2, e62.	1.5	165
682	Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcription and organismic complexity. <i>Genome Research</i> , 2006, 16, 922-933.	2.4	40
683	Bioinformatics of alternative splicing and its regulation. <i>Briefings in Bioinformatics</i> , 2006, 7, 55-69.	3.2	29
684	In Vivo Requirement of the Small Subunit of U2AF for Recognition of a Weak 5' Splice Site. <i>Molecular and Cellular Biology</i> , 2006, 26, 8183-8190.	1.1	56
685	A computational screen for mammalian pseudouridylation guide H/ACA RNAs. <i>Rna</i> , 2006, 12, 15-25.	1.6	84
686	Conserved distances between vertebrate highly conserved elements. <i>Human Molecular Genetics</i> , 2006, 15, 2911-2922.	1.4	28
687	U1-like snRNAs lacking complementarity to canonical 5' splice sites. <i>Rna</i> , 2006, 12, 1603-1611.	1.6	28
688	Water stress-responsive genes in loblolly pine ( <i>Pinus taeda</i> ) roots identified by analyses of expressed sequence tag libraries. <i>Tree Physiology</i> , 2006, 26, 1-16.	1.4	84
689	MYC-containing double minutes in hematologic malignancies: evidence in favor of the episome model and exclusion of MYC as the target gene. <i>Human Molecular Genetics</i> , 2006, 15, 933-942.	1.4	116
690	Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure. <i>Genome Research</i> , 2006, 16, 885-889.	2.4	148
691	Targeted disruption of glycerol kinase gene in mice: expression analysis in liver shows alterations in network partners related to glycerol kinase activity. <i>Human Molecular Genetics</i> , 2006, 15, 405-415.	1.4	31
692	Genome-wide analysis of mRNAs bound to the histone stem-loop binding protein. <i>Rna</i> , 2006, 12, 1853-1867.	1.6	66
693	Gene Expression and Protein Length Influence Codon Usage and Rates of Sequence Evolution in <i>Populus tremula</i> . <i>Molecular Biology and Evolution</i> , 2006, 24, 836-844.	3.5	121
694	TOPAAS, a Tomato and Potato Assembly Assistance System for Selection and Finishing of Bacterial Artificial Chromosomes. <i>Plant Physiology</i> , 2006, 140, 805-817.	2.3	13
695	Decoding the fine-scale structure of a breast cancer genome and transcriptome. <i>Genome Research</i> , 2006, 16, 394-404.	2.4	49

#	ARTICLE	IF	CITATIONS
696	Foamy virus vector integration sites in normal human cells. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1498-1503.	3.3	226
697	Common origin of the human synovial sarcoma associated <i>SS18</i> and <i>SS18L1</i> gene loci. Cytogenetic and Genome Research, 2006, 112, 222-226.	0.6	8
698	Isolation and functional analysis of human HMBOX1, a homeobox containing protein with transcriptional repressor activity. Cytogenetic and Genome Research, 2006, 114, 131-136.	0.6	44
699	Genome-wide in silico identification and analysis of cis natural antisense transcripts (cis-NATs) in ten species. Nucleic Acids Research, 2006, 34, 3465-3475.	6.5	155
700	Evolution of the vertebrate DNMT3 gene family: a possible link between existence of <i>DNMT3L</i> and genomic imprinting. Cytogenetic and Genome Research, 2006, 113, 75-80.	0.6	67
701	GenRate: A Generative Model that Reveals Novel Transcripts in Genome-Tiling Microarray Data. Journal of Computational Biology, 2006, 13, 200-214.	0.8	1
702	AGRIS and AtRegNet. A Platform to Link cis-Regulatory Elements and Transcription Factors into Regulatory Networks. Plant Physiology, 2006, 140, 818-829.	2.3	249
703	Mammalian $\hat{\text{A}}$ -spectrin is a neofunctionalized polypeptide adapted to small highly deformable erythrocytes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 643-648.	3.3	43
704	SyMAP: A system for discovering and viewing syntenic regions of FPC maps. Genome Research, 2006, 16, 1159-1168.	2.4	176
705	Characterization of a cancer/testis (CT) antigen gene family capable of eliciting humoral response in cancer patients. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18066-18071.	3.3	32
706	Sequence analysis of the complete mitochondrial DNA in 10 commonly used inbred rat strains. American Journal of Physiology - Cell Physiology, 2006, 291, C1183-C1192.	2.1	39
707	A UNIFYING FRAMEWORK FOR SEED SENSITIVITY AND ITS APPLICATION TO SUBSET SEEDS. Journal of Bioinformatics and Computational Biology, 2006, 04, 553-569.	0.3	58
709	A high throughput method for genome-wide analysis of retroviral integration. Nucleic Acids Research, 2006, 34, e134-e134.	6.5	8
710	Computational methods for alternative splicing prediction. Briefings in Functional Genomics & Proteomics, 2006, 5, 46-51.	3.8	16
711	Identification and Characterization of Functional Rat Arylamine N-Acetyltransferase 3: Comparisons with Rat Arylamine N-Acetyltransferases 1 and 2. Journal of Pharmacology and Experimental Therapeutics, 2006, 319, 369-375.	1.3	33
712	A First-Generation Metric Linkage Disequilibrium Map of Bovine Chromosome 6. Genetics, 2006, 174, 79-85.	1.2	35
713	Flexibility and constraint in the nucleosome core landscape of <i>Caenorhabditis elegans</i> chromatin. Genome Research, 2006, 16, 1505-1516.	2.4	169
714	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14959-14964.	3.3	286

#	ARTICLE	IF	CITATIONS
715	Gallus GBrowse: a unified genomic database for the chicken. <i>Nucleic Acids Research</i> , 2007, 36, D719-D723.	6.5	9
716	OVERLAPPING ALTERNATIVE DONOR SPLICE SITES IN THE HUMAN GENOME. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 991-1004.	0.3	8
717	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	3.3	563
718	MicroRNA genes are frequently located near mouse cancer susceptibility loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8017-8022.	3.3	138
719	Alternative Splicing Yields Protein Arginine Methyltransferase 1 Isoforms with Distinct Activity, Substrate Specificity, and Subcellular Localization. <i>Journal of Biological Chemistry</i> , 2007, 282, 33009-33021.	1.6	156
720	Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , 2007, 17, 1763-1773.	2.4	42
721	Distinct mechanisms for trans-mediated mobilization of cellular RNAs by the LINE-1 reverse transcriptase. <i>Genome Research</i> , 2007, 17, 602-611.	2.4	111
722	A recurrent inversion on the eutherian X chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18571-18576.	3.3	45
723	Widely variable endogenous retroviral methylation levels in human placenta. <i>Nucleic Acids Research</i> , 2007, 35, 4743-4754.	6.5	86
724	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. <i>Nucleic Acids Research</i> , 2007, 36, D787-D792.	6.5	33
725	A Cytogenetically Characterized, Genome-Anchored 10-Mb BAC Set and CGH Array for the Domestic Dog. <i>Journal of Heredity</i> , 2007, 98, 474-484.	1.0	32
726	Sampling the Arabidopsis Transcriptome with Massively Parallel Pyrosequencing. <i>Plant Physiology</i> , 2007, 144, 32-42.	2.3	298
727	Genetic analysis of albuminuria in a cross between C57BL/6J and DBA/2J mice. <i>American Journal of Physiology - Renal Physiology</i> , 2007, 293, F1649-F1656.	1.3	35
728	Alu Recombination-Mediated Structural Deletions in the Chimpanzee Genome. <i>PLoS Genetics</i> , 2007, 3, e184.	1.5	94
729	Evolutionary Conservation of UTR Intron Boundaries in <i>Cryptococcus</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 1140-1148.	3.5	18
730	Genome-Wide Expression Profiling of the Arabidopsis Female Gametophyte Identifies Families of Small, Secreted Proteins. <i>PLoS Genetics</i> , 2007, 3, e171.	1.5	165
731	Finding association rules of cis-regulatory elements involved in alternative splicing. , 2007, , .		0
732	An integrative genomics strategy for systematic characterization of genetic loci modulating phenotypes. <i>Human Molecular Genetics</i> , 2007, 16, 1381-1390.	1.4	18

#	ARTICLE	IF	CITATIONS
733	Genome browsing with Ensembl: a practical overview. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2007, 6, 202-219.	3.8	31
734	Population Genomics: Whole-Genome Analysis of Polymorphism and Divergence in <i>Drosophila simulans</i> . <i>PLoS Biology</i> , 2007, 5, e310.	2.6	583
735	Divergent Evolution of Human p53 Binding Sites: Cell Cycle Versus Apoptosis. <i>PLoS Genetics</i> , 2007, 3, e127.	1.5	88
736	A Screen for Retrotransposed Imprinted Genes Reveals an Association between X Chromosome Homology and Maternal Germ-Line Methylation. <i>PLoS Genetics</i> , 2007, 3, e20.	1.5	103
737	GeneHub-GEPIS: digital expression profiling for normal and cancer tissues based on an integrated gene database. <i>Nucleic Acids Research</i> , 2007, 35, W152-W158.	6.5	30
738	FK506, a Calcineurin Inhibitor, Prevents Cadmium-Induced Testicular Toxicity in Mice. <i>Toxicological Sciences</i> , 2007, 100, 474-485.	1.4	23
739	cGMP-dependent protein kinase I interacts with TRIM39R, a novel Rpp21 domain-containing TRIM protein. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2007, 293, L903-L912.	1.3	15
740	Improving the <i>Caenorhabditis elegans</i> Genome Annotation Using Machine Learning. <i>PLoS Computational Biology</i> , 2007, 3, e20.	1.5	57
741	Comparative Genomics Search for Losses of Long-Established Genes on the Human Lineage. <i>PLoS Computational Biology</i> , 2007, 3, e247.	1.5	103
742	A High-Resolution Map of Segmental DNA Copy Number Variation in the Mouse Genome. <i>PLoS Genetics</i> , 2007, 3, e3.	1.5	196
743	Genome Analysis of <i>Minibacterium massiliensis</i> Highlights the Convergent Evolution of Water-Living Bacteria. <i>PLoS Genetics</i> , 2007, 3, e138.	1.5	64
744	Adaptive Evolution of Conserved Noncoding Elements in Mammals. <i>PLoS Genetics</i> , 2007, 3, e147.	1.5	79
745	Extragenic Accumulation of RNA Polymerase II Enhances Transcription by RNA Polymerase III. <i>PLoS Genetics</i> , 2007, 3, e212.	1.5	56
746	Transcriptional Interferences in cis Natural Antisense Transcripts of Humans and Mice. <i>Genetics</i> , 2007, 176, 1299-1306.	1.2	124
747	Comparative Physical Mapping Between <i>Oryza sativa</i> (AA Genome Type) and <i>O. punctata</i> (BB Genome) Tj ETQq0 0,0,rgBT /Overlock 10	1.2	49
748	Sex-specific regulation of gene expression in the aging monkey aorta. <i>Physiological Genomics</i> , 2007, 29, 169-180.	1.0	43
749	Hairpin structure within the 3'UTR of DNA polymerase $\beta$ mRNA acts as a post-transcriptional regulatory element and interacts with Hax-1. <i>Nucleic Acids Research</i> , 2007, 35, 5499-5510.	6.5	43
750	Context Dependence, Ancestral Misidentification, and Spurious Signatures of Natural Selection. <i>Molecular Biology and Evolution</i> , 2007, 24, 1792-1800.	3.5	162

#	ARTICLE	IF	CITATIONS
751	Mapping Human Genetic Ancestry. <i>Molecular Biology and Evolution</i> , 2007, 24, 2266-2276.	3.5	117
752	The TIGR Plant Transcript Assemblies database. <i>Nucleic Acids Research</i> , 2007, 35, D846-D851.	6.5	173
753	The UCSC genome browser database: update 2007. <i>Nucleic Acids Research</i> , 2007, 35, D668-D673.	6.5	260
754	A role for microRNAs in maintenance of mouse mammary epithelial progenitor cells. <i>Genes and Development</i> , 2007, 21, 3238-3243.	2.7	195
755	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). <i>Genome Research</i> , 2007, 17, 828-838.	2.4	86
756	Differing patterns of selection in alternative and constitutive splice sites. <i>Genome Research</i> , 2007, 17, 1015-1022.	2.4	32
757	VectorBase: a home for invertebrate vectors of human pathogens. <i>Nucleic Acids Research</i> , 2007, 35, D503-D505.	6.5	107
758	Bird and Mammal Sex-Chromosome Orthologs Map to the Same Autosomal Region in a Salamander ( <i>Ambystoma</i> ). <i>Genetics</i> , 2007, 177, 607-613.	1.2	25
759	Drosophila Polymorphism Database (DPDB) A Portal for Nucleotide Polymorphism in <i>Drosophila</i> . <i>Fly</i> , 2007, 1, 205-211.	0.9	3
760	Ro-Associated Y RNAs in Metazoans: Evolution and Diversification. <i>Molecular Biology and Evolution</i> , 2007, 24, 1678-1689.	3.5	93
761	Systematic variation in mRNA 3' processing signals during mouse spermatogenesis. <i>Nucleic Acids Research</i> , 2007, 35, 234-246.	6.5	114
762	PolyA_DB 2: mRNA polyadenylation sites in vertebrate genes. <i>Nucleic Acids Research</i> , 2007, 35, D165-D168.	6.5	156
763	Comparison of HIV-derived Lentiviral and MLV-based Gammaretroviral Vector Integration Sites in Primate Repopulating Cells. <i>Molecular Therapy</i> , 2007, 15, 1356-1365.	3.7	104
764	Common Functions for Diverse Small RNAs of Land Plants. <i>Plant Cell</i> , 2007, 19, 1750-1769.	3.1	387
765	Identification of the circadian transcriptome in adult mouse skeletal muscle. <i>Physiological Genomics</i> , 2007, 31, 86-95.	1.0	300
766	Diploid genome reconstruction of <i>Ciona intestinalis</i> and comparative analysis with <i>Ciona savignyi</i> . <i>Genome Research</i> , 2007, 17, 1101-1110.	2.4	65
767	Towards pathogenomics: a web-based resource for pathogenicity islands. <i>Nucleic Acids Research</i> , 2007, 35, D395-D400.	6.5	84
768	Differential Regulation of Serum- and Glucocorticoid-Inducible Kinase 1 (SGK1) Splice Variants Based on Alternative Initiation of Transcription. <i>Cellular Physiology and Biochemistry</i> , 2007, 20, 715-728.	1.1	48

#	ARTICLE	IF	CITATIONS
769	Large-scale Discovery of Regulatory Motifs Involved in Alternative Splicing. , 2007, , .		0
770	Correcting Base-Assignment Errors in Repeat Regions of Shotgun Assembly. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 54-64.	1.9	9
771	Generalized Correlation Functions and Their Applications in Selection of Optimal Multiple Spaced Seeds for Homology Search. Journal of Computational Biology, 2007, 14, 238-254.	0.8	10
772	EFCBP1/NECAB1, a brain-specifically expressed gene with highest abundance in temporal lobe, encodes a protein containing EF-hand and antibiotic biosynthesis monooxygenase domains. DNA Sequence, 2007, 18, 73-79.	0.7	7
773	Bayesian Inference of MicroRNA Targets from Sequence and Expression Data. Journal of Computational Biology, 2007, 14, 550-563.	0.8	106
774	A complex system of small RNAs in the unicellular green alga Chlamydomonas reinhardtii. Genes and Development, 2007, 21, 1190-1203.	2.7	367
775	Widespread mRNA polyadenylation events in introns indicate dynamic interplay between polyadenylation and splicing. Genome Research, 2007, 17, 156-165.	2.4	184
776	Comparative Cross-Species Alternative Splicing in Plants. Plant Physiology, 2007, 144, 1632-1641.	2.3	73
777	Adaptive Evolution of Recently Duplicated Accessory Gland Protein Genes in Desert Drosophila. Genetics, 2007, 177, 1023-1030.	1.2	45
778	Analysis of the Unassembled Part of the Dog Genome Sequence: Chromosomal Localization of 115 Genes Inferred from Multispecies Comparative Genomics. Journal of Heredity, 2007, 98, 461-467.	1.0	5
779	Toward a universal microarray: prediction of gene expression through nearest-neighbor probe sequence identification. Nucleic Acids Research, 2007, 35, e99-e99.	6.5	63
780	Functional Analysis of the Human N-Acetyltransferase 1 Major Promoter: Quantitation of Tissue Expression and Identification of Critical Sequence Elements. Drug Metabolism and Disposition, 2007, 35, 1649-1656.	1.7	49
781	Homology search for genes. Bioinformatics, 2007, 23, i97-i103.	1.8	13
782	A Primary Assembly of a Bovine Haplotype Block Map Based on a 15,036-Single-Nucleotide Polymorphism Panel Genotyped in Holsteinâ€“Friesian Cattle. Genetics, 2007, 176, 763-772.	1.2	77
783	Phylogenetic Footprinting Analysis in the Upstream Regulatory Regions of the Drosophila <i>Enhancer of split</i> Genes. Genetics, 2007, 177, 1377-1394.	1.2	22
784	Quantitating tissue specificity of human genes to facilitate biomarker discovery. Bioinformatics, 2007, 23, 1348-1355.	1.8	19
785	Dual-specificity splice sites function alternatively as 5â€² and 3â€² splice sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15028-15033.	3.3	36
786	Dual Modes of Natural Selection on Upstream Open Reading Frames. Molecular Biology and Evolution, 2007, 24, 1744-1751.	3.5	46

#	ARTICLE	IF	CITATIONS
787	Assessing the need for sequence-based normalization in tiling microarray experiments. <i>Bioinformatics</i> , 2007, 23, 988-997.	1.8	36
788	The UCSC Genome Browser Database: 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D773-D779.	6.5	459
789	Identification of N-Acetyltransferase 2 (NAT2) Transcription Start Sites and Quantitation of NAT2-Specific mRNA in Human Tissues. <i>Drug Metabolism and Disposition</i> , 2007, 35, 721-727.	1.7	83
790	Context-Dependent Mutation Rates May Cause Spurious Signatures of a Fixation Bias Favoring Higher GC-Content in Humans. <i>Molecular Biology and Evolution</i> , 2007, 24, 2196-2202.	3.5	50
791	Discovering and detecting transposable elements in genome sequences. <i>Briefings in Bioinformatics</i> , 2007, 8, 382-392.	3.2	189
792	Multiple whole genome alignments and novel biomedical applications at the VISTA portal. <i>Nucleic Acids Research</i> , 2007, 35, W669-W674.	6.5	30
793	Tissue Expression and Genomic Sequences of Rat N-acetyltransferases rNat1, rNat2, rNat3, and Functional Characterization of a Novel rNat3*2 Genetic Variant. <i>Toxicological Sciences</i> , 2007, 99, 413-421.	1.4	22
794	Underlying Mechanisms of Pharmacology and Toxicity of a Novel PPAR Agonist Revealed Using Rodent and Canine Hepatocytes. <i>Toxicological Sciences</i> , 2007, 96, 294-309.	1.4	30
795	Optimized design and assessment of whole genome tiling arrays. <i>Bioinformatics</i> , 2007, 23, i195-i204.	1.8	53
796	A correlation with exon expression approach to identify cis-regulatory elements for tissue-specific alternative splicing. <i>Nucleic Acids Research</i> , 2007, 35, 4845-4857.	6.5	75
797	LINE-1 retrotransposition in human embryonic stem cells. <i>Human Molecular Genetics</i> , 2007, 16, 1569-1577.	1.4	204
798	UTRome.org: a platform for 3'UTR biology in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2007, 36, D57-D62.	6.5	20
799	CTCFBSDB: a CTCF-binding site database for characterization of vertebrate genomic insulators. <i>Nucleic Acids Research</i> , 2007, 36, D83-D87.	6.5	98
800	<i>C. elegans</i> sequences that control <i>trans</i>-splicing and operon pre-mRNA processing. <i>Rna</i> , 2007, 13, 1409-1426.	1.6	37
801	Analysis of SNP markers for chicken blue-shelled gene using PCR-SSCP. <i>Chinese Journal of Agricultural Biotechnology</i> , 2007, 4, 53-56.	0.1	4
802	PALMA: mRNA to genome alignments using large margin algorithms. <i>Bioinformatics</i> , 2007, 23, 1892-1900.	1.8	12
803	A high-resolution linkage map for the Z chromosome in chicken reveals hot spots for recombination. <i>Cytogenetic and Genome Research</i> , 2007, 117, 22-29.	0.6	26
804	Biodiversity of 20 chicken breeds assessed by SNPs located in gene regions. <i>Cytogenetic and Genome Research</i> , 2007, 117, 319-326.	0.6	22

#	ARTICLE	IF	CITATIONS
805	Purifying Selection Maintains Highly Conserved Noncoding Sequences in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 2222-2234.	3.5	63
806	EST assembly supported by a draft genome sequence: an analysis of the <i>Chlamydomonas reinhardtii</i> transcriptome. <i>Nucleic Acids Research</i> , 2007, 35, 2074-2083.	6.5	34
807	CG dinucleotide clustering is a species-specific property of the genome. <i>Nucleic Acids Research</i> , 2007, 35, 6798-6807.	6.5	74
808	Novel rapidly evolving hominid RNAs bind nuclear factor 90 and display tissue-restricted distribution. <i>Nucleic Acids Research</i> , 2007, 35, 6249-6258.	6.5	75
809	Functional Characterization of Spliceosomal Introns and Identification of U2, U4, and U5 snRNAs in the Deep-Branching Eukaryote <i>Entamoeba histolytica</i> . <i>Eukaryotic Cell</i> , 2007, 6, 940-948.	3.4	24
810	A tale of two templates: Automatically resolving double traces has many applications, including efficient PCR-based elucidation of alternative splices. <i>Genome Research</i> , 2007, 17, 212-218.	2.4	13
811	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. <i>Genome Research</i> , 2007, 17, 1296-1303.	2.4	180
812	Finding Protein-coding Genes. , 0, , 129-158.		1
813	Finding Repeats in Genome Sequences. , 0, , 197-233.		3
814	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2007, 17, Unit 1.4.	25.8	41
815	A gene signature of 8 genes could identify the risk of recurrence and progression in Dukes' B colon cancer patients. <i>Oncology Reports</i> , 0, , .	1.2	15
816	MapToGenome: A Comparative Genomic Tool that Aligns Transcript Maps to Sequenced Genomes. <i>Evolutionary Bioinformatics</i> , 2007, 3, 117693430700300.	0.6	2
818	Comparative and evolutionary pharmacogenetics of ABCB1: complex signatures of positive selection on coding and regulatory regions. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 667-678.	0.7	21
819	A map of nuclear matrix attachment regions within the breast cancer loss-of-heterozygosity region on human chromosome 16q22.1. <i>Genomics</i> , 2007, 89, 354-361.	1.3	18
820	Characteristics of oligonucleotide tiling arrays measured by hybridizing full-length cDNA clones: Causes of signal variation and false positive signals. <i>Genomics</i> , 2007, 89, 541-551.	1.3	5
821	Patterns of gene duplication and intron loss in the ENCODE regions suggest a confounding factor. <i>Genomics</i> , 2007, 90, 44-48.	1.3	5
822	Identification of six putative human transporters with structural similarity to the drug transporter SLC22 family. <i>Genomics</i> , 2007, 90, 595-609.	1.3	78
823	A complex rearrangement in GBE1 causes both perinatal hypoglycemic collapse and late-juvenile-onset neuromuscular degeneration in glycogen storage disease type IV of Norwegian forest cats. <i>Molecular Genetics and Metabolism</i> , 2007, 90, 383-392.	0.5	29

#	ARTICLE	IF	CITATIONS
824	Molecular determinants of AMPA receptor subunit assembly. <i>Trends in Neurosciences</i> , 2007, 30, 407-416.	4.2	169
825	Characterization of alternatively spliced isoforms of the type I interleukin-1 receptor on iNOS induction in rat hepatocytes. <i>Nitric Oxide - Biology and Chemistry</i> , 2007, 17, 98-105.	1.2	29
826	Identification and characterization of novel polymorphic LINE-1 insertions through comparison of two human genome sequence assemblies. <i>Gene</i> , 2007, 390, 28-38.	1.0	35
827	Mavericks, a novel class of giant transposable elements widespread in eukaryotes and related to DNA viruses. <i>Gene</i> , 2007, 390, 3-17.	1.0	213
828	Identification of three mouse $\mu$ -opioid receptor (MOR) gene (Oprm1) splice variants containing a newly identified alternatively spliced exon. <i>Gene</i> , 2007, 388, 135-147.	1.0	30
829	Comparative analysis of cis-encoded antisense RNAs in eukaryotes. <i>Gene</i> , 2007, 392, 134-141.	1.0	29
830	Identification of five mouse $\mu$ -opioid receptor (MOR) gene (Oprm1) splice variants containing a newly identified alternatively spliced exon. <i>Gene</i> , 2007, 395, 98-107.	1.0	38
831	Mapping of chimpanzee full-length cDNAs onto the human genome unveils large potential divergence of the transcriptome. <i>Gene</i> , 2007, 399, 1-10.	1.0	13
832	Origin and evolution of vertebrate ABCA genes: A story from Amphioxus. <i>Gene</i> , 2007, 405, 88-95.	1.0	7
833	The Zinc Finger Proteins ZXDA and ZXDC Form a Complex that Binds CIITA and Regulates MHC II Gene Transcription. <i>Journal of Molecular Biology</i> , 2007, 369, 1175-1187.	2.0	21
834	Exon-based mapping of microarray probes: Recovering differential gene expression signal in underpowered hypoxia experiment. <i>Molecular and Cellular Probes</i> , 2007, 21, 134-139.	0.9	8
835	ZXDC, a novel zinc finger protein that binds CIITA and activates MHC gene transcription. <i>Molecular Immunology</i> , 2007, 44, 311-321.	1.0	20
836	Bioinformatic analysis of post-transcriptional regulation by uORF in human and mouse. <i>FEBS Letters</i> , 2007, 581, 4184-4188.	1.3	64
837	The Strength of Selection on Ultraconserved Elements in the Human Genome. <i>American Journal of Human Genetics</i> , 2007, 80, 692-704.	2.6	62
838	Restauro-G: A Rapid Genome Re-Annotation System for Comparative Genomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 53-58.	3.0	17
839	Gene copy number variation spanning 60 million years of human and primate evolution. <i>Genome Research</i> , 2007, 17, 1266-1277.	2.4	153
840	A cross-species alignment tool (CAT). <i>BMC Bioinformatics</i> , 2007, 8, 349.	1.2	4
841	Genome-wide Detection and Analysis of Alternative Splicing for Nucleotide Binding Site-Leucine-Rich Repeats Sequences in Rice. <i>Journal of Genetics and Genomics</i> , 2007, 34, 247-257.	1.7	17

#	ARTICLE	IF	CITATIONS
842	Origin and Evolution of Human microRNAs From Transposable Elements. <i>Genetics</i> , 2007, 176, 1323-1337.	1.2	311
843	CONTRAST: a discriminative, phylogeny-free approach to multiple informant de novo gene prediction. <i>Genome Biology</i> , 2007, 8, R269.	13.9	79
844	Contribution of telomerase RNA retrotranscription to DNA double-strand break repair during mammalian genome evolution. <i>Genome Biology</i> , 2007, 8, R260.	13.9	68
845	The ribosomal protein genes and Minute loci of <i>Drosophila melanogaster</i> . <i>Genome Biology</i> , 2007, 8, R216.	13.9	330
846	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	13.9	73
847	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007, 8, R171.	13.9	170
848	Genome position and gene amplification. <i>Genome Biology</i> , 2007, 8, R120.	13.9	24
849	Morphine effects on striatal transcriptome in mice. <i>Genome Biology</i> , 2007, 8, R128.	13.9	74
850	Large-scale identification of human genes implicated in epidermal barrier function. <i>Genome Biology</i> , 2007, 8, R107.	13.9	130
851	LongSAGE profiling of nine human embryonic stem cell lines. <i>Genome Biology</i> , 2007, 8, R113.	13.9	21
852	cis-Decoder discovers constellations of conserved DNA sequences shared among tissue-specific enhancers. <i>Genome Biology</i> , 2007, 8, R75.	13.9	24
853	Regulatory conservation of protein coding and microRNA genes in vertebrates: lessons from the opossum genome. <i>Genome Biology</i> , 2007, 8, R84.	13.9	26
854	Discovery of tissue-specific exons using comprehensive human exon microarrays. <i>Genome Biology</i> , 2007, 8, R64.	13.9	255
855	Sense-antisense pairs in mammals: functional and evolutionary considerations. <i>Genome Biology</i> , 2007, 8, R40.	13.9	55
856	CAGE-TSSchip: promoter-based expression profiling using the 5'-leading label of capped transcripts. <i>Genome Biology</i> , 2007, 8, R42.	13.9	3
857	A haplome alignment and reference sequence of the highly polymorphic <i>Ciona savignyi</i> genome. <i>Genome Biology</i> , 2007, 8, R41.	13.9	90
858	PennCNV: An integrated hidden Markov model designed for high-resolution copy number variation detection in whole-genome SNP genotyping data. <i>Genome Research</i> , 2007, 17, 1665-1674.	2.4	1,586
859	Finding cis-regulatory modules in <i>Drosophila</i> using phylogenetic hidden Markov models. <i>Bioinformatics</i> , 2007, 23, 2031-2037.	1.8	9

#	ARTICLE	IF	CITATIONS
860	Unique Integration Profiles in a Canine Model of Long-Term Repopulating Cells Transduced with Gammaretrovirus, Lentivirus, or Foamy Virus. <i>Human Gene Therapy</i> , 2007, 18, 423-434.	1.4	73
861	Comparing Compressed Sequences for Faster Nucleotide BLAST Searches. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 349-364.	1.9	16
862	Superiority of Spaced Seeds for Homology Search. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 496-505.	1.9	13
863	A practical guide to the art of RNA gene prediction. <i>Briefings in Bioinformatics</i> , 2007, 8, 396-414.	3.2	37
864	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
865	SmedGD: the <i>Schmidtea mediterranea</i> genome database. <i>Nucleic Acids Research</i> , 2007, 36, D599-D606.	6.5	251
866	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
867	Variation of CNV distribution in five different ethnic populations. <i>Cytogenetic and Genome Research</i> , 2007, 118, 19-30.	0.6	46
868	Designing Sensitive and Specific Spaced Seeds for Cross-Species mRNA-to-Genome Alignment. <i>Journal of Computational Biology</i> , 2007, 14, 113-130.	0.8	8
869	&lt;i>Ellobius lutescens&/i>: Sex Determination and Sex Chromosome. <i>Sexual Development</i> , 2007, 1, 211-221.	1.1	46
870	A chromosome inversion near the &lt;i>KIT&/i> gene and the Tobiano spotting pattern in horses. <i>Cytogenetic and Genome Research</i> , 2007, 119, 225-230.	0.6	96
871	Aligning Multiple Whole Genomes with Mercator and MAVID. <i>Methods in Molecular Biology</i> , 2007, 395, 221-235.	0.4	83
872	Automated Querying of Genome Databases. <i>PLoS Computational Biology</i> , 2007, 3, e1.	1.5	17
873	A Family of Human MicroRNA Genes from Miniature Inverted-Repeat Transposable Elements. <i>PLoS ONE</i> , 2007, 2, e203.	1.1	264
874	Extensive Polycistronism and Antisense Transcription in the Mammalian Hox Clusters. <i>PLoS ONE</i> , 2007, 2, e356.	1.1	78
875	Gene Organization in Rice Revealed by Full-Length cDNA Mapping and Gene Expression Analysis through Microarray. <i>PLoS ONE</i> , 2007, 2, e1235.	1.1	51
876	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. <i>Genome Research</i> , 2007, 17, 720-731.	2.4	31
877	BLAST-off for genomes. <i>Nature Reviews Genetics</i> , 2007, 8, S14-S14.	7.7	1

#	ARTICLE	IF	CITATIONS
878	In silico-initiated cloning and molecular characterization of cortexin 3, a novel human gene specifically expressed in the kidney and brain, and well conserved in vertebrates. <i>International Journal of Molecular Medicine</i> , 0, , .	1.8	5
881	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007, 28, 554-562.	1.1	79
882	Complex genomic rearrangement in CCS-LacZ transgenic mice. <i>Genesis</i> , 2007, 45, 76-82.	0.8	15
883	FluoMEP: A new genotyping method combining the advantages of randomly amplified polymorphic DNA and amplified fragment length polymorphism. <i>Electrophoresis</i> , 2007, 28, 525-534.	1.3	14
884	Review of the literature examining the correlation among DNA microarray technologies. <i>Environmental and Molecular Mutagenesis</i> , 2007, 48, 380-394.	0.9	75
885	A high performance grid-web service framework for the identification of "conserved sequence tags"™. <i>Future Generation Computer Systems</i> , 2007, 23, 371-381.	4.9	0
886	Indexing schemes for similarity search in datasets of short protein fragments. <i>Information Systems</i> , 2007, 32, 1145-1165.	2.4	16
887	Rod-derived Cone Viability Factor-2 is a novel bifunctional-thioredoxin-like protein with therapeutic potential. <i>BMC Molecular Biology</i> , 2007, 8, 74.	3.0	58
888	DNA microarray data integration by ortholog gene analysis reveals potential molecular mechanisms of estrogen-dependent growth of human uterine fibroids. <i>BMC Women's Health</i> , 2007, 7, 5.	0.8	24
889	Comparative analysis of structured RNAs in <i>S. cerevisiae</i> indicates a multitude of different functions. <i>BMC Biology</i> , 2007, 5, 25.	1.7	32
890	A mobile element-based evolutionary history of guenons (tribe Cercopithecini). <i>BMC Biology</i> , 2007, 5, 5.	1.7	58
891	Asymptotic behaviour and optimal word size for exact and approximate word matches between random sequences. <i>Proceedings in Applied Mathematics and Mechanics</i> , 2007, 7, 1121801-1121802.	0.2	0
892	Global DNA methylation profiling reveals silencing of a secreted form of Epha7 in mouse and human germinal center B-cell lymphomas. <i>Oncogene</i> , 2007, 26, 4243-4252.	2.6	40
893	ACTuDB, a new database for the integrated analysis of array-CGH and clinical data for tumors. <i>Oncogene</i> , 2007, 26, 6641-6652.	2.6	12
894	Recurrent DNA copy number variation in the laboratory mouse. <i>Nature Genetics</i> , 2007, 39, 1384-1389.	9.4	129
895	A retroviral strategy that efficiently creates chromosomal deletions in mammalian cells. <i>Nature Methods</i> , 2007, 4, 263-268.	9.0	14
896	Processing of intronic microRNAs. <i>EMBO Journal</i> , 2007, 26, 775-783.	3.5	714
897	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467.	13.7	3,384

#	ARTICLE	IF	CITATIONS
898	Constraint and turnover in sex-biased gene expression in the genus <i>Drosophila</i> . <i>Nature</i> , 2007, 450, 233-237.	13.7	269
899	Laser capture microdissection and microarray analysis of dividing neural progenitor cells from the adult rat hippocampus. <i>European Journal of Neuroscience</i> , 2007, 26, 1079-1090.	1.2	16
900	Differential gene expression in an elite hybrid rice cultivar ( <i>Oryza sativa</i> , L) and its parental lines based on SAGE data. <i>BMC Plant Biology</i> , 2007, 7, 49.	1.6	41
901	Interpretation of multiple probe sets mapping to the same gene in Affymetrix GeneChips. <i>BMC Bioinformatics</i> , 2007, 8, 13.	1.2	66
902	antiCODE: a natural sense-antisense transcripts database. <i>BMC Bioinformatics</i> , 2007, 8, 319.	1.2	24
903	Considerations in the identification of functional RNA structural elements in genomic alignments. <i>BMC Bioinformatics</i> , 2007, 8, 33.	1.2	56
904	How accurately is ncRNA aligned within whole-genome multiple alignments?. <i>BMC Bioinformatics</i> , 2007, 8, 417.	1.2	20
905	SpliceMiner: a high-throughput database implementation of the NCBI Evidence Viewer for microarray splice variant analysis. <i>BMC Bioinformatics</i> , 2007, 8, 75.	1.2	23
906	Gene models from ESTs (GeneModelEST): an application on the <i>Solanum lycopersicum</i> genome. <i>BMC Bioinformatics</i> , 2007, 8, S9.	1.2	10
907	Accurate splice site prediction using support vector machines. <i>BMC Bioinformatics</i> , 2007, 8, S7.	1.2	135
908	Simultaneous identification of long similar substrings in large sets of sequences. <i>BMC Bioinformatics</i> , 2007, 8, S7.	1.2	4
909	Analysis of the features and source gene composition of the AluYg6 subfamily of human retrotransposons. <i>BMC Evolutionary Biology</i> , 2007, 7, 102.	3.2	3
910	Conserved and species-specific alternative splicing in mammalian genomes. <i>BMC Evolutionary Biology</i> , 2007, 7, 249.	3.2	26
911	A cricket Gene Index: a genomic resource for studying neurobiology, speciation, and molecular evolution. <i>BMC Genomics</i> , 2007, 8, 109.	1.2	32
912	Gene-resolution analysis of DNA copy number variation using oligonucleotide expression microarrays. <i>BMC Genomics</i> , 2007, 8, 111.	1.2	19
913	Global repeat discovery and estimation of genomic copy number in a large, complex genome using a high-throughput 454 sequence survey. <i>BMC Genomics</i> , 2007, 8, 132.	1.2	84
914	Development of the first marmoset-specific DNA microarray (EUMAMA): a new genetic tool for large-scale expression profiling in a non-human primate. <i>BMC Genomics</i> , 2007, 8, 190.	1.2	22
915	WASP: a Web-based Allele-Specific PCR assay designing tool for detecting SNPs and mutations. <i>BMC Genomics</i> , 2007, 8, 275.	1.2	107

#	ARTICLE	IF	CITATIONS
916	The G protein-coupled receptor subset of the rat genome. <i>BMC Genomics</i> , 2007, 8, 338.	1.2	170
917	Short sequence motifs, overrepresented in mammalian conserved non-coding sequences. <i>BMC Genomics</i> , 2007, 8, 378.	1.2	7
918	A screen for nuclear transcripts identifies two linked noncoding RNAs associated with SC35 splicing domains. <i>BMC Genomics</i> , 2007, 8, 39.	1.2	836
919	Large-scale analysis by SAGE reveals new mechanisms of v-erbA oncogene action. <i>BMC Genomics</i> , 2007, 8, 390.	1.2	15
920	Exonization of active mouse L1s: a driver of transcriptome evolution?. <i>BMC Genomics</i> , 2007, 8, 392.	1.2	41
921	Mapping of transcription start sites of human retina expressed genes. <i>BMC Genomics</i> , 2007, 8, 42.	1.2	14
922	A gene-based radiation hybrid map of the gilthead sea bream <i>Sparus aurata</i> refines and exploits conserved synteny with <i>Tetraodon nigroviridis</i> . <i>BMC Genomics</i> , 2007, 8, 44.	1.2	52
923	Ashbya Genome Database 3.0: a cross-species genome and transcriptome browser for yeast biologists. <i>BMC Genomics</i> , 2007, 8, 9.	1.2	46
924	Bacterial flora-typing with targeted, chip-based Pyrosequencing. <i>BMC Microbiology</i> , 2007, 7, 108.	1.3	205
925	Isolation, sequencing, and functional analysis of the TATA-less murine ATPase II promoter and structural analysis of the ATPase II gene. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2007, 1769, 61-75.	2.4	7
926	Translational regulation of human methionine synthase by upstream open reading frames. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2007, 1769, 532-540.	2.4	24
927	Physical mapping of distinct 7q22 deletions in uterine leiomyoma and analysis of a recently annotated 7q22 candidate gene. <i>Cancer Genetics and Cytogenetics</i> , 2007, 174, 116-120.	1.0	19
928	SGA: A grammar-based alignment algorithm. <i>Computer Methods and Programs in Biomedicine</i> , 2007, 86, 17-20.	2.6	2
929	GRAT" genome-scale rapid alignment tool. <i>Computer Methods and Programs in Biomedicine</i> , 2007, 86, 87-92.	2.6	3
930	Chaperonomics, a new tool to study ageing and associated diseases. <i>Mechanisms of Ageing and Development</i> , 2007, 128, 125-136.	2.2	18
931	Reciprocal gene loss between <i>Tetraodon</i> and zebrafish after whole genome duplication in their ancestor. <i>Trends in Genetics</i> , 2007, 23, 108-112.	2.9	116
932	Reconsidering the significance of genomic word frequencies. <i>Trends in Genetics</i> , 2007, 23, 543-546.	2.9	31
933	Gross Genomic Rearrangement Involving the TSC2-PKD1 Contiguous Deletion Syndrome: Characterization of the Deletion Event by Quantitative Polymerase Chain Reaction Deletion Assay. <i>American Journal of Kidney Diseases</i> , 2007, 49, e11-e21.	2.1	17

#	ARTICLE	IF	CITATIONS
934	BGI-RIS V2. , 2007, 406, 275-299.		4
935	An Introduction to BioPerl. , 2007, 406, 535-548.		39
936	Evolution of the Metazoan Protein Phosphatase 2C Superfamily. Journal of Molecular Evolution, 2007, 64, 61-70.	0.8	38
937	Evolutionary Pathways of the tirant LTR Retrotransposon in the Drosophila melanogaster Subgroup of Species. Journal of Molecular Evolution, 2007, 64, 438-447.	0.8	9
938	Comparative genomics reveals functional transcriptional control sequences in the Prop1 gene. Mammalian Genome, 2007, 18, 521-537.	1.0	21
939	A Reconfigurable Index FLASH Memory tailored to Seed-Based Genomic Sequence Comparison Algorithms. Journal of Signal Processing Systems, 2007, 48, 255-269.	1.0	11
940	Biosequence Similarity Search on the Mercury System. Journal of Signal Processing Systems, 2007, 49, 101-121.	1.0	27
941	Ion Channel Gene Expression in the Inner Ear. JARO - Journal of the Association for Research in Otolaryngology, 2007, 8, 305-328.	0.9	56
942	Non-random genomic divergence in repetitive sequences of human and chimpanzee in genes of different functional categories. Molecular Genetics and Genomics, 2007, 277, 441-455.	1.0	8
943	Evaluation of an extended set of 15 candidate STR loci for paternity and kinship analysis in an Austrian population sample. International Journal of Legal Medicine, 2007, 121, 85-89.	1.2	32
944	Genomic organization and sequence analysis of the vomeronasal receptor V2R genes in mouse genome. Science Bulletin, 2007, 52, 336-342.	1.7	5
945	Focus on the intermediate state: immature mRNA of cytochromes P450â€”methods and insights. Analytical and Bioanalytical Chemistry, 2008, 392, 1109-1122.	1.9	13
946	Different Evolutionary Strategies for the Origin of Caspase-1 Inhibitors. Journal of Molecular Evolution, 2008, 66, 591-597.	0.8	14
947	Gene Duplication in Early Vertebrates Results in Tissue-Specific Subfunctionalized Adaptor Proteins: CASP and GRASP. Journal of Molecular Evolution, 2008, 67, 168-178.	0.8	5
948	Evolution, expression and effectiveness in a cluster of novel bovine Î²-defensins. Immunogenetics, 2008, 60, 147-156.	1.2	73
949	The effect of temperature on Natural Antisense Transcript (NAT) expression in Aspergillus flavus. Current Genetics, 2008, 54, 241-269.	0.8	41
950	An imputed genotype resource for the laboratory mouse. Mammalian Genome, 2008, 19, 199-208.	1.0	79
951	Characterization of mouse Dactylaplasia mutations: a model for human ectrodactyly SHFM3. Mammalian Genome, 2008, 19, 272-278.	1.0	23

#	ARTICLE	IF	CITATIONS
952	An epigenetic aberration increased in intergenic regions of cloned mice. <i>Mammalian Genome</i> , 2008, 19, 667-674.	1.0	5
953	The Genome Browser at UCSC for Locating Genes, and Much More!. <i>Molecular Biotechnology</i> , 2008, 38, 269-275.	1.3	15
954	Linking the Genomes of Nonmodel Teleosts Through Comparative Genomics. <i>Marine Biotechnology</i> , 2008, 10, 227-233.	1.1	83
955	Comparative genomic analysis of the arthropod muscle myosin heavy chain genes allows ancestral gene reconstruction and reveals a new type of 'partially' processed pseudogene. <i>BMC Molecular Biology</i> , 2008, 9, 21.	3.0	24
956	Lentiviral integration preferences in transgenic mice. <i>Genesis</i> , 2008, 46, 711-718.	0.8	22
957	Genotype-phenotype correlations in MYCN-related Feingold syndrome. <i>Human Mutation</i> , 2008, 29, 1125-1132.	1.1	72
958	An unusual haplotype structure on human chromosome 8p23 derived from the inversion polymorphism. <i>Human Mutation</i> , 2008, 29, 1209-1216.	1.1	30
959	Characterization of TRIM31, upregulated in gastric adenocarcinoma, as a novel RBCC protein. <i>Journal of Cellular Biochemistry</i> , 2008, 105, 1081-1091.	1.2	40
960	Polymorphic microsatellite loci for the common marmoset ( <i>Callithrix jacchus</i> ) designed using a cost-effective and time-efficient method. <i>American Journal of Primatology</i> , 2008, 70, 906-910.	0.8	8
961	An automated, high-throughput sequence read classification pipeline for preliminary genome characterization. <i>Analytical Biochemistry</i> , 2008, 373, 78-87.	1.1	5
962	A small trip in the untranquil world of genomes. <i>Theoretical Computer Science</i> , 2008, 395, 171-192.	0.5	4
963	Mouse ES cells express endogenous shRNAs, siRNAs, and other Microprocessor-independent, Dicer-dependent small RNAs. <i>Genes and Development</i> , 2008, 22, 2773-2785.	2.7	739
964	A novel insertion variant of the human IL-23 receptor-1 chain transcript. <i>Genes and Immunity</i> , 2008, 9, 566-569.	2.2	12
965	Automated analysis of viral integration sites in gene therapy research using the SeqMap web resource. <i>Gene Therapy</i> , 2008, 15, 1294-1298.	2.3	12
966	Proportionally more deleterious genetic variation in European than in African populations. <i>Nature</i> , 2008, 451, 994-997.	13.7	365
967	A discontinuous hammerhead ribozyme embedded in a mammalian messenger RNA. <i>Nature</i> , 2008, 454, 899-902.	13.7	156
968	The impact of microRNAs on protein output. <i>Nature</i> , 2008, 455, 64-71.	13.7	3,270
969	Design and analysis of ChIP-seq experiments for DNA-binding proteins. <i>Nature Biotechnology</i> , 2008, 26, 1351-1359.	9.4	825

#	ARTICLE	IF	CITATIONS
970	Primary microRNA transcripts are processed co-transcriptionally. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 902-909.	3.6	335
971	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , 2008, 5, 613-619.	9.0	952
972	Steady progress and recent breakthroughs in the accuracy of automated genome annotation. <i>Nature Reviews Genetics</i> , 2008, 9, 62-73.	7.7	133
973	Towards a cyberinfrastructure for the biological sciences: progress, visions and challenges. <i>Nature Reviews Genetics</i> , 2008, 9, 678-688.	7.7	145
974	The DISC locus in psychiatric illness. <i>Molecular Psychiatry</i> , 2008, 13, 36-64.	4.1	554
975	Identification of the sensory neuron specific regulatory region for the mouse gene encoding the voltage-gated sodium channel Na <sup>v</sup> 1.8. <i>Journal of Neurochemistry</i> , 2008, 106, 1209-1224.	2.1	14
976	Development of an <i>in silico</i> coding gene SNP map in pigs. <i>Animal Genetics</i> , 2008, 39, 446-450.	0.6	4
977	The mouse hairy ears mutation exhibits an extended growth (anagen) phase in hair follicles and altered <i>Hoxc</i> gene expression in the ears. <i>Veterinary Dermatology</i> , 2008, 19, 358-367.	0.4	10
978	Multiple organism algorithm for finding ultraconserved elements. <i>BMC Bioinformatics</i> , 2008, 9, 15.	1.2	10
979	Finding sequence motifs with Bayesian models incorporating positional information: an application to transcription factor binding sites. <i>BMC Bioinformatics</i> , 2008, 9, 262.	1.2	25
980	Scipio: Using protein sequences to determine the precise exon/intron structures of genes and their orthologs in closely related species. <i>BMC Bioinformatics</i> , 2008, 9, 278.	1.2	137
981	SynBlast: Assisting the analysis of conserved synteny information. <i>BMC Bioinformatics</i> , 2008, 9, 351.	1.2	12
982	Identification and correction of abnormal, incomplete and mispredicted proteins in public databases. <i>BMC Bioinformatics</i> , 2008, 9, 353.	1.2	55
983	SQUAT: A web tool to mine human, murine and avian SAGE data. <i>BMC Bioinformatics</i> , 2008, 9, 378.	1.2	7
984	Optimal neighborhood indexing for protein similarity search. <i>BMC Bioinformatics</i> , 2008, 9, 534.	1.2	3
985	Supervised Lowess normalization of comparative genome hybridization data – application to lactococcal strain comparisons. <i>BMC Bioinformatics</i> , 2008, 9, 93.	1.2	20
986	Functional analysis of novel SNPs and mutations in human and mouse genomes. <i>BMC Bioinformatics</i> , 2008, 9, S10.	1.2	16
987	hsp70 genes in the human genome: Conservation and differentiation patterns predict a wide array of overlapping and specialized functions. <i>BMC Evolutionary Biology</i> , 2008, 8, 19.	3.2	224

#	ARTICLE	IF	CITATIONS
988	A genomic view of the NOD-like receptor family in teleost fish: identification of a novel NLR subfamily in zebrafish. <i>BMC Evolutionary Biology</i> , 2008, 8, 42.	3.2	199
989	Opossum carboxylesterases: sequences, phylogeny and evidence for CES gene duplication events predating the marsupial-eutherian common ancestor. <i>BMC Evolutionary Biology</i> , 2008, 8, 54.	3.2	12
990	The amphioxus ( <i>Branchiostoma floridae</i> ) genome contains a highly diversified set of G protein-coupled receptors. <i>BMC Evolutionary Biology</i> , 2008, 8, 9.	3.2	87
991	Rapid detection and curation of conserved DNA via enhanced-BLAT and EvoPrinterHD analysis. <i>BMC Genomics</i> , 2008, 9, 106.	1.2	31
992	A novel method of differential gene expression analysis using multiple cDNA libraries applied to the identification of tumour endothelial genes. <i>BMC Genomics</i> , 2008, 9, 153.	1.2	47
993	Detailed characterization of the mouse embryonic stem cell transcriptome reveals novel genes and intergenic splicing associated with pluripotency. <i>BMC Genomics</i> , 2008, 9, 155.	1.2	13
994	Hidden layers of human small RNAs. <i>BMC Genomics</i> , 2008, 9, 157.	1.2	255
995	How many human genes can be defined as housekeeping with current expression data?. <i>BMC Genomics</i> , 2008, 9, 172.	1.2	125
996	Non-random retention of protein-coding overlapping genes in Metazoa. <i>BMC Genomics</i> , 2008, 9, 174.	1.2	26
997	Comparative analysis of sequence features involved in the recognition of tandem splice sites. <i>BMC Genomics</i> , 2008, 9, 202.	1.2	9
998	Repeats and EST analysis for new organisms. <i>BMC Genomics</i> , 2008, 9, 23.	1.2	12
999	The RHNumtS compilation: Features and bioinformatics approaches to locate and quantify Human NumtS. <i>BMC Genomics</i> , 2008, 9, 267.	1.2	34
1000	Genome-wide identification of coding and non-coding conserved sequence tags in human and mouse genomes. <i>BMC Genomics</i> , 2008, 9, 277.	1.2	3
1001	Genome-wide analysis of alternative promoters of human genes using a custom promoter tiling array. <i>BMC Genomics</i> , 2008, 9, 349.	1.2	50
1002	Expression patterns of transcribed human endogenous retrovirus HERV-K(HML-2) loci in human tissues and the need for a HERV Transcriptome Project. <i>BMC Genomics</i> , 2008, 9, 354.	1.2	95
1003	Human MLPA Probe Design (H-MAPD): a probe design tool for both electrophoresis-based and bead-coupled human multiplex ligation-dependent probe amplification assays. <i>BMC Genomics</i> , 2008, 9, 407.	1.2	28
1004	WebScipio: An online tool for the determination of gene structures using protein sequences. <i>BMC Genomics</i> , 2008, 9, 422.	1.2	30
1005	Retrocopy contributions to the evolution of the human genome. <i>BMC Genomics</i> , 2008, 9, 466.	1.2	93

#	ARTICLE	IF	CITATIONS
1006	Analysis of the <i>Pythium ultimum</i> transcriptome using Sanger and Pyrosequencing approaches. <i>BMC Genomics</i> , 2008, 9, 542.	1.2	78
1007	LTR retrotransposons reveal recent extensive inter-subspecies nonreciprocal recombination in Asian cultivated rice. <i>BMC Genomics</i> , 2008, 9, 565.	1.2	5
1008	Analysis of 4,664 high-quality sequence-finished poplar full-length cDNA clones and their utility for the discovery of genes responding to insect feeding. <i>BMC Genomics</i> , 2008, 9, 57.	1.2	68
1009	ProSeeK: A web server for MLPA probe design. <i>BMC Genomics</i> , 2008, 9, 573.	1.2	6
1010	Methylation-sensitive linking libraries enhance gene-enriched sequencing of complex genomes and map DNA methylation domains. <i>BMC Genomics</i> , 2008, 9, 621.	1.2	11
1011	Identification of novel homologous microRNA genes in the rhesus macaque genome. <i>BMC Genomics</i> , 2008, 9, 8.	1.2	38
1012	Complementary RNA amplification methods enhance microarray identification of transcripts expressed in the <i>C. elegans</i> nervous system. <i>BMC Genomics</i> , 2008, 9, 84.	1.2	34
1013	Gene conversion in the rice genome. <i>BMC Genomics</i> , 2008, 9, 93.	1.2	42
1014	xMAN: extreme MApping of OligoNucleotides. <i>BMC Genomics</i> , 2008, 9, S20.	1.2	19
1015	Fast comparison of DNA sequences by oligonucleotide profiling. <i>BMC Research Notes</i> , 2008, 1, 5.	0.6	7
1016	Identification and classification of genes regulated by phosphatidylinositol 3-kinase- and TRKB-mediated signalling pathways during neuronal differentiation in two subtypes of the human neuroblastoma cell line SH-SY5Y. <i>BMC Research Notes</i> , 2008, 1, 95.	0.6	36
1017	Patterns of Codon Usage in two Ciliates that Reassign the Genetic Code: <i>Tetrahymena thermophila</i> and <i>Paramecium tetraurelia</i> . <i>Protist</i> , 2008, 159, 283-298.	0.6	32
1018	Effect of ergot alkaloids associated with fescue toxicosis on hepatic cytochrome P450 and antioxidant proteins. <i>Toxicology and Applied Pharmacology</i> , 2008, 227, 347-356.	1.3	25
1019	Bioinformatics challenges of new sequencing technology. <i>Trends in Genetics</i> , 2008, 24, 142-149.	2.9	438
1020	The impact of next-generation sequencing technology on genetics. <i>Trends in Genetics</i> , 2008, 24, 133-141.	2.9	1,848
1021	<i>Cassandra</i> retrotransposons carry independently transcribed 5S RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5833-5838.	3.3	127
1022	HTLV-1 Integration into Transcriptionally Active Genomic Regions Is Associated with Proviral Expression and with HAM/TSP. <i>PLoS Pathogens</i> , 2008, 4, e1000027.	2.1	91
1024	Clinical Uses of Microarrays in Cancer Research. <i>Methods in Molecular Medicine</i> , 2008, 141, 87-113.	0.8	18

#	ARTICLE	IF	CITATIONS
1025	Group I Metabotropic Glutamate Receptors (mGlu1 and mGlu5)., 2008, , 387-463.		7
1026	Clustering exact matches of pairwise sequence alignments by weighted linear regression. BMC Bioinformatics, 2008, 9, 102.	1.2	3
1027	HIV-1 latency in actively dividing human T cell lines. Retrovirology, 2008, 5, 37.	0.9	45
1028	Splign: algorithms for computing spliced alignments with identification of paralogs. Biology Direct, 2008, 3, 20.	1.9	329
1029	Molecular Identification and Functional Characterization of the Kisspeptin/Kisspeptin Receptor System in Lower Vertebrates1. Biology of Reproduction, 2008, 79, 776-786.	1.2	211
1030	Genome-Wide Association of Histone H3 Lysine Nine Methylation with CHG DNA Methylation in Arabidopsis thaliana. PLoS ONE, 2008, 3, e3156.	1.1	293
1031	Genome Annotation. Methods in Molecular Biology, 2008, 452, 125-139.	0.4	7
1032	Essential Concepts in Toxicogenomics. Methods in Molecular Biology, 2008, , .	0.4	1
1033	CompostBin: A DNA Composition-Based Algorithm for Binning Environmental Shotgun Reads. Lecture Notes in Computer Science, 2008, , 17-28.	1.0	85
1034	Improved genome assembly and evidence-based global gene model set for the chordate Ciona intestinalis: new insight into intron and operon populations. Genome Biology, 2008, 9, R152.	13.9	192
1035	Genomic analysis of the relationship between gene expression variation and DNA polymorphism in Drosophila simulans. Genome Biology, 2008, 9, R125.	13.9	17
1036	Cross-kingdom patterns of alternative splicing and splice recognition. Genome Biology, 2008, 9, R50.	13.9	126
1037	Transcriptional analysis of highly syntenic regions between Medicago truncatula and Glycine max using tiling microarrays. Genome Biology, 2008, 9, R57.	13.9	13
1038	A sequence-based survey of the complex structural organization of tumor genomes. Genome Biology, 2008, 9, R59.	13.9	31
1039	Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus Oryza. Genome Biology, 2008, 9, R45.	13.9	82
1040	The Groucho/TLE/Grg family of transcriptional co-repressors. Genome Biology, 2008, 9, 205.	13.9	141
1041	Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. Genome Biology, 2008, 9, R3.	13.9	53
1042	Automated eukaryotic gene structure annotation using EvidenceModeler and the Program to Assemble Spliced Alignments. Genome Biology, 2008, 9, R7.	13.9	2,484

#	ARTICLE	IF	CITATIONS
1043	Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008, 18, 1851-1858.	2.4	2,275
1044	Inferring Function from Homology. <i>Methods in Molecular Biology</i> , 2008, 453, 149-168.	0.4	9
1045	Bioinformatics Detection of Alternative Splicing. <i>Methods in Molecular Biology</i> , 2008, 452, 179-197.	0.4	15
1046	Conservation of inter-protein binding sites in RUSH and RFBP, an ATP11B isoform. <i>Molecular and Cellular Endocrinology</i> , 2008, 292, 79-86.	1.6	6
1047	Global identification and comparative analysis of SOCS genes in fish: Insights into the molecular evolution of SOCS family. <i>Molecular Immunology</i> , 2008, 45, 1258-1268.	1.0	77
1048	Combinatorial effects of four histone modifications in transcription and differentiation. <i>Genomics</i> , 2008, 91, 41-51.	1.3	45
1049	UCSC genome browser tutorial. <i>Genomics</i> , 2008, 92, 75-84.	1.3	108
1050	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008, 9, R175.	13.9	210
1051	Retrotransposition as a Source of New Promoters. <i>Molecular Biology and Evolution</i> , 2008, 25, 1231-1238.	3.5	38
1052	Molecular cloning and analysis of breakpoints on ring chromosome 17 in a patient with autism. <i>Gene</i> , 2008, 407, 186-192.	1.0	14
1053	Bioinformatic prediction and analysis of eukaryotic protein kinases in the rat genome. <i>Gene</i> , 2008, 410, 147-153.	1.0	20
1054	Zebrafish U6 small nuclear RNA gene promoters contain a SPH element in an unusual location. <i>Gene</i> , 2008, 421, 89-94.	1.0	11
1055	Comparative analysis of an unusual gene arrangement in the human chromosome 1. <i>Gene</i> , 2008, 423, 172-179.	1.0	6
1056	Structure and regulation of the cystic fibrosis transmembrane conductance regulator (CFTR) gene in killifish: A comparative genomics approach. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2008, 3, 172-185.	0.4	10
1057	A putative protein structurally related to zygote arrest 1 (Zar1), Zar1-like, is encoded by a novel gene conserved in the vertebrate lineage. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2008, 150, 233-239.	0.7	15
1058	High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322.	13.5	1,246
1059	Human Chromosomal Translocations at CpG Sites and a Theoretical Basis for Their Lineage and Stage Specificity. <i>Cell</i> , 2008, 135, 1130-1142.	13.5	207
1060	Unfolded Protein Response Genes Regulated by CED-1 Are Required for <i>Caenorhabditis elegans</i> Innate Immunity. <i>Developmental Cell</i> , 2008, 15, 87-97.	3.1	79

#	ARTICLE	IF	CITATIONS
1061	Translational control of intron splicing in eukaryotes. <i>Nature</i> , 2008, 451, 359-362.	13.7	200
1062	Combining Virtual Machine migration with process migration for HPC on multi-clusters and Grids. , 2008, , .		21
1063	Bioinformatics and Database of the Rice Genome. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 13-21.	0.2	0
1064	Whole population, genome-wide mapping of hidden relatedness. <i>Genome Research</i> , 2009, 19, 318-326.	2.4	411
1065	The KLAB Toolbox: A Suite of In-house Software Applications for Epigenetic Analysis. <i>Systems Biology in Reproductive Medicine</i> , 2008, 54, 97-108.	1.0	2
1066	Anytime K-Nearest Neighbor Search for Database Applications. , 2008, , .		1
1067	<i>Helmsman</i> Is Expressed in Both Trachea and Photoreceptor Development: Partial Inactivation Alters Tracheal Morphology and Visually Guided Behavior. <i>Journal of Neurogenetics</i> , 2008, 22, 117-137.	0.6	2
1068	UCSC Genome Browser: Deep support for molecular biomedical research. <i>Biotechnology Annual Review</i> , 2008, 14, 63-108.	2.1	19
1069	Genome Alignments Using MPI-LAGAN. , 2008, , .		0
1070	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. <i>Genome Research</i> , 2008, 18, 1433-1445.	2.4	698
1071	Comparative and Evolutionary Genomics of Globin Genes in Fish. <i>Methods in Enzymology</i> , 2008, 436, 511-538.	0.4	6
1072	Conserved chromosomal clustering of genes governed by chromatin regulators in <i>Drosophila</i> . <i>Genome Biology</i> , 2008, 9, R134.	13.9	16
1073	Chromatin structure analyses identify miRNA promoters. <i>Genes and Development</i> , 2008, 22, 3172-3183.	2.7	541
1074	Designating eukaryotic orthology via processed transcription units. <i>Nucleic Acids Research</i> , 2008, 36, 3436-3442.	6.5	4
1075	Species-specific Differences among KCNMB3 BK $\hat{2}$ Auxiliary Subunits: Some $\hat{2}$ N-terminal Variants May Be Primate-specific Subunits. <i>Journal of General Physiology</i> , 2008, 132, 115-129.	0.9	20
1076	SeqMap: mapping massive amount of oligonucleotides to the genome. <i>Bioinformatics</i> , 2008, 24, 2395-2396.	1.8	459
1077	OREST: the online resource for EST analysis. <i>Nucleic Acids Research</i> , 2008, 36, W140-W144.	6.5	6
1078	Tissue-specific splicing factor gene expression signatures. <i>Nucleic Acids Research</i> , 2008, 36, 4823-4832.	6.5	172

#	ARTICLE	IF	CITATIONS
1079	Gene prediction in novel fungal genomes using an ab initio algorithm with unsupervised training. <i>Genome Research</i> , 2008, 18, 1979-1990.	2.4	800
1080	Predicting functional regulatory polymorphisms. <i>Bioinformatics</i> , 2008, 24, 1787-1792.	1.8	21
1081	Database indexing for production MegaBLAST searches. <i>Bioinformatics</i> , 2008, 24, 1757-1764.	1.8	993
1082	Large-scale gene trapping in C57BL/6N mouse embryonic stem cells. <i>Genome Research</i> , 2008, 18, 1670-1679.	2.4	117
1083	Organization and transcriptional output of a novel mRNA-like piRNA gene (<i>mpiR</i>) located on mouse chromosome 10. <i>Rna</i> , 2008, 14, 1005-1011.	1.6	9
1084	Comparative expression analysis uncovers novel features of endogenous antisense transcription. <i>Human Molecular Genetics</i> , 2008, 17, 1631-1640.	1.4	45
1085	Gene Expression Levels Are a Target of Recent Natural Selection in the Human Genome. <i>Molecular Biology and Evolution</i> , 2008, 26, 649-658.	3.5	96
1086	WAMIDEX: A web atlas of murine genomic imprinting and differential expression. <i>Epigenetics</i> , 2008, 3, 89-96.	1.3	51
1087	Using whole genome presence/absence data to untangle function in 12 <i>Drosophila</i> genomes. <i>Fly</i> , 2008, 2, 291-299.	0.9	10
1088	Run Probabilities of Seed-Like Patterns and Identifying Good Transition Seeds. <i>Journal of Computational Biology</i> , 2008, 15, 1295-1313.	0.8	16
1089	G9a Histone Methyltransferase Contributes to Imprinting in the Mouse Placenta. <i>Molecular and Cellular Biology</i> , 2008, 28, 1104-1113.	1.1	172
1090	Alternative splicing of the G protein-coupled receptor superfamily in human airway smooth muscle diversifies the complement of receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5230-5235.	3.3	70
1091	Transcriptional Autoregulation Controls Pancreatic <i>Ptf1a</i> Expression during Development and Adulthood. <i>Molecular and Cellular Biology</i> , 2008, 28, 5458-5468.	1.1	93
1092	A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. <i>Genome Research</i> , 2009, 19, 510-519.	2.4	261
1093	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.	2.4	456
1094	Nested Patch PCR enables highly multiplexed mutation discovery in candidate genes. <i>Genome Research</i> , 2008, 18, 1844-1850.	2.4	55
1095	Molecular profiling in the age of cancer genomics. <i>Expert Review of Molecular Diagnostics</i> , 2008, 8, 263-276.	1.5	8
1096	FishMap: A Community Resource for Zebrafish Genomics. <i>Zebrafish</i> , 2008, 5, 125-130.	0.5	20

#	ARTICLE	IF	CITATIONS
1097	FINDING ALTERNATIVE SPLICING PATTERNS WITH STRONG SUPPORT FROM EXPRESSED SEQUENCES ON INDIVIDUAL EXONS/INTRONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 1021-1033.	0.3	4
1098	Whole-genome expression profiling of the marine diatom <i>Thalassiosira pseudonana</i> identifies genes involved in silicon bioprocesses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1579-1584.	3.3	247
1099	Genome-Wide Pattern of TCF7L2/TCF4 Chromatin Occupancy in Colorectal Cancer Cells. <i>Molecular and Cellular Biology</i> , 2008, 28, 2732-2744.	1.1	208
1100	Insertional mutagenesis by the <i>Tol2</i> transposon-mediated enhancer trap approach generated mutations in two developmental genes: <i>tcf7</i> and <i>synembryn-like</i> . <i>Development (Cambridge)</i> , 2008, 135, 159-169.	1.2	142
1101	Unexpected complexity at breakpoint junctions in phenotypically normal individuals and mechanisms involved in generating balanced translocations t(1;22)(p36;q13). <i>Genome Research</i> , 2008, 18, 1733-1742.	2.4	26
1102	Acetylcholinesterase Expression in Muscle Is Specifically Controlled by a Promoter-Selective Enhancesome in the First Intron. <i>Journal of Neuroscience</i> , 2008, 28, 2459-2470.	1.7	26
1103	Characterization of genome-wide p53-binding sites upon stress response. <i>Nucleic Acids Research</i> , 2008, 36, 3639-3654.	6.5	199
1104	DNAlive: a tool for the physical analysis of DNA at the genomic scale. <i>Bioinformatics</i> , 2008, 24, 1731-1732.	1.8	28
1105	Navigating the genome. <i>Journal of Cell Science</i> , 2008, 121, 921-923.	1.2	0
1106	Using retroviruses as a mutagenesis tool to explore the zebrafish genome. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2008, 7, 427-443.	3.8	29
1107	Characterization, chromosomal location, and genomic neighborhood of a ratite ortholog of a gene with gonadal expression in mammals. <i>Integrative and Comparative Biology</i> , 2008, 48, 505-511.	0.9	3
1108	Multilocus Patterns of Nucleotide Polymorphism and the Demographic History of <i>Populus tremula</i> . <i>Genetics</i> , 2008, 180, 329-340.	1.2	173
1109	Genotypic Features of Lentivirus Transgenic Mice. <i>Journal of Virology</i> , 2008, 82, 7111-7119.	1.5	30
1110	A microRNA catalog of the developing chicken embryo identified by a deep sequencing approach. <i>Genome Research</i> , 2008, 18, 957-964.	2.4	282
1111	ZOOM! Zillions of oligos mapped. <i>Bioinformatics</i> , 2008, 24, 2431-2437.	1.8	187
1112	Fast Evolution of Core Promoters in Primate Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1239-1244.	3.5	15
1113	Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. <i>PLoS Genetics</i> , 2008, 4, e1000271.	1.5	143
1114	Direct mapping and alignment of protein sequences onto genomic sequence. <i>Bioinformatics</i> , 2008, 24, 2438-2444.	1.8	53

#	ARTICLE	IF	CITATIONS
1115	High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. <i>PLoS Genetics</i> , 2008, 4, e1000249.	1.5	99
1116	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. <i>PLoS Genetics</i> , 2008, 4, e1000214.	1.5	510
1117	Near Intron Positions Are Reliable Phylogenetic Markers: An Application to Holometabolous Insects. <i>Molecular Biology and Evolution</i> , 2008, 25, 821-830.	3.5	39
1118	A robust framework for detecting structural variations in a genome. <i>Bioinformatics</i> , 2008, 24, i59-i67.	1.8	49
1119	Agglomerative Epigenetic Aberrations Are a Common Event in Human Breast Cancer. <i>Cancer Research</i> , 2008, 68, 8616-8625.	0.4	146
1120	Using native and syntenically mapped cDNA alignments to improve <i>de novo</i> gene finding. <i>Bioinformatics</i> , 2008, 24, 637-644.	1.8	1,618
1121	Origin, Evolution, and Biological Role of miRNA Cluster in DLK-DIO3 Genomic Region in Placental Mammals. <i>Molecular Biology and Evolution</i> , 2008, 25, 939-948.	3.5	127
1122	The Subtelomere of <i>Oryza sativa</i> Chromosome 3 Short Arm as a Hot Bed of New Gene Origination in Rice. <i>Molecular Plant</i> , 2008, 1, 839-850.	3.9	36
1123	Chromosomal Gene Movements Reflect the Recent Origin and Biology of Therian Sex Chromosomes. <i>PLoS Biology</i> , 2008, 6, e80.	2.6	182
1124	Genome-Wide Assessments Reveal Extremely High Levels of Polymorphism of Two Active Families of Mouse Endogenous Retroviral Elements. <i>PLoS Genetics</i> , 2008, 4, e1000007.	1.5	90
1125	Sepsid even-skipped Enhancers Are Functionally Conserved in <i>Drosophila</i> Despite Lack of Sequence Conservation. <i>PLoS Genetics</i> , 2008, 4, e1000106.	1.5	262
1126	The Status of Dosage Compensation in the Multiple X Chromosomes of the Platypus. <i>PLoS Genetics</i> , 2008, 4, e1000140.	1.5	102
1127	Identification of ancient remains through genomic sequencing. <i>Genome Research</i> , 2008, 18, 1347-1353.	2.4	47
1128	genBlastA: Enabling BLAST to identify homologous gene sequences. <i>Genome Research</i> , 2009, 19, 143-149.	2.4	249
1129	Genome level analysis of rice mRNA 3' end processing signals and alternative polyadenylation. <i>Nucleic Acids Research</i> , 2008, 36, 3150-3161.	6.5	163
1130	Patterns and changes in gene expression following neo-adjuvant anti-estrogen treatment in estrogen receptor-positive breast cancer. <i>Endocrine-Related Cancer</i> , 2008, 15, 439-449.	1.6	16
1131	Splicing factor SFRS1 recognizes a functionally diverse landscape of RNA transcripts. <i>Genome Research</i> , 2009, 19, 381-394.	2.4	284
1132	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	2.4	117

#	ARTICLE	IF	CITATIONS
1133	Analysis of Alternative Splicing in Plants with Bioinformatics Tools. <i>Current Topics in Microbiology and Immunology</i> , 2008, 326, 17-37.	0.7	11
1134	How Segmental Duplications Shape Our Genome: Recent Evolution of ABCC6 and PKD1 Mendelian Disease Genes. <i>Molecular Biology and Evolution</i> , 2008, 25, 2601-2613.	3.5	34
1135	A Member of the p38 Mitogen-Activated Protein Kinase Family Is Responsible for Transcriptional Induction of <i>Dopa decarboxylase</i> in the Epidermis of <i>Drosophila melanogaster</i> during the Innate Immune Response. <i>Molecular and Cellular Biology</i> , 2008, 28, 4883-4895.	1.1	60
1136	Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. <i>Rna</i> , 2008, 14, 2455-2459.	1.6	133
1137	A space-efficient and accurate method for mapping and aligning cDNA sequences onto genomic sequence. <i>Nucleic Acids Research</i> , 2008, 36, 2630-2638.	6.5	91
1138	On the origin of new genes in <i>Drosophila</i> . <i>Genome Research</i> , 2008, 18, 1446-1455.	2.4	240
1139	Phylogenetic analysis of mRNA polyadenylation sites reveals a role of transposable elements in evolution of the 3' end of genes. <i>Nucleic Acids Research</i> , 2008, 36, 5581-5590.	6.5	100
1140	Epigenetic Silencing of Human Immunodeficiency Virus (HIV) Transcription by Formation of Restrictive Chromatin Structures at the Viral Long Terminal Repeat Drives the Progressive Entry of HIV into Latency. <i>Journal of Virology</i> , 2008, 82, 12291-12303.	1.5	266
1141	Aryl Hydrocarbon Receptor-Dependent Induction of Flavin-Containing Monooxygenase mRNAs in Mouse Liver. <i>Drug Metabolism and Disposition</i> , 2008, 36, 2499-2505.	1.7	45
1142	Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009, 15, 85-96.	1.6	90
1143	The protist, <i>Monosiga brevicollis</i> , has a tyrosine kinase signaling network more elaborate and diverse than found in any known metazoan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9674-9679.	3.3	191
1144	A Genome-Wide Transcription Analysis Reveals a Close Correlation of Promoter INDEL Polymorphism and Heterotic Gene Expression in Rice Hybrids. <i>Molecular Plant</i> , 2008, 1, 720-731.	3.9	101
1145	Expressed Sequence Tags With cDNA Termini: Previously Overlooked Resources for Gene Annotation and Transcriptome Exploration in <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008, 179, 83-93.	1.2	15
1146	De novo assembly using low-coverage short read sequence data from the rice pathogen <i>Pseudomonas syringae</i> pv. <i>oryzae</i> . <i>Genome Research</i> , 2009, 19, 294-305.	2.4	129
1147	Dispensability of mammalian DNA. <i>Genome Research</i> , 2008, 18, 1743-1751.	2.4	42
1148	Properties of Wild-Type and Fluorescent Protein-Tagged Mouse Tetrodotoxin-Resistant Sodium Channel (Na <sup>V</sup> 1.8) Heterologously Expressed in Rat Sympathetic Neurons. <i>Journal of Neurophysiology</i> , 2008, 99, 1917-1927.	0.9	12
1149	SOX17 directly activates <i>Zfp202</i> transcription during in vitro endoderm differentiation. <i>Physiological Genomics</i> , 2008, 34, 277-284.	1.0	8
1150	Haplotype sorting using human fosmid clone end-sequence pairs. <i>Genome Research</i> , 2008, 18, 2016-2023.	2.4	25

#	ARTICLE	IF	CITATIONS
1151	Specific expression of long noncoding RNAs in the mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 716-721.	3.3	1,081
1152	An efficient algorithm for local sequence alignment. , 2008, 2008, 1367-72.		4
1153	The <i>hobo</i> -related elements in the <i>melanogaster</i> species group. Genetical Research, 2008, 90, 243-252.	0.3	18
1154	Mutation Detection Using Automated Fluorescence-Based Sequencing. Current Protocols in Human Genetics, 2008, 57, Unit7.9.	3.5	5
1155	¼ mutation patterns suggest different progression pathways in follicular lymphoma: early direct or late from FL progenitor cells. Blood, 2008, 112, 1951-1959.	0.6	54
1156	Calcitonin receptor-like receptor guides arterial differentiation in zebrafish. Blood, 2008, 111, 4965-4972.	0.6	38
1157	Global Sequencing: A Review of Current Molecular Data and New Methods Available to Assess Microbial Diversity. Microbes and Environments, 2008, 23, 253-268.	0.7	64
1158	CoCoNUT: an efficient system for the comparison and analysis of genomes. BMC Bioinformatics, 2008, 9, 476.	1.2	23
1159	Strategies for Reliable Exploitation of Evolutionary Concepts in High Throughput Biology. Evolutionary Bioinformatics, 2008, 4, EBO.S597.	0.6	15
1160	On the Extent and Origins of Genic Novelty in the Phylum Nematoda. PLoS Neglected Tropical Diseases, 2008, 2, e258.	1.3	68
1161	GPCR Genes Are Preferentially Retained after Whole Genome Duplication. PLoS ONE, 2008, 3, e1903.	1.1	22
1162	Width of Gene Expression Profile Drives Alternative Splicing. PLoS ONE, 2008, 3, e3587.	1.1	13
1163	The Human Microbiome and Infectious Diseases: Beyond Koch. Interdisciplinary Perspectives on Infectious Diseases, 2008, 2008, 1-2.	0.6	11
1164	The Human Vaginal Bacterial Biota and Bacterial Vaginosis. Interdisciplinary Perspectives on Infectious Diseases, 2008, 2008, 1-22.	0.6	185
1165	Affymetrix Whole-Transcript Human Gene 1.0 ST array is highly concordant with standard 3' expression arrays. BioTechniques, 2008, 44, 759-762.	0.8	31
1166	Large-scale Discovery of Gene-Enriched SNPs. Plant Genome, 2009, 2, .	1.6	55
1167	High Performance Protein Sequence Database Scanning on the Cell Broadband Engine. Scientific Programming, 2009, 17, 97-111.	0.5	5
1168	A novel L1 retrotransposon marker for HeLa cell line identification. BioTechniques, 2009, 46, 277-284.	0.8	115

#	ARTICLE	IF	CITATIONS
1169	High-throughput verification of transcriptional starting sites by Deep-RACE. <i>BioTechniques</i> , 2009, 46, 130-132.	0.8	33
1170	Structural Fingerprints of Transcription Factor Binding Site Regions. <i>Algorithms</i> , 2009, 2, 448-469.	1.2	1
1171	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2009, 4, e6524.	1.1	568
1172	Fine-Scale Phylogenetic Discordance across the House Mouse Genome. <i>PLoS Genetics</i> , 2009, 5, e1000729.	1.5	104
1173	Sequencing, Mapping, and Analysis of 27,455 Maize Full-Length cDNAs. <i>PLoS Genetics</i> , 2009, 5, e1000740.	1.5	145
1174	Big Genomes Facilitate the Comparative Identification of Regulatory Elements. <i>PLoS ONE</i> , 2009, 4, e4688.	1.1	41
1175	A Scalable Method for Analysis and Display of DNA Sequences. <i>PLoS ONE</i> , 2009, 4, e7051.	1.1	23
1176	BFAST: An Alignment Tool for Large Scale Genome Resequencing. <i>PLoS ONE</i> , 2009, 4, e7767.	1.1	444
1177	A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2009, 5, e1000551.	1.5	554
1178	Identification of Lympho-Epithelial Kazal-Type Inhibitor 2 in Human Skin as a Kallikrein-Related Peptidase 5-Specific Protease Inhibitor. <i>PLoS ONE</i> , 2009, 4, e4372.	1.1	60
1179	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	2.4	125
1180	Mapping short reads to a genome without using hash look-up table algorithm and Burrows Wheeler Transformation. , 2009, , .		2
1181	VectorBase: a data resource for invertebrate vector genomics. <i>Nucleic Acids Research</i> , 2009, 37, D583-D587.	6.5	234
1182	Recent de novo origin of human protein-coding genes. <i>Genome Research</i> , 2009, 19, 1752-1759.	2.4	256
1183	Parallel short sequence mapping for high throughput genome sequencing. , 2009, , .		15
1184	Prediction of novel microRNA genes in cancer-associated genomic regions—a combined computational and experimental approach. <i>Nucleic Acids Research</i> , 2009, 37, 3276-3287.	6.5	60
1185	RazerSâ€”fast read mapping with sensitivity control. <i>Genome Research</i> , 2009, 19, 1646-1654.	2.4	125
1186	Cell contact-dependent acquisition of cellular and viral nonautonomously encoded small RNAs. <i>Genes and Development</i> , 2009, 23, 1971-1979.	2.7	106

#	ARTICLE	IF	CITATIONS
1187	A Domestic cat X Chromosome Linkage Map and the Sex-Linked <i>orange</i> Locus: Mapping of <i>orange</i> , Multiple Origins and Epistasis Over <i>nonagouti</i> . <i>Genetics</i> , 2009, 181, 1415-1425.	1.2	30
1188	Identification and Characterization of a Novel Gene, <i>dapr</i> , Involved in Skeletal Muscle Differentiation and Protein Kinase B Signaling. <i>Journal of Biological Chemistry</i> , 2009, 284, 1636-1643.	1.6	3
1189	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. <i>Journal of Immunology</i> , 2009, 182, 7738-7748.	0.4	221
1190	mGene: Accurate SVM-based gene finding with an application to nematode genomes. <i>Genome Research</i> , 2009, 19, 2133-2143.	2.4	79
1191	Blimp-1/Prdm1 Alternative Promoter Usage during Mouse Development and Plasma Cell Differentiation. <i>Molecular and Cellular Biology</i> , 2009, 29, 5813-5827.	1.1	57
1192	Response of Gastric Epithelial Progenitors to <i>Helicobacter pylori</i> Isolates Obtained from Swedish Patients with Chronic Atrophic Gastritis. <i>Journal of Biological Chemistry</i> , 2009, 284, 30383-30394.	1.6	25
1193	Genetic Regulatory Network Analysis for <i>App</i> Based on Genetical Genomics Approach. <i>Experimental Aging Research</i> , 2009, 36, 79-93.	0.6	14
1194	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. <i>Molecular Biology and Evolution</i> , 2009, 26, 2865-2875.	3.5	50
1195	Detection of intergenic non-coding RNAs expressed in the main developmental stages in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2009, 37, 4308-4314.	6.5	21
1196	Exon-trapping mediated by the human retrotransposon SVA. <i>Genome Research</i> , 2009, 19, 1983-1991.	2.4	94
1197	Translation of an STR-based biomarker into a clinically compatible SNP-based platform for loss of heterozygosity. <i>Cancer Biomarkers</i> , 2009, 5, 143-158.	0.8	8
1198	Analysis of Transcriptome Changes Induced by <i>Ptr ToxA</i> in Wheat Provides Insights into the Mechanisms of Plant Susceptibility. <i>Molecular Plant</i> , 2009, 2, 1067-1083.	3.9	54
1199	PerM: efficient mapping of short sequencing reads with periodic full sensitive spaced seeds. <i>Bioinformatics</i> , 2009, 25, 2514-2521.	1.8	95
1200	Discovery of <i>Plasmodium</i> modulators by genome-wide analysis of circulating hemocytes in <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21270-21275.	3.3	91
1201	Four histone variants mark the boundaries of polycistronic transcription units in <i>Trypanosoma brucei</i> . <i>Genes and Development</i> , 2009, 23, 1063-1076.	2.7	312
1202	Proteomics and Comparative Genomic Investigations Reveal Heterogeneity in Evolutionary Rate of Male Reproductive Proteins in Mice ( <i>Mus domesticus</i> ). <i>Molecular Biology and Evolution</i> , 2009, 26, 1733-1743.	3.5	93
1203	TARGeT: a web-based pipeline for retrieving and characterizing gene and transposable element families from genomic sequences. <i>Nucleic Acids Research</i> , 2009, 37, e78-e78.	6.5	33
1204	HAPLOWSER: a whole-genome haplotype browser for personal genome and metagenome. <i>Bioinformatics</i> , 2009, 25, 2430-2431.	1.8	2

#	ARTICLE	IF	CITATIONS
1205	Finding genes in <i>Schistosoma japonicum</i> : annotating novel genomes with help of extrinsic evidence. <i>Nucleic Acids Research</i> , 2009, 37, e52-e52.	6.5	13
1206	The UCSC Genome Browser Database: update 2009. <i>Nucleic Acids Research</i> , 2009, 37, D755-D761.	6.5	329
1207	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2009, 28, Unit1.4.	25.8	149
1208	Systematic identification and characterization of chicken ( <i>Gallus gallus</i> ) ncRNAs. <i>Nucleic Acids Research</i> , 2009, 37, 6562-6574.	6.5	25
1209	RBF-TSS: Identification of Transcription Start Site in Human Using Radial Basis Functions Network and Oligonucleotide Positional Frequencies. <i>PLoS ONE</i> , 2009, 4, e4878.	1.1	12
1210	A Modified <i>Sleeping Beauty</i> Transposon System That Can Be Used to Model a Wide Variety of Human Cancers in Mice. <i>Cancer Research</i> , 2009, 69, 8150-8156.	0.4	156
1211	A High-Density Single Nucleotide Polymorphism Map for <i>Neurospora crassa</i> . <i>Genetics</i> , 2009, 181, 767-781.	1.2	54
1212	Identification, sequencing, and cellular localization of hepcidin in guinea pig ( <i>Cavia porcellus</i> ). <i>Journal of Endocrinology</i> , 2009, 202, 389-396.	1.2	9
1213	Characterizing the D2 Statistic: Word Matches in Biological Sequences. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-21.	0.2	20
1214	Genome-Wide Discovery of <i>cis</i> -Elements in Promoter Sequences Using Gene Expression. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 139-151.	1.0	32
1215	Transcriptional Enhancers Induce Insertional Gene Deregulation Independently From the Vector Type and Design. <i>Molecular Therapy</i> , 2009, 17, 851-856.	3.7	79
1216	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731.	2.4	295
1217	High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. <i>Genome Research</i> , 2009, 19, 1133-1140.	2.4	69
1218	Extensive Structural Renovation of Retrogenes in the Evolution of the <i>Populus</i> Genome. <i>Plant Physiology</i> , 2009, 151, 1943-1951.	2.3	66
1219	SNP-o-matic. <i>Bioinformatics</i> , 2009, 25, 2434-2435.	1.8	23
1220	Evolutionary Breakpoints in the Gibbon Suggest Association between Cytosine Methylation and Karyotype Evolution. <i>PLoS Genetics</i> , 2009, 5, e1000538.	1.5	81
1221	GASZ Is Essential for Male Meiosis and Suppression of Retrotransposon Expression in the Male Germline. <i>PLoS Genetics</i> , 2009, 5, e1000635.	1.5	151
1222	WebGMAP: a web service for mapping and aligning cDNA sequences to genomes. <i>Nucleic Acids Research</i> , 2009, 37, W77-W83.	6.5	5

#	ARTICLE	IF	CITATIONS
1223	Using microarrays to identify positional candidate genes for QTL: the case study of ACTH response in pigs. BMC Proceedings, 2009, 3, S14.	1.8	10
1224	A Genome-Wide Association Study of Pulmonary Function Measures in the Framingham Heart Study. PLoS Genetics, 2009, 5, e1000429.	1.5	292
1225	Comparison of three microarray probe annotation pipelines: differences in strategies and their effect on downstream analysis. BMC Proceedings, 2009, 3, S1.	1.8	7
1226	Evolutionary Processes Acting on Candidate cis-Regulatory Regions in Humans Inferred from Patterns of Polymorphism and Divergence. PLoS Genetics, 2009, 5, e1000592.	1.5	123
1227	MFEprimer: multiple factor evaluation of the specificity of PCR primers. Bioinformatics, 2009, 25, 276-278.	1.8	62
1228	Global discovery of primate-specific genes in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12019-12024.	3.3	66
1229	Fine-Scale Variation and Genetic Determinants of Alternative Splicing across Individuals. PLoS Genetics, 2009, 5, e1000766.	1.5	81
1230	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. Bioinformatics, 2009, 25, 1587-1593.	1.8	6
1231	G-compass: a web-based comparative genome browser between human and other vertebrate genomes. Bioinformatics, 2009, 25, 3321-3322.	1.8	7
1232	A comprehensive in silico expression analysis of RNA binding proteins in normal and tumor tissue; identification of potential players in tumor formation. RNA Biology, 2009, 6, 426-433.	1.5	51
1233	Age-Associated Inflammation and Toll-Like Receptor Dysfunction Prime the Lungs for Pneumococcal Pneumonia. Journal of Infectious Diseases, 2009, 200, 546-554.	1.9	131
1234	k-link EST clustering: evaluating error introduced by chimeric sequences under different degrees of linkage. Bioinformatics, 2009, 25, 2302-2308.	1.8	4
1235	Conserved introns reveal novel transcripts in <i>Drosophila melanogaster</i> . Genome Research, 2009, 19, 1289-1300.	2.4	38
1236	Seq-SNPing: Multiple-Alignment Tool for SNP Discovery, SNP ID Identification, and RFLP Genotyping. OMICS A Journal of Integrative Biology, 2009, 13, 253-260.	1.0	13
1237	Modulation of gene expression in U251 glioblastoma cells by binding of mutant p53 R273H to intronic and intergenic sequences. Nucleic Acids Research, 2009, 37, 1486-1500.	6.5	56
1238	<i>Caenorhabditis elegans</i> RNA-Directed RNA Polymerase in Sperm Development and Endogenous RNA Interference. Genetics, 2009, 183, 1297-1314.	1.2	80
1239	Lowly Expressed Human MicroRNA Genes Evolve Rapidly. Molecular Biology and Evolution, 2009, 26, 1195-1198.	3.5	86
1240	RiceGeneThresher: a web-based application for mining genes underlying QTL in rice genome. Nucleic Acids Research, 2009, 37, D996-D1000.	6.5	10

#	ARTICLE	IF	CITATIONS
1241	Dynamic Evolution of <i>Oryza</i> Genomes Is Revealed by Comparative Genomic Analysis of a Genus-Wide Vertical Data Set. <i>Plant Cell</i> , 2009, 20, 3191-3209.	3.1	128
1242	MachiBase: a <i>Drosophila melanogaster</i> 5'-end mRNA transcription database. <i>Nucleic Acids Research</i> , 2009, 37, D49-D53.	6.5	23
1243	Evolution of Vault RNAs. <i>Molecular Biology and Evolution</i> , 2009, 26, 1975-1991.	3.5	130
1244	Gramene QTL database: development, content and applications. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap005.	1.4	95
1245	Sim4cc: a cross-species spliced alignment program. <i>Nucleic Acids Research</i> , 2009, 37, e80-e80.	6.5	16
1246	Computational and analytical framework for small RNA profiling by high-throughput sequencing. <i>Rna</i> , 2009, 15, 992-1002.	1.6	112
1247	Orphelia: predicting genes in metagenomic sequencing reads. <i>Nucleic Acids Research</i> , 2009, 37, W101-W105.	6.5	114
1248	The Serum Response Factor and a Putative Novel Transcription Factor Regulate Expression of the Immediate-Early Gene <i>Arc/Arg3.1</i> in Neurons. <i>Journal of Neuroscience</i> , 2009, 29, 1525-1537.	1.7	75
1249	Conservation of Domain Structure in a Fast-Evolving Heterochromatic SUUR Protein in <i>Drosophilids</i> . <i>Genetics</i> , 2009, 183, 119-129.	1.2	4
1250	Multiple whole-genome alignments without a reference organism. <i>Genome Research</i> , 2009, 19, 682-689.	2.4	63
1251	Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009, 37, D136-D140.	6.5	820
1252	The apolipoprotein L family of programmed cell death and immunity genes rapidly evolved in primates at discrete sites of host-pathogen interactions. <i>Genome Research</i> , 2009, 19, 850-858.	2.4	135
1253	Local alignment of two-base encoded DNA sequence. <i>BMC Bioinformatics</i> , 2009, 10, 175.	1.2	32
1254	miRExpress: Analyzing high-throughput sequencing data for profiling microRNA expression. <i>BMC Bioinformatics</i> , 2009, 10, 328.	1.2	165
1255	BLAST+: architecture and applications. <i>BMC Bioinformatics</i> , 2009, 10, 421.	1.2	14,935
1256	QSRA – a quality-value guided de novo short read assembler. <i>BMC Bioinformatics</i> , 2009, 10, 69.	1.2	53
1257	CNV-seq, a new method to detect copy number variation using high-throughput sequencing. <i>BMC Bioinformatics</i> , 2009, 10, 80.	1.2	495
1258	Short read DNA fragment anchoring algorithm. <i>BMC Bioinformatics</i> , 2009, 10, S17.	1.2	12

#	ARTICLE	IF	CITATIONS
1259	EasyCluster: a fast and efficient gene-oriented clustering tool for large-scale transcriptome data. BMC Bioinformatics, 2009, 10, S10.	1.2	15
1260	Statistical assessment of discriminative features for protein-coding and non coding cross-species conserved sequence elements. BMC Bioinformatics, 2009, 10, S2.	1.2	2
1261	Source gene composition and gene conversion of the AluYh and AluYi lineages of retrotransposons. BMC Evolutionary Biology, 2009, 9, 102.	3.2	7
1262	Rodent-specific alternative exons are more frequent in rapidly evolving genes and in paralogs. BMC Evolutionary Biology, 2009, 9, 142.	3.2	7
1263	Identifying concerted evolution and gene conversion in mammalian gene pairs lasting over 100 million years. BMC Evolutionary Biology, 2009, 9, 156.	3.2	14
1264	HaMStR: Profile hidden markov model based search for orthologs in ESTs. BMC Evolutionary Biology, 2009, 9, 157.	3.2	269
1265	The sea lamprey <i>Petromyzon marinus</i> genome reveals the early origin of several chemosensory receptor families in the vertebrate lineage. BMC Evolutionary Biology, 2009, 9, 180.	3.2	58
1266	Genetic variation at hair length candidate genes in elephants and the extinct woolly mammoth. BMC Evolutionary Biology, 2009, 9, 232.	3.2	18
1267	Positive selection for the male functionality of a co-retroposed gene in the hominoids. BMC Evolutionary Biology, 2009, 9, 252.	3.2	14
1268	Nme protein family evolutionary history, a vertebrate perspective. BMC Evolutionary Biology, 2009, 9, 256.	3.2	94
1269	Transcription and splicing regulation in human umbilical vein endothelial cells under hypoxic stress conditions by exon array. BMC Genomics, 2009, 10, 126.	1.2	47
1270	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. BMC Genomics, 2009, 10, 163.	1.2	205
1271	ESTPiper – a web-based analysis pipeline for expressed sequence tags. BMC Genomics, 2009, 10, 174.	1.2	17
1272	An examination of positive selection and changing effective population size in Angus and Holstein cattle populations ( <i>Bos taurus</i> ) using a high density SNP genotyping platform and the contribution of ancient polymorphism to genomic diversity in Domestic cattle. BMC Genomics, 2009, 10, 181.	1.2	72
1273	Genic regions of a large salamander genome contain long introns and novel genes. BMC Genomics, 2009, 10, 19.	1.2	81
1274	Improving Gene-finding in <i>Chlamydomonas reinhardtii</i> : GreenGenie2. BMC Genomics, 2009, 10, 210.	1.2	18
1275	The G protein-coupled receptor subset of the dog genome is more similar to that in humans than rodents. BMC Genomics, 2009, 10, 24.	1.2	47
1276	Primate phylogenomics: developing numerous nuclear non-coding, non-repetitive markers for ecological and phylogenetic applications and analysis of evolutionary rate variation. BMC Genomics, 2009, 10, 247.	1.2	27

#	ARTICLE	IF	CITATIONS
1277	In silico identification of a core regulatory network of OCT4 in human embryonic stem cells using an integrated approach. BMC Genomics, 2009, 10, 314.	1.2	41
1278	Characterization of the <i>Zoarces viviparus</i> liver transcriptome using massively parallel pyrosequencing. BMC Genomics, 2009, 10, 345.	1.2	65
1279	Mining for single nucleotide polymorphisms in pig genome sequence data. BMC Genomics, 2009, 10, 4.	1.2	32
1280	A BAC-based physical map of <i>Brachypodium distachyon</i> and its comparative analysis with rice and wheat. BMC Genomics, 2009, 10, 496.	1.2	42
1281	Computational prediction of splicing regulatory elements shared by Tetrapoda organisms. BMC Genomics, 2009, 10, 508.	1.2	5
1282	Genome and gene alterations by insertions and deletions in the evolution of human and chimpanzee chromosome 22. BMC Genomics, 2009, 10, 51.	1.2	17
1283	An expression database for roots of the model legume <i>Medicago truncatula</i> under salt stress. BMC Genomics, 2009, 10, 517.	1.2	65
1284	The effect of sequencing errors on metagenomic gene prediction. BMC Genomics, 2009, 10, 520.	1.2	84
1285	Correlation of microsynteny conservation and disease gene distribution in mammalian genomes. BMC Genomics, 2009, 10, 521.	1.2	5
1286	Detection of pathogenic copy number variants in children with idiopathic intellectual disability using 500 K SNP array genomic hybridization. BMC Genomics, 2009, 10, 526.	1.2	30
1287	Complexity of genome evolution by segmental rearrangement in <i>Brassica rapa</i> revealed by sequence-level analysis. BMC Genomics, 2009, 10, 539.	1.2	33
1288	Expression profiling of rainbow trout testis development identifies evolutionary conserved genes involved in spermatogenesis. BMC Genomics, 2009, 10, 546.	1.2	76
1289	Combining next-generation pyrosequencing with microarray for large scale expression analysis in non-model species. BMC Genomics, 2009, 10, 555.	1.2	72
1290	FragIdent – Automatic identification and characterisation of cDNA-fragments. BMC Genomics, 2009, 10, 95.	1.2	0
1291	MapNext: a software tool for spliced and unspliced alignments and SNP detection of short sequence reads. BMC Genomics, 2009, 10, S13.	1.2	14
1292	BOAT: Basic Oligonucleotide Alignment Tool. BMC Genomics, 2009, 10, S2.	1.2	7
1293	An empirical study of choosing efficient discriminative seeds for oligonucleotide design. BMC Genomics, 2009, 10, S3.	1.2	3
1294	PDbase: a database of Parkinson's Disease-related genes and genetic variation using substantia nigra ESTs. BMC Genomics, 2009, 10, S32.	1.2	20

#	ARTICLE	IF	CITATIONS
1295	COMUS: Clinician-Oriented locus-specific MUtation detection and deposition System. BMC Genomics, 2009, 10, S35.	1.2	2
1296	RExPrimer: an integrated primer designing tool increases PCR effectiveness by avoiding 3' SNP-in-primer and mis-priming from structural variation. BMC Genomics, 2009, 10, S4.	1.2	22
1297	Genomic analysis of Campylobacter fetus subspecies: identification of candidate virulence determinants and diagnostic assay targets. BMC Microbiology, 2009, 9, 86.	1.3	51
1298	A newly-developed community microarray resource for transcriptome profiling in Brassica species enables the confirmation of Brassica-specific expressed sequences. BMC Plant Biology, 2009, 9, 50.	1.6	55
1299	ECRG4 is a candidate tumor suppressor gene frequently hypermethylated in colorectal carcinoma and glioma. BMC Cancer, 2009, 9, 447.	1.1	77
1300	Collection of Macaca fascicularis cDNAs derived from bone marrow, kidney, liver, pancreas, spleen, and thymus. BMC Research Notes, 2009, 2, 199.	0.6	11
1301	MicroRNAs and Cancer—The Search Begins!. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 67-77.	3.6	18
1302	An expanded clade of rodent Trim5 genes. Virology, 2009, 385, 473-483.	1.1	68
1303	Advanced in silico analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance — Fundamental insights toward biotechnological outcomes. Biotechnology Advances, 2009, 27, 439-448.	6.0	29
1304	Functional Identification of Tumor-Suppressor Genes through an In Vivo RNA Interference Screen in a Mouse Lymphoma Model. Cancer Cell, 2009, 16, 324-335.	7.7	155
1305	Xq13.2q21.1 duplication encompassing the <i>ATRXL</i> gene in a man with mental retardation, minor facial and genital anomalies, short stature and broad thorax. American Journal of Medical Genetics, Part A, 2009, 149A, 760-766.	0.7	17
1306	Distribution and neuronal expression of phosphatidylinositol phosphate kinase $II\beta$ in the mouse brain. Journal of Comparative Neurology, 2009, 517, 296-312.	0.9	48
1307	Regucalcin is underexpressed in human breast and prostate cancers: Effect of sex steroid hormones. Journal of Cellular Biochemistry, 2009, 107, 667-676.	1.2	47
1308	Zebrafish <i>cnbp</i> intron1 plays a fundamental role in controlling spatiotemporal gene expression during embryonic development. Journal of Cellular Biochemistry, 2009, 108, 1364-1375.	1.2	7
1309	Methylation analysis by DNA immunoprecipitation. Journal of Cellular Physiology, 2010, 222, 522-531.	2.0	23
1310	Hematopoietic immortalizing function of the NKX6 subclass homeobox gene <i>TLX1</i> . Genes Chromosomes and Cancer, 2010, 49, 119-131.	1.5	2
1311	Drosophila P transposons of the urochordata <i>Ciona intestinalis</i> . Molecular Genetics and Genomics, 2009, 282, 165-172.	1.0	8
1312	Evolution of Tom, 297, 17.6 and rover retrotransposons in Drosophilidae species. Molecular Genetics and Genomics, 2009, 282, 351-362.	1.0	15

#	ARTICLE	IF	CITATIONS
1313	Meiotic behavior of aneuploid chromatin in mouse models of Down syndrome. <i>Chromosoma</i> , 2009, 118, 723-736.	1.0	20
1314	Identification of a novel human lactate dehydrogenase gene LDHAL6A, which activates transcriptional activities of AP1(PMA). <i>Molecular Biology Reports</i> , 2009, 36, 669-676.	1.0	4
1315	Influence of genetic background on tumor karyotypes: Evidence for breed-associated cytogenetic aberrations in canine appendicular osteosarcoma. <i>Chromosome Research</i> , 2009, 17, 365-377.	1.0	74
1316	Microarray-based cytogenetic profiling reveals recurrent and subtype-associated genomic copy number aberrations in feline sarcomas. <i>Chromosome Research</i> , 2009, 17, 987-1000.	1.0	14
1317	Isolation of Plant Gene Space-Related Sequence Elements by High C+G Patch (HCGP) Filtration: Model Study on Rice. <i>Plant Molecular Biology Reporter</i> , 2009, 27, 79-85.	1.0	2
1318	Characterization of new hAT transposable elements in 12 <i>Drosophila</i> genomes. <i>Genetica</i> , 2009, 135, 67-75.	0.5	22
1319	Search for informative polymorphisms in candidate genes: clock genes and circadian behaviour in blue tits. <i>Genetica</i> , 2009, 136, 109-117.	0.5	42
1320	The role of gene DCDC2 in German dyslexics. <i>Annals of Dyslexia</i> , 2009, 59, 1-11.	1.2	64
1321	Computational evidence of A-to-I RNA editing in nucleus transcriptome of <i>Arabidopsis thaliana</i> . <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2009, 4, 349-361.	0.6	0
1322	Gene structures, biochemical characterization and distribution of rat melatonin receptors. <i>Journal of Physiological Sciences</i> , 2009, 59, 37-47.	0.9	56
1323	Single feature polymorphisms between two rice cultivars detected using a median polish method. <i>Theoretical and Applied Genetics</i> , 2009, 119, 151-164.	1.8	13
1324	Short Homologous Sequences Are Strongly Associated with the Generation of Chimeric RNAs in Eukaryotes. <i>Journal of Molecular Evolution</i> , 2009, 68, 56-65.	0.8	77
1325	Tandem Stop Codons in Ciliates That Reassign Stop Codons. <i>Journal of Molecular Evolution</i> , 2009, 68, 424-431.	0.8	28
1326	A Comparative Approach Shows Differences in Patterns of Numt Insertion During Hominoid Evolution. <i>Journal of Molecular Evolution</i> , 2009, 68, 688-699.	0.8	39
1327	Non-coding RNAs revealed during identification of genes involved in chicken immune responses. <i>Immunogenetics</i> , 2009, 61, 55-70.	1.2	17
1328	Porcine EPCs downregulate stem cell markers and upregulate endothelial maturation markers during <i>in vitro</i> cultivation. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2009, 3, 512-520.	1.3	7
1329	Natural antisense transcript of natriuretic peptide precursor A (NPPA): structural organization and modulation of NPPA expression. <i>BMC Molecular Biology</i> , 2009, 10, 81.	3.0	64
1330	Mapping the human membrane proteome: a majority of the human membrane proteins can be classified according to function and evolutionary origin. <i>BMC Biology</i> , 2009, 7, 50.	1.7	497

#	ARTICLE	IF	CITATIONS
1331	Genetical genomic determinants of alcohol consumption in rats and humans. <i>BMC Biology</i> , 2009, 7, 70.	1.7	148
1332	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. <i>BMC Biology</i> , 2009, 7, 78.	1.7	155
1333	Conservation of core gene expression in vertebrate tissues. <i>Journal of Biology</i> , 2009, 8, 33.	2.7	165
1334	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009, 58, 1068-1082.	2.8	273
1335	The transcriptionally active regions in the genome of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2009, 73, 1043-1057.	1.2	146
1336	Whole genome scan to detect quantitative trait loci for bovine milk protein composition. <i>Animal Genetics</i> , 2009, 40, 524-537.	0.6	27
1337	Novel SLC7A7 large rearrangements in lysinuric protein intolerance patients involving the same AluY repeat. <i>European Journal of Human Genetics</i> , 2009, 17, 71-79.	1.4	29
1338	Genotype-phenotype correlations in Down syndrome identified by array CGH in 30 cases of partial trisomy and partial monosomy chromosome 21. <i>European Journal of Human Genetics</i> , 2009, 17, 454-466.	1.4	240
1339	QuickMap: a public tool for large-scale gene therapy vector insertion site mapping and analysis. <i>Gene Therapy</i> , 2009, 16, 885-893.	2.3	45
1340	Retroviral vector integration in post-transplant hematopoiesis in mice conditioned with either submyeloablative or ablative irradiation. <i>Gene Therapy</i> , 2009, 16, 1452-1464.	2.3	9
1341	Transcriptome sequencing to detect gene fusions in cancer. <i>Nature</i> , 2009, 458, 97-101.	13.7	791
1342	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858.	13.7	1,526
1343	Copy number variation at 1q21.1 associated with neuroblastoma. <i>Nature</i> , 2009, 459, 987-991.	13.7	329
1344	Direct RNA sequencing. <i>Nature</i> , 2009, 461, 814-818.	13.7	409
1345	An integrative approach to reveal driver gene fusions from paired-end sequencing data in cancer. <i>Nature Biotechnology</i> , 2009, 27, 1005-1011.	9.4	69
1346	Comprehensive genomic access to vector integration in clinical gene therapy. <i>Nature Medicine</i> , 2009, 15, 1431-1436.	15.2	173
1347	Somatic cell nuclear transfer in zebrafish. <i>Nature Methods</i> , 2009, 6, 733-735.	9.0	42
1348	Application of 'next-generation' sequencing technologies to microbial genetics. <i>Nature Reviews Microbiology</i> , 2009, 7, 96-97.	13.6	269

#	ARTICLE	IF	CITATIONS
1349	In the News. <i>Nature Reviews Microbiology</i> , 2009, 7, 260-261.	13.6	158
1350	The evolutionary history of the SSX family of human C/T-antigens. <i>Molecular Biology</i> , 2009, 43, 954-960.	0.4	2
1351	Detecting positive selection in the budding yeast genome. <i>Journal of Evolutionary Biology</i> , 2009, 22, 2430-2437.	0.8	19
1352	SNP Discovery and Haplotype Analysis in the Segmentally Duplicated <i>DRD5</i> Coding Region. <i>Annals of Human Genetics</i> , 2009, 73, 274-282.	0.3	10
1353	The <i>Populus</i> Genome Integrative Explorer (PopGenIE): a new resource for exploring the <i>Populus</i> genome. <i>New Phytologist</i> , 2009, 182, 1013-1025.	3.5	208
1354	Acceleration of ungapped extension in Mercury BLAST. <i>Microprocessors and Microsystems</i> , 2009, 33, 281-289.	1.8	18
1355	A fully resolved genus level phylogeny of neotropical primates (Platyrrhini). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 694-702.	1.2	102
1356	Computational identification of novel microRNA homologs in the chimpanzee genome. <i>Computational Biology and Chemistry</i> , 2009, 33, 62-70.	1.1	39
1357	Sequence assembly. <i>Computational Biology and Chemistry</i> , 2009, 33, 121-136.	1.1	39
1358	Molecular mechanisms regulating bovine ovarian follicular selection. <i>Molecular Reproduction and Development</i> , 2009, 76, 351-366.	1.0	28
1359	TopHat: discovering splice junctions with RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1105-1111.	1.8	11,265
1360	On Subset Seeds for Protein Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 483-494.	1.9	20
1361	“Changing by doubling”, the impact of Whole Genome Duplications in the evolution of eukaryotes. <i>Comptes Rendus - Biologies</i> , 2009, 332, 241-253.	0.1	48
1362	The avian Toll-Like receptor pathway—Subtle differences amidst general conformity. <i>Developmental and Comparative Immunology</i> , 2009, 33, 967-973.	1.0	103
1363	A Hierarchy of H3K4me3 and H3K27me3 Acquisition in Spatial Gene Regulation in <i>Xenopus</i> Embryos. <i>Developmental Cell</i> , 2009, 17, 425-434.	3.1	206
1364	A Systems Approach Reveals that the Myogenesis Genome Network Is Regulated by the Transcriptional Repressor RP58. <i>Developmental Cell</i> , 2009, 17, 836-848.	3.1	259
1365	Characterisation of circulating DNA by parallel tagged sequencing on the 454 platform. <i>Clinica Chimica Acta</i> , 2009, 409, 21-27.	0.5	32
1366	Dissecting Regulatory Networks in Host-Pathogen Interaction Using ChIP-on-chip Technology. <i>Cell Host and Microbe</i> , 2009, 5, 430-437.	5.1	14

#	ARTICLE	IF	CITATIONS
1367	Comparative genomics of gene regulation—conservation and divergence of cis-regulatory information. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 565-570.	1.5	76
1368	UTR dinucleotide simple sequence repeat evolution exhibits recurring patterns including regulatory sequence motif replacements. <i>Gene</i> , 2009, 429, 80-86.	1.0	28
1369	Spatial and temporal preferences for trans-splicing in <i>Ciona intestinalis</i> revealed by EST-based gene expression analysis. <i>Gene</i> , 2009, 430, 44-49.	1.0	4
1370	Internal priming: An opportunistic pathway for L1 and Alu retrotransposition in hominins. <i>Gene</i> , 2009, 448, 233-241.	1.0	21
1371	Loss of epigenetic silencing in tumors preferentially affects primate-specific retroelements. <i>Gene</i> , 2009, 448, 151-167.	1.0	108
1372	Identification of an ancient <i>Bmp4</i> mesoderm enhancer located 46 kb from the promoter. <i>Developmental Biology</i> , 2009, 327, 590-602.	0.9	30
1373	Cis-regulation and chromosomal rearrangement of the <i>fgf8</i> locus after the teleost/tetrapod split. <i>Developmental Biology</i> , 2009, 336, 301-312.	0.9	39
1374	A high-resolution cat radiation hybrid and integrated FISH mapping resource for phylogenomic studies across Felidae. <i>Genomics</i> , 2009, 93, 299-304.	1.3	44
1375	An alternative pathway for Alu retrotransposition suggests a role in DNA double-strand break repair. <i>Genomics</i> , 2009, 93, 205-212.	1.3	36
1376	Characterization and functional analysis of cis-acting elements of the human farnesyl diphosphate synthetase (FDPS) gene 5' flanking region. <i>Genomics</i> , 2009, 93, 227-234.	1.3	21
1377	Identification of a high frequency transposon induced by tissue culture, nDaiZ, a member of the hAT family in rice. <i>Genomics</i> , 2009, 93, 274-281.	1.3	34
1378	Critical evaluation of the FANTOM3 non-coding RNA transcripts. <i>Genomics</i> , 2009, 94, 169-176.	1.3	15
1379	Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. <i>Genomics</i> , 2009, 94, 308-316.	1.3	11
1380	Genome-wide high throughput analysis of DNA methylation in eukaryotes. <i>Methods</i> , 2009, 47, 142-150.	1.9	178
1381	Integration of genetic and genomic methods for identification of genes and gene variants encoding QTLs in the nonhuman primate. <i>Methods</i> , 2009, 49, 63-69.	1.9	9
1382	Photoperiod modifies the diurnal expression profile of <i>VvPHYA</i> and <i>VvPHYB</i> transcripts in field-grown grapevine leaves. <i>Journal of Plant Physiology</i> , 2009, 166, 1172-1180.	1.6	42
1383	Overexpression of <i>Nrp/b</i> (nuclear restrict protein in brain) suppresses the malignant phenotype in the C6/ST1 glioma cell line. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2009, 117, 107-116.	1.2	5
1384	Phylogenetic Relationships and Classification of Didelphid Marsupials, an Extant Radiation of New World Metatherian Mammals. <i>Bulletin of the American Museum of Natural History</i> , 2009, 322, 1-177.	1.2	255

#	ARTICLE	IF	CITATIONS
1385	Mining SNPs from DNA Sequence Data; Computational Approaches to SNP Discovery and Analysis. <i>Methods in Molecular Biology</i> , 2009, 578, 73-91.	0.4	16
1386	The first Korean genome sequence and analysis: Full genome sequencing for a socio-ethnic group. <i>Genome Research</i> , 2009, 19, 1622-1629.	2.4	282
1387	Sequence Comparison Tools. , 2009, , 13-37.		4
1388	DNA Sudoku“harnessing high-throughput sequencing for multiplexed specimen analysis. <i>Genome Research</i> , 2009, 19, 1243-1253.	2.4	141
1389	A Parallel Pairwise Local Sequence Alignment Algorithm. <i>IEEE Transactions on Nanobioscience</i> , 2009, 8, 139-146.	2.2	7
1390	Genes targeted by the estrogen and progesterone receptors in the human endometrial cell lines HEC1A and RL95-2. <i>Reproductive Biology and Endocrinology</i> , 2009, 7, 150.	1.4	22
1391	Analysis of transcribed human endogenous retrovirus W env loci clarifies the origin of multiple sclerosis-associated retrovirus env sequences. <i>Retrovirology</i> , 2009, 6, 37.	0.9	65
1392	The DAWGPAWS pipeline for the annotation of genes and transposable elements in plant genomes. <i>Plant Methods</i> , 2009, 5, 8.	1.9	21
1393	The Role of CLCA Proteins in Inflammatory Airway Disease. <i>Annual Review of Physiology</i> , 2009, 71, 425-449.	5.6	105
1394	Finding Similar Nucleotide Sequences Using Network BLAST Searches. <i>Current Protocols in Bioinformatics</i> , 2009, 26, Unit 3.3.	25.8	16
1395	Pairwise sequence alignment algorithms. , 2009, , .		31
1396	Applications of Ultra-high-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2009, 553, 79-108.	0.4	72
1397	Proteolytic Systems: Constructing Degradomes. <i>Methods in Molecular Biology</i> , 2009, 539, 33-47.	0.4	15
1399	iTriplet, a rule-based nucleic acid sequence motif finder. <i>Algorithms for Molecular Biology</i> , 2009, 4, 14.	0.3	25
1400	Tandem repeats modify the structure of human genes hosted in segmental duplications. <i>Genome Biology</i> , 2009, 10, R137.	13.9	32
1401	High resolution discovery and confirmation of copy number variants in 90 Yoruba Nigerians. <i>Genome Biology</i> , 2009, 10, R125.	13.9	53
1402	Transcriptome analysis of functional differentiation between haploid and diploid cells of <i>Emiliania huxleyi</i> , a globally significant photosynthetic calcifying cell. <i>Genome Biology</i> , 2009, 10, R114.	13.9	105
1403	Genome-wide comparative analysis of the <i>Brassica rapa</i> gene space reveals genome shrinkage and differential loss of duplicated genes after whole genome triplication. <i>Genome Biology</i> , 2009, 10, R111.	13.9	183

#	ARTICLE	IF	CITATIONS
1404	Many LINE1 elements contribute to the transcriptome of human somatic cells. <i>Genome Biology</i> , 2009, 10, R100.	3.8	84
1405	The bovine lactation genome: insights into the evolution of mammalian milk. <i>Genome Biology</i> , 2009, 10, R43.	13.9	164
1406	Widespread evidence for horizontal transfer of transposable elements across <i>Drosophila</i> genomes. <i>Genome Biology</i> , 2009, 10, R22.	13.9	128
1407	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. <i>Genome Biology</i> , 2009, 10, R23.	13.9	223
1408	Identification of Novel Alternative Splice Isoforms of Circulating Proteins in a Mouse Model of Human Pancreatic Cancer. <i>Cancer Research</i> , 2009, 69, 300-309.	0.4	67
1409	Pan-vertebrate conserved non-coding sequences associated with developmental regulation. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2009, 8, 256-265.	3.8	17
1410	An overview of recent developments in genomics and associated statistical methods. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2009, 367, 4313-4337.	1.6	27
1411	Molecular cloning, sequence characteristics, and polymorphism analyses of the tyrosinase-related protein 2 / DOPAchrome tautomerase gene of black-boned sheep ( <i>Ovis aries</i> ). <i>Genome</i> , 2009, 52, 1001-1011.	0.9	14
1412	xIP-seq Platform: An Integrative Framework for High-Throughput Sequencing Data Analysis. , 2009, , .		2
1413	Complete Alternative Splicing Events Are Bubbles in Splicing Graphs. <i>Journal of Computational Biology</i> , 2009, 16, 1117-1140.	0.8	46
1414	A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 180-189.	1.9	14
1415	Geometric Aspects of Biological Sequence Comparison. <i>Journal of Computational Biology</i> , 2009, 16, 579-610.	0.8	10
1416	Dynamic Programming for Single Nucleotide Polymorphism ID Identification in Systematic Association Studies. <i>Kaohsiung Journal of Medical Sciences</i> , 2009, 25, 165-176.	0.8	1
1417	Bioinformatic analysis of microRNA biogenesis and function related proteins in eleven animal genomes. <i>Journal of Genetics and Genomics</i> , 2009, 36, 591-601.	1.7	16
1418	EvoOligo: Oligonucleotide Probe Design With Multiobjective Evolutionary Algorithms. <i>IEEE Transactions on Systems, Man, and Cybernetics</i> , 2009, 39, 1606-1616.	5.5	11
1419	Setting CAGE Tags in a Genomic Context. , 2009, , 93-100.		0
1420	Orientation, distance, regulation and function of neighbouring genes. <i>Human Genomics</i> , 2009, 3, 143-56.	1.4	22
1421	Evolution of a Bitter Taste Receptor Gene Cluster in a New World Sparrow. <i>Genome Biology and Evolution</i> , 2010, 2, 358-370.	1.1	38

#	ARTICLE	IF	CITATIONS
1422	Quantitative Gene Expression Profiles in Real Time From Expressed Sequence Tag Databases. <i>Gene Expression</i> , 2010, 14, 321-336.	0.5	4
1423	Validation of Rearrangement Break Points Identified by Paired-End Sequencing in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 83-101.	1.1	46
1424	Gene Duplication and Environmental Adaptation within Yeast Populations. <i>Genome Biology and Evolution</i> , 2010, 2, 591-601.	1.1	44
1425	Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. <i>Standards in Genomic Sciences</i> , 2010, 2, 142-148.	1.5	509
1426	Whole-Genome Positive Selection and Habitat-Driven Evolution in a Shallow and a Deep-Sea Urchin. <i>Genome Biology and Evolution</i> , 2010, 2, 800-814.	1.1	52
1427	Alterations in Gene Expression in MEN1-Associated Insulinoma Development. <i>Pancreas</i> , 2010, 39, 1140-1146.	0.5	7
1428	Heritability in the Efficiency of Nonsense-Mediated mRNA Decay in Humans. <i>PLoS ONE</i> , 2010, 5, e11657.	1.1	17
1433	<i>Agrobacterium</i> -mediated gene disruption using split-marker in <i>Grosmanina clavigera</i> , a mountain pine beetle associated pathogen. <i>Current Genetics</i> , 2010, 56, 297-307.	0.8	39
1434	Characterization of the zebrafish T cell receptor $\hat{1}^2$ locus. <i>Immunogenetics</i> , 2010, 62, 23-29.	1.2	46
1435	Organization of the variable region of the immunoglobulin heavy-chain gene locus of the rat. <i>Immunogenetics</i> , 2010, 62, 479-486.	1.2	13
1436	Reducing non-determinism of k-NN searching in non-ordered discrete data spaces. <i>Information Processing Letters</i> , 2010, 110, 420-423.	0.4	0
1437	Positional variations among heterogeneous nucleosome maps give dynamical information on chromatin. <i>Chromosoma</i> , 2010, 119, 391-404.	1.0	8
1438	Large intron 14 rearrangement in APC results in splice defect and attenuated FAP. <i>Human Genetics</i> , 2010, 127, 359-369.	1.8	17
1439	Contributions of three-site mutations in acetylcholinesterase and cytochrome P450 to genetic variation in susceptibility to organophosphate insecticides within a natural population of <i>Drosophila melanogaster</i> . <i>Population Ecology</i> , 2010, 52, 159-169.	0.7	6
1440	A comprehensive analysis of protein phosphatases in rice and Arabidopsis. <i>Plant Systematics and Evolution</i> , 2010, 289, 111-126.	0.3	7
1441	Prediction and identification of tumor-specific noncoding RNAs from human UniGene. <i>Medical Oncology</i> , 2010, 27, 894-898.	1.2	7
1442	An N- and C-terminal truncated isoform of zinc finger X-linked duplicated C protein represses MHC class II transcription. <i>Molecular and Cellular Biochemistry</i> , 2010, 337, 1-7.	1.4	4
1443	Characterization of a novel human HMBOX1 splicing variant lacking the homeodomain and with attenuated transcription repressor activity. <i>Molecular Biology Reports</i> , 2010, 37, 2767-2772.	1.0	5

#	ARTICLE	IF	CITATIONS
1444	Strategies to develop polymorphic markers for <i>Coffea arabica</i> L.. <i>Euphytica</i> , 2010, 173, 243-253.	0.6	2
1445	hAT transposable elements and their derivatives: an analysis in the 12 <i>Drosophila</i> genomes. <i>Genetica</i> , 2010, 138, 649-655.	0.5	13
1446	Genome-wide SNP association-based localization of a dwarfism gene in Friesian dwarf horses. <i>Animal Genetics</i> , 2010, 41, 2-7.	0.6	31
1447	Transcription of LINE-derived sequences in exercise-induced stress in horses. <i>Animal Genetics</i> , 2010, 41, 23-27.	0.6	22
1448	Mitochondrial DNA insertions in the nuclear horse genome. <i>Animal Genetics</i> , 2010, 41, 176-185.	0.6	35
1449	Histone H3 trimethylated at lysine 4 is enriched at probable transcription start sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 172, 141-144.	0.5	77
1450	BS Seeker: precise mapping for bisulfite sequencing. <i>BMC Bioinformatics</i> , 2010, 11, 203.	1.2	212
1451	A method of predicting changes in human gene splicing induced by genetic variants in context of cis-acting elements. <i>BMC Bioinformatics</i> , 2010, 11, 22.	1.2	15
1452	Cgaln: fast and space-efficient whole-genome alignment. <i>BMC Bioinformatics</i> , 2010, 11, 224.	1.2	14
1453	eHive: An Artificial Intelligence workflow system for genomic analysis. <i>BMC Bioinformatics</i> , 2010, 11, 240.	1.2	37
1454	Analysing 454 amplicon resequencing experiments using the modular and database oriented Variant Identification Pipeline. <i>BMC Bioinformatics</i> , 2010, 11, 269.	1.2	15
1455	Improving de novo sequence assembly using machine learning and comparative genomics for overlap correction. <i>BMC Bioinformatics</i> , 2010, 11, 33.	1.2	16
1456	Local alignment of generalized k-base encoded DNA sequence. <i>BMC Bioinformatics</i> , 2010, 11, 347.	1.2	1
1457	Geoseq: a tool for dissecting deep-sequencing datasets. <i>BMC Bioinformatics</i> , 2010, 11, 506.	1.2	4
1458	Gen Htr : a tool for comparative assessment of genetic heterogeneity in microbial genomes generated by massive short-read sequencing. <i>BMC Bioinformatics</i> , 2010, 11, 508.	1.2	4
1459	Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. <i>BMC Bioinformatics</i> , 2010, 11, 572.	1.2	48
1460	Initial steps towards a production platform for DNA sequence analysis on the grid. <i>BMC Bioinformatics</i> , 2010, 11, 598.	1.2	7
1461	A computational screen for site selective A-to-I editing detects novel sites in neuron specific Hu proteins. <i>BMC Bioinformatics</i> , 2010, 11, 6.	1.2	35

#	ARTICLE	IF	CITATIONS
1462	Parameters for accurate genome alignment. <i>BMC Bioinformatics</i> , 2010, 11, 80.	1.2	180
1463	Quail Genomics: a knowledgebase for Northern bobwhite. <i>BMC Bioinformatics</i> , 2010, 11, S13.	1.2	14
1464	Assessment of genetic variation for the LINE-1 retrotransposon from next generation sequence data. <i>BMC Bioinformatics</i> , 2010, 11, S12.	1.2	7
1465	The molecular evolution of PL10 homologs. <i>BMC Evolutionary Biology</i> , 2010, 10, 127.	3.2	26
1466	Some novel intron positions in conserved <i>Drosophila</i> genes are caused by intron sliding or tandem duplication. <i>BMC Evolutionary Biology</i> , 2010, 10, 156.	3.2	17
1467	Periostin shows increased evolutionary plasticity in its alternatively spliced region. <i>BMC Evolutionary Biology</i> , 2010, 10, 30.	3.2	87
1468	Evolution of Rhizaria: new insights from phylogenomic analysis of uncultivated protists. <i>BMC Evolutionary Biology</i> , 2010, 10, 377.	3.2	130
1469	Evolution of spliceosomal introns following endosymbiotic gene transfer. <i>BMC Evolutionary Biology</i> , 2010, 10, 57.	3.2	23
1470	Chaperonin genes on the rise: new divergent classes and intense duplication in human and other vertebrate genomes. <i>BMC Evolutionary Biology</i> , 2010, 10, 64.	3.2	30
1471	Genomic organization of duplicated short wave-sensitive and long wave-sensitive opsin genes in the green swordtail, <i>Xiphophorus helleri</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 87.	3.2	32
1472	Genome-wide analysis of alternative splicing in <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2010, 11, 114.	1.2	69
1473	An EST resource for tilapia based on 17 normalized libraries and assembly of 116,899 sequence tags. <i>BMC Genomics</i> , 2010, 11, 278.	1.2	39
1474	A manual collection of Syt, Esyt, Rph3a, Rph3al, Doc2, and Dblc2 genes from 46 metazoan genomes - an open access resource for neuroscience and evolutionary biology. <i>BMC Genomics</i> , 2010, 11, 37.	1.2	53
1475	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. <i>BMC Genomics</i> , 2010, 11, 383.	1.2	97
1476	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. <i>BMC Genomics</i> , 2010, 11, 384.	1.2	161
1477	Gene discovery for the bark beetle-vectored fungal tree pathogen <i>Grosmannia clavigera</i> . <i>BMC Genomics</i> , 2010, 11, 536.	1.2	25
1478	Gene expression in a paleopolyploid: a transcriptome resource for the ciliate <i>Paramecium tetraurelia</i> . <i>BMC Genomics</i> , 2010, 11, 547.	1.2	64
1479	Expression proteomics of UPF1 knockdown in HeLa cells reveals autoregulation of hnRNP A2/B1 mediated by alternative splicing resulting in nonsense-mediated mRNA decay. <i>BMC Genomics</i> , 2010, 11, 565.	1.2	67

#	ARTICLE	IF	CITATIONS
1480	Comparing de novo assemblers for 454 transcriptome data. BMC Genomics, 2010, 11, 571.	1.2	217
1481	Annotation and comparative analysis of the glycoside hydrolase genes in <i>Brachypodium distachyon</i> . BMC Genomics, 2010, 11, 600.	1.2	53
1482	Genomic tools development for <i>Aquilegia</i> : construction of a BAC-based physical map. BMC Genomics, 2010, 11, 621.	1.2	13
1483	The rapid generation of chimerical genes expanding protein diversity in zebrafish. BMC Genomics, 2010, 11, 657.	1.2	36
1484	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. BMC Genomics, 2010, 11, 663.	1.2	201
1485	Genomic and transcriptomic analysis of the AP2/ERF superfamily in <i>Vitis vinifera</i> . BMC Genomics, 2010, 11, 719.	1.2	307
1486	Gallin; an antimicrobial peptide member of a new avian defensin family, the ovodefensins, has been subject to recent gene duplication. BMC Immunology, 2010, 11, 12.	0.9	67
1487	Analysis of the genome content of <i>Lactococcus garvieae</i> by genomic interspecies microarray hybridization. BMC Microbiology, 2010, 10, 79.	1.3	11
1488	Long noncoding RNAs in neuronal-glia fate specification and oligodendrocyte lineage maturation. BMC Neuroscience, 2010, 11, 14.	0.8	381
1489	Transcriptional profiles underlying parent-of-origin effects in seeds of <i>Arabidopsis thaliana</i> . BMC Plant Biology, 2010, 10, 72.	1.6	71
1490	Expression profiling in canine osteosarcoma: identification of biomarkers and pathways associated with outcome. BMC Cancer, 2010, 10, 506.	1.1	47
1491	Alterations in the steroid hormone receptor co-chaperone FKBP1 are associated with male infertility: a case-control study. Reproductive Biology and Endocrinology, 2010, 8, 22.	1.4	31
1492	Cloning and characterization of a novel alternatively spliced transcript of the human CHD7 putative helicase. BMC Research Notes, 2010, 3, 252.	0.6	7
1493	Rapid pair-wise synteny analysis of large bacterial genomes using web-based GeneOrder4.0. BMC Research Notes, 2010, 3, 41.	0.6	15
1494	Vertebrate $\beta$ -thymosins: Conserved synteny reveals the relationship between those of bony fish and of land vertebrates. FEBS Letters, 2010, 584, 1047-1053.	1.3	5
1495	Inherited neuroaxonal dystrophy in dogs causing lethal, fetal-onset motor system dysfunction and cerebellar hypoplasia. Journal of Comparative Neurology, 2010, 518, 3771-3784.	0.9	16
1496	Telomere healing following DNA polymerase arrest-induced breakages is likely the main mechanism generating chromosome 4p terminal deletions. Human Mutation, 2010, 31, 1343-1351.	1.1	21
1497	Tissue-specific regulatory regions of the <i>PTH</i> gene localized by novel chromosome 11 rearrangement breakpoints in a parathyroid adenoma. Journal of Bone and Mineral Research, 2010, 25, 2606-2612.	3.1	12

#	ARTICLE	IF	CITATIONS
1498	Validation and application of normalization factors for gene expression studies in rubella virus-infected cell lines with quantitative real-time PCR. <i>Journal of Cellular Biochemistry</i> , 2010, 110, 118-128.	1.2	25
1499	OCT3/4 regulates transcription of histone deacetylase 4 ( <i>Hdac4</i> ) in mouse embryonic stem cells. <i>Journal of Cellular Biochemistry</i> , 2010, 111, 391-401.	1.2	10
1500	Cabin1 expression suggests roles in neuronal development. <i>Developmental Dynamics</i> , 2010, 239, 2443-2451.	0.8	19
1501	Recurrent interstitial 1p36 deletions: Evidence for germline mosaicism and complex rearrangement breakpoints. <i>American Journal of Medical Genetics, Part A</i> , 2010, 152A, 3074-3083.	0.7	31
1502	Intracisternal A particle genes: Distribution in the mouse genome, active subtypes, and potential roles as species-specific mediators of susceptibility to cancer. <i>Molecular Carcinogenesis</i> , 2010, 49, 54-67.	1.3	44
1503	Hox expression in the American alligator and evolution of archosaurian axial patterning. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2010, 314B, 629-644.	0.6	38
1504	Quantitative erythrocyte membrane proteome analysis with Blue-Native/SDS PAGE. <i>Journal of Proteomics</i> , 2010, 73, 456-465.	1.2	60
1505	Computational identification and characterization of primate-specific microRNAs in human genome. <i>Computational Biology and Chemistry</i> , 2010, 34, 232-241.	1.1	57
1506	Human T-cell memory consists mainly of unexpanded clones. <i>Immunology Letters</i> , 2010, 133, 42-48.	1.1	89
1507	Characterization of the first beta-class carbonic anhydrase from an arthropod ( <i>Drosophila</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Biochemistry</i> , 2010, 11, 28.	4.4	72
1508	A genome-wide association study on androstenone levels in pigs reveals a cluster of candidate genes on chromosome 6. <i>BMC Genetics</i> , 2010, 11, 42.	2.7	96
1509	Identifying novel genes in <i>C. elegans</i> using SAGE tags. <i>BMC Molecular Biology</i> , 2010, 11, 96.	3.0	5
1510	Serious limitations of the QTL/Microarray approach for QTL gene discovery. <i>BMC Biology</i> , 2010, 8, 96.	1.7	29
1511	Phylogenetic comparative assembly. <i>Algorithms for Molecular Biology</i> , 2010, 5, 3.	0.3	15
1512	Heads or tails: L1 insertion-associated 5' homopolymeric sequences. <i>Mobile DNA</i> , 2010, 1, 7.	1.3	10
1513	Computational analysis of unassigned high-quality MS/MS spectra in proteomic data sets. <i>Proteomics</i> , 2010, 10, 2712-2718.	1.3	58
1514	Detecting Gene Duplications in the Human Lineage. <i>Annals of Human Genetics</i> , 2010, 74, 555-565.	0.3	6
1515	Characterization of the <i>Arabidopsis thaliana</i> exocyst complex gene families by phylogenetic, expression profiling, and subcellular localization studies. <i>New Phytologist</i> , 2010, 185, 401-419.	3.5	77

#	ARTICLE	IF	CITATIONS
1516	Increased vitamin D-driven signalling and expression of the vitamin D receptor, MSX2, and RANKL in tooth resorption in cats. <i>European Journal of Oral Sciences</i> , 2010, 118, 39-46.	0.7	22
1517	A genetic linkage map of red drum, <i>Sciaenops ocellatus</i> . <i>Animal Genetics</i> , 2010, 41, 630-641.	0.6	12
1518	Comparative analysis of nuclear tRNA genes of <i>Nasonia vitripennis</i> and other arthropods, and relationships to codon usage bias. <i>Insect Molecular Biology</i> , 2010, 19, 49-58.	1.0	32
1519	Molecular Evolution of the Thyrotrophin-Releasing Hormone Precursor in Vertebrates: Insights From Comparative Genomics. <i>Journal of Neuroendocrinology</i> , 2010, 22, 608-619.	1.2	19
1520	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. <i>Molecular Ecology</i> , 2010, 19, 266-276.	2.0	105
1521	A syndrome of short stature, microcephaly and speech delay is associated with duplications reciprocal to the common Sotos syndrome deletion. <i>European Journal of Human Genetics</i> , 2010, 18, 258-261.	1.4	41
1522	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
1523	Building the sequence map of the human pan-genome. <i>Nature Biotechnology</i> , 2010, 28, 57-63.	9.4	237
1524	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010, 63, 990-1003.	2.8	47
1525	Mutation spectrum revealed by breakpoint sequencing of human germline CNVs. <i>Nature Genetics</i> , 2010, 42, 385-391.	9.4	211
1526	Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010, 42, 1053-1059.	9.4	987
1527	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010, 7, 909-912.	9.0	886
1528	Defining transcribed regions using RNA-seq. <i>Nature Protocols</i> , 2010, 5, 255-266.	5.5	70
1529	Genome-wide high-throughput integrome analyses by nrLAM-PCR and next-generation sequencing. <i>Nature Protocols</i> , 2010, 5, 1379-1395.	5.5	161
1530	A microsatellite linkage map for <i>Drosophila montana</i> shows large variation in recombination rates, and a courtship song trait maps to an area of low recombination. <i>Journal of Evolutionary Biology</i> , 2010, 23, 518-527.	0.8	15
1531	Testing the Coding Potential of Conserved Short Genomic Sequences. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-8.	5.7	0
1532	Endothelial Cell Processing and Alternatively Spliced Transcripts of Factor VIII: Potential Implications for Coagulation Cascades and Pulmonary Hypertension. <i>PLoS ONE</i> , 2010, 5, e9154.	1.1	44
1533	A Novel Role for Minimal Introns: Routing mRNAs to the Cytosol. <i>PLoS ONE</i> , 2010, 5, e10144.	1.1	27

#	ARTICLE	IF	CITATIONS
1534	HMMSplicer: A Tool for Efficient and Sensitive Discovery of Known and Novel Splice Junctions in RNA-Seq Data. PLoS ONE, 2010, 5, e13875.	1.1	50
1535	Multiplexed DNA Sequence Capture of Mitochondrial Genomes Using PCR Products. PLoS ONE, 2010, 5, e14004.	1.1	471
1536	Analyses of Copy Number Variation of GK Rat Reveal New Putative Type 2 Diabetes Susceptibility Loci. PLoS ONE, 2010, 5, e14077.	1.1	10
1537	Nme Gene Family Evolutionary History Reveals Pre-Metazoan Origins and High Conservation between Humans and the Sea Anemone, <i>Nematostella vectensis</i> . PLoS ONE, 2010, 5, e15506.	1.1	29
1538	Microarray probes and probe sets. <i>Frontiers in Bioscience - Elite</i> , 2010, E2, 325-338.	0.9	45
1539	Scaffolding a <i>Caenorhabditis</i> nematode genome with RNA-seq. <i>Genome Research</i> , 2010, 20, 1740-1747.	2.4	83
1540	Analysis of Human Small Nucleolar RNAs (snoRNA) and the Development of snoRNA Modulator of Gene Expression Vectors. <i>Molecular Biology of the Cell</i> , 2010, 21, 1569-1584.	0.9	40
1541	Mutation@A Glance: An Integrative Web Application for Analysing Mutations from Human Genetic Diseases. <i>DNA Research</i> , 2010, 17, 197-208.	1.5	26
1542	Classification of DNA sequences using Bloom filters. <i>Bioinformatics</i> , 2010, 26, 1595-1600.	1.8	57
1543	BAGEL2: mining for bacteriocins in genomic data. <i>Nucleic Acids Research</i> , 2010, 38, W647-W651.	6.5	144
1544	ChimerDB 2.0—a knowledgebase for fusion genes updated. <i>Nucleic Acids Research</i> , 2010, 38, D81-D85.	6.5	78
1545	Rapid identification of heterozygous mutations in <i>Drosophila melanogaster</i> using genomic capture sequencing. <i>Genome Research</i> , 2010, 20, 981-988.	2.4	30
1546	Genome-wide synteny through highly sensitive sequence alignment: <i>Satsuma</i> . <i>Bioinformatics</i> , 2010, 26, 1145-1151.	1.8	258
1547	Targeted next-generation sequencing of DNA regions proximal to a conserved GXGXXG signaling motif enables systematic discovery of tyrosine kinase fusions in cancer. <i>Nucleic Acids Research</i> , 2010, 38, 6985-6996.	6.5	39
1548	Evidence for bacterial origin of heat shock RNA-1. <i>Rna</i> , 2010, 16, 274-279.	1.6	14
1549	Fine-mapping and mutation analysis of TRPM1: a candidate gene for leopard complex (LP) spotting and congenital stationary night blindness in horses. <i>Briefings in Functional Genomics</i> , 2010, 9, 193-207.	1.3	49
1550	Cost-Effective Sequencing of Full-Length cDNA Clones Powered by a De Novo-Reference Hybrid Assembly. PLoS ONE, 2010, 5, e10517.	1.1	11
1551	SFmap: a web server for motif analysis and prediction of splicing factor binding sites. <i>Nucleic Acids Research</i> , 2010, 38, W281-W285.	6.5	89

#	ARTICLE	IF	CITATIONS
1552	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. <i>Bioinformatics</i> , 2010, 26, 2076-2084.	1.8	7
1553	Genome-wide mapping and assembly of structural variant breakpoints in the mouse genome. <i>Genome Research</i> , 2010, 20, 623-635.	2.4	257
1554	DARNED: a DAtabase of RNA EDiting in humans. <i>Bioinformatics</i> , 2010, 26, 1772-1776.	1.8	225
1555	PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 623-634.	2.5	72
1556	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, e17-e17.	6.5	200
1557	A network of conserved co-occurring motifs for the regulation of alternative splicing. <i>Nucleic Acids Research</i> , 2010, 38, 7916-7926.	6.5	12
1558	Characterization of C1q in Teleosts. <i>Journal of Biological Chemistry</i> , 2010, 285, 28777-28786.	1.6	45
1559	Genome of <i>Helicobacter pylori</i> Strain 908. <i>Journal of Bacteriology</i> , 2010, 192, 6488-6489.	1.0	25
1560	FragGeneScan: predicting genes in short and error-prone reads. <i>Nucleic Acids Research</i> , 2010, 38, e191-e191.	6.5	760
1561	Unconstrained mining of transcript data reveals increased alternative splicing complexity in the human transcriptome. <i>Nucleic Acids Research</i> , 2010, 38, 4740-4754.	6.5	55
1562	Metagenomics: seeking for the human gut microbial communities. <i>Reviews in Medical Microbiology</i> , 2010, 21, 51-55.	0.4	1
1563	Challenges of sequencing human genomes. <i>Briefings in Bioinformatics</i> , 2010, 11, 484-498.	3.2	134
1564	Detection, Validation, and Downstream Analysis of Allelic Variation in Gene Expression. <i>Genetics</i> , 2010, 184, 119-128.	1.2	60
1565	Population dynamics of PIWI-interacting RNAs (piRNAs) and their targets in <i>Drosophila</i> . <i>Genome Research</i> , 2010, 20, 212-227.	2.4	89
1566	Allele-specific methylation is prevalent and is contributed by CpG-SNPs in the human genome. <i>Genome Research</i> , 2010, 20, 883-889.	2.4	343
1567	Provirus Selected for High and Stable Expression of Transduced Genes Accumulate in Broadly Transcribed Genome Areas. <i>Journal of Virology</i> , 2010, 84, 4204-4211.	1.5	15
1568	Degeneration of an Intracellular Ion Channel in the Primate Lineage by Relaxation of Selective Constraints. <i>Molecular Biology and Evolution</i> , 2010, 27, 2352-2359.	3.5	56
1569	The UCSC Genome Browser database: update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D613-D619.	6.5	537

#	ARTICLE	IF	CITATIONS
1570	Dynamic Proteomics: a database for dynamics and localizations of endogenous fluorescently-tagged proteins in living human cells. <i>Nucleic Acids Research</i> , 2010, 38, D508-D512.	6.5	28
1571	Chromosomal position effects on AAV-mediated gene targeting. <i>Nucleic Acids Research</i> , 2010, 38, 3582-3594.	6.5	14
1572	Efficient k-nearest neighbor searching in nonordered discrete data spaces. <i>ACM Transactions on Information Systems</i> , 2010, 28, 1-33.	3.8	7
1573	Detection of human interchromosomal trans-splicing in sequence databanks. <i>Briefings in Bioinformatics</i> , 2010, 11, 198-209.	3.2	33
1574	Molecular Genetic Analysis of <i>Chd3</i> and Polycomb Chromosome Region 76B-D in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2010, 185, 811-822.	1.2	11
1575	High-throughput sequence analysis of <i>Ciona intestinalis</i> SL trans-spliced mRNAs: Alternative expression modes and gene function correlates. <i>Genome Research</i> , 2010, 20, 636-645.	2.4	40
1576	MicroRNA Gene Evolution in <i>Arabidopsis lyrata</i> and <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2010, 22, 1074-1089.	3.1	234
1577	Different Phylogenomic Approaches to Resolve the Evolutionary Relationships among Model Fish Species. <i>Molecular Biology and Evolution</i> , 2010, 27, 2757-2774.	3.5	18
1578	Genome Analysis of <i>Moraxella catarrhalis</i> Strain RH4, a Human Respiratory Tract Pathogen. <i>Journal of Bacteriology</i> , 2010, 192, 3574-3583.	1.0	78
1579	A generalized sequence pattern matching algorithm using complementary dual-seeding. , 2010, , .		1
1580	pFANGS: Parallel high speed sequence mapping for Next Generation 454-roche Sequencing reads. , 2010, , .		3
1581	Time-frequency based biological sequence querying. , 2010, , .		4
1582	BeetleBase in 2010: revisions to provide comprehensive genomic information for <i>Tribolium castaneum</i> . <i>Nucleic Acids Research</i> , 2010, 38, D437-D442.	6.5	138
1583	GPU-RMAP: Accelerating Short-Read Mapping on Graphics Processors. , 2010, , .		19
1584	Reinforcement Learning Method for BioAgents. , 2010, , .		4
1585	Error Tolerant Indexing and Alignment of Short Reads with Covering Template Families. <i>Journal of Computational Biology</i> , 2010, 17, 1397-1411.	0.8	23
1586	Network of Cancer Genes: a web resource to analyze duplicability, orthology and network properties of cancer genes. <i>Nucleic Acids Research</i> , 2010, 38, D670-D675.	6.5	28
1587	PanCGHweb: a web tool for genotype calling in pangenome CGH data. <i>Bioinformatics</i> , 2010, 26, 1256-1257.	1.8	20

#	ARTICLE	IF	CITATIONS
1589	Conserved long noncoding RNAs transcriptionally regulated by Oct4 and Nanog modulate pluripotency in mouse embryonic stem cells. <i>Rna</i> , 2010, 16, 324-337.	1.6	306
1590	MicroRNA Regulation of IFN- $\beta$ Protein Expression: Rapid and Sensitive Modulation of the Innate Immune Response. <i>Journal of Immunology</i> , 2010, 184, 2369-2376.	0.4	167
1591	Transcriptomic Analyses of Xylan Degradation by <i>Prevotella bryantii</i> and Insights into Energy Acquisition by Xylanolytic Bacteroidetes. <i>Journal of Biological Chemistry</i> , 2010, 285, 30261-30273.	1.6	114
1592	Isolation of SPINK6 in Human Skin. <i>Journal of Biological Chemistry</i> , 2010, 285, 32174-32181.	1.6	75
1593	Targets of the Tal1 Transcription Factor in Erythrocytes. <i>Journal of Biological Chemistry</i> , 2010, 285, 5338-5346.	1.6	16
1594	Discovery and Characterization of Mammalian Endogenous Parvoviruses. <i>Journal of Virology</i> , 2010, 84, 12628-12635.	1.5	68
1595	PLANdbAffy: probe-level annotation database for Affymetrix expression microarrays. <i>Nucleic Acids Research</i> , 2010, 38, D726-D730.	6.5	25
1596	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	2.4	239
1597	MouseIndelDB: a database integrating genomic indel polymorphisms that distinguish mouse strains. <i>Nucleic Acids Research</i> , 2010, 38, D600-D606.	6.5	19
1598	The Role of Nucleosome Positioning in the Evolution of Gene Regulation. <i>PLoS Biology</i> , 2010, 8, e1000414.	2.6	202
1599	The Parental Non-Equivalence of Imprinting Control Regions during Mammalian Development and Evolution. <i>PLoS Genetics</i> , 2010, 6, e1001214.	1.5	61
1600	Human and Non-Human Primate Genomes Share Hotspots of Positive Selection. <i>PLoS Genetics</i> , 2010, 6, e1000840.	1.5	58
1601	r2cat: synteny plots and comparative assembly. <i>Bioinformatics</i> , 2010, 26, 570-571.	1.8	134
1602	Genome-Wide Interrogation of Mammalian Stem Cell Fate Determinants by Nested Chromosome Deletions. <i>PLoS Genetics</i> , 2010, 6, e1001241.	1.5	5
1603	Six RNA Viruses and Forty-One Hosts: Viral Small RNAs and Modulation of Small RNA Repertoires in Vertebrate and Invertebrate Systems. <i>PLoS Pathogens</i> , 2010, 6, e1000764.	2.1	234
1604	Smed454 dataset: unravelling the transcriptome of <i>Schmidtea mediterranea</i> . <i>BMC Genomics</i> , 2010, 11, 731.	1.2	48
1605	Genome-wide analysis of mRNA abundance in two life-cycle stages of <i>Trypanosoma brucei</i> and identification of splicing and polyadenylation sites. <i>Nucleic Acids Research</i> , 2010, 38, 4946-4957.	6.5	276
1606	Integration Preferences of Wildtype AAV-2 for Consensus Rep-Binding Sites at Numerous Loci in the Human Genome. <i>PLoS Pathogens</i> , 2010, 6, e1000985.	2.1	72

#	ARTICLE	IF	CITATIONS
1607	The Evolutionary Analysis of Emerging Low Frequency HIV-1 CXCR4 Using Variants through Time—An Ultra-Deep Approach. <i>PLoS Computational Biology</i> , 2010, 6, e1001022.	1.5	72
1608	Deletion of CREB1 from the Dorsal Telencephalon Reduces Motivational Properties of Cocaine. <i>Cerebral Cortex</i> , 2010, 20, 941-952.	1.6	24
1609	Evolution of an X-Linked Primate-Specific Micro RNA Cluster. <i>Molecular Biology and Evolution</i> , 2010, 27, 671-683.	3.5	64
1610	GenomeRNAi: a database for cell-based RNAi phenotypes. 2009 update. <i>Nucleic Acids Research</i> , 2010, 38, D448-D452.	6.5	37
1611	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	2.4	84
1612	E-RNAi: a web application for the multi-species design of RNAi reagents—2010 update. <i>Nucleic Acids Research</i> , 2010, 38, W332-W339.	6.5	136
1613	KRAB—Zinc Finger Proteins and KAP1 Can Mediate Long-Range Transcriptional Repression through Heterochromatin Spreading. <i>PLoS Genetics</i> , 2010, 6, e1000869.	1.5	309
1614	inGAP: an integrated next-generation genome analysis pipeline. <i>Bioinformatics</i> , 2010, 26, 127-129.	1.8	58
1615	Semi-Automated Library Preparation for High-Throughput DNA Sequencing Platforms. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-8.	3.0	31
1616	Targeted deep resequencing of the human cancer genome using next-generation technologies. <i>Biotechnology and Genetic Engineering Reviews</i> , 2010, 27, 135-158.	2.4	11
1617	FANGS. , 2010, , .		4
1618	REAL. , 2010, , .		24
1619	EuG—ne-maize: a web site for maize gene prediction. <i>Bioinformatics</i> , 2010, 26, 1254-1255.	1.8	1
1620	RNA-Seq Analysis of Sulfur-Deprived <i>Chlamydomonas</i> Cells Reveals Aspects of Acclimation Critical for Cell Survival. <i>Plant Cell</i> , 2010, 22, 2058-2084.	3.1	253
1621	mRNA deep sequencing reveals 75 new genes and a complex transcriptional landscape in Mimivirus. <i>Genome Research</i> , 2010, 20, 664-674.	2.4	160
1622	Gene Family Size Conservation Is a Good Indicator of Evolutionary Rates. <i>Molecular Biology and Evolution</i> , 2010, 27, 1750-1758.	3.5	31
1623	An annotatedk-deep prefix tree for (1-k)-mer based sequence comparisons. , 2010, , .		0
1624	Natural selection on <i>cis</i> and <i>trans</i> regulation in yeasts. <i>Genome Research</i> , 2010, 20, 826-836.	2.4	156

#	ARTICLE	IF	CITATIONS
1625	A SNP discovery method to assess variant allele probability from next-generation resequencing data. <i>Genome Research</i> , 2010, 20, 273-280.	2.4	168
1626	The FLIGHT <i>Drosophila</i> RNAi database. <i>Fly</i> , 2010, 4, 344-348.	0.9	4
1627	miRBase: microRNA Sequences and Annotation. <i>Current Protocols in Bioinformatics</i> , 2010, 29, Unit 12.9.1-10.	25.8	171
1628	RNA-Seq: A Method for Comprehensive Transcriptome Analysis. <i>Current Protocols in Molecular Biology</i> , 2010, 89, Unit 4.11.1-13.	2.9	218
1629	Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. <i>Standards in Genomic Sciences</i> , 2010, 2, 117-134.	1.5	1,442
1630	Marsupial Sequencing Projects and Bioinformatics Challenges. , 2010, , 121-132.		1
1631	An Integrated Physical, Genetic and Cytogenetic Map of <i>Brachypodium distachyon</i> , a Model System for Grass Research. <i>PLoS ONE</i> , 2010, 5, e13461.	1.1	45
1632	Exploring Zebrafish Genomic, Functional and Phenotypic Data Using ZFIN. <i>Current Protocols in Bioinformatics</i> , 2010, 31, Unit 1.18.	25.8	5
1633	Identification and analysis of unitary pseudogenes: historic and contemporary gene losses in humans and other primates. <i>Genome Biology</i> , 2010, 11, R26.	13.9	150
1634	Epigenetic Databases and Computational Methodologies in the Analysis of Epigenetic Datasets. <i>Advances in Genetics</i> , 2010, 71, 259-295.	0.8	4
1635	Gilthead sea bream ( <i>Sparus auratus</i> ) and European sea bass ( <i>Dicentrarchus labrax</i> ) expressed sequence tags: Characterization, tissue-specific expression and gene markers. <i>Marine Genomics</i> , 2010, 3, 179-191.	0.4	25
1636	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. <i>Genome Biology</i> , 2010, 11, R104.	3.8	137
1637	Prevalence of alternative splicing choices in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2010, 10, 102.	1.6	34
1638	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010, 7, 111.	0.9	141
1639	Replacement of Rbpj With Rbpjl in the PTF1 Complex Controls the Final Maturation of Pancreatic Acinar Cells. <i>Gastroenterology</i> , 2010, 139, 270-280.	0.6	85
1640	A Restriction Enzyme-PCR-Based Technique to Determine Transgene Insertion Sites. <i>Methods in Molecular Biology</i> , 2010, 597, 287-299.	0.4	12
1641	DNA barcoding: a six-question tour to improve users' awareness about the method. <i>Briefings in Bioinformatics</i> , 2010, 11, 440-453.	3.2	129
1642	A Hybrid, <i>de Novo</i> Based, Genome-Wide Database Search Approach Applied to the Sea Urchin Neuropeptidome. <i>Journal of Proteome Research</i> , 2010, 9, 990-996.	1.8	37

#	ARTICLE	IF	CITATIONS
1643	Insights from the Comparison of Plant Genome Sequences. <i>Annual Review of Plant Biology</i> , 2010, 61, 349-372.	8.6	202
1644	Ensembl Genome Browser. , 2010, , 923-939.		31
1645	Distinct Phases of siRNA Synthesis in an Endogenous RNAi Pathway in <i>C. elegans</i> Soma. <i>Molecular Cell</i> , 2010, 37, 679-689.	4.5	177
1646	A novel single cDNA amplicon pyrosequencing method for high-throughput, cost-effective sequence-based HLA class I genotyping. <i>Human Immunology</i> , 2010, 71, 1011-1017.	1.2	50
1647	Magnesium sulfate treatment alters fetal cerebellar gene expression responses to hypoxia. <i>International Journal of Developmental Neuroscience</i> , 2010, 28, 207-216.	0.7	6
1648	Alternative promoter usage and alternative splicing of the rat estrogen receptor $\beta$ gene generate numerous mRNA variants with distinct 5' ends. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2010, 118, 59-69.	1.2	30
1649	tsORFdb: Theoretical Small Open Reading Frames (ORFs) database and massProphet: Peptide Mass Fingerprinting (PMF) tool for unknown small functional ORFs. <i>Biochemical and Biophysical Research Communications</i> , 2010, 397, 120-126.	1.0	6
1650	The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. <i>Cell</i> , 2010, 140, 631-642.	13.5	399
1651	LINE-1 Retrotransposition Activity in Human Genomes. <i>Cell</i> , 2010, 141, 1159-1170.	13.5	531
1652	Efficient discovery of ASCL1 regulatory sequences through transgene pooling. <i>Genomics</i> , 2010, 95, 363-369.	1.3	3
1653	A radiation hybrid map of the European sea bass ( <i>Dicentrarchus labrax</i> ) based on 1581 markers: Synteny analysis with model fish genomes. <i>Genomics</i> , 2010, 96, 228-238.	1.3	32
1654	Genomic SELEX: A discovery tool for genomic aptamers. <i>Methods</i> , 2010, 52, 125-132.	1.9	55
1655	MetaBioME: a database to explore commercially useful enzymes in metagenomic datasets. <i>Nucleic Acids Research</i> , 2010, 38, D468-D472.	6.5	66
1656	What can next generation sequencing do for you? Next generation sequencing as a valuable tool in plant research. <i>Plant Biology</i> , 2010, 12, 831-841.	1.8	140
1657	Runx2 regulates survivin expression in prostate cancer cells. <i>Laboratory Investigation</i> , 2010, 90, 222-233.	1.7	72
1658	Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. <i>Nature</i> , 2010, 466, 612-616.	13.7	210
1659	A survey of sequence alignment algorithms for next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 473-483.	3.2	765
1660	Fast and SNP-tolerant detection of complex variants and splicing in short reads. <i>Bioinformatics</i> , 2010, 26, 873-881.	1.8	1,774

#	ARTICLE	IF	CITATIONS
1661	Databases and Genome Browsers. , 2010, , 905-921.		0
1662	Cell-type specific analysis of translating RNAs in developing flowers reveals new levels of control. <i>Molecular Systems Biology</i> , 2010, 6, 419.	3.2	155
1663	Computational Gene Prediction in Eukaryotic Genomes. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , 291-306.	0.3	0
1664	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 181-197.	3.2	141
1665	Characterization of microRNAs encoded by the bovine herpesvirus 1 genome. <i>Journal of General Virology</i> , 2010, 91, 32-41.	1.3	44
1666	Computational Methods for Ab Initio and Comparative Gene Finding. <i>Methods in Molecular Biology</i> , 2010, 609, 269-284.	0.4	45
1667	Bioinformatics for Next Generation Sequencing Data. <i>Genes</i> , 2010, 1, 294-307.	1.0	65
1668	Sequencing and Genome Assembly Using Next-Generation Technologies. <i>Methods in Molecular Biology</i> , 2010, 673, 1-17.	0.4	47
1669	Genetic diversity in India and the inference of Eurasian population expansion. <i>Genome Biology</i> , 2010, 11, R113.	3.8	60
1670	Design and evaluation of genome-wide libraries for RNA interference screens. <i>Genome Biology</i> , 2010, 11, R61.	13.9	69
1671	Towards a comprehensive structural variation map of an individual human genome. <i>Genome Biology</i> , 2010, 11, R52.	13.9	261
1672	Genomic and small RNA sequencing of <i>Miscanthus Ã— giganteus</i> shows the utility of sorghum as a reference genome sequence for Andropogoneae grasses. <i>Genome Biology</i> , 2010, 11, R12.	13.9	93
1673	SL RNA Genes of the Ascidian Tunicates <i>Ciona intestinalis</i> and <i>Ciona savignyi</i> . <i>Zoological Science</i> , 2010, 27, 171-180.	0.3	7
1674	Fast and accurate long-read alignment with Burrows-Wheeler transform. <i>Bioinformatics</i> , 2010, 26, 589-595.	1.8	10,002
1675	Whole-genome sequencing and intensive analysis of the undomesticated soybean ( <i>Glycine soja</i> ) in America, 2010, 107, 22032-22037.	3.3	299
1676	Development of a DNA Microarray to Detect Antimicrobial Resistance Genes Identified in the National Center for Biotechnology Information Database. <i>Microbial Drug Resistance</i> , 2010, 16, 9-19.	0.9	55
1677	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010, 38, D211-D222.	6.5	2,693
1678	Integrative Deep Sequencing of the Mouse Lung Transcriptome Reveals Differential Expression of Diverse Classes of Small RNAs in Response to Respiratory Virus Infection. <i>MBio</i> , 2011, 2, .	1.8	86

#	ARTICLE	IF	CITATIONS
1679	Sequencing and disease variation detection tools and techniques. , 2011, , .		1
1680	The human gut virome: Inter-individual variation and dynamic response to diet. <i>Genome Research</i> , 2011, 21, 1616-1625.	2.4	825
1681	Evolution of C4 Photosynthesis in the Genus <i>Flaveria</i> : How Many and Which Genes Does It Take to Make C4?. <i>Plant Cell</i> , 2011, 23, 2087-2105.	3.1	185
1682	Rigid region pairwise sequence alignment. , 2011, , .		2
1683	Analysis of Transcriptome Complexity Through RNA Sequencing in Normal and Failing Murine Hearts. <i>Circulation Research</i> , 2011, 109, 1332-1341.	2.0	194
1684	CUDA-BLASTP: Accelerating BLASTP on CUDA-Enabled Graphics Hardware. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1678-1684.	1.9	69
1685	Comparative analysis of RNA-Seq alignment algorithms and the RNA-Seq unified mapper (RUM). <i>Bioinformatics</i> , 2011, 27, 2518-2528.	1.8	298
1686	GnomCmp: a quantitative approach for comparative analysis of closely related genomes of bacterial pathogens. <i>Genome</i> , 2011, 54, 402-418.	0.9	1
1687	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011, 12, R10.	3.8	754
1688	Evaluation of normalization methods for RNA-Seq gene expression estimation. , 2011, 2011, 50-57.		4
1689	Langerhans cell histiocytosis in a pediatric patient with thrombocytopenia-absent radius syndrome and 1q21.1 deletion: case report and proposal of a rapid molecular diagnosis of 1q21.1 deletion. <i>Immunopharmacology and Immunotoxicology</i> , 2011, 33, 754-758.	1.1	9
1690	Alternative Splicing in the Fly and the Worm: Splicing Databases for <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> . , 2011, , .		0
1691	Sequence Analysis of the Genome of an Oil-Bearing Tree, <i>Jatropha curcas</i> L.. <i>DNA Research</i> , 2011, 18, 65-76.	1.5	294
1692	The Galaxy Track Browser: Transforming the genome browser from visualization tool to analysis tool. , 2011, , .		1
1693	Polycomb preferentially targets stalled promoters of coding and noncoding transcripts. <i>Genome Research</i> , 2011, 21, 216-226.	2.4	146
1694	Three Periods of Regulatory Innovation During Vertebrate Evolution. <i>Science</i> , 2011, 333, 1019-1024.	6.0	127
1695	<i>Drosophila</i> Duplication Hotspots Are Associated with Late-Replicating Regions of the Genome. <i>PLoS Genetics</i> , 2011, 7, e1002340.	1.5	31
1696	Capturing cold-stress-related sequence diversity from a wild relative of common bean ( <i>Phaseolus</i> ) Tj ETQq1 1 0.784314 rgBT 5/Overloc	0.9	5

#	ARTICLE	IF	CITATIONS
1697	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. <i>Nature Biotechnology</i> , 2011, 29, 723-730.	9.4	113
1699	Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. <i>Nature Genetics</i> , 2011, 43, 956-963.	9.4	910
1700	Discovery of lost diversity of paternal horse lineages using ancient DNA. <i>Nature Communications</i> , 2011, 2, 450.	5.8	72
1701	Mesozoic retroposons reveal parrots as the closest living relatives of passerine birds. <i>Nature Communications</i> , 2011, 2, 443.	5.8	175
1702	Genome wide SNP discovery, analysis and evaluation in mallard ( <i>Anas platyrhynchos</i> ). <i>BMC Genomics</i> , 2011, 12, 150.	1.2	63
1703	Comparative analysis of the ATRX promoter and 5' regulatory region reveals conserved regulatory elements which are linked to roles in neurodevelopment, alpha-globin regulation and testicular function. <i>BMC Research Notes</i> , 2011, 4, 200.	0.6	6
1704	The complexity of <i>Rhipicephalus (Boophilus) microplus</i> genome characterised through detailed analysis of two BAC clones. <i>BMC Research Notes</i> , 2011, 4, 254.	0.6	6
1705	Cross-species protein sequence and gene structure prediction with fine-tuned Webscipio 2.0 and Scipio. <i>BMC Research Notes</i> , 2011, 4, 265.	0.6	38
1706	Integrating fragmented software applications into holistic solutions: focus on drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2011, 6, 383-392.	2.5	1
1707	Next generation sequencing has lower sequence coverage and poorer SNP-detection capability in the regulatory regions. <i>Scientific Reports</i> , 2011, 1, 55.	1.6	67
1708	Transcriptome Sequencing Demonstrates that Human Papillomavirus Is Not Active in Cutaneous Squamous Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2011, 131, 1745-1753.	0.3	127
1709	Probabilistic Analysis of Probe Reliability in Differential Gene Expression Studies with Short Oligonucleotide Arrays. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 217-225.	1.9	29
1710	Post-transcriptional exon shuffling events in humans can be evolutionarily conserved and abundant. <i>Genome Research</i> , 2011, 21, 1788-1799.	2.4	56
1711	Waveform Mapping and Time-Frequency Processing of DNA and Protein Sequences. <i>IEEE Transactions on Signal Processing</i> , 2011, 59, 4210-4224.	3.2	7
1712	Plant Reverse Genetics. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	7
1713	CREST maps somatic structural variation in cancer genomes with base-pair resolution. <i>Nature Methods</i> , 2011, 8, 652-654.	9.0	451
1714	Mapping of BLASTP Algorithm onto GPU Clusters. , 2011, , .		10
1715	The draft genome of the carcinogenic human liver fluke <i>Clonorchis sinensis</i> . <i>Genome Biology</i> , 2011, 12, R107.	13.9	183

#	ARTICLE	IF	CITATIONS
1716	The draft genome and transcriptome of <i>Cannabis sativa</i> . <i>Genome Biology</i> , 2011, 12, R102.	13.9	479
1717	TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. <i>Genome Biology</i> , 2011, 12, R72.	13.9	670
1718	The head-regeneration transcriptome of the planarian <i>Schmidtea mediterranea</i> . <i>Genome Biology</i> , 2011, 12, R76.	13.9	109
1719	Refinement of primate copy number variation hotspots identifies candidate genomic regions evolving under positive selection. <i>Genome Biology</i> , 2011, 12, R52.	3.8	58
1720	A vertebrate case study of the quality of assemblies derived from next-generation sequences. <i>Genome Biology</i> , 2011, 12, R31.	13.9	32
1721	Genome sequence of the stramenopile <i>Blastocystis</i> , a human anaerobic parasite. <i>Genome Biology</i> , 2011, 12, R29.	13.9	159
1722	A cost-effective and universal strategy for complete prokaryotic genome sequencing proposed by computer simulation. <i>Genome Biology</i> , 2011, 12, .	13.9	1
1723	Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi. <i>Genome Biology</i> , 2011, 12, R7.	13.9	181
1724	Identification and characterisation of the BPI/LBP/PLUNC-like gene repertoire in chickens reveals the absence of a LBP gene. <i>Developmental and Comparative Immunology</i> , 2011, 35, 285-295.	1.0	28
1725	Bioinformatics challenges for personalized medicine. <i>Bioinformatics</i> , 2011, 27, 1741-1748.	1.8	223
1726	Development and characterization of two mini-X chromosomal short tandem repeat multiplexes. <i>Forensic Science International: Genetics</i> , 2011, 5, 415-421.	1.6	29
1727	Dating Primate Divergences through an Integrated Analysis of Palaeontological and Molecular Data. <i>Systematic Biology</i> , 2011, 60, 16-31.	2.7	195
1728	Activation-Induced Cytidine Deaminase Induces Reproducible DNA Breaks at Many Non-Ig Loci in Activated B Cells. <i>Molecular Cell</i> , 2011, 41, 232-242.	4.5	77
1729	Identification of novel splicing events and post-transcriptional regulation of human estrogen receptor $\beta$ isoforms. <i>Molecular and Cellular Endocrinology</i> , 2011, 333, 55-61.	1.6	24
1730	Identification of C-terminally and N-terminally truncated estrogen receptor $\beta$ variants in the mouse. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2011, 124, 38-46.	1.2	14
1731	Complex organization of the 5'-untranslated region of the mouse estrogen receptor $\beta$ gene: Identification of numerous mRNA transcripts with distinct 5'-ends. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2011, 125, 211-218.	1.2	18
1732	Mapping in vivo protein-RNA interactions at single-nucleotide resolution from HITS-CLIP data. <i>Nature Biotechnology</i> , 2011, 29, 607-614.	9.4	384
1733	Sequence overlap between autosomal and sex-linked probes on the Illumina HumanMethylation27 microarray. <i>Genomics</i> , 2011, 97, 214-222.	1.3	67

#	ARTICLE	IF	CITATIONS
1734	Identification and analysis of novel microRNAs from fragile sites of human cervical cancer: Computational and experimental approach. <i>Genomics</i> , 2011, 97, 333-340.	1.3	20
1735	Computational Analysis of Drought Stress-Associated miRNAs and miRNA Co-Regulation Network in <i>Physcomitrella patens</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 37-44.	3.0	26
1736	Identification of Alternatively Spliced Transcripts Using a Proteomic Informatics Approach. <i>Methods in Molecular Biology</i> , 2011, 696, 319-326.	0.4	14
1737	Omics, Bioinformatics, and Infectious Disease Research. , 2011, , 523-539.		1
1738	An unbiased genome-wide analysis of zinc-finger nuclease specificity. <i>Nature Biotechnology</i> , 2011, 29, 816-823.	9.4	488
1739	Weak seed-pairing stability and high target-site abundance decrease the proficiency of lsy-6 and other microRNAs. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1139-1146.	3.6	803
1740	Museum genomics: low-cost and high-accuracy genetic data from historical specimens. <i>Molecular Ecology Resources</i> , 2011, 11, 1082-1092.	2.2	122
1741	An Introduction to the Informatics of "Next-Generation" Sequencing. <i>Current Protocols in Bioinformatics</i> , 2011, 36, Unit 11.1..	25.8	12
1742	Designing, Performing, and Interpreting a Microarray-Based Gene Expression Study. <i>Methods in Molecular Biology</i> , 2011, 793, 417-439.	0.4	22
1743	Deep Sequencing of the Human TCR $\beta$ and TCR $\alpha$ Repertoires Suggests that TCR $\alpha$ Rearranges After $\beta$ T Cell Commitment. <i>Science Translational Medicine</i> , 2011, 3, 90ra61.	5.8	132
1744	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	9.4	428
1745	Using Bacterial Artificial Chromosomes to Refine Genome Assemblies and to Build Virtual Genomes. , 0, , .		0
1746	Predicting Tandemly Arrayed Gene Duplicates with WebScipio. , 0, , .		2
1747	Gene Expression Analysis Using RNA-Seq from Organisms Lacking Substantial Genomic Resources. , 2011, , .		0
1748	Phosphorylation network rewiring by gene duplication. <i>Molecular Systems Biology</i> , 2011, 7, 504.	3.2	32
1749	Adaptation of the AFLP technique as a new tool to detect genetic instability and transposition in interspecific hybrids. <i>BioTechniques</i> , 2011, 50, 247-250.	0.8	12
1750	Identification of Disease-Causing Mutations in Autosomal Dominant Retinitis Pigmentosa (adRP) Using Next-Generation DNA Sequencing. , 2011, 52, 494.		80
1751	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	1.7	396

#	ARTICLE	IF	CITATIONS
1752	Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont <i>Piriformospora indica</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002290.	2.1	361
1753	Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two <i>Bos Taurus</i> Assemblies. <i>PLoS ONE</i> , 2011, 6, e21400.	1.1	65
1754	Phylogenetic Comparison of F-Box (FBX) Gene Superfamily within the Plant Kingdom Reveals Divergent Evolutionary Histories Indicative of Genomic Drift. <i>PLoS ONE</i> , 2011, 6, e16219.	1.1	116
1755	Considering Transposable Element Diversification in De Novo Annotation Approaches. <i>PLoS ONE</i> , 2011, 6, e16526.	1.1	477
1756	Quantitative Trait Loci Involved in Sex Determination and Body Growth in the Gilthead Sea Bream ( <i>Sparus aurata</i> L.) through Targeted Genome Scan. <i>PLoS ONE</i> , 2011, 6, e16599.	1.1	70
1757	Genome-Wide Linkage Analysis of Global Gene Expression in Loin Muscle Tissue Identifies Candidate Genes in Pigs. <i>PLoS ONE</i> , 2011, 6, e16766.	1.1	45
1758	Fast Identification and Removal of Sequence Contamination from Genomic and Metagenomic Datasets. <i>PLoS ONE</i> , 2011, 6, e17288.	1.1	630
1759	CORE: A Phylogenetically-Curated 16S rDNA Database of the Core Oral Microbiome. <i>PLoS ONE</i> , 2011, 6, e19051.	1.1	154
1760	The First Sequenced Carnivore Genome Shows Complex Host-Endogenous Retrovirus Relationships. <i>PLoS ONE</i> , 2011, 6, e19832.	1.1	32
1761	Towards the Human Colorectal Cancer Microbiome. <i>PLoS ONE</i> , 2011, 6, e20447.	1.1	470
1762	Nuclear Outsourcing of RNA Interference Components to Human Mitochondria. <i>PLoS ONE</i> , 2011, 6, e20746.	1.1	249
1763	Poly (A)+ Transcriptome Assessment of ERBB2-Induced Alterations in Breast Cell Lines. <i>PLoS ONE</i> , 2011, 6, e21022.	1.1	17
1764	Microbial Diversity in the Midguts of Field and Lab-Reared Populations of the European Corn Borer <i>Ostrinia nubilalis</i> . <i>PLoS ONE</i> , 2011, 6, e21751.	1.1	71
1765	The Fat Body Transcriptomes of the Yellow Fever Mosquito <i>Aedes aegypti</i> , Pre- and Post- Blood Meal. <i>PLoS ONE</i> , 2011, 6, e22573.	1.1	77
1766	Addressing Inter-Gene Heterogeneity in Maximum Likelihood Phylogenomic Analysis: Yeasts Revisited. <i>PLoS ONE</i> , 2011, 6, e22783.	1.1	24
1767	Protein-Binding Microarray Analysis of Tumor Suppressor AP2 Target Gene Specificity. <i>PLoS ONE</i> , 2011, 6, e22895.	1.1	5
1768	Very Few RNA and DNA Sequence Differences in the Human Transcriptome. <i>PLoS ONE</i> , 2011, 6, e25842.	1.1	69
1769	Regional Selection Acting on the OFD1 Gene Family. <i>PLoS ONE</i> , 2011, 6, e26195.	1.1	9

#	ARTICLE	IF	CITATIONS
1770	Neuroglobin-Deficiency Exacerbates Hif1A and c-FOS Response, but Does Not Affect Neuronal Survival during Severe Hypoxia In Vivo. PLoS ONE, 2011, 6, e28160.	1.1	45
1771	Genome-Wide Signatures of "Rearrangement Hotspots"™ within Segmental Duplications in Humans. PLoS ONE, 2011, 6, e28853.	1.1	14
1772	A genomic approach to investigate expression profiles in Slovenian patients with gastric cancer. Oncology Letters, 2011, 2, 1003-1014.	0.8	7
1773	Evolution of Synonymous Codon Usage in Neurospora tetrasperma and Neurospora discreta. Genome Biology and Evolution, 2011, 3, 332-343.	1.1	32
1774	Familial hemophagocytic lymphohistiocytosis type 3 (FHL3) caused by deep intronic mutation and inversion in UNC13D. Blood, 2011, 118, 5783-5793.	0.6	115
1775	Disease and Phenotype Data at Ensembl. Current Protocols in Human Genetics, 2011, 69, Unit 6.11.	3.5	3
1777	Identification of true EST alignments for recognising transcribed regions. International Journal of Data Mining and Bioinformatics, 2011, 5, 465.	0.1	2
1778	The UCSC Genome Browser. Current Protocols in Human Genetics, 2011, 71, Unit18.6.	3.5	38
1779	Getting a Full Dose? Reconsidering Sex Chromosome Dosage Compensation in the Silkworm, Bombyx mori. Genome Biology and Evolution, 2011, 3, 491-504.	1.1	53
1780	Characterization of a divergent chromosome region in the willow warbler Phylloscopus trochilus using avian genomic resources. Journal of Evolutionary Biology, 2011, 24, 1241-1253.	0.8	8
1781	Comparative deep transcriptional profiling of four developing oilseeds. Plant Journal, 2011, 68, 1014-1027.	2.8	241
1782	Characterization of a genomic divergence island between black and yellow and gopher <i>Sebastes</i> rockfishes. Molecular Ecology, 2011, 20, 2603-2618.	2.0	14
1783	Isolation and gene flow: inferring the speciation history of European house mice. Molecular Ecology, 2011, 20, 5248-5264.	2.0	99
1784	Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. Journal of Neurochemistry, 2011, 116, 459-466.	2.1	152
1785	Understanding the pathogenesis of Alzheimer's disease: will RNA-Seq realize the promise of transcriptomics?. Journal of Neurochemistry, 2011, 116, 937-946.	2.1	65
1786	Expression Profiling of Cassava Storage Roots Reveals an Active Process of Glycolysis/Gluconeogenesis <sup>F</sup> . Journal of Integrative Plant Biology, 2011, 53, 193-211.	4.1	89
1787	A CASE-BY-CASE EVOLUTIONARY ANALYSIS OF FOUR IMPRINTED RETROGENES. Evolution; International Journal of Organic Evolution, 2011, 65, 1413-1427.	1.1	26
1788	Soil-specific limitations for access and analysis of soil microbial communities by metagenomics. FEMS Microbiology Ecology, 2011, 78, 31-49.	1.3	185

#	ARTICLE	IF	CITATIONS
1789	The mega-matrix tree of life: using genome-scale horizontal gene transfer and sequence evolution data as information about the vertical history of life. <i>Cladistics</i> , 2011, 27, 417-427.	1.5	6
1790	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	9.4	814
1791	Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.	9.0	919
1792	Next-generation transcriptome assembly. <i>Nature Reviews Genetics</i> , 2011, 12, 671-682.	7.7	1,073
1793	De novo genome sequencing and comparative genomics of date palm ( <i>Phoenix dactylifera</i> ). <i>Nature Biotechnology</i> , 2011, 29, 521-527.	9.4	356
1794	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
1795	Identification of <i>Salmonella enterica</i> species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2151-2161.	1.0	10
1796	Gene expression in <i>Trypanosoma brucei</i> : lessons from high-throughput RNA sequencing. <i>Trends in Parasitology</i> , 2011, 27, 434-441.	1.5	71
1797	Effects of genome-wide copy number variation on expression in mammalian cells. <i>BMC Genomics</i> , 2011, 12, 562.	1.2	19
1798	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. <i>BMC Genomics</i> , 2011, 12, 590.	1.2	34
1799	Analysis of expression sequence tags from a full-length-enriched cDNA library of developing sesame seeds ( <i>Sesamum indicum</i> ). <i>BMC Plant Biology</i> , 2011, 11, 180.	1.6	25
1800	Spliceosomal intron size expansion in domesticated grapevine ( <i>Vitis vinifera</i> ). <i>BMC Research Notes</i> , 2011, 4, 52.	0.6	16
1801	The physiological, transcriptional and genetic responses of an ozone-sensitive and an ozone tolerant poplar and selected extremes of their F2 progeny. <i>Environmental Pollution</i> , 2011, 159, 45-54.	3.7	32
1802	Analysis of High-Throughput Sequencing Data. <i>Methods in Molecular Biology</i> , 2011, 678, 1-11.	0.4	6
1803	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533.	13.7	246
1804	Next-generation sequencing and its applications in molecular diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 333-343.	1.5	146
1805	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638.	9.4	567
1806	A Boundary Element Between <i>Tsix</i> and <i>Xist</i> Binds the Chromatin Insulator Ctfc and Contributes to Initiation of X-Chromosome Inactivation. <i>Genetics</i> , 2011, 189, 441-454.	1.2	41

#	ARTICLE	IF	CITATIONS
1807	Bioinformatic identification of novel protein phosphatases in the dog genome. <i>Molecular and Cellular Biochemistry</i> , 2011, 351, 149-156.	1.4	1
1808	Pseudogene: lessons from PCR bias, identification and resurrection. <i>Molecular Biology Reports</i> , 2011, 38, 3709-3715.	1.0	10
1809	A novel mitofusin 2 mutation causes canine fetal-onset neuroaxonal dystrophy. <i>Neurogenetics</i> , 2011, 12, 223-232.	0.7	24
1810	Functional Divergences of GAPDH Isoforms During Early Development in Two Perciform Fish Species. <i>Marine Biotechnology</i> , 2011, 13, 1115-1124.	1.1	11
1811	Ecological genetics of invasive alien species. <i>BioControl</i> , 2011, 56, 409-428.	0.9	244
1812	Fine genetic mapping localizes cucumber scab resistance gene Ccu into an R gene cluster. <i>Theoretical and Applied Genetics</i> , 2011, 122, 795-803.	1.8	43
1813	Gene Duplication and Divergence of Long Wavelength-Sensitive Opsin Genes in the Guppy, <i>Poecilia reticulata</i> . <i>Journal of Molecular Evolution</i> , 2011, 72, 240-252.	0.8	47
1814	Investigation of the Origin and Spread of a Mammalian Transposable Element Based on Current Sequence Diversity. <i>Journal of Molecular Evolution</i> , 2011, 73, 287-296.	0.8	4
1815	Reproductive tissue-specific expression profiling and genetic variation across a 19 gene bovine $\beta$ -defensin cluster. <i>Immunogenetics</i> , 2011, 63, 641-651.	1.2	33
1816	Finding Cancer-Associated miRNAs: Methods and Tools. <i>Molecular Biotechnology</i> , 2011, 49, 97-107.	1.3	7
1817	De novo transcriptome assembly of RNA-Seq reads with different strategies. <i>Science China Life Sciences</i> , 2011, 54, 1129-1133.	2.3	16
1818	Mitochondrial genome sequences illuminate maternal lineages of conservation concern in a rare carnivore. <i>BMC Ecology</i> , 2011, 11, 10.	3.0	66
1819	Identification, characterization, and comparative genomic distribution of the HERV-K (HML-2) group of human endogenous retroviruses. <i>Retrovirology</i> , 2011, 8, 90.	0.9	340
1820	Fast local fragment chaining using sum-of-pair gap costs. <i>Algorithms for Molecular Biology</i> , 2011, 6, 4.	0.3	15
1821	Enhancing genome assemblies by integrating non-sequence based data. <i>BMC Proceedings</i> , 2011, 5, S7.	1.8	5
1822	Identification of gene fusion transcripts by transcriptome sequencing in BRCA1-mutated breast cancers and cell lines. <i>BMC Medical Genomics</i> , 2011, 4, 75.	0.7	40
1823	Distinct influences of tandem repeats and retrotransposons on CENH3 nucleosome positioning. <i>Epigenetics and Chromatin</i> , 2011, 4, 3.	1.8	30
1824	Alu pair exclusions in the human genome. <i>Mobile DNA</i> , 2011, 2, 10.	1.3	15

#	ARTICLE	IF	CITATIONS
1825	RAPSearch: a fast protein similarity search tool for short reads. BMC Bioinformatics, 2011, 12, 159.	1.2	128
1826	Parallelized short read assembly of large genomes using de Bruijn graphs. BMC Bioinformatics, 2011, 12, 354.	1.2	64
1827	Support vector machines-based identification of alternative splicing in Arabidopsis thaliana from whole-genome tiling arrays. BMC Bioinformatics, 2011, 12, 55.	1.2	21
1828	Optimizing de novo transcriptome assembly from short-read RNA-Seq data: a comparative study. BMC Bioinformatics, 2011, 12, S2.	1.2	462
1829	ClipCrop: a tool for detecting structural variations with single-base resolution using soft-clipping information. BMC Bioinformatics, 2011, 12, S7.	1.2	41
1830	STELLAR: fast and exact local alignments. BMC Bioinformatics, 2011, 12, S15.	1.2	28
1831	Human teneurin-1 is a direct target of the homeobox transcription factor EMX2 at a novel alternate promoter. BMC Developmental Biology, 2011, 11, 35.	2.1	15
1832	The sequence, structure and evolutionary features of HOTAIR in mammals. BMC Evolutionary Biology, 2011, 11, 102.	3.2	118
1833	Rhythms and synchronization patterns in gene expression in the Aedes aegypti mosquito. BMC Genomics, 2011, 12, 153.	1.2	47
1834	Rice-Map: a new-generation rice genome browser. BMC Genomics, 2011, 12, 165.	1.2	10
1835	A high-resolution linkage map for comparative genome analysis and QTL fine mapping in Asian seabass, Lates calcarifer. BMC Genomics, 2011, 12, 174.	1.2	93
1836	Building a model: developing genomic resources for common milkweed (Asclepias syriaca) with low coverage genome sequencing. BMC Genomics, 2011, 12, 211.	1.2	104
1837	A systematic evaluation of expression of HERV-W elements; influence of genomic context, viral structure and orientation. BMC Genomics, 2011, 12, 22.	1.2	21
1838	Comprehensive assessment of sequence variation within the copy number variable defensin cluster on 8p23 by target enriched in-depth 454 sequencing. BMC Genomics, 2011, 12, 243.	1.2	7
1839	Evolutionary conserved microRNAs are ubiquitously expressed compared to tick-specific miRNAs in the cattle tick Rhipicephalus (Boophilus) microplus. BMC Genomics, 2011, 12, 328.	1.2	33
1840	Exome-wide DNA capture and next generation sequencing in domestic and wild species. BMC Genomics, 2011, 12, 347.	1.2	88
1841	Identification of genomic indels and structural variations using split reads. BMC Genomics, 2011, 12, 375.	1.2	57
1842	Deep sequencing reveals as-yet-undiscovered small RNAs in Escherichia coli. BMC Genomics, 2011, 12, 428.	1.2	51

#	ARTICLE	IF	CITATIONS
1843	A comparative physical map reveals the pattern of chromosomal evolution between the turkey ( <i>Meleagris gallopavo</i> ) and chicken ( <i>Gallus gallus</i> ) genomes. <i>BMC Genomics</i> , 2011, 12, 447.	1.2	24
1844	De novo sequence assembly of <i>Albugo candida</i> reveals a small genome relative to other biotrophic oomycetes. <i>BMC Genomics</i> , 2011, 12, 503.	1.2	123
1845	RNA-Seq improves annotation of protein-coding genes in the cucumber genome. <i>BMC Genomics</i> , 2011, 12, 540.	1.2	232
1846	The repertoire of G protein-coupled receptors in the human parasite <i>Schistosoma mansoni</i> and the model organism <i>Schmidtea mediterranea</i> . <i>BMC Genomics</i> , 2011, 12, 596.	1.2	72
1847	The mosquito <i>Aedes aegypti</i> has a large genome size and high transposable element load but contains a low proportion of transposon-specific piRNAs. <i>BMC Genomics</i> , 2011, 12, 606.	1.2	99
1848	Genomic sequencing and analysis of a Chinese hamster ovary cell line using Illumina sequencing technology. <i>BMC Genomics</i> , 2011, 12, 67.	1.2	37
1849	Interrogation of alternative splicing events in duplicated genes during evolution. <i>BMC Genomics</i> , 2011, 12, S16.	1.2	13
1850	Profiling ascidian promoters as the primordial type of vertebrate promoter. <i>BMC Genomics</i> , 2011, 12, S7.	1.2	7
1851	Mutational analysis of 12 patients with the phenotype of Ehlers-Danlos syndrome type VIB shows no linkage to the zinc transporter gene <i>SLC39A13</i> . <i>American Journal of Medical Genetics, Part A</i> , 2011, 155, 2011-2014.	0.7	0
1852	An experience report: porting the MG-RAST rapid metagenomics analysis pipeline to the cloud. <i>Concurrency Computation Practice and Experience</i> , 2011, 23, 2250-2257.	1.4	13
1853	In silico bioinformatic tools for determining core genes from sets of genomes. <i>Drug Development Research</i> , 2011, 72, 147-152.	1.4	0
1854	SNP uniqueness problem: a proof-of-principle in HapMap SNPs. <i>Human Mutation</i> , 2011, 32, 355-357.	1.1	7
1855	Genome-wide identification of conserved regulatory function in diverged sequences. <i>Genome Research</i> , 2011, 21, 1139-1149.	2.4	72
1856	A method for visualization of economic datasets for sphingolipid metabolism to predict potentially interesting differences. <i>Journal of Lipid Research</i> , 2011, 52, 1073-1083.	2.0	24
1857	Identifying viral integration sites using SeqMap 2.0. <i>Bioinformatics</i> , 2011, 27, 720-722.	1.8	33
1858	Adaptive seeds tame genomic sequence comparison. <i>Genome Research</i> , 2011, 21, 487-493.	2.4	1,120
1859	Computational Genomic Signatures. <i>Synthesis Lectures on Biomedical Engineering</i> , 2011, 6, 1-129.	0.1	3
1860	The <i>Drosophila melanogaster</i> transcriptome by paired-end RNA sequencing. <i>Genome Research</i> , 2011, 21, 315-324.	2.4	123

#	ARTICLE	IF	CITATIONS
1861	Using inversion signatures to generate draft genome sequence scaffolds. , 2011, , .		1
1862	Identification of a Genomic Reservoir for New TRIM Genes in Primate Genomes. <i>PLoS Genetics</i> , 2011, 7, e1002388.	1.5	98
1863	Evidence-Based Annotation of Transcripts and Proteins in the Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2011, 193, 5716-5727.	1.0	28
1864	Evolutionary divergence of intrinsic and <i>trans</i> -regulated nucleosome positioning sequences reveals plastic rules for chromatin organization. <i>Genome Research</i> , 2011, 21, 1851-1862.	2.4	74
1865	An mRNA Blueprint for C4 Photosynthesis Derived from Comparative Transcriptomics of Closely Related C3 and C4 Species. <i>Plant Physiology</i> , 2011, 155, 142-156.	2.3	222
1866	Genome of Multidrug-Resistant Uropathogenic <i>Escherichia coli</i> Strain NA114 from India. <i>Journal of Bacteriology</i> , 2011, 193, 4272-4273.	1.0	63
1867	Interval Trees for Detection of Overlapping Genetic Entities. , 2011, , .		1
1868	Sequence-specific error profile of Illumina sequencers. <i>Nucleic Acids Research</i> , 2011, 39, e90-e90.	6.5	513
1869	Multimodal RNA-seq using single-strand, double-strand, and CirLigase-based capture yields a refined and extended description of the <i>C. elegans</i> transcriptome. <i>Genome Research</i> , 2011, 21, 265-275.	2.4	38
1870	Expression, Splicing, and Evolution of the Myosin Gene Family in Plants. <i>Plant Physiology</i> , 2011, 155, 1191-1204.	2.3	78
1871	Inhibition of RNA Interference and Modulation of Transposable Element Expression by Cell Death in <i>Drosophila</i> . <i>Genetics</i> , 2011, 188, 823-834.	1.2	9
1872	Identification of piRNAs in the central nervous system. <i>Rna</i> , 2011, 17, 1090-1099.	1.6	265
1873	Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. <i>Bioinformatics</i> , 2011, 27, 1481-1488.	1.8	39
1874	PE-Assembler: <i>de novo</i> assembler using short paired-end reads. <i>Bioinformatics</i> , 2011, 27, 167-174.	1.8	98
1875	The effects of EBV transformation on gene expression levels and methylation profiles. <i>Human Molecular Genetics</i> , 2011, 20, 1643-1652.	1.4	124
1876	Meta-IDBA: a <i>de Novo</i> assembler for metagenomic data. <i>Bioinformatics</i> , 2011, 27, i94-i101.	1.8	267
1877	Epigenetic Control of Retrotransposon Expression in Human Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2011, 31, 300-316.	1.1	128
1878	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. <i>Nucleic Acids Research</i> , 2011, 39, W551-W556.	6.5	114

#	ARTICLE	IF	CITATIONS
1879	RNA-Seq analysis of splicing in <i>Plasmodium falciparum</i> uncovers new splice junctions, alternative splicing and splicing of antisense transcripts. <i>Nucleic Acids Research</i> , 2011, 39, 3820-3835.	6.5	123
1880	Zygomycetes, Microsporidia, and the Evolutionary Ancestry of Sex Determination. <i>Genome Biology and Evolution</i> , 2011, 3, 186-194.	1.1	24
1881	Genome-wide analysis of retrogene polymorphisms in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011, 21, 2087-2095.	2.4	58
1882	Anatomy of a hash-based long read sequence mapping algorithm for next generation DNA sequencing. <i>Bioinformatics</i> , 2011, 27, 189-195.	1.8	24
1883	Genomic mRNA Profiling Reveals Compensatory Mechanisms for the Requirement of the Essential Splicing Factor U2AF. <i>Molecular and Cellular Biology</i> , 2011, 31, 652-661.	1.1	20
1884	Annotating genes and genomes with DNA sequences extracted from biomedical articles. <i>Bioinformatics</i> , 2011, 27, 980-986.	1.8	23
1885	S-Adenosylmethionine Decreases Lipopolysaccharide-Induced Phosphodiesterase 4B2 and Attenuates Tumor Necrosis Factor Expression via cAMP/Protein Kinase A Pathway. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2011, 337, 433-443.	1.3	42
1886	Whole Genome Sequence Comparisons in Taxonomy. <i>Methods in Microbiology</i> , 2011, 38, 409-436.	0.4	8
1887	Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq. <i>Nucleic Acids Research</i> , 2011, 39, 1408-1418.	6.5	19
1888	Cell envelope gene expression in phosphate-limited <i>Bacillus subtilis</i> cells. <i>Microbiology (United Kingdom)</i> 10.1093/mic/dqr355	0.7	35
1889	Silencing, Positive Selection and Parallel Evolution: Busy History of Primate Cytochromes c. <i>PLoS ONE</i> , 2011, 6, e26269.	1.1	14
1890	A Genome-Wide Study of DNA Methylation Patterns and Gene Expression Levels in Multiple Human and Chimpanzee Tissues. <i>PLoS Genetics</i> , 2011, 7, e1001316.	1.5	196
1891	T1DBase: update 2011, organization and presentation of large-scale data sets for type 1 diabetes research. <i>Nucleic Acids Research</i> , 2011, 39, D997-D1001.	6.5	68
1892	Genome of a Novel Isolate of <i>Paracoccus denitrificans</i> Capable of Degrading N,N-Dimethylformamide. <i>Journal of Bacteriology</i> , 2011, 193, 5598-5599.	1.0	42
1893	dbDNV: a resource of duplicated gene nucleotide variants in human genome. <i>Nucleic Acids Research</i> , 2011, 39, D920-D925.	6.5	13
1894	Structure-Function Analyses Point to a Polynucleotide-Accommodating Groove Essential for APOBEC3A Restriction Activities. <i>Journal of Virology</i> , 2011, 85, 1765-1776.	1.5	67
1895	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. <i>Genome Research</i> , 2011, 21, 634-641.	2.4	105
1896	Molecular Description and Industrial Potential of Tn 6098 Conjugative Transfer Conferring Alpha-Galactoside Metabolism in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 555-563.	1.4	30

#	ARTICLE	IF	CITATIONS
1897	Expression of Type II Chorionic Gonadotropin Genes Supports a Role in the Male Reproductive System. <i>Molecular and Cellular Biology</i> , 2011, 31, 287-299.	1.1	12
1898	<tt>Sim4db</tt> and <tt>Leaff</tt>: utilities for fast batch spliced alignment and sequence indexing. <i>Bioinformatics</i> , 2011, 27, 1869-1870.	1.8	18
1899	Methods and strategies for gene structure curation in WormBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, baq039-baq039.	1.4	15
1900	Transcriptome Analysis of <i>Sarracenia</i> , an Insectivorous Plant. <i>DNA Research</i> , 2011, 18, 253-261.	1.5	28
1901	Seventy Million Years of Concerted Evolution of a Homoeologous Chromosome Pair, in Parallel, in Major Poaceae Lineages. <i>Plant Cell</i> , 2011, 23, 27-37.	3.1	80
1902	Extraordinary Sequence Divergence at Tsga8, an X-linked Gene Involved in Mouse Spermiogenesis. <i>Molecular Biology and Evolution</i> , 2011, 28, 1675-1686.	3.5	22
1903	Cross-validated methods for promoter/transcription start site mapping in SL trans-spliced genes, established using the <i>Ciona intestinalis</i> troponin I gene. <i>Nucleic Acids Research</i> , 2011, 39, 2638-2648.	6.5	5
1904	Analysis of Leaf and Root Transcriptomes of Soil-Grown <i>Avena barbata</i> Plants. <i>Plant and Cell Physiology</i> , 2011, 52, 317-332.	1.5	34
1905	Kaviar: an accessible system for testing SNV novelty. <i>Bioinformatics</i> , 2011, 27, 3216-3217.	1.8	187
1906	Enrichment of mRNA-like Noncoding RNAs in the Divergence of <i>Drosophila</i> Males. <i>Molecular Biology and Evolution</i> , 2011, 28, 1339-1348.	3.5	11
1907	AGE: defining breakpoints of genomic structural variants at single-nucleotide resolution, through optimal alignments with gap excision. <i>Bioinformatics</i> , 2011, 27, 595-603.	1.8	84
1908	Computational challenges of sequence classification in microbiomic data. <i>Briefings in Bioinformatics</i> , 2011, 12, 614-625.	3.2	15
1909	The Solute Carrier Families Have a Remarkably Long Evolutionary History with the Majority of the Human Families Present before Divergence of Bilaterian Species. <i>Molecular Biology and Evolution</i> , 2011, 28, 1531-1541.	3.5	182
1910	<i>In Silico</i> Reconstruction of Viral Genomes from Small RNAs Improves Virus-Derived Small Interfering RNA Profiling. <i>Journal of Virology</i> , 2011, 85, 11016-11021.	1.5	48
1911	Massive Changes in Genome Architecture Accompany the Transition to Self-Fertility in the Filamentous Fungus <i>Neurospora tetrasperma</i>. <i>Genetics</i> , 2011, 189, 55-69.	1.2	69
1912	SyMAP v3.4: a turnkey synteny system with application to plant genomes. <i>Nucleic Acids Research</i> , 2011, 39, e68-e68.	6.5	304
1913	piRNA profiling during specific stages of mouse spermatogenesis. <i>Rna</i> , 2011, 17, 1191-1203.	1.6	94
1914	Genomes of Two Chronological Isolates ( <i>Helicobacter pylori</i> 2017 and 2018) of the West African <i>Helicobacter pylori</i> Strain 908 Obtained from a Single Patient. <i>Journal of Bacteriology</i> , 2011, 193, 3385-3386.	1.0	29

#	ARTICLE	IF	CITATIONS
1915	Evolution of the V, D, and J gene segments used in the primate $\alpha$ T-cell receptor reveals a dichotomy of conservation and diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E332-40.	3.3	49
1916	Activation of the Glucocorticoid Receptor Is Associated with Poor Prognosis in Estrogen Receptor-Negative Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6360-6370.	0.4	219
1917	FoSTeS, MMBIR and NAHR at the human proximal Xp region and the mechanisms of human Xq isochromosome formation. <i>Human Molecular Genetics</i> , 2011, 20, 1925-1936.	1.4	34
1918	The evolution and expression of the snaR family of small non-coding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, 1485-1500.	6.5	59
1919	Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain H44/76. <i>Journal of Bacteriology</i> , 2011, 193, 2371-2372.	1.0	30
1920	Distinct patterns of somatic alterations in a lymphoblastoid and a tumor genome derived from the same individual. <i>Nucleic Acids Research</i> , 2011, 39, 6056-6068.	6.5	19
1921	Whole genome sequencing of multiple <i>Leishmania donovani</i> clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , 2011, 21, 2143-2156.	2.4	381
1922	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <i>Genome Research</i> , 2011, 21, 1193-1200.	2.4	100
1923	Sequence Alignment as Hypothesis Testing. <i>Journal of Computational Biology</i> , 2011, 18, 677-691.	0.8	8
1924	The UCSC Genome Browser database: update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D876-D882.	6.5	958
1925	Metagenomic detection of phage-encoded platelet-binding factors in the human oral cavity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4547-4553.	3.3	123
1926	The Plant Cell Wall "Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
1927	A novel hybrid gene prediction method employing protein multiple sequence alignments. <i>Bioinformatics</i> , 2011, 27, 757-763.	1.8	468
1928	FR-HIT, a very fast program to recruit metagenomic reads to homologous reference genomes. <i>Bioinformatics</i> , 2011, 27, 1704-1705.	1.8	76
1929	Gene Gain and Loss during Evolution of Obligate Parasitism in the White Rust Pathogen of <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2011, 9, e1001094.	2.6	271
1930	MicroRNA-Driven Developmental Remodeling in the Brain Distinguishes Humans from Other Primates. <i>PLoS Biology</i> , 2011, 9, e1001214.	2.6	198
1931	MicroRNA Expression and Regulation in Human, Chimpanzee, and Macaque Brains. <i>PLoS Genetics</i> , 2011, 7, e1002327.	1.5	126
1932	A Deep Sequencing Approach to Comparatively Analyze the Transcriptome of Lifecycle Stages of the Filarial Worm, <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1409.	1.3	86

#	ARTICLE	IF	CITATIONS
1933	Estimated Comparative Integration Hotspots Identify Different Behaviors of Retroviral Gene Transfer Vectors. <i>PLoS Computational Biology</i> , 2011, 7, e1002292.	1.5	17
1934	Independent HHsearch, Needleman-Wunsch-Based, and Motif Analyses Reveal the Overall Hierarchy for Most of the G Protein-Coupled Receptor Families. <i>Molecular Biology and Evolution</i> , 2011, 28, 2471-2480.	3.5	145
1935	TparvaDB: a database to support <i>Theileria parva</i> vaccine development. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar015-bar015.	1.4	1
1936	Narrowing a region on rat chromosome 13 that protects against hypertension in Dahl SS-13 <sup>BN</sup> congenic strains. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2011, 300, H1530-H1535.	1.5	27
1937	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. <i>PLoS Genetics</i> , 2011, 7, e1002236.	1.5	278
1938	RNA-Seq Assembly “Are We There Yet?”. <i>Frontiers in Plant Science</i> , 2012, 3, 220.	1.7	112
1939	Tethering of the Conserved piggyBac Transposase Fusion Protein CSB-PGBD3 to Chromosomal AP-1 Proteins Regulates Expression of Nearby Genes in Humans. <i>PLoS Genetics</i> , 2012, 8, e1002972.	1.5	30
1940	Virus Identification in Unknown Tropical Febrile Illness Cases Using Deep Sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1485.	1.3	148
1941	Joint Analysis of Multiple Metagenomic Samples. <i>PLoS Computational Biology</i> , 2012, 8, e1002373.	1.5	23
1942	A Forward Genetic Screen Reveals that Calcium-dependent Protein Kinase 3 Regulates Egress in <i>Toxoplasma</i> . <i>PLoS Pathogens</i> , 2012, 8, e1003049.	2.1	118
1943	Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. <i>Bioinformatics</i> , 2012, 28, 3232-3239.	1.8	154
1944	UniPrimer: A Web-Based Primer Design Tool for Comparative Analyses of Primate Genomes. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-8.	2.0	4
1945	A SEL1L Mutation Links a Canine Progressive Early-Onset Cerebellar Ataxia to the Endoplasmic Reticulum-Associated Protein Degradation (ERAD) Machinery. <i>PLoS Genetics</i> , 2012, 8, e1002759.	1.5	52
1946	A nucleosomal surface defines an integration hotspot for the <i>Saccharomyces cerevisiae</i> Ty1 retrotransposon. <i>Genome Research</i> , 2012, 22, 704-713.	2.4	61
1947	Tissue-Restricted Transcription from a Conserved Intragenic CpG Island in the Klf1 Gene in Mice1. <i>Biology of Reproduction</i> , 2012, 87, 108.	1.2	9
1948	Microarray Analysis of LTR Retrotransposon Silencing Identifies Hdac1 as a Regulator of Retrotransposon Expression in Mouse Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2012, 8, e1002486.	1.5	64
1949	Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1002692.	1.5	80
1950	A Novel Rhabdovirus Associated with Acute Hemorrhagic Fever in Central Africa. <i>PLoS Pathogens</i> , 2012, 8, e1002924.	2.1	181

#	ARTICLE	IF	CITATIONS
1951	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. <i>PLoS Pathogens</i> , 2012, 8, e1003037.	2.1	595
1952	The Paramecium Germline Genome Provides a Niche for Intragenic Parasitic DNA: Evolutionary Dynamics of Internal Eliminated Sequences. <i>PLoS Genetics</i> , 2012, 8, e1002984.	1.5	154
1953	Variants Affecting Exon Skipping Contribute to Complex Traits. <i>PLoS Genetics</i> , 2012, 8, e1002998.	1.5	53
1954	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. <i>PLoS Genetics</i> , 2012, 8, e1003127.	1.5	166
1955	Hundreds of conserved non-coding genomic regions are independently lost in mammals. <i>Nucleic Acids Research</i> , 2012, 40, 11463-11476.	6.5	48
1956	Tachyon search speeds up retrieval of similar sequences by several orders of magnitude. <i>Bioinformatics</i> , 2012, 28, 1645-1646.	1.8	12
1957	High Levels of Sequence Diversity in the 5' UTRs of Human-Specific L1 Elements. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-8.	2.0	11
1958	Tools for mapping high-throughput sequencing data. <i>Bioinformatics</i> , 2012, 28, 3169-3177.	1.8	269
1959	The genome of <i>Prunus mume</i> . <i>Nature Communications</i> , 2012, 3, 1318.	5.8	441
1960	Dr.VIS: a database of human disease-related viral integration sites. <i>Nucleic Acids Research</i> , 2012, 40, D1041-D1046.	6.5	14
1961	Complete Resequencing and Reannotation of the <i>Lactobacillus plantarum</i> WCFS1 Genome. <i>Journal of Bacteriology</i> , 2012, 194, 195-196.	1.0	109
1962	RAPSearch2: a fast and memory-efficient protein similarity search tool for next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 125-126.	1.8	386
1963	Expression Quantitative Trait Loci for Extreme Host Response to Influenza A in Pre-Collaborative Cross Mice. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 213-221.	0.8	78
1964	Deep-sequencing of endothelial cells exposed to hypoxia reveals the complexity of known and novel microRNAs. <i>Rna</i> , 2012, 18, 472-484.	1.6	121
1965	Whole Genome Expression Differences in Human Left and Right Atria Ascertained by RNA Sequencing. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 327-335.	5.1	53
1966	Methylation of L1Hs promoters is lower on the inactive X, has a tendency of being higher on autosomes in smaller genomes and shows inter-individual variability at some loci. <i>Human Molecular Genetics</i> , 2012, 21, 219-235.	1.4	27
1967	GGRNA: an ultrafast, transcript-oriented search engine for genes and transcripts. <i>Nucleic Acids Research</i> , 2012, 40, W592-W596.	6.5	9
1968	VarioWatch: providing large-scale and comprehensive annotations on human genomic variants in the next generation sequencing era. <i>Nucleic Acids Research</i> , 2012, 40, W76-W81.	6.5	39

#	ARTICLE	IF	CITATIONS
1969	Comment on "Widespread RNA and DNA Sequence Differences in the Human Transcriptome" Science, 2012, 335, 1302-1302.	6.0	155
1970	lobSTR: A short tandem repeat profiler for personal genomes. Genome Research, 2012, 22, 1154-1162.	2.4	294
1971	Copy number variation at 6q13 functions as a long-range regulator and is associated with pancreatic cancer risk. Carcinogenesis, 2012, 33, 94-100.	1.3	34
1972	Reverse engineering biomolecular systems using -omic data: challenges, progress and opportunities. Briefings in Bioinformatics, 2012, 13, 430-445.	3.2	19
1973	Ionising irradiation alters the dynamics of human long interspersed nuclear elements 1 (LINE1) retrotransposon. Mutagenesis, 2012, 27, 599-607.	1.0	21
1974	FoxO-Dependent Regulation of Diacylglycerol Kinase $\beta$ Gene Expression. Molecular and Cellular Biology, 2012, 32, 4168-4180.	1.1	32
1975	Response to Comments on "Widespread RNA and DNA Sequence Differences in the Human Transcriptome" Science, 2012, 335, 1302-1302.	6.0	98
1976	Conditional CD8 <sup>+</sup> T Cell Escape during Acute Simian Immunodeficiency Virus Infection. Journal of Virology, 2012, 86, 605-609.	1.5	29
1977	Navigating the tip of the genomic iceberg: Next-generation sequencing for plant systematics. American Journal of Botany, 2012, 99, 349-364.	0.8	558
1978	YAHA: fast and flexible long-read alignment with optimal breakpoint detection. Bioinformatics, 2012, 28, 2417-2424.	1.8	62
1979	Double Digest RADseq: An Inexpensive Method for De Novo SNP Discovery and Genotyping in Model and Non-Model Species. PLoS ONE, 2012, 7, e37135.	1.1	2,836
1980	Genotypic and Phenotypic Evaluation of the Evolution of High-Level Daptomycin Nonsusceptibility in Vancomycin-Resistant Enterococcus faecium. Antimicrobial Agents and Chemotherapy, 2012, 56, 6051-6053.	1.4	55
1981	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. Nucleic Acids Research, 2012, 41, D142-D151.	6.5	47
1982	Identification of allele-specific alternative mRNA processing via transcriptome sequencing. Nucleic Acids Research, 2012, 40, e104-e104.	6.5	74
1983	Genome Update of Botrytis cinerea Strains B05.10 and T4. Eukaryotic Cell, 2012, 11, 1413-1414.	3.4	124
1984	YOABS: yet other aligner of biological sequences—an efficient linearly scaling nucleotide aligner. Bioinformatics, 2012, 28, 1070-1077.	1.8	11
1985	Genome-Wide Selection on Codon Usage at the Population Level in the Fungal Model Organism Neurospora crassa. Molecular Biology and Evolution, 2012, 29, 1975-1986.	3.5	21
1986	Accurate identification of A-to-I RNA editing in human by transcriptome sequencing. Genome Research, 2012, 22, 142-150.	2.4	297

#	ARTICLE	IF	CITATIONS
1987	SCOREM: statistical consolidation of redundant expression measures. <i>Nucleic Acids Research</i> , 2012, 40, e46-e46.	6.5	8
1988	Dynamic Intra-Japonica Subspecies Variation and Resource Application. <i>Molecular Plant</i> , 2012, 5, 218-230.	3.9	23
1989	Spatio-temporal regulation of ADAR editing during development in porcine neural tissues. <i>RNA Biology</i> , 2012, 9, 1054-1065.	1.5	38
1990	Databases and software to make your research life easier. , 2012, , 7-47.		0
1991	Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene Structure and Coding Sequence Evolution in Polyploid Wheat $\ddot{A}$ . <i>Plant Physiology</i> , 2012, 161, 252-265.	2.3	113
1992	A Rickettsia Genome Overrun by Mobile Genetic Elements Provides Insight into the Acquisition of Genes Characteristic of an Obligate Intracellular Lifestyle. <i>Journal of Bacteriology</i> , 2012, 194, 376-394.	1.0	152
1993	High-Resolution Analysis of Intrahost Genetic Diversity in Dengue Virus Serotype 1 Infection Identifies Mixed Infections. <i>Journal of Virology</i> , 2012, 86, 835-843.	1.5	52
1994	Evolutionary History and Functional Characterization of the Amphibian Xenosensor CAR. <i>Molecular Endocrinology</i> , 2012, 26, 14-26.	3.7	26
1995	A quantitative atlas of polyadenylation in five mammals. <i>Genome Research</i> , 2012, 22, 1173-1183.	2.4	557
1996	A mini-library of sequenced human DNA fragments: linking bench experiments with informatics. <i>Journal of Biological Education</i> , 2012, 46, 193-198.	0.8	0
1997	Detection of Base Substitution-Type Somatic Mosaicism of the NLRP3 Gene with >99.9% Statistical Confidence by Massively Parallel Sequencing. <i>DNA Research</i> , 2012, 19, 143-152.	1.5	51
1998	SPLOOCE. <i>RNA Biology</i> , 2012, 9, 1339-1343.	1.5	7
1999	Statistical assessment of gene fusion detection algorithms using RNA Sequencing Data. , 2012, , .		1
2000	FANSe: an accurate algorithm for quantitative mapping of large scale sequencing reads. <i>Nucleic Acids Research</i> , 2012, 40, e83-e83.	6.5	39
2001	Evaluation of GPU-based Seed Generation for Computational Genomics Using Burrows-Wheeler Transform. , 2012, , .		7
2002	Sex-Biased Transcriptome Evolution in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 1189-1200.	1.1	159
2003	SUITE OF TOOLS FOR STATISTICAL N-GRAM LANGUAGE MODELING FOR PATTERN MINING IN WHOLE GENOME SEQUENCES. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250016.	0.3	3
2004	Complementary Proteome and Transcriptome Profiling in Phosphate-deficient <i>Arabidopsis</i> Roots Reveals Multiple Levels of Gene Regulation. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1156-1166.	2.5	266

#	ARTICLE	IF	CITATIONS
2005	Functional RNA Interference (RNAi) Screen Identifies System A Neutral Amino Acid Transporter 2 (SNAT2) as a Mediator of Arsenic-induced Endoplasmic Reticulum Stress. <i>Journal of Biological Chemistry</i> , 2012, 287, 6025-6034.	1.6	29
2006	Identification and Properties of 1,119 Candidate LincRNA Loci in the <i>Drosophila melanogaster</i> Genome. <i>Genome Biology and Evolution</i> , 2012, 4, 427-442.	1.1	217
2007	Conserved epigenetic sensitivity to early life experience in the rat and human hippocampus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17266-17272.	3.3	285
2008	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. <i>Nucleic Acids Research</i> , 2012, 40, D91-D97.	6.5	179
2009	PARALLEL ALGORITHMS FOR MAPPING SHORT DEGENERATE AND WEIGHTED DNA SEQUENCES TO A REFERENCE GENOME. <i>International Journal of Foundations of Computer Science</i> , 2012, 23, 249-259.	0.8	1
2010	Transcriptomic Evidence for the Expression of Horizontally Transferred Algal Nuclear Genes in the Photosynthetic Sea Slug, <i>Elysia chlorotica</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1545-1556.	3.5	54
2011	Phenotype-specific effect of chromosome 1q21.1 rearrangements and GJA5 duplications in 2436 congenital heart disease patients and 6760 controls. <i>Human Molecular Genetics</i> , 2012, 21, 1513-1520.	1.4	101
2012	Strong signatures of selection in the domestic pig genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19529-19536.	3.3	548
2013	Comparative Analysis of Genome Sequences Covering the Seven <i>Cronobacter</i> Species. <i>PLoS ONE</i> , 2012, 7, e49455.	1.1	130
2014	CADRE: the Central <i>Aspergillus</i> Data REpository 2012. <i>Nucleic Acids Research</i> , 2012, 40, D660-D666.	6.5	55
2015	Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. <i>PLoS ONE</i> , 2012, 7, e30087.	1.1	360
2016	Genome-Wide Analysis of DNA Methylation Differences in Muscle and Fat from Monozygotic Twins Discordant for Type 2 Diabetes. <i>PLoS ONE</i> , 2012, 7, e51302.	1.1	171
2017	Novel domain combinations in proteins encoded by chimeric transcripts. <i>Bioinformatics</i> , 2012, 28, i67-i74.	1.8	35
2018	Regulated Expression of Chromobox Homolog 5 Revealed in Tumors of <i>ApcMin/+</i> ROSA11 Gene Trap Mice. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 569-578.	0.8	4
2019	Rapid identification of non-human sequences in high-throughput sequencing datasets. <i>Bioinformatics</i> , 2012, 28, 1174-1175.	1.8	88
2020	Entry of Human T-Cell Leukemia Virus Type 1 Is Augmented by Heparin Sulfate Proteoglycans Bearing Short Heparin-Like Structures. <i>Journal of Virology</i> , 2012, 86, 2959-2969.	1.5	16
2021	Genomic Analysis of the Hydrocarbon-Producing, Cellulolytic, Endophytic Fungus <i>Ascocoryne sarcoides</i> . <i>PLoS Genetics</i> , 2012, 8, e1002558.	1.5	76
2022	RecountDB: a database of mapped and count corrected transcribed sequences. <i>Nucleic Acids Research</i> , 2012, 40, D1089-D1092.	6.5	0

#	ARTICLE	IF	CITATIONS
2023	MetaCluster 5.0: a two-round binning approach for metagenomic data for low-abundance species in a noisy sample. <i>Bioinformatics</i> , 2012, 28, i356-i362.	1.8	106
2024	Whole-genome resequencing of two elite sires for the detection of haplotypes under selection in dairy cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7693-7698.	3.3	67
2025	Dissect: detection and characterization of novel structural alterations in transcribed sequences. <i>Bioinformatics</i> , 2012, 28, i179-i187.	1.8	13
2026	Xenomeâ€”a tool for classifying reads from xenograft samples. <i>Bioinformatics</i> , 2012, 28, i172-i178.	1.8	211
2027	Finding differentially expressed regions of arbitrary length in quantitative genomic data based on marked point process model. <i>Bioinformatics</i> , 2012, 28, i633-i639.	1.8	1
2028	Transcriptome Analysis of a North American Songbird, <i>Melospiza melodia</i> . <i>DNA Research</i> , 2012, 19, 325-333.	1.5	16
2029	Elephant Transcriptome Provides Insights into the Evolution of Eutherian Placentation. <i>Genome Biology and Evolution</i> , 2012, 4, 713-725.	1.1	27
2030	RNASEQQRâ€”a streamlined and accurate RNA-seq sequence analysis program. <i>Nucleic Acids Research</i> , 2012, 40, e42-e42.	6.5	33
2031	jpHMM: recombination analysis in viruses with circular genomes such as the hepatitis B virus. <i>Nucleic Acids Research</i> , 2012, 40, W193-W198.	6.5	67
2032	Sequencing of the smallest Apicomplexan genome from the human pathogen <i>Babesia microti</i> â€. <i>Nucleic Acids Research</i> , 2012, 40, 9102-9114.	6.5	179
2033	Transcriptome sequencing of black grouse ( <i>Tetrao tetrix</i> ) for immune gene discovery and microsatellite development. <i>Open Biology</i> , 2012, 2, 120054.	1.5	26
2034	Dynamic regulation of HIV-1 mRNA populations analyzed by single-molecule enrichment and long-read sequencing. <i>Nucleic Acids Research</i> , 2012, 40, 10345-10355.	6.5	114
2035	Two new large deletions of the AVPR2 gene causing nephrogenic diabetes insipidus and a review of previously published deletions. <i>Nephrology Dialysis Transplantation</i> , 2012, 27, 3705-3712.	0.4	15
2036	Bioinformatic Tools Identify Chromosome-Specific DNA Probes and Facilitate Risk Assessment by Detecting Aneusomies in Extra-embryonic Tissues. <i>Current Genomics</i> , 2012, 13, 438-445.	0.7	5
2037	Rat <i>Mcs1b</i> Is Concordant to the Genome-Wide Association-Identified Breast Cancer Risk Locus at Human 5q11.2 and <i>MIER3</i> is a Candidate Cancer Susceptibility Gene. <i>Cancer Research</i> , 2012, 72, 6002-6012.	0.4	24
2039	Detection of fixed length web spambot using REAL (read aligner). , 2012, , .		2
2040	MGOS: Development of a Community Annotation Database for <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 271-278.	1.4	2
2041	Population Genomic Analysis of Model and Nonmodel Organisms Using Sequenced RAD Tags. <i>Methods in Molecular Biology</i> , 2012, 888, 235-260.	0.4	56

#	ARTICLE	IF	CITATIONS
2042	Detection of Chromosomal Alterations in the Circulation of Cancer Patients with Whole-Genome Sequencing. <i>Science Translational Medicine</i> , 2012, 4, 162ra154.	5.8	557
2043	The genome of flax ( <i>Linum usitatissimum</i> ) assembled <i>de novo</i> from short shotgun sequence reads. <i>Plant Journal</i> , 2012, 72, 461-473.	2.8	415
2044	Field Monitoring of Avian Influenza Viruses: Whole-Genome Sequencing and Tracking of Neuraminidase Evolution Using 454 Pyrosequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2881-2887.	1.8	25
2045	Lentiviral Hematopoietic Cell Gene Therapy for X-Linked Adrenoleukodystrophy. <i>Methods in Enzymology</i> , 2012, 507, 187-198.	0.4	100
2046	A <i>de novo</i> metagenomic assembly program for shotgun DNA reads. <i>Bioinformatics</i> , 2012, 28, 1455-1462.	1.8	42
2047	Genome-Wide Analysis Uncovers Regulation of Long Intergenic Noncoding RNAs in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 4333-4345.	3.1	656
2048	Targeted genome enrichment for efficient purification of endosymbiont DNA from host DNA. <i>Symbiosis</i> , 2012, 58, 201-207.	1.2	31
2049	The Rice Genome Knowledgebase (RGKbase): an annotation database for rice comparative genomics and evolutionary biology. <i>Nucleic Acids Research</i> , 2012, 41, D1199-D1205.	6.5	25
2050	Computational tools for viral metagenomics and their application in clinical research. <i>Virology</i> , 2012, 434, 162-174.	1.1	59
2051	Identification and Functional Analysis of Three Isoforms of Bovine BST-2. <i>PLoS ONE</i> , 2012, 7, e41483.	1.1	18
2052	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. <i>Science</i> , 2012, 338, 1587-1593.	6.0	905
2053	A Living Fossil in the Genome of a Living Fossil: Harbinger Transposons in the Coelacanth Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 985-993.	3.5	36
2054	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. <i>Bioinformatics</i> , 2012, 28, 1923-1924.	1.8	54
2055	Bioinformatics tools and databases for analysis of next-generation sequence data. <i>Briefings in Functional Genomics</i> , 2012, 11, 12-24.	1.3	73
2056	Chromosome conformation capture assays in bacteria. <i>Methods</i> , 2012, 58, 212-220.	1.9	7
2057	SpliceGrapher: detecting patterns of alternative splicing from RNA-Seq data in the context of gene models and EST data. <i>Genome Biology</i> , 2012, 13, R4.	13.9	140
2058	The GENCODE pseudogene resource. <i>Genome Biology</i> , 2012, 13, R51.	13.9	273
2059	Exploring the <i>Schistosoma mansoni</i> adult male transcriptome using RNA-seq. <i>Experimental Parasitology</i> , 2012, 132, 22-31.	0.5	35

#	ARTICLE	IF	CITATIONS
2060	Characterisation of retroviruses in the horse genome and their transcriptional activity via transcriptome sequencing. <i>Virology</i> , 2012, 433, 55-63.	1.1	14
2061	Molecular evolution of the neurohypophysial hormone precursors in mammals: Comparative genomics reveals novel mammalian oxytocin and vasopressin analogues. <i>General and Comparative Endocrinology</i> , 2012, 179, 313-318.	0.8	40
2062	RCDA: A highly sensitive and specific alternatively spliced transcript assembly tool featuring upstream consecutive exon structures. <i>Genomics</i> , 2012, 100, 357-362.	1.3	1
2063	Data Management Challenges in Next Generation Sequencing. <i>Datenbank-Spektrum</i> , 2012, 12, 161-171.	1.2	25
2064	Development of EST database and transcriptome analysis in the leaves of <i>Brassica rapa</i> using a newly developed pipeline. <i>Genes and Genomics</i> , 2012, 34, 671-679.	0.5	4
2065	Next-Generation Sequencing and De Novo Assembly, Genome Organization, and Comparative Genomic Analyses of the Genomes of Two <i>Helicobacter pylori</i> Isolates from Duodenal Ulcer Patients in India. <i>Journal of Bacteriology</i> , 2012, 194, 5963-5964.	1.0	14
2066	SKIP Is a Component of the Spliceosome Linking Alternative Splicing and the Circadian Clock in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 3278-3295.	3.1	198
2067	Long noncoding RNAs are rarely translated in two human cell lines. <i>Genome Research</i> , 2012, 22, 1646-1657.	2.4	346
2068	Gene Assembly from Chip-synthesized Oligonucleotides. <i>Current Protocols in Chemical Biology</i> , 2012, 4, 1-17.	1.7	19
2069	Investigating Memory Optimization of Hash-index for Next Generation Sequencing on Multi-core Architecture. , 2012, , .		7
2070	Radiation and Functional Diversification of Alpha Keratins during Early Vertebrate Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 995-1004.	3.5	73
2071	Using GPUs for the Exact Alignment of Short-Read Genetic Sequences by Means of the Burrows-Wheeler Transform. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1245-1256.	1.9	28
2072	A multi-omic map of the lipid-producing yeast <i>Rhodospiridium toruloides</i> . <i>Nature Communications</i> , 2012, 3, 1112.	5.8	324
2073	Probabilistic Arithmetic Automata and Their Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1737-1750.	1.9	11
2074	R-SAP: a multi-threading computational pipeline for the characterization of high-throughput RNA-sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, e67-e67.	6.5	6
2075	A New Efficient Data Structure for Storage and Retrieval of Multiple Biosequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 345-357.	1.9	11
2076	Grabfast: A CUDA based GPU accelerated fast short sequence alignment algorithm. , 2012, , .		0
2077	Accelerating Millions of Short Reads Mapping on a Heterogeneous Architecture with FPGA Accelerator. , 2012, , .		43

#	ARTICLE	IF	CITATIONS
2078	Restricted Gene Flow among Hospital Subpopulations of <i>Enterococcus faecium</i> . <i>MBio</i> , 2012, 3, e00151-12.	1.8	177
2079	Miniature Inverted-Repeat Transposable Elements (MITEs) Have Been Accumulated through Amplification Bursts and Play Important Roles in Gene Expression and Species Diversity in <i>Oryza sativa</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1005-1017.	3.5	191
2080	Genomic analysis of DNA binding and gene regulation by homologous nucleoid-associated proteins IHF and HU in <i>Escherichia coli</i> K12. <i>Nucleic Acids Research</i> , 2012, 40, 3524-3537.	6.5	140
2081	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , 2012, 22, 1231-1242.	2.4	143
2082	Oases: robust <i>de novo</i> RNA-seq assembly across the dynamic range of expression levels. <i>Bioinformatics</i> , 2012, 28, 1086-1092.	1.8	1,351
2083	Ultrafast clustering algorithms for metagenomic sequence analysis. <i>Briefings in Bioinformatics</i> , 2012, 13, 656-668.	3.2	403
2084	Interactions Between Commensal Fungi and the C-Type Lectin Receptor Dectin-1 Influence Colitis. <i>Science</i> , 2012, 336, 1314-1317.	6.0	886
2085	A differential sequencing-based analysis of the <i>C. elegans</i> noncoding transcriptome. <i>Rna</i> , 2012, 18, 626-639.	1.6	11
2086	Integrase-Deficient Lentiviral Vectors Mediate Efficient Gene Transfer to Human Vascular Smooth Muscle Cells with Minimal Genotoxic Risk. <i>Human Gene Therapy</i> , 2012, 23, 1247-1257.	1.4	16
2087	Mapsembler, targeted and micro assembly of large NGS datasets on a desktop computer. <i>BMC Bioinformatics</i> , 2012, 13, 48.	1.2	31
2088	OSA: a fast and accurate alignment tool for RNA-Seq. <i>Bioinformatics</i> , 2012, 28, 1933-1934.	1.8	119
2089	The Minimal Active Human SVA Retrotransposon Requires Only the 5'-Hexamer and Alu-Like Domains. <i>Molecular and Cellular Biology</i> , 2012, 32, 4718-4726.	1.1	28
2090	Mapping single molecule sequencing reads using basic local alignment with successive refinement (BLASR): application and theory. <i>BMC Bioinformatics</i> , 2012, 13, 238.	1.2	1,075
2091	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	3.5	210
2092	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	3.2	23
2093	Classification of metagenomic sequences: methods and challenges. <i>Briefings in Bioinformatics</i> , 2012, 13, 669-681.	3.2	184
2094	MFEprimer-2.0: a fast thermodynamics-based program for checking PCR primer specificity. <i>Nucleic Acids Research</i> , 2012, 40, W205-W208.	6.5	80
2095	The genome of the xerotolerant mold <i>Wallemia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. <i>Fungal Genetics and Biology</i> , 2012, 49, 217-226.	0.9	103

#	ARTICLE	IF	CITATIONS
2096	Identification of a HMGA2-EFCAB6 gene rearrangement following next-generation sequencing in a patient with a t(12;22)(q14.3;q13.2) and JAK2V617F-positive myeloproliferative neoplasm. <i>Cancer Genetics</i> , 2012, 205, 295-303.	0.2	10
2097	Differential expression and intrachromosomal evolution of the sghC1q genes in zebrafish ( <i>Danio</i> ) Tj ETQq1 1 0.784314 rgBT /Overloc 11	1.0	11
2098	6â€“10 <sup>5</sup> — pyrosequencing is a practical approach for whole prokaryote genome studies. <i>Gene</i> , 2012, 494, 57-64.	1.0	10
2099	CR1 retroposons provide a new insight into the phylogeny of Phasianidae species (Aves: Galliformes). <i>Gene</i> , 2012, 502, 125-132.	1.0	16
2100	KGBassembler: a karyotype-based genome assembler for Brassicaceae species. <i>Bioinformatics</i> , 2012, 28, 3141-3143.	1.8	12
2101	An Alu-Based Phylogeny of Gibbons ( <i>Hylobatidae</i> ). <i>Molecular Biology and Evolution</i> , 2012, 29, 3441-3450.	3.5	41
2102	CLIP-seq of eIF4AIII reveals transcriptome-wide mapping of the human exon junction complex. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1124-1131.	3.6	197
2103	Application of metatranscriptomics to soil environments. <i>Journal of Microbiological Methods</i> , 2012, 91, 246-251.	0.7	142
2104	A genome resource to address mechanisms of developmental programming: determination of the fetal sheep heart transcriptome. <i>Journal of Physiology</i> , 2012, 590, 2873-2884.	1.3	15
2105	The M5nr: a novel non-redundant database containing protein sequences and annotations from multiple sources and associated tools. <i>BMC Bioinformatics</i> , 2012, 13, 141.	1.2	291
2106	Short-read reading-frame predictors are not created equal: sequence error causes loss of signal. <i>BMC Bioinformatics</i> , 2012, 13, 183.	1.2	39
2107	CaPSID: A bioinformatics platform for computational pathogen sequence identification in human genomes and transcriptomes. <i>BMC Bioinformatics</i> , 2012, 13, 206.	1.2	41
2108	AbsIDconvert: An absolute approach for converting genetic identifiers at different granularities. <i>BMC Bioinformatics</i> , 2012, 13, 229.	1.2	8
2109	ncRNAclassifier: a tool for detection and classification of transposable element sequences in RNA hairpins. <i>BMC Bioinformatics</i> , 2012, 13, 246.	1.2	25
2110	SIS: a program to generate draft genome sequence scaffolds for prokaryotes. <i>BMC Bioinformatics</i> , 2012, 13, 96.	1.2	29
2111	Separating the wheat from the chaff: mitigating the effects of noise in a plastome phylogenomic data set from <i>Pinus</i> L. ( <i>Pinaceae</i> ). <i>BMC Evolutionary Biology</i> , 2012, 12, 100.	3.2	96
2112	Comparative genomics of eukaryotic small nucleolar RNAs reveals deep evolutionary ancestry amidst ongoing intragenomic mobility. <i>BMC Evolutionary Biology</i> , 2012, 12, 183.	3.2	30
2113	ENU mutagenesis reveals that Notchless homolog 1 ( <i>Drosophila</i> ) affects Cdkn1a and several members of the Wnt pathway during murine pre-implantation development. <i>BMC Genetics</i> , 2012, 13, 106.	2.7	10

#	ARTICLE	IF	CITATIONS
2114	Whole genome comparisons of <i>Fragaria</i> , <i>Prunus</i> and <i>Malus</i> reveal different modes of evolution between Rosaceous subfamilies. BMC Genomics, 2012, 13, 129.	1.2	77
2115	A framework genetic map for <i>Miscanthus sinensis</i> from RNAseq-based markers shows recent tetraploidy. BMC Genomics, 2012, 13, 142.	1.2	87
2116	A high-resolution map of the Nile tilapia genome: a resource for studying cichlids and other percomorphs. BMC Genomics, 2012, 13, 222.	1.2	104
2117	Developing the anemone <i>Aiptasia</i> as a tractable model for cnidarian-dinoflagellate symbiosis: the transcriptome of aposymbiotic <i>A. pallida</i> . BMC Genomics, 2012, 13, 271.	1.2	99
2118	Comparative transcriptome analysis between planarian <i>Dugesia japonica</i> and other platyhelminth species. BMC Genomics, 2012, 13, 289.	1.2	34
2119	Oomycete transcriptomics database: A resource for oomycete transcriptomes. BMC Genomics, 2012, 13, 303.	1.2	7
2120	Genetic changes during a laboratory adaptive evolution process that allowed fast growth in glucose to an <i>Escherichia coli</i> strain lacking the major glucose transport system. BMC Genomics, 2012, 13, 385.	1.2	45
2121	Optimizing de novo common wheat transcriptome assembly using short-read RNA-Seq data. BMC Genomics, 2012, 13, 392.	1.2	104
2122	Transcriptome-based exon capture enables highly cost-effective comparative genomic data collection at moderate evolutionary scales. BMC Genomics, 2012, 13, 403.	1.2	253
2123	Personal receptor repertoires: olfaction as a model. BMC Genomics, 2012, 13, 414.	1.2	92
2124	Identification and analysis of pig chimeric mRNAs using RNA sequencing data. BMC Genomics, 2012, 13, 429.	1.2	15
2125	Comparative genomics of the white-rot fungi, <i>Phanerochaete carmosa</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. BMC Genomics, 2012, 13, 444.	1.2	125
2126	Genome sequencing and genetic breeding of a bioethanol <i>Saccharomyces cerevisiae</i> strain YJS329. BMC Genomics, 2012, 13, 479.	1.2	36
2127	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. BMC Genomics, 2012, 13, 586.	1.2	150
2128	Toward understanding the genetic basis of adaptation to high-elevation life in poikilothermic species: A comparative transcriptomic analysis of two ranid frogs, <i>Rana chensinensis</i> and <i>R. kukunoris</i> . BMC Genomics, 2012, 13, 588.	1.2	55
2129	Identification, characterization and distribution of transposable elements in the flax ( <i>Linum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	30
2130	Structural analysis of the genome of breast cancer cell line ZR-75-30 identifies twelve expressed fusion genes. BMC Genomics, 2012, 13, 719.	1.2	32
2131	A genomic scale map of genetic diversity in <i>Trypanosoma cruzi</i> . BMC Genomics, 2012, 13, 736.	1.2	16

#	ARTICLE	IF	CITATIONS
2132	Cutoffs and k-mers: implications from a transcriptome study in allopolyploid plants. <i>BMC Genomics</i> , 2012, 13, 92.	1.2	52
2133	RON is not a prognostic marker for resectable pancreatic cancer. <i>BMC Cancer</i> , 2012, 12, 395.	1.1	17
2134	Integrative transcriptome analysis suggest processing of a subset of long non-coding RNAs to small RNAs. <i>Biology Direct</i> , 2012, 7, 25.	1.9	71
2135	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. <i>BMC Medical Genomics</i> , 2012, 5, 17.	0.7	49
2136	Bisquinolinium compounds induce quadruplex-specific transcriptome changes in HeLa S3 cell lines. <i>BMC Research Notes</i> , 2012, 5, 138.	0.6	42
2137	Evolutionary patterns of RNA-based gene duplicates in <i>Caenorhabditis nematodes</i> coincide with their genomic features. <i>BMC Research Notes</i> , 2012, 5, 398.	0.6	7
2138	Rapid phylogenetic and functional classification of short genomic fragments with signature peptides. <i>BMC Research Notes</i> , 2012, 5, 460.	0.6	24
2139	Next-generation sequencing coupled with a cell-free display technology for high-throughput production of reliable interactome data. <i>Scientific Reports</i> , 2012, 2, 691.	1.6	25
2140	Performance Comparison of Multiple Microarray Platforms for Gene Expression Profiling. <i>Methods in Molecular Biology</i> , 2012, 802, 141-155.	0.4	13
2141	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit1.4.	25.8	86
2142	Molecular aspects of the antagonistic interaction of smoke-derived butenolides on the germination process of <i>Gallium aparine</i> and <i>Raphanus sativus</i> lettuce ( <i>Lactuca sativa</i> ) achenes. <i>New Phytologist</i> , 2012, 196, 1060-1073.	3.5	29
2144	Draft genome sequence of pigeonpea ( <i>Cajanus cajan</i> ), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89.	9.4	788
2145	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. <i>Journal of Cystic Fibrosis</i> , 2012, 11, 511-517.	0.3	17
2146	A randomized Numerical Aligner (rNA). <i>Journal of Computer and System Sciences</i> , 2012, 78, 1868-1882.	0.9	7
2147	A Survey of Copy Number Variation Detection Tools Based on High-Throughput Sequencing Data. <i>Current Protocols in Human Genetics</i> , 2012, 75, Unit7.19.	3.5	18
2149	Using BLAT to Find Sequence Similarity in Closely Related Genomes. , 2012, Chapter 10, Unit10.8.		36
2150	Evolution, Expression, and Developmental Function of Hox-Embedded miRNAs. <i>Current Topics in Developmental Biology</i> , 2012, 99, 31-57.	1.0	21
2151	Gene Prediction. <i>Methods in Molecular Biology</i> , 2012, 855, 175-201.	0.4	14

#	ARTICLE	IF	CITATIONS
2152	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	9.4	818
2154	A Draft Genome Sequence of <i>Nicotiana benthamiana</i> to Enhance Molecular Plant-Microbe Biology Research. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1523-1530.	1.4	411
2155	Role of Genomics and RNA-seq in Studies of Fungal Virulence. <i>Current Fungal Infection Reports</i> , 2012, 6, 267-274.	0.9	3
2156	High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57.		0
2157	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	13.7	1,204
2161	Compressive genomics. <i>Nature Biotechnology</i> , 2012, 30, 627-630.	9.4	99
2162	Comparing Fungal Genomes: Insight into Functional and Evolutionary Processes. <i>Methods in Molecular Biology</i> , 2012, 835, 531-548.	0.4	7
2163	Genomic Variation in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2012, 192, 533-598.	1.2	325
2164	Flexible and efficient genome tiling design with penalized uniqueness score. <i>BMC Bioinformatics</i> , 2012, 13, 323.	1.2	2
2165	Highly improved homopolymer aware nucleotide-protein alignments with 454 data. <i>BMC Bioinformatics</i> , 2012, 13, 230.	1.2	7
2166	The evolution of the class A scavenger receptors. <i>BMC Evolutionary Biology</i> , 2012, 12, 227.	3.2	52
2167	Newly evolved introns in human retrogenes provide novel insights into their evolutionary roles. <i>BMC Evolutionary Biology</i> , 2012, 12, 128.	3.2	19
2168	Meta-analytical biomarker search of EST expression data reveals three differentially expressed candidates. <i>BMC Genomics</i> , 2012, 13, S12.	1.2	9
2169	An integrated approach of comparative genomics and heritability analysis of pig and human on obesity trait: evidence for candidate genes on human chromosome 2. <i>BMC Genomics</i> , 2012, 13, 711.	1.2	28
2170	Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse <i>Escherichia coli</i> genomes. <i>BMC Genomics</i> , 2012, 13, 577.	1.2	205
2171	Genetic structure of community acquired methicillin-resistant <i>Staphylococcus aureus</i> USA300. <i>BMC Genomics</i> , 2012, 13, 508.	1.2	24
2172	High-resolution genotyping and mapping of recombination and gene conversion in the protozoan <i>Theileria parva</i> using whole genome sequencing. <i>BMC Genomics</i> , 2012, 13, 503.	1.2	41
2173	Ultra-high resolution HLA genotyping and allele discovery by highly multiplexed cDNA amplicon pyrosequencing. <i>BMC Genomics</i> , 2012, 13, 378.	1.2	38

#	ARTICLE	IF	CITATIONS
2174	Mutation spectrum of <i>Drosophila</i> CNVs revealed by breakpoint sequencing. <i>Genome Biology</i> , 2012, 13, R119.	13.9	15
2175	Orangutan Alu quiescence reveals possible source element: support for ancient backseat drivers. <i>Mobile DNA</i> , 2012, 3, 8.	1.3	11
2176	Activity-Dependent Human Brain Coding/Noncoding Gene Regulatory Networks. <i>Genetics</i> , 2012, 192, 1133-1148.	1.2	175
2177	Hospital and Community Ampicillin-Resistant <i>Enterococcus faecium</i> Are Evolutionarily Closely Linked but Have Diversified through Niche Adaptation. <i>PLoS ONE</i> , 2012, 7, e30319.	1.1	45
2178	CAPRG: Sequence Assembling Pipeline for Next Generation Sequencing of Non-Model Organisms. <i>PLoS ONE</i> , 2012, 7, e30370.	1.1	4
2179	Organizational Heterogeneity of Vertebrate Genomes. <i>PLoS ONE</i> , 2012, 7, e32076.	1.1	7
2180	Fast and Accurate Taxonomic Assignments of Metagenomic Sequences Using MetaBin. <i>PLoS ONE</i> , 2012, 7, e34030.	1.1	27
2181	Characterisation of Bovine Leukocyte Ig-like Receptors. <i>PLoS ONE</i> , 2012, 7, e34291.	1.1	22
2182	The <i>Chlamydia psittaci</i> Genome: A Comparative Analysis of Intracellular Pathogens. <i>PLoS ONE</i> , 2012, 7, e35097.	1.1	87
2183	Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS. <i>PLoS ONE</i> , 2012, 7, e35333.	1.1	50
2184	Experimental Verification of a Predicted Intronic MicroRNA in Human NGFR Gene with a Potential Pro-Apoptotic Function. <i>PLoS ONE</i> , 2012, 7, e35561.	1.1	29
2185	GHOSTM: A GPU-Accelerated Homology Search Tool for Metagenomics. <i>PLoS ONE</i> , 2012, 7, e36060.	1.1	22
2186	Transcript Profiling Identifies Dynamic Gene Expression Patterns and an Important Role for Nrf2/Keap1 Pathway in the Developing Mouse Esophagus. <i>PLoS ONE</i> , 2012, 7, e36504.	1.1	28
2187	The Molecular Mechanism of Action of the CR6261-Azichromycin Combination Found through Computational Analysis. <i>PLoS ONE</i> , 2012, 7, e37790.	1.1	1
2188	Multi-Locus Phylogeographic and Population Genetic Analysis of <i>Anolis carolinensis</i> : Historical Demography of a Genomic Model Species. <i>PLoS ONE</i> , 2012, 7, e38474.	1.1	40
2189	Large-Scale Transcriptome Analysis of Retroelements in the Migratory Locust, <i>Locusta migratoria</i> . <i>PLoS ONE</i> , 2012, 7, e40532.	1.1	30
2190	The Natural History of Class I Primate Alcohol Dehydrogenases Includes Gene Duplication, Gene Loss, and Gene Conversion. <i>PLoS ONE</i> , 2012, 7, e41175.	1.1	16
2191	Mating of the Stichotrichous Ciliate <i>Oxytricha trifallax</i> Induces Production of a Class of 27 nt Small RNAs Derived from the Parental Macronucleus. <i>PLoS ONE</i> , 2012, 7, e42371.	1.1	43

#	ARTICLE	IF	CITATIONS
2192	Identification of 34 Novel Proinflammatory Proteins in a Genome-Wide Macrophage Functional Screen. PLoS ONE, 2012, 7, e42388.	1.1	9
2193	SAPâ€™A Sequence Mapping and Analyzing Program for Long Sequence Reads Alignment and Accurate Variants Discovery. PLoS ONE, 2012, 7, e42887.	1.1	1
2194	Ruler Arrays Reveal Haploid Genomic Structural Variation. PLoS ONE, 2012, 7, e43210.	1.1	0
2195	Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of Salmonella Paratyphi A. PLoS ONE, 2012, 7, e45346.	1.1	26
2196	A Fish-Specific Transposable Element Shapes the Repertoire of p53 Target Genes in Zebrafish. PLoS ONE, 2012, 7, e46642.	1.1	17
2197	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	1.1	61
2198	Gene and Genome Parameters of Mammalian Liver Circadian Genes (LCGs). PLoS ONE, 2012, 7, e46961.	1.1	10
2199	A Hybrid Distance Measure for Clustering Expressed Sequence Tags Originating from the Same Gene Family. PLoS ONE, 2012, 7, e47216.	1.1	5
2200	A Streamlined Method for Detecting Structural Variants in Cancer Genomes by Short Read Paired-End Sequencing. PLoS ONE, 2012, 7, e48314.	1.1	21
2201	The Î¸,CstF-64 Polyadenylation Protein Controls Genome Expression in Testis. PLoS ONE, 2012, 7, e48373.	1.1	26
2202	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat ( <i>Artibeus jamaicensis</i> ). PLoS ONE, 2012, 7, e48472.	1.1	77
2203	Comprehensive Human Transcription Factor Binding Site Map for Combinatory Binding Motifs Discovery. PLoS ONE, 2012, 7, e49086.	1.1	5
2204	Exploring Pandora's Box: Potential and Pitfalls of Low Coverage Genome Surveys for Evolutionary Biology. PLoS ONE, 2012, 7, e49202.	1.1	31
2205	Mutation at the Human DIS80 Minisatellite Locus. Scientific World Journal, The, 2012, 2012, 1-8.	0.8	3
2206	The Human Transcriptome: An Unfinished Story. Genes, 2012, 3, 344-360.	1.0	121
2207	On the Analysis of the Illumina 450k Array Data: Probes Ambiguously Mapped to the Human Genome. Frontiers in Genetics, 2012, 3, 73.	1.1	45
2208	Diversity of Antisense and Other Non-Coding RNAs in Archaea Revealed by Comparative Small RNA Sequencing in Four <i>Pyrobaculum</i> Species. Frontiers in Microbiology, 2012, 3, 231.	1.5	46
2209	Comparative genomic and transcriptional analyses of CRISPR systems across the genus <i>Pyrobaculum</i> . Frontiers in Microbiology, 2012, 3, 251.	1.5	28

#	ARTICLE	IF	CITATIONS
2210	Characteristics of nucleosomes and linker DNA regions on the genome of the basidiomycete <i>Mixia osmundae</i> revealed by mono- and dinucleosome mapping. <i>Open Biology</i> , 2012, 2, 120043.	1.5	11
2211	A Transcriptome- and Marker-Based Systemic Analysis of Cervical Cancer. , 2012, , .		2
2213	Evolutionary history of <i>Myx</i> in teleosts and characterization of the duplicated <i>Myx</i> genes in goldfish embryos. <i>Molecular Reproduction and Development</i> , 2012, 79, 85-96.	1.0	20
2214	Probe mapping across multiple microarray platforms. <i>Briefings in Bioinformatics</i> , 2012, 13, 547-554.	3.2	25
2215	Bioinformatic Clonality Analysis of Next-Generation Sequencing-Derived Viral Vector Integration Sites. <i>Human Gene Therapy Methods</i> , 2012, 23, 111-118.	2.1	43
2216	Extended Survival of Glioblastoma Patients After Chemoprotective HSC Gene Therapy. <i>Science Translational Medicine</i> , 2012, 4, 133ra57.	5.8	91
2217	A beginner's guide to eukaryotic genome annotation. <i>Nature Reviews Genetics</i> , 2012, 13, 329-342.	7.7	553
2218	Effect of Periodontal Pathogens on the Metatranscriptome of a Healthy Multispecies Biofilm Model. <i>Journal of Bacteriology</i> , 2012, 194, 2082-2095.	1.0	85
2219	The banana ( <i>Musa acuminata</i> ) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	13.7	1,049
2220	Functional assignment of metagenomic data: challenges and applications. <i>Briefings in Bioinformatics</i> , 2012, 13, 711-727.	3.2	150
2221	A Universal Method for the Study of CR1 Retroposons in Nonmodel Bird Genomes. <i>Molecular Biology and Evolution</i> , 2012, 29, 2899-2903.	3.5	27
2222	Proviral loads of human T-cell lymphotropic virus Type 1 in asymptomatic carriers with different infection routes. <i>International Journal of Cancer</i> , 2012, 130, 2318-2326.	2.3	16
2223	Analysis of Metagenomics Data. , 2012, , 219-229.		1
2224	Short-Read Mapping. , 2012, , 107-125.		2
2225	Designing a transcriptome next-generation sequencing project for a nonmodel plant species. <i>American Journal of Botany</i> , 2012, 99, 257-266.	0.8	192
2226	Expressed Pseudogenes in the Transcriptional Landscape of Human Cancers. <i>Cell</i> , 2012, 149, 1622-1634.	13.5	250
2227	Meta-analysis of genetic association studies on bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 508-518.	1.1	64
2228	Genome sequence of foxtail millet ( <i>Setaria italica</i> ) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012, 30, 549-554.	9.4	636

#	ARTICLE	IF	CITATIONS
2229	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	9.4	864
2230	SEQuel: improving the accuracy of genome assemblies. <i>Bioinformatics</i> , 2012, 28, i188-i196.	1.8	56
2231	Analysis of High-Throughput Ancient DNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 840, 197-228.	0.4	177
2232	Graph concordance of next-generation sequence assemblies. <i>Bioinformatics</i> , 2012, 28, 13-16.	1.8	51
2233	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	9.4	946
2234	A tumour suppressor network relying on the polyamineâ€“hypusine axis. <i>Nature</i> , 2012, 487, 244-248.	13.7	133
2235	Large-scale collection and annotation of gene models for date palm ( <i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012, 79, 521-536.	2.0	26
2236	The chimpanzee GH locus: composition, organization, and evolution. <i>Mammalian Genome</i> , 2012, 23, 387-398.	1.0	6
2237	A pronounced evolutionary shift of the pseudoautosomal region boundary in house mice. <i>Mammalian Genome</i> , 2012, 23, 454-466.	1.0	37
2238	Polymorphic NumtS trace human population relationships. <i>Human Genetics</i> , 2012, 131, 757-771.	1.8	40
2239	Molecular cloning of large alternative transcripts based on comparative phylogenetic analysis and exploration of an EST database. <i>Analytical Biochemistry</i> , 2012, 424, 140-141.	1.1	1
2240	Hematopoietic stem cell expansion facilitates multilineage engraftment in a nonhuman primate cord blood transplantation model. <i>Experimental Hematology</i> , 2012, 40, 187-196.	0.2	19
2241	The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. <i>International Journal of Food Microbiology</i> , 2012, 157, 202-209.	2.1	102
2242	From genomics to metagenomics. <i>Current Opinion in Biotechnology</i> , 2012, 23, 72-76.	3.3	77
2243	A comparative transcriptome analysis reveals expression profiles conserved across three <i>Eimeria</i> spp. of domestic fowl and associated with multiple developmental stages. <i>International Journal for Parasitology</i> , 2012, 42, 39-48.	1.3	30
2244	CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus (Boophilus) microplus</i> . <i>International Journal for Parasitology</i> , 2012, 42, 161-169.	1.3	55
2245	Genome sequence of <i>Wickerhamomyces anomalus</i> DSM 6766 reveals genetic basis of biotechnologically important antimicrobial activities. <i>FEMS Yeast Research</i> , 2012, 12, 382-386.	1.1	40
2246	Characterizing complex structural variation in germline and somatic genomes. <i>Trends in Genetics</i> , 2012, 28, 43-53.	2.9	93

#	ARTICLE	IF	CITATIONS
2247	Search for an aetiological virus candidate in chronic lymphocytic leukaemia by extensive transcriptome analysis. <i>British Journal of Haematology</i> , 2012, 157, 709-717.	1.2	6
2248	Plntron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. <i>BMC Bioinformatics</i> , 2012, 13, S2.	1.2	8
2249	KIS SPLICE: de-novo calling alternative splicing events from RNA-seq data. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	85
2250	A context-based approach to identify the most likely mapping for RNA-seq experiments. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	14
2251	A recurrent translocation is mediated by homologous recombination between HERV-H elements. <i>Molecular Cytogenetics</i> , 2012, 5, 6.	0.4	25
2252	A cost-effective and universal strategy for complete prokaryotic genomic sequencing proposed by computer simulation. <i>BMC Research Notes</i> , 2012, 5, 80.	0.6	4
2253	Metagenomics - a guide from sampling to data analysis. <i>Microbial Informatics and Experimentation</i> , 2012, 2, 3.	7.6	680
2254	Discovery of <i>ALK</i> gene fusion from human non-small cell lung carcinoma cell line using next generation RNA sequencing. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 590-597.	1.5	80
2255	Adrenal androgen production in catarrhine primates and the evolution of adrenarche. <i>American Journal of Physical Anthropology</i> , 2012, 147, 389-400.	2.1	44
2256	Analysis of ESTs from a Normalized cDNA Library of the Rhizome Tip of <i>Oryza longistaminata</i> . <i>Journal of Plant Biology</i> , 2012, 55, 33-42.	0.9	5
2257	Molecular mechanisms of EGF signaling-dependent regulation of pipe, a gene crucial for dorsoventral axis formation in <i>Drosophila</i> . <i>Development Genes and Evolution</i> , 2012, 222, 1-17.	0.4	9
2258	Genome-wide expression profiling of schizophrenia using a large combined cohort. <i>Molecular Psychiatry</i> , 2013, 18, 215-225.	4.1	88
2259	Ratite Nonmonophyly: Independent Evidence from 40 Novel Loci. <i>Systematic Biology</i> , 2013, 62, 35-49.	2.7	73
2260	Epigenetics in the Human Brain. <i>Neuropsychopharmacology</i> , 2013, 38, 183-197.	2.8	65
2261	Microbial and viral metagenomes of a subtropical freshwater reservoir subject to climatic disturbances. <i>ISME Journal</i> , 2013, 7, 2374-2386.	4.4	81
2262	TNPO3 protects HIV-1 replication from CPSF6-mediated capsid stabilization in the host cell cytoplasm. <i>Retrovirology</i> , 2013, 10, 20.	0.9	129
2263	RECOT: a tool for the coordinate transformation of next-generation sequencing reads for comparative genomics and transcriptomics. <i>Source Code for Biology and Medicine</i> , 2013, 8, 6.	1.7	1
2264	Reference genomes and transcriptomes of <i>Nicotiana sylvestris</i> and <i>Nicotiana tomentosiformis</i> . <i>Genome Biology</i> , 2013, 14, R60.	3.8	192

#	ARTICLE	IF	CITATIONS
2265	Mapping gene activity of Arabidopsis root hairs. <i>Genome Biology</i> , 2013, 14, R67.	3.8	89
2266	Integrated analysis of recurrent properties of cancer genes to identify novel drivers. <i>Genome Biology</i> , 2013, 14, R52.	13.9	33
2267	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	13.9	276
2268	Retrotransposition of gene transcripts leads to structural variation in mammalian genomes. <i>Genome Biology</i> , 2013, 14, R22.	13.9	102
2269	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate <i>Salpingoeca rosetta</i> . <i>Genome Biology</i> , 2013, 14, R15.	13.9	219
2270	Additional annotation enhances potential for biologically-relevant analysis of the Illumina Infinium HumanMethylation450 BeadChip array. <i>Epigenetics and Chromatin</i> , 2013, 6, 4.	1.8	412
2271	Tumor-associated copy number changes in the circulation of patients with prostate cancer identified through whole-genome sequencing. <i>Genome Medicine</i> , 2013, 5, 30.	3.6	306
2272	<i>Populus euphratica</i> : the transcriptomic response to drought stress. <i>Plant Molecular Biology</i> , 2013, 83, 539-557.	2.0	84
2273	Transduction-Specific ATLAS Reveals a Cohort of Highly Active L1 Retrotransposons in Human Populations. <i>Human Mutation</i> , 2013, 34, 974-985.	1.1	38
2274	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013, 31, 759-765.	9.4	340
2275	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 2013, 45, 891-898.	9.4	350
2276	Instability at the FRA8I common fragile site disrupts the genomic integrity of the KIAA0146, CEBPD and PRKDC genes in colorectal cancer. <i>Cancer Letters</i> , 2013, 336, 85-95.	3.2	10
2277	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. <i>Statistics in Biosciences</i> , 2013, 5, 3-25.	0.6	15
2278	Bellerophon: a hybrid method for detecting interchromo-somal rearrangements at base pair resolution using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, S6.	1.2	16
2279	A multispecies polyadenylation site model. <i>BMC Bioinformatics</i> , 2013, 14, S9.	1.2	4
2280	Mobilomics in <i>Saccharomyces cerevisiae</i> strains. <i>BMC Bioinformatics</i> , 2013, 14, 102.	1.2	9
2281	Genome sequence-based species delimitation with confidence intervals and improved distance functions. <i>BMC Bioinformatics</i> , 2013, 14, 60.	1.2	5,139
2282	Phylogenomics of stronglycentrotid sea urchins. <i>BMC Evolutionary Biology</i> , 2013, 13, 88.	3.2	42

#	ARTICLE	IF	CITATIONS
2283	Genomics analysis of potassium channel genes in songbirds reveals molecular specializations of brain circuits for the maintenance and production of learned vocalizations. <i>BMC Genomics</i> , 2013, 14, 470.	1.2	31
2284	Genetic heterogeneity revealed by sequence analysis of <i>Mycobacterium tuberculosis</i> isolates from extra-pulmonary tuberculosis patients. <i>BMC Genomics</i> , 2013, 14, 404.	1.2	15
2285	Phase-defined complete sequencing of the HLA genes by next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 355.	1.2	121
2286	Optimizing de novo assembly of short-read RNA-seq data for phylogenomics. <i>BMC Genomics</i> , 2013, 14, 328.	1.2	189
2287	TRACER: a resource to study the regulatory architecture of the mouse genome. <i>BMC Genomics</i> , 2013, 14, 215.	1.2	15
2288	Construction of a plant-transformation-competent BIBAC library and genome sequence analysis of polyploid Upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2013, 14, 208.	1.2	15
2289	Prediction of constitutive A-to-I editing sites from human transcriptomes in the absence of genomic sequences. <i>BMC Genomics</i> , 2013, 14, 206.	1.2	32
2290	Transcriptome analyses reveal protein and domain families that delineate stage-related development in the economically important parasitic nematodes, <i>Ostertagia ostertagi</i> and <i>Cooperia oncophora</i> . <i>BMC Genomics</i> , 2013, 14, 118.	1.2	31
2291	Phylogenetic patterns of emergence of new genes support a model of frequent de novo evolution. <i>BMC Genomics</i> , 2013, 14, 117.	1.2	218
2292	Draft genome sequence of the rubber tree <i>Hevea brasiliensis</i> . <i>BMC Genomics</i> , 2013, 14, 75.	1.2	222
2293	Genome-wide identification, characterization, and expression analysis of lineage-specific genes within zebrafish. <i>BMC Genomics</i> , 2013, 14, 65.	1.2	39
2294	Genome reannotation of the lizard <i>Anolis carolinensis</i> based on 14 adult and embryonic deep transcriptomes. <i>BMC Genomics</i> , 2013, 14, 49.	1.2	55
2295	HDAM: a resource of human disease associated mutations from next generation sequencing studies. <i>BMC Medical Genomics</i> , 2013, 6, S16.	0.7	3
2296	Draft genome sequence of chickpea ( <i>Cicer arietinum</i> ) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	9.4	1,049
2297	MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. <i>Human Genetics</i> , 2013, 132, 1235-1243.	1.8	68
2298	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. <i>Human Genetics</i> , 2013, 132, 899-911.	1.8	13
2299	Latent Regulatory Potential of Human-Specific Repetitive Elements. <i>Molecular Cell</i> , 2013, 49, 262-272.	4.5	62
2300	The first genetic map of the American cranberry: exploration of synteny conservation and quantitative trait loci. <i>Theoretical and Applied Genetics</i> , 2013, 126, 673-692.	1.8	47

#	ARTICLE	IF	CITATIONS
2301	Directional RNA-seq reveals highly complex condition-dependent transcriptomes in <i>E. coli</i> K12 through accurate full-length transcripts assembling. <i>BMC Genomics</i> , 2013, 14, 520.	1.2	31
2302	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1131-1139.	3.6	1,416
2303	Accuracy and coverage assessment of <i>Oryctolagus cuniculus</i> (rabbit) genes encoding immunoglobulins in the whole genome sequence assembly (OryCun2.0) and localization of the IGH locus to chromosome 20. <i>Immunogenetics</i> , 2013, 65, 749-762.	1.2	19
2304	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. <i>Nature Genetics</i> , 2013, 45, 1232-1237.	9.4	334
2305	Resistance gene enrichment sequencing (R-Seq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. <i>Plant Journal</i> , 2013, 76, 530-544.	2.8	367
2306	PECONPI: A novel software for uncovering pathogenic copy number variations in non-syndromic sensorineural hearing loss and other genetically heterogeneous disorders. <i>American Journal of Medical Genetics, Part A</i> , 2013, 161, 2134-2147.	0.7	5
2307	Comparative study of de novo assembly and genome-guided assembly strategies for transcriptome reconstruction based on RNA-Seq. <i>Science China Life Sciences</i> , 2013, 56, 143-155.	2.3	55
2308	IDBA-MT: <i>De Novo</i> Assembler for Metatranscriptomic Data Generated from Next-Generation Sequencing Technology. <i>Journal of Computational Biology</i> , 2013, 20, 540-550.	0.8	45
2309	Transcriptional regulation of teleost <i>Aicda</i> genes. Part 1 – Suppressors of promiscuous promoters. <i>Fish and Shellfish Immunology</i> , 2013, 35, 1981-1987.	1.6	4
2310	Recessive Cancer Genes Engage in Negative Genetic Interactions with Their Functional Paralogs. <i>Cell Reports</i> , 2013, 5, 1519-1526.	2.9	19
2311	SSP: An interval integer linear programming for de novo transcriptome assembly and isoform discovery of RNA-seq reads. <i>Genomics</i> , 2013, 102, 507-514.	1.3	11
2312	No TAP63 promoter mutation is detected in bladder exstrophy-epispadias complex patients. <i>Journal of Pediatric Surgery</i> , 2013, 48, 2393-2400.	0.8	3
2313	Nuclear Wave1 Is Required for Reprogramming Transcription in Oocytes and for Normal Development. <i>Science</i> , 2013, 341, 1002-1005.	6.0	82
2314	BRANCH: boosting RNA-Seq assemblies with partial or related genomic sequences. <i>Bioinformatics</i> , 2013, 29, 1250-1259.	1.8	28
2315	Conservation and Functional Element Discovery in 20 Angiosperm Plant Genomes. <i>Molecular Biology and Evolution</i> , 2013, 30, 1729-1744.	3.5	60
2316	Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. <i>Nature Genetics</i> , 2013, 45, 937-941.	9.4	203
2317	Large-scale detection of in vivo transcription errors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18584-18589.	3.3	94
2318	Sequencing Y Chromosomes Resolves Discrepancy in Time to Common Ancestor of Males Versus Females. <i>Science</i> , 2013, 341, 562-565.	6.0	235

#	ARTICLE	IF	CITATIONS
2319	Reconstructing the Microbial Diversity and Function of Pre-Agricultural Tallgrass Prairie Soils in the United States. <i>Science</i> , 2013, 342, 621-624.	6.0	480
2320	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	9.0	467
2321	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat ( <i>Capra</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	9.4	479
2322	Enrichment of processed pseudogene transcripts in L1-ribonucleoprotein particles. <i>Human Molecular Genetics</i> , 2013, 22, 3730-3748.	1.4	50
2323	The High Polyphenol Content of Grapevine Cultivar Tannat Berries Is Conferred Primarily by Genes That Are Not Shared with the Reference Genome. <i>Plant Cell</i> , 2013, 25, 4777-4788.	3.1	138
2324	Assembler for de novo assembly of large genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3417-24.	3.3	41
2325	BlastGraph: a comparative genomics tool based on BLAST and graph algorithms. <i>Bioinformatics</i> , 2013, 29, 3222-3224.	1.8	10
2326	RNAâ€DNA differences in human mitochondria restore ancestral form of 16S ribosomal RNA. <i>Genome Research</i> , 2013, 23, 1789-1796.	2.4	49
2327	Inference of Alternative Splicing from Tiling Array Data. <i>Methods in Molecular Biology</i> , 2013, 1067, 143-164.	0.4	0
2328	Comprehensive Analysis of Human Endogenous Retrovirus Group HERV-W Locus Transcription in Multiple Sclerosis Brain Lesions by High-Throughput Amplicon Sequencing. <i>Journal of Virology</i> , 2013, 87, 13837-13852.	1.5	59
2329	A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225.	9.4	472
2330	Sex-specific expression, synthesis and localization of aromatase regulators in one-year-old Atlantic salmon ovaries and testes. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2013, 164, 236-246.	0.7	21
2331	An integrative bioinformatics pipeline for the genomewide identification of novel porcine microRNA genes. <i>Journal of Genetics</i> , 2013, 92, 587-593.	0.4	2
2332	Environmental bio-monitoring with high-throughput sequencing. <i>Briefings in Bioinformatics</i> , 2013, 14, 575-588.	3.2	26
2333	Iron availability modulates aberrant splicing of ferrochelatase through the iron- and 2-oxoglutarate dependent dioxygenase Jmjd6 and U2AF65. <i>Blood Cells, Molecules, and Diseases</i> , 2013, 51, 151-161.	0.6	31
2334	Transparency tools in gene patenting for informing policy and practice. <i>Nature Biotechnology</i> , 2013, 31, 1086-1093.	9.4	22
2335	Transcriptome-wide identification of RNA binding sites by CLIP-seq. <i>Methods</i> , 2013, 63, 32-40.	1.9	28
2336	CruzDB: software for annotation of genomic intervals with UCSC genome-browser database. <i>Bioinformatics</i> , 2013, 29, 3003-3006.	1.8	22

#	ARTICLE	IF	CITATIONS
2337	Genome-block expression-assisted association studies discover malaria resistance genes in <i>Anopheles gambiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20675-20680.	3.3	37
2338	An evaluation of the PacBio RS platform for sequencing and de novo assembly of a chloroplast genome. BMC Genomics, 2013, 14, 670.	1.2	146
2339	Construction of a high-density genetic map for sesame based on large scale marker development by specific length amplified fragment (SLAF) sequencing. BMC Plant Biology, 2013, 13, 141.	1.6	256
2340	Web Apollo: a web-based genomic annotation editing platform. Genome Biology, 2013, 14, R93.	13.9	329
2341	A SNP profiling panel for sample tracking in whole-exome sequencing studies. Genome Medicine, 2013, 5, 89.	3.6	57
2342	Transcriptome analyses of a Chinese hazelnut species <i>Corylus mandshurica</i> . BMC Plant Biology, 2013, 13, 152.	1.6	24
2343	HIV latency and integration site placement in five cell-based models. Retrovirology, 2013, 10, 90.	0.9	104
2344	Mena/VASP and $\beta$ -II-Spectrin complexes regulate cytoplasmic actin networks in cardiomyocytes and protect from conduction abnormalities and dilated cardiomyopathy. Cell Communication and Signaling, 2013, 11, 56.	2.7	38
2345	L_RNA_scaffolder: scaffolding genomes with transcripts. BMC Genomics, 2013, 14, 604.	1.2	129
2346	Fine mapping of V(D)J recombinase mediated rearrangements in human lymphoid malignancies. BMC Genomics, 2013, 14, 565.	1.2	9
2347	Endonuclease-containing Penelope retrotransposons in the bdelloid rotifer <i>Adineta vaga</i> exhibit unusual structural features and play a role in expansion of host gene families. Mobile DNA, 2013, 4, 19.	1.3	18
2348	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. BMC Genomics, 2013, 14, 550.	1.2	12
2349	De novo transcriptome assembly of drought tolerant CAM plants, <i>Agave deserti</i> and <i>Agave tequilana</i> . BMC Genomics, 2013, 14, 563.	1.2	115
2350	EGN: a wizard for construction of gene and genome similarity networks. BMC Evolutionary Biology, 2013, 13, 146.	3.2	50
2351	Obligate mutualism within a host drives the extreme specialization of a fig wasp genome. Genome Biology, 2013, 14, R141.	13.9	85
2352	The genome of <i>Romanomermis culicivorax</i> : revealing fundamental changes in the core developmental genetic toolkit in Nematoda. BMC Genomics, 2013, 14, 923.	1.2	43
2353	Biochemical and molecular characterization of <i>Treponema phagedenis</i> -like spirochetes isolated from a bovine digital dermatitis lesion. BMC Microbiology, 2013, 13, 280.	1.3	26
2354	Genome sequence and analysis of methylotrophic yeast <i>Hansenula polymorpha</i> DL1. BMC Genomics, 2013, 14, 837.	1.2	81

#	ARTICLE	IF	CITATIONS
2355	Detection limit of intragenic deletions with targeted array comparative genomic hybridization. BMC Genetics, 2013, 14, 116.	2.7	15
2356	OMACC: an Optical-Map-Assisted Contig Connector for improving de novo genome assembly. BMC Systems Biology, 2013, 7, S7.	3.0	4
2357	A detailed gene expression study of the Miscanthus genus reveals changes in the transcriptome associated with the rejuvenation of spring rhizomes. BMC Genomics, 2013, 14, 864.	1.2	27
2358	Spatial-temporal targeting of lung-specific mesenchyme by a Tbx4 enhancer. BMC Biology, 2013, 11, 111.	1.7	74
2359	Exploration of the gene fusion landscape of glioblastoma using transcriptome sequencing and copy number data. BMC Genomics, 2013, 14, 818.	1.2	72
2360	Efficient cellular fractionation improves RNA sequencing analysis of mature and nascent transcripts from human tissues. BMC Biotechnology, 2013, 13, 99.	1.7	47
2361	Development of SSR markers by next-generation sequencing of Korean landraces of chamoë (Cucumis) Tj ETQq0 0 0 rgBT /Overlock 10	1.0	7
2362	Genomic divergence between nine- and three-spined sticklebacks. BMC Genomics, 2013, 14, 756.	1.2	42
2363	A base composition analysis of natural patterns for the preprocessing of metagenome sequences. BMC Bioinformatics, 2013, 14, S5.	1.2	4
2364	The landscape of somatic mutations in Down syndrome-related myeloid disorders. Nature Genetics, 2013, 45, 1293-1299.	9.4	324
2365	A Metagenomics Portal for a Democratized Sequencing World. Methods in Enzymology, 2013, 531, 487-523.	0.4	16
2366	Methylation-specific digital karyotyping of HPV16E6E7-expressing human keratinocytes identifies novel methylation events in cervical carcinogenesis. Journal of Pathology, 2013, 231, 53-62.	2.1	48
2367	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. Methods in Enzymology, 2013, 531, 525-547.	0.4	28
2368	Genome-wide sequencing of <i>Phytophthora lateralis</i> reveals genetic variation among isolates from Lawson cypress ( <i>Chamaecyparis lawsoniana</i> ) in Northern Ireland. FEMS Microbiology Letters, 2013, 344, 179-185.	0.7	47
2369	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	0.4	553
2370	Reliable Identification of Genomic Variants from RNA-Seq Data. American Journal of Human Genetics, 2013, 93, 641-651.	2.6	319
2371	De novo assembly methods for next generation sequencing data. Tsinghua Science and Technology, 2013, 18, 500-514.	4.1	15
2374	Human Analysts at Superhuman Scales: What Has Friendly Software To Do?. Big Data, 2013, 1, 227-236.	2.1	1

#	ARTICLE	IF	CITATIONS
2375	The genome of the pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
2376	WebAUGUSTUS--a web service for training AUGUSTUS and predicting genes in eukaryotes. <i>Nucleic Acids Research</i> , 2013, 41, W123-W128.	6.5	253
2377	Estimating the Nucleotide Diversity in <i>Ceratodon purpureus</i> (Ditrichaceae) from 218 Conserved Exon-Primed, Intron-Spanning Nuclear Loci. <i>Applications in Plant Sciences</i> , 2013, 1, 1200387.	0.8	17
2378	The chemical interactome space between the human host and the genetically defined gut metabotypes. <i>ISME Journal</i> , 2013, 7, 730-742.	4.4	21
2379	Association of Intron Loss with High Mutation Rate in <i>Arabidopsis</i> : Implications for Genome Size Evolution. <i>Genome Biology and Evolution</i> , 2013, 5, 723-733.	1.1	39
2380	IDBA-tran: a more robust de novo de Bruijn graph assembler for transcriptomes with uneven expression levels. <i>Bioinformatics</i> , 2013, 29, i326-i334.	1.8	233
2381	Novel splicing events and post-transcriptional regulation of human estrogen receptor $\alpha$ E isoforms. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2013, 133, 120-128.	1.2	15
2382	gKaKs: the pipeline for genome-level Ka/Ks calculation. <i>Bioinformatics</i> , 2013, 29, 645-646.	1.8	47
2383	The UCSC genome browser and associated tools. <i>Briefings in Bioinformatics</i> , 2013, 14, 144-161.	3.2	736
2384	Next-generation sequencing meets genetic diagnostics: development of a comprehensive workflow for the analysis of BRCA1 and BRCA2 genes. <i>European Journal of Human Genetics</i> , 2013, 21, 864-870.	1.4	94
2385	neXtProt: Organizing Protein Knowledge in the Context of Human Proteome Projects. <i>Journal of Proteome Research</i> , 2013, 12, 293-298.	1.8	116
2386	Discovery of cross-reactive probes and polymorphic CpGs in the Illumina Infinium HumanMethylation450 microarray. <i>Epigenetics</i> , 2013, 8, 203-209.	1.3	1,276
2387	Current analysis platforms and methods for detecting copy number variation. <i>Physiological Genomics</i> , 2013, 45, 1-16.	1.0	64
2388	Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460.	6.0	522
2389	The Sorghum Genome Sequence: A Core Resource for Saccharinae Genomics. , 2013, , 105-119.		1
2390	Characterization of the Standard and Recommended <scp>CODIS</scp> Markers*. <i>Journal of Forensic Sciences</i> , 2013, 58, S169-72.	0.9	31
2391	The SNPs in the human genetic blueprint era. <i>New Biotechnology</i> , 2013, 30, 475-484.	2.4	10
2392	Structural organization and classification of cytochrome P450 genes in flax ( <i>Linum usitatissimum</i> L.). <i>Gene</i> , 2013, 513, 156-162.	1.0	37

#	ARTICLE	IF	CITATIONS
2393	A guide to in silico vaccine discovery for eukaryotic pathogens. <i>Briefings in Bioinformatics</i> , 2013, 14, 753-774.	3.2	29
2394	Decombinator: a tool for fast, efficient gene assignment in T-cell receptor sequences using a finite state machine. <i>Bioinformatics</i> , 2013, 29, 542-550.	1.8	101
2395	Mutation Detection by Clonal Sequencing of PCR Amplicons and Grouped Read Typing is Applicable to Clinical Diagnostics. <i>Human Mutation</i> , 2013, 34, 248-254.	1.1	8
2396	Mechanisms of Formation of Structural Variation in a Fully Sequenced Human Genome. <i>Human Mutation</i> , 2013, 34, 345-354.	1.1	34
2397	Microarray analysis of <i>Drosophila dicer</i> mutants reveals potential regulation of mitochondrial metabolism by endogenous siRNAs. <i>Journal of Cellular Biochemistry</i> , 2013, 114, 418-427.	1.2	10
2398	Detection of FLT3 Internal Tandem Duplication in Targeted, Short-Read-Length, Next-Generation Sequencing Data. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 81-93.	1.2	119
2399	Genome-wide, whole mount in situ analysis of transcriptional regulators in zebrafish embryos. <i>Developmental Biology</i> , 2013, 380, 351-362.	0.9	54
2400	Exploring the utility of human DNA methylation arrays for profiling mouse genomic DNA. <i>Genomics</i> , 2013, 102, 38-46.	1.3	36
2401	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. <i>Cell Reports</i> , 2013, 5, 1469-1478.	2.9	113
2402	Establishment and interpretation of the genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB isolate 7/3/14. <i>Journal of Biotechnology</i> , 2013, 167, 142-155.	1.9	93
2403	Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2013, 45, 1431-1438.	9.4	472
2404	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial $\alpha 5$ Integrin. <i>Cancer Research</i> , 2013, 73, 4579-4590.	0.4	97
2405	A Computational Workflow to Identify Allele-specific Expression and Epigenetic Modification in Maize. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 247-252.	3.0	10
2406	Building a Genome Analysis Pipeline to Predict Disease Risk and Prevent Disease. <i>Journal of Molecular Biology</i> , 2013, 425, 3993-4005.	2.0	31
2407	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013, 93, 876-890.	2.6	330
2408	The plasmidome of a <i>Salmonella enterica</i> serovar Derby isolated from pork meat. <i>Plasmid</i> , 2013, 69, 202-210.	0.4	20
2409	Hoxa-5 acts in segmented somites to regulate cervical vertebral morphology. <i>Mechanisms of Development</i> , 2013, 130, 226-240.	1.7	20
2410	Genomic Pathology of SLE-Associated Copy-Number Variation at the FCGR2C/FCGR3B/FCGR2B Locus. <i>American Journal of Human Genetics</i> , 2013, 92, 28-40.	2.6	63

#	ARTICLE	IF	CITATIONS
2411	Whole genome association of SNP with newborn calf cannon bone length. <i>Livestock Science</i> , 2013, 155, 186-196.	0.6	10
2412	Exome sequencing reveals a homozygous mutation in TWINKLE as the cause of multisystemic failure including renal tubulopathy in three siblings. <i>Molecular Genetics and Metabolism</i> , 2013, 108, 190-194.	0.5	22
2413	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. <i>Nature Methods</i> , 2013, 10, 122-124.	9.0	66
2414	Alternative Polyadenylation in Glioblastoma Multiforme and Changes in Predicted RNA Binding Protein Profiles. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 136-149.	1.0	14
2415	A specific family of interspersed repeats (SINEs) facilitates meiotic synapsis in mammals. <i>Molecular Cytogenetics</i> , 2013, 6, 1.	0.4	17
2416	Delimiting species in recent radiations with low levels of morphological divergence: A case study in Australian <i>Gehyra</i> geckos. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 135-143.	1.2	33
2417	The Coding and the Non-coding Transcriptome. , 2013, , 27-41.		3
2418	Beyond an <sc>AFLP</sc> genome scan towards the identification of immune genes involved in plague resistance in <i>Rattus rattus</i> from Madagascar. <i>Molecular Ecology</i> , 2013, 22, 354-367.	2.0	11
2419	Untangling the transcriptome from fungus-infected plant tissues. <i>Gene</i> , 2013, 519, 238-244.	1.0	6
2420	Saccharinae Bioinformatics Resources. , 2013, , 303-330.		0
2421	Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 12-17.	9.4	374
2422	Comparative Analysis of MicroRNA Promoters in <i>Arabidopsis</i> and Rice. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 56-60.	3.0	21
2423	Transcriptome analysis of Inbred Long Sleep and Inbred Short Sleep mice. <i>Genes, Brain and Behavior</i> , 2013, 12, 263-274.	1.1	15
2424	Circular RNAs are a large class of animal RNAs with regulatory potency. <i>Nature</i> , 2013, 495, 333-338.	13.7	6,474
2425	The cytochrome P450 genesis locus: the origin and evolution of animal cytochrome P450s. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120474.	1.8	147
2426	MosaicFinder: identification of fused gene families in sequence similarity networks. <i>Bioinformatics</i> , 2013, 29, 837-844.	1.8	29
2427	Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. <i>Science</i> , 2013, 339, 1063-1067.	6.0	230
2428	Whole transcriptome analysis using next-generation sequencing of model species <i>Setaria viridis</i> to support C4 photosynthesis research. <i>Plant Molecular Biology</i> , 2013, 83, 77-87.	2.0	53

#	ARTICLE	IF	CITATIONS
2429	<i>De novo</i> transcriptomic analyses for non-model organisms: an evaluation of methods across a multi-species data set. <i>Molecular Ecology Resources</i> , 2013, 13, 403-416.	2.2	71
2430	Integration of Genome-wide Approaches Identifies lncRNAs of Adult Neural Stem Cells and Their Progeny In Vivo. <i>Cell Stem Cell</i> , 2013, 12, 616-628.	5.2	224
2431	Computational solutions for omics data. <i>Nature Reviews Genetics</i> , 2013, 14, 333-346.	7.7	288
2432	Regional Modulation of a Stochastically Expressed Factor Determines Photoreceptor Subtypes in the <i>Drosophila</i> Retina. <i>Developmental Cell</i> , 2013, 25, 93-105.	3.1	44
2433	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to <i>Phytophthora infestans</i> . <i>Genomics</i> , 2013, 101, 249-255.	1.3	7
2434	Metagenomic study of the viruses of African straw-coloured fruit bats: Detection of a chiropteran poxvirus and isolation of a novel adenovirus. <i>Virology</i> , 2013, 441, 95-106.	1.1	121
2435	siRNA Screen Identifies the Phosphatase Acting on the G Protein-Coupled Thyrotropin-Releasing Hormone Receptor. <i>ACS Chemical Biology</i> , 2013, 8, 588-598.	1.6	5
2436	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013, 45, 701-706.	9.4	409
2437	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	9.4	364
2438	Bioclimatic, ecological, and phenotypic intermediacy and high genetic admixture in a natural hybrid of octoploid strawberries. <i>American Journal of Botany</i> , 2013, 100, 939-950.	0.8	36
2439	The high-quality draft genome of peach ( <i>Prunus persica</i> ) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	9.4	1,031
2440	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. <i>C3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63.	0.8	167
2441	Transcriptome of the <i>Lymantria dispar</i> (Gypsy Moth) Larval Midgut in Response to Infection by <i>Bacillus thuringiensis</i> . <i>PLoS ONE</i> , 2013, 8, e61190.	1.1	46
2442	A Practical Approach to Reconstruct Evolutionary History of Animal Sialyltransferases and Gain Insights into the Sequence-Function Relationships of Golgi-Glycosyltransferases. <i>Methods in Molecular Biology</i> , 2013, 1022, 73-97.	0.4	9
2443	Nucleotide resolution analysis of <i>TMPRSS2</i> and <i>ERG</i> rearrangements in prostate cancer. <i>Journal of Pathology</i> , 2013, 230, 174-183.	2.1	41
2444	Reversal of an ancient sex chromosome to an autosome in <i>Drosophila</i> . <i>Nature</i> , 2013, 499, 332-335.	13.7	201
2445	Sequence Alignment, Analysis, and Bioinformatic Pipelines. , 2013, , 59-77.		0
2446	Identification of novel exons and transcripts by comprehensive RNA-Seq of horn cancer transcriptome in <i>Bos indicus</i> . <i>Journal of Biotechnology</i> , 2013, 165, 37-44.	1.9	13

#	ARTICLE	IF	CITATIONS
2447	Ground tit genome reveals avian adaptation to living at high altitudes in the Tibetan plateau. <i>Nature Communications</i> , 2013, 4, 2071.	5.8	229
2448	Integrated molecular analysis of clear-cell renal cell carcinoma. <i>Nature Genetics</i> , 2013, 45, 860-867.	9.4	955
2449	Somatic Alterations Contributing to Metastasis of a Castration-Resistant Prostate Cancer. <i>Human Mutation</i> , 2013, 34, 1231-1241.	1.1	52
2450	Divergent low water potential response in <i>Arabidopsis thaliana</i> accessions Landsberg <i>erecta</i> and Shahdara. <i>Plant, Cell and Environment</i> , 2013, 36, 994-1008.	2.8	29
2451	CD34+ Expansion With Delta-1 and HOXB4 Promotes Rapid Engraftment and Transfusion Independence in a <i>Macaca nemestrina</i> Cord Blood Transplant Model. <i>Molecular Therapy</i> , 2013, 21, 1270-1278.	3.7	9
2452	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013, 45, 767-775.	9.4	176
2453	Clinical and cytogenetic features of a Potocki-Lupski syndrome with the shortest 0.25Mb microduplication in 17p11.2 including RAI1. <i>Brain and Development</i> , 2013, 35, 681-685.	0.6	13
2454	Better spaced seeds using Quadratic Residues. <i>Journal of Computer and System Sciences</i> , 2013, 79, 1144-1155.	0.9	17
2455	Analysis of western lowland gorilla ( <i>Gorilla gorilla gorilla</i> ) specific Alu repeats. <i>Mobile DNA</i> , 2013, 4, 26.	1.3	13
2456	Resequencing and Comparative Genomics of <i>Stagonospora nodorum</i> : Sectional Gene Absence and Effector Discovery. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 959-969.	0.8	66
2457	Development and Characterization of cDNA Resources for the Common Marmoset: One of the Experimental Primate Models. <i>DNA Research</i> , 2013, 20, 255-262.	1.5	12
2458	The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. <i>Nature Genetics</i> , 2013, 45, 567-572.	9.4	251
2459	High Occurrence of Functional New Chimeric Genes in Survey of Rice Chromosome 3 Short Arm Genome Sequences. <i>Genome Biology and Evolution</i> , 2013, 5, 1038-1048.	1.1	11
2460	Birth, decay, and reconstruction of an ancient <i>TRIMCyp</i> gene fusion in primate genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E583-92.	3.3	44
2461	Acquired Genetic Mechanisms of a Multiresistant Bacterium Isolated from a Treatment Plant Receiving Wastewater from Antibiotic Production. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7256-7263.	1.4	52
2462	The perfect neuroimaging-genetics-computation storm: collision of petabytes of data, millions of hardware devices and thousands of software tools. <i>Brain Imaging and Behavior</i> , 2014, 8, 311-22.	1.1	15
2463	STAR: ultrafast universal RNA-seq aligner. <i>Bioinformatics</i> , 2013, 29, 15-21.	1.8	35,376
2464	Design of RNAi Reagents for Invertebrate Model Organisms and Human Disease Vectors. <i>Methods in Molecular Biology</i> , 2013, 942, 315-346.	0.4	4

#	ARTICLE	IF	CITATIONS
2465	Reading between the lines: molecular characterization of five widely used canine lymphoid tumour cell lines. <i>Veterinary and Comparative Oncology</i> , 2013, 11, 30-50.	0.8	25
2466	PRICE: Software for the Targeted Assembly of Components of (Meta) Genomic Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 865-880.	0.8	250
2467	Transcriptome analyses of the human retina identify unprecedented transcript diversity and 3.5 Mb of novel transcribed sequence via significant alternative splicing and novel genes. <i>BMC Genomics</i> , 2013, 14, 486.	1.2	151
2468	Genome Sequences of Six Wheat-Infecting <i>Fusarium</i> Species Isolates. <i>Genome Announcements</i> , 2013, 1, .	0.8	38
2469	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. <i>MBio</i> , 2013, 4, .	1.8	106
2470	Steric antisense inhibition of AMPA receptor Q/R editing reveals tight coupling to intronic editing sites and splicing. <i>Nucleic Acids Research</i> , 2013, 41, 1113-1123.	6.5	29
2471	Insertional Mutagenesis Using <i>Tnt1</i> Retrotransposon in Potato. <i>Plant Physiology</i> , 2013, 163, 21-29.	2.3	30
2472	Microbiome in Human Health and Disease. <i>Science Progress</i> , 2013, 96, 153-170.	1.0	18
2473	Activity-regulated RNA editing in select neuronal subfields in hippocampus. <i>Nucleic Acids Research</i> , 2013, 41, 1124-1134.	6.5	73
2474	Analysis and design of RNA sequencing experiments for identifying RNA editing and other single-nucleotide variants. <i>Rna</i> , 2013, 19, 725-732.	1.6	60
2475	Integrated analysis of microRNA and mRNA expression: adding biological significance to microRNA target predictions. <i>Nucleic Acids Research</i> , 2013, 41, e146-e146.	6.5	58
2476	Substantial Loss of Conserved and Gain of Novel MicroRNA Families in Flatworms. <i>Molecular Biology and Evolution</i> , 2013, 30, 2619-2628.	3.5	84
2477	Inferring the choreography of parental genomes during fertilization from ultralarge-scale whole-transcriptome analysis. <i>Genes and Development</i> , 2013, 27, 2736-2748.	2.7	86
2478	A second-generation assembly of the <i>Drosophila simulans</i> genome provides new insights into patterns of lineage-specific divergence. <i>Genome Research</i> , 2013, 23, 89-98.	2.4	157
2479	A large-scale in vivo analysis reveals that TALENs are significantly more mutagenic than ZFNs generated using context-dependent assembly. <i>Nucleic Acids Research</i> , 2013, 41, 2769-2778.	6.5	115
2480	Low-Bandwidth and Non-Compute Intensive Remote Identification of Microbes from Raw Sequencing Reads. <i>PLoS ONE</i> , 2013, 8, e83784.	1.1	5
2481	Henipavirus Pathogenesis in Human Respiratory Epithelial Cells. <i>Journal of Virology</i> , 2013, 87, 3284-3294.	1.5	46
2482	nhmmer: DNA homology search with profile HMMs. <i>Bioinformatics</i> , 2013, 29, 2487-2489.	1.8	735

#	ARTICLE	IF	CITATIONS
2483	Exaptation of Transposable Elements into Novel Cis-Regulatory Elements: Is the Evidence Always Strong?. <i>Molecular Biology and Evolution</i> , 2013, 30, 1239-1251.	3.5	153
2484	DDBJ Read Annotation Pipeline: A Cloud Computing-Based Pipeline for High-Throughput Analysis of Next-Generation Sequencing Data. <i>DNA Research</i> , 2013, 20, 383-390.	1.5	68
2485	ASPic-GeneID: A Lightweight Pipeline for Gene Prediction and Alternative Isoforms Detection. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	8
2486	Transposable Elements Are Major Contributors to the Origin, Diversification, and Regulation of Vertebrate Long Noncoding RNAs. <i>PLoS Genetics</i> , 2013, 9, e1003470.	1.5	574
2487	The transcriptional response of Arabidopsis leaves to Fe deficiency. <i>Frontiers in Plant Science</i> , 2013, 4, 276.	1.7	152
2488	Evolutionary Dynamics of Sex-Biased Genes in a Hermaphrodite Fungus. <i>Molecular Biology and Evolution</i> , 2013, 30, 2435-2446.	3.5	27
2489	Probabilistic Inference of Biochemical Reactions in Microbial Communities from Metagenomic Sequences. <i>PLoS Computational Biology</i> , 2013, 9, e1002981.	1.5	17
2490	Detection of Human Endogenous Retrovirus K (HERV-K) Transcripts in Human Prostate Cancer Cell Lines. <i>Frontiers in Oncology</i> , 2013, 3, 180.	1.3	65
2491	Geneticâ€¦Genomic Replication to Identify Candidate Mouse Atherosclerosis Modifier Genes. <i>Journal of the American Heart Association</i> , 2013, 2, e005421.	1.6	16
2492	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	1.7	198
2493	ToPS: A Framework to Manipulate Probabilistic Models of Sequence Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003234.	1.5	6
2494	Genome-Wide Analysis Reveals Origin of Transfer RNA Genes from tRNA Halves. <i>Molecular Biology and Evolution</i> , 2013, 30, 2087-2098.	3.5	20
2495	The <i>Oxytricha trifallax</i> Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. <i>PLoS Biology</i> , 2013, 11, e1001473.	2.6	198
2496	Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003242.	1.5	88
2497	Microhomology-Mediated Mechanisms Underlie Non-Recurrent Disease-Causing Microdeletions of the FOXL2 Gene or Its Regulatory Domain. <i>PLoS Genetics</i> , 2013, 9, e1003358.	1.5	72
2498	The Diversity of Class II Transposable Elements in Mammalian Genomes Has Arisen from Ancestral Phylogenetic Splits during Ancient Waves of Proliferation through the Genome. <i>Molecular Biology and Evolution</i> , 2013, 30, 100-108.	3.5	15
2499	Systems Approaches to Modeling Chronic Mucosal Inflammation. <i>BioMed Research International</i> , 2013, 2013, 1-17.	0.9	34
2500	Identification of Novel MicroRNAs in Primates by Using the Synteny Information and Small RNA Deep Sequencing Data. <i>International Journal of Molecular Sciences</i> , 2013, 14, 20820-20832.	1.8	1

#	ARTICLE	IF	CITATIONS
2501	MGMT expression: insights into its regulation. 2. Single nucleotide polymorphisms. <i>Biopolymers and Cell</i> , 2013, 29, 367-374.	0.1	1
2502	Comparative Sex Chromosome Genomics in Snakes: Differentiation, Evolutionary Strata, and Lack of Global Dosage Compensation. <i>PLoS Biology</i> , 2013, 11, e1001643.	2.6	270
2503	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	1.5	232
2504	An Evolutionary Screen Highlights Canonical and Noncanonical Candidate Antiviral Genes within the Primate TRIM Gene Family. <i>Genome Biology and Evolution</i> , 2013, 5, 2141-2154.	1.1	45
2505	Automated design of paralogue ratio test assays for the accurate and rapid typing of copy number variation. <i>Bioinformatics</i> , 2013, 29, 1997-2003.	1.8	8
2506	Dual Host-Virus Arms Races Shape an Essential Housekeeping Protein. <i>PLoS Biology</i> , 2013, 11, e1001571.	2.6	116
2507	Comprehensive Analysis of Transcriptome Variation Uncovers Known and Novel Driver Events in T-Cell Acute Lymphoblastic Leukemia. <i>PLoS Genetics</i> , 2013, 9, e1003997.	1.5	110
2508	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. <i>PLoS Pathogens</i> , 2013, 9, e1003196.	2.1	183
2509	Trivalent Live Attenuated Influenza-Simian Immunodeficiency Virus Vaccines: Efficacy and Evolution of Cytotoxic T Lymphocyte Escape in Macaques. <i>Journal of Virology</i> , 2013, 87, 4146-4160.	1.5	17
2510	Identification of Biologically Relevant Enhancers in Human Erythroid Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 8433-8444.	1.6	49
2511	Mutually Exclusive Alterations in Secondary Metabolism Are Critical for the Uptake of Insoluble Iron Compounds by <i>Arabidopsis</i> and <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2013, 162, 1473-1485.	2.3	212
2512	Genome-Wide Detection of Condition-Sensitive Alternative Splicing in <i>Arabidopsis</i> Roots. <i>Plant Physiology</i> , 2013, 162, 1750-1763.	2.3	113
2513	Characterization of insertion sites and development of locus-specific assays for three broiler-derived subgroup E avian leukosis virus proviruses. <i>Avian Pathology</i> , 2013, 42, 373-378.	0.8	8
2514	Suppressor Analysis Reveals a Role for SecY in the SecA2-Dependent Protein Export Pathway of <i>Mycobacteria</i> . <i>Journal of Bacteriology</i> , 2013, 195, 4456-4465.	1.0	20
2515	Hominoid fission of chromosome 14/15 and the role of segmental duplications. <i>Genome Research</i> , 2013, 23, 1763-1773.	2.4	14
2516	Composition-based classification of short metagenomic sequences elucidates the landscapes of taxonomic and functional enrichment of microorganisms. <i>Nucleic Acids Research</i> , 2013, 41, e3-e3.	6.5	54
2517	OLEgo: fast and sensitive mapping of spliced mRNA-Seq reads using small seeds. <i>Nucleic Acids Research</i> , 2013, 41, 5149-5163.	6.5	116
2518	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e89-e89.	6.5	177

#	ARTICLE	IF	CITATIONS
2519	WebScipio: reconstructing alternative splice variants of eukaryotic proteins. <i>Nucleic Acids Research</i> , 2013, 41, W504-W509.	6.5	15
2520	Sex-biased gene expression at homomorphic sex chromosomes in emus and its implication for sex chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6453-6458.	3.3	146
2521	OikoBase: a genomics and developmental transcriptomics resource for the urochordate <i>Oikopleura dioica</i> . <i>Nucleic Acids Research</i> , 2013, 41, D845-D853.	6.5	53
2522	The Use of RelocaTE and Unassembled Short Reads to Produce High-Resolution Snapshots of Transposable Element Generated Diversity in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 949-957.	0.8	44
2523	Bacterial DNA Sifted from the <i>Trichoplax adhaerens</i> (Animalia: Placozoa) Genome Project Reveals a Putative Rickettsial Endosymbiont. <i>Genome Biology and Evolution</i> , 2013, 5, 621-645.	1.1	72
2524	Genome-Wide Characterization of Adaptation and Speciation in Tiger Swallowtail Butterflies Using De Novo Transcriptome Assemblies. <i>Genome Biology and Evolution</i> , 2013, 5, 1233-1245.	1.1	29
2525	SlopMap: A Software Application Tool for Quick and Flexible Identification of Similar Sequences Using Exact K-Mer Matching. <i>Journal of Data Mining in Genomics &amp; Proteomics</i> , 2013, 04, .	0.5	2
2526	Genomic Diversity and Fitness of <i>E. coli</i> Strains Recovered from the Intestinal and Urinary Tracts of Women with Recurrent Urinary Tract Infection. <i>Science Translational Medicine</i> , 2013, 5, 184ra60.	5.8	148
2527	Identification of Stanniocalcin 2 as a Novel Aryl Hydrocarbon Receptor Target Gene. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2013, 344, 579-588.	1.3	27
2528	MGAviewer: a desktop visualization tool for analysis of metagenomics alignment data. <i>Bioinformatics</i> , 2013, 29, 122-123.	1.8	18
2529	Lizards and LINEs: Selection and Demography Affect the Fate of L1 Retrotransposons in the Genome of the Green Anole ( <i>Anolis carolinensis</i> ). <i>Genome Biology and Evolution</i> , 2013, 5, 1754-1768.	1.1	29
2530	TrueSight: a new algorithm for splice junction detection using RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e51-e51.	6.5	31
2531	Reprever: resolving low-copy duplicated sequences using template driven assembly. <i>Nucleic Acids Research</i> , 2013, 41, e128-e128.	6.5	7
2532	Boosting the Detection of Transposable Elements Using Machine Learning. <i>Advances in Intelligent Systems and Computing</i> , 2013, , 85-91.	0.5	8
2533	ReviSTER: an automated pipeline to revise misaligned reads to simple tandem repeats. <i>Bioinformatics</i> , 2013, 29, 1734-1741.	1.8	21
2534	GnpIS: an information system to integrate genetic and genomic data from plants and fungi. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat058.	1.4	43
2535	Horizontal Transfer of DNA from the Mitochondrial to the Plastid Genome and Its Subsequent Evolution in Milkweeds (Apocynaceae). <i>Genome Biology and Evolution</i> , 2013, 5, 1872-1885.	1.1	129
2536	VirusFinder: Software for Efficient and Accurate Detection of Viruses and Their Integration Sites in Host Genomes through Next Generation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e64465.	1.1	139

#	ARTICLE	IF	CITATIONS
2537	Genome sequence of ground tit <i>Pseudopodoces humilis</i> and its adaptation to high altitude. <i>Genome Biology</i> , 2013, 14, R29.	13.9	81
2538	Separating homeologs by phasing in the tetraploid wheat transcriptome. <i>Genome Biology</i> , 2013, 14, R66.	3.8	126
2539	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89.	13.9	192
2540	Genome-wide analysis of light-regulated alternative splicing mediated by photoreceptors in <i>Physcomitrella patens</i> . <i>Genome Biology</i> , 2013, 15, R10.	13.9	89
2541	rDNA-directed integration by an HIV-1 integrase- $\Psi$ I-Ppol fusion protein. <i>Nucleic Acids Research</i> , 2013, 41, e61-e61.	6.5	20
2542	TriageTools: tools for partitioning and prioritizing analysis of high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e86-e86.	6.5	7
2543	Compensation of the Metabolic Costs of Antibiotic Resistance by Physiological Adaptation in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3752-3762.	1.4	68
2544	Endogenous Gammaretrovirus Acquisition in <i>Mus musculus</i> Subspecies Carrying Functional Variants of the XPR1 Virus Receptor. <i>Journal of Virology</i> , 2013, 87, 9845-9855.	1.5	16
2545	A Guide to Bioinformatics for Immunologists. <i>Frontiers in Immunology</i> , 2013, 4, 416.	2.2	10
2546	Probabilistic error correction for RNA sequencing. <i>Nucleic Acids Research</i> , 2013, 41, e109-e109.	6.5	68
2547	Bioinformatic and molecular characterization of cathelicidin-like peptides isolated from the green lizard <i>Anolis carolinensis</i> (Reptilia: Lepidosauria: Iguanidae). <i>Italian Journal of Zoology</i> , 2013, 80, 177-186.	0.6	16
2548	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	5.8	229
2549	Genotypic adaptations associated with prolonged persistence of <i>Lactobacillus plantarum</i> in the murine digestive tract. <i>Biotechnology Journal</i> , 2013, 8, 895-904.	1.8	19
2550	Lack of evidence for existence of noncanonical RNA editing. <i>Nature Biotechnology</i> , 2013, 31, 19-20.	9.4	87
2551	Reconfigurable Accelerator for the Word-Matching Stage of BLASTN. <i>IEEE Transactions on Very Large Scale Integration (VLSI) Systems</i> , 2013, 21, 659-669.	2.1	18
2552	Rice Annotation Project Database (RAP-DB): An Integrative and Interactive Database for Rice Genomics. <i>Plant and Cell Physiology</i> , 2013, 54, e6-e6.	1.5	614
2553	Defining the Functional Potential and Active Community Members of a Sediment Microbial Community in a High-Arctic Hypersaline Subzero Spring. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3637-3648.	1.4	51
2554	Building localized bioinformatics platform based on Galaxy and high performance computing cluster. , 2013, , .		1

#	ARTICLE	IF	CITATIONS
2555	A scalable data analysis platform for metagenomics. , 2013, , .		25
2556	Contrasting Patterns of Transposable Element and Satellite Distribution on Sex Chromosomes (XY1Y2) in the Dioecious Plant <i>Rumex acetosa</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 769-782.	1.1	55
2557	RCpedia: a database of retrocopied genes. <i>Bioinformatics</i> , 2013, 29, 1235-1237.	1.8	32
2558	Using Chimaeric Expression Sequence Tag as the Reference to Identify Three-Dimensional Chromosome Contacts. <i>DNA Research</i> , 2013, 20, 45-53.	1.5	2
2559	The shared genomic architecture of human nucleolar organizer regions. <i>Genome Research</i> , 2013, 23, 2003-2012.	2.4	107
2560	Draft genome of the kiwifruit <i>Actinidia chinensis</i> . <i>Nature Communications</i> , 2013, 4, 2640.	5.8	423
2561	Landscape of DNA Virus Associations across Human Malignant Cancers: Analysis of 3,775 Cases Using RNA-Seq. <i>Journal of Virology</i> , 2013, 87, 8916-8926.	1.5	187
2562	Inactivation of the RB family prevents thymus involution and promotes thymic function by direct control of <i>Foxn1</i> expression. <i>Journal of Experimental Medicine</i> , 2013, 210, 1087-1097.	4.2	59
2564	Human GGT2 Does Not Autocleave into a Functional Enzyme: A Cautionary Tale for Interpretation of Microarray Data on Redox Signaling. <i>Antioxidants and Redox Signaling</i> , 2013, 19, 1877-1888.	2.5	13
2565	Genomics of <i>Loa loa</i> , a <i>Wolbachia</i> -free filarial parasite of humans. <i>Nature Genetics</i> , 2013, 45, 495-500.	9.4	173
2566	The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013, 4, 2433.	5.8	217
2567	Spliced DNA Sequences in the <i>Paramecium</i> Germline: Their Properties and Evolutionary Potential. <i>Genome Biology and Evolution</i> , 2013, 5, 1200-1211.	1.1	19
2568	Genome Sequencing Identifies Two Nearly Unchanged Strains of Persistent <i>Listeria monocytogenes</i> Isolated at Two Different Fish Processing Plants Sampled 6 Years Apart. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2944-2951.	1.4	110
2569	Noncoder: a web interface for exon array-based detection of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2013, 41, e20-e20.	6.5	54
2570	Targeted-capture massively-parallel sequencing enables robust detection of clinically informative mutations from formalin-fixed tumours. <i>Scientific Reports</i> , 2013, 3, 3494.	1.6	44
2571	Phenotypic Plasticity, CYP19A1 Pleiotropy, and Maladaptive Selection in Developmental Disorders. <i>SAGE Open</i> , 2013, 3, 215824401348447.	0.8	0
2572	Combined methylation mapping of 5mC and 5hmC during early embryonic stages in bovine. <i>BMC Genomics</i> , 2013, 14, 406.	1.2	15
2573	Data compression for sequencing data. <i>Algorithms for Molecular Biology</i> , 2013, 8, 25.	0.3	82

#	ARTICLE	IF	CITATIONS
2574	Answering biological questions by querying k�mer databases. <i>Concurrency Computation Practice and Experience</i> , 2013, 25, 497-509.	1.4	21
2575	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. <i>Genome Biology</i> , 2013, 14, r53.	3.8	225
2576	MisPred: a resource for identification of erroneous protein sequences in public databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat053.	1.4	17
2577	Global regulation of alternative splicing by adenosine deaminase acting on RNA (ADAR). <i>Rna</i> , 2013, 19, 591-604.	1.6	125
2578	Sequencing of the Dutch Elm Disease Fungus Genome Using the Roche/454 GS-FLX Titanium System in a Comparison of Multiple Genomics Core Facilities. <i>Journal of Biomolecular Techniques</i> , 2013, 24, jbt.12-2401-005.	0.8	47
2579	Deep Sequencing of RNA from Ancient Maize Kernels. <i>PLoS ONE</i> , 2013, 8, e50961.	1.1	38
2580	Cloning, Annotation and Developmental Expression of the Chicken Intestinal MUC2 Gene. <i>PLoS ONE</i> , 2013, 8, e53781.	1.1	37
2581	Genetic Diversity, Linkage Disequilibrium and Selection Signatures in Chinese and Western Pigs Revealed by Genome-Wide SNP Markers. <i>PLoS ONE</i> , 2013, 8, e56001.	1.1	234
2582	Transforming Growth Factor Beta Receptor 2 (TGFB2) Changes Sialylation in the Microsatellite Unstable (MSI) Colorectal Cancer Cell Line HCT116. <i>PLoS ONE</i> , 2013, 8, e57074.	1.1	28
2583	Analysis of Metagenomic Data Containing High Biodiversity Levels. <i>PLoS ONE</i> , 2013, 8, e58118.	1.1	12
2584	PSimScan: Algorithm and Utility for Fast Protein Similarity Search. <i>PLoS ONE</i> , 2013, 8, e58505.	1.1	7
2585	Contradiction between Plastid Gene Transcription and Function Due to Complex Posttranscriptional Splicing: An Exemplary Study of <i>yfc15</i> Function and Evolution in Angiosperms. <i>PLoS ONE</i> , 2013, 8, e59620.	1.1	55
2586	Construction of Customized Sub-Databases from NCBI-nr Database for Rapid Annotation of Huge Metagenomic Datasets Using a Combined BLAST and MEGAN Approach. <i>PLoS ONE</i> , 2013, 8, e59831.	1.1	49
2587	Transcriptome Analysis of the Differentially Expressed Genes in the Male and Female Shrub Willows ( <i>Salix suchowensis</i> ). <i>PLoS ONE</i> , 2013, 8, e60181.	1.1	38
2588	Overexpression of Full-Length Centrobin Rescues Limb Malformation but Not Male Fertility of the Hypodactylous (hd) Rats. <i>PLoS ONE</i> , 2013, 8, e60859.	1.1	7
2589	Mechanisms of Intron Loss and Gain in the Fission Yeast <i>Schizosaccharomyces</i> . <i>PLoS ONE</i> , 2013, 8, e61683.	1.1	27
2590	Simultaneous Transcriptome Analysis of Sorghum and <i>Bipolaris sorghicola</i> by Using RNA-seq in Combination with De Novo Transcriptome Assembly. <i>PLoS ONE</i> , 2013, 8, e62460.	1.1	79
2591	High-Throughput miRNA and mRNA Sequencing of Paired Colorectal Normal, Tumor and Metastasis Tissues and Bioinformatic Modeling of miRNA-1 Therapeutic Applications. <i>PLoS ONE</i> , 2013, 8, e67461.	1.1	53

#	ARTICLE	IF	CITATIONS
2592	Complete Genome Analysis of a <i>Haemophilus parasuis</i> Serovar 12 Strain from China. PLoS ONE, 2013, 8, e68350.	1.1	12
2593	A Systems-Genetics Approach and Data Mining Tool to Assist in the Discovery of Genes Underlying Complex Traits in <i>Oryza sativa</i> . PLoS ONE, 2013, 8, e68551.	1.1	26
2594	Genomic Treasure Troves: Complete Genome Sequencing of Herbarium and Insect Museum Specimens. PLoS ONE, 2013, 8, e69189.	1.1	215
2595	Analysis of Unannotated Equine Transcripts Identified by mRNA Sequencing. PLoS ONE, 2013, 8, e70125.	1.1	16
2596	Comprehensive Genomic Characterization of <i>Campylobacter</i> Genus Reveals Some Underlying Mechanisms for its Genomic Diversification. PLoS ONE, 2013, 8, e70241.	1.1	16
2597	RNA-Seq Reveals Infection-Related Gene Expression Changes in <i>Phytophthora capsici</i> . PLoS ONE, 2013, 8, e74588.	1.1	49
2598	Signatures of Rapid Evolution in Urban and Rural Transcriptomes of White-Footed Mice ( <i>Peromyscus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	68
2599	Variant Splicing and Influence of Ionizing Radiation on Human Endogenous Retrovirus K (HERV-K) Transcripts in Cancer Cell Lines. PLoS ONE, 2013, 8, e76472.	1.1	18
2600	Evaluation of Alignment Algorithms for Discovery and Identification of Pathogens Using RNA-Seq. PLoS ONE, 2013, 8, e76935.	1.1	37
2601	Optimal Scaling of Digital Transcriptomes. PLoS ONE, 2013, 8, e77885.	1.1	44
2602	Cross-Platform Prediction of Gene Expression Signatures. PLoS ONE, 2013, 8, e79228.	1.1	9
2603	Comparative Transcriptome Analysis of Two Rice Varieties in Response to Rice Stripe Virus and Small Brown Planthoppers during Early Interaction. PLoS ONE, 2013, 8, e82126.	1.1	94
2604	Genome-Wide Survey of Cold Stress Regulated Alternative Splicing in <i>Arabidopsis thaliana</i> with Tiling Microarray. PLoS ONE, 2013, 8, e66511.	1.1	64
2605	Development of Peptide Nucleic Acid Probes for Detection of the HER2 Oncogene. PLoS ONE, 2013, 8, e58870.	1.1	19
2606	SLAF-seq: An Efficient Method of Large-Scale De Novo SNP Discovery and Genotyping Using High-Throughput Sequencing. PLoS ONE, 2013, 8, e58700.	1.1	791
2607	MATCHCLIP: locate precise breakpoints for copy number variation using CIGAR string by matching soft clipped reads. <i>Frontiers in Genetics</i> , 2013, 4, 157.	1.1	16
2608	Sense-antisense gene pairs: sequence, transcription, and structure are not conserved between human and mouse. <i>Frontiers in Genetics</i> , 2013, 4, 183.	1.1	46
2609	The spliced leader trans-splicing mechanism in different organisms: molecular details and possible biological roles. <i>Frontiers in Genetics</i> , 2013, 4, 199.	1.1	29

#	ARTICLE	IF	CITATIONS
2610	A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. <i>Frontiers in Genetics</i> , 2013, 4, 209.	1.1	10
2611	Metagenomic evidence for sulfur lithotrophy by Epsilonproteobacteria as the major energy source for primary productivity in a sub-aerial arctic glacial deposit, Borup Fiord Pass. <i>Frontiers in Microbiology</i> , 2013, 4, 63.	1.5	42
2612	Monocular inhibition reveals temporal and spatial changes in gene expression in the primary visual cortex of marmoset. <i>Frontiers in Neural Circuits</i> , 2013, 7, 43.	1.4	15
2613	Trapping DNA Replication Origins from the Human Genome. <i>Genes</i> , 2013, 4, 198-225.	1.0	0
2614	Shared and Unique Proteins in Human, Mouse and Rat Saliva Proteomes: Footprints of Functional Adaptation. <i>Proteomes</i> , 2013, 1, 275-289.	1.7	16
2615	Comprehensive Analysis of Alternative Splicing in <i>Digitalis purpurea</i> by Strand-Specific RNA-Seq. <i>PLoS ONE</i> , 2014, 9, e106001.	1.1	12
2616	De Novo Sequencing, Assembly, and Analysis of the Root Transcriptome of <i>Persea americana</i> (Mill.) in Response to <i>Phytophthora cinnamomi</i> and Flooding. <i>PLoS ONE</i> , 2014, 9, e86399.	1.1	38
2617	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. <i>PLoS ONE</i> , 2014, 9, e85568.	1.1	57
2618	C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. <i>PLoS ONE</i> , 2014, 9, e86476.	1.1	19
2619	Single Cell Genomics of Uncultured, Health-Associated <i>Tannerella</i> BU063 (Oral Taxon 286) and Comparison to the Closely Related Pathogen <i>Tannerella forsythia</i> . <i>PLoS ONE</i> , 2014, 9, e89398.	1.1	29
2620	The Impacts of Read Length and Transcriptome Complexity for De Novo Assembly: A Simulation Study. <i>PLoS ONE</i> , 2014, 9, e94825.	1.1	32
2621	A Method for Detecting Long Non-Coding RNAs with Tiled RNA Expression Microarrays. <i>PLoS ONE</i> , 2014, 9, e99899.	1.1	12
2622	Repair of Oxidative DNA Base Damage in the Host Genome Influences the HIV Integration Site Sequence Preference. <i>PLoS ONE</i> , 2014, 9, e103164.	1.1	12
2623	SNP Identification by Transcriptome Sequencing and Candidate Gene-Based Association Analysis for Heat Tolerance in the Bay Scallop <i>Argopecten irradians</i> . <i>PLoS ONE</i> , 2014, 9, e104960.	1.1	20
2624	LncRBase: An Enriched Resource for lncRNA Information. <i>PLoS ONE</i> , 2014, 9, e108010.	1.1	60
2625	NSIT: Novel Sequence Identification Tool. <i>PLoS ONE</i> , 2014, 9, e108011.	1.1	1
2626	Effective Extraction and Assembly Methods for Simultaneously Obtaining Plastid and Mitochondrial Genomes. <i>PLoS ONE</i> , 2014, 9, e108291.	1.1	13
2627	Evaluation of a Hybrid Approach Using UBLAST and BLASTX for Metagenomic Sequences Annotation of Specific Functional Genes. <i>PLoS ONE</i> , 2014, 9, e110947.	1.1	36

#	ARTICLE	IF	CITATIONS
2628	RADIA: RNA and DNA Integrated Analysis for Somatic Mutation Detection. PLoS ONE, 2014, 9, e111516.	1.1	90
2629	Detection Theory in Identification of RNA-DNA Sequence Differences Using RNA-Sequencing. PLoS ONE, 2014, 9, e112040.	1.1	7
2630	Comparative Genomic Analysis Shows That Avian Pathogenic Escherichia coli Isolate IMT5155 (O2:K1:H5;) Tj ETQq0 0 0 rgBT /Overlock PLoS ONE, 2014, 9, e112048.	1.1	75
2631	Integrated Analysis of Whole Genome and Transcriptome Sequencing Reveals Diverse Transcriptomic Aberrations Driven by Somatic Genomic Changes in Liver Cancers. PLoS ONE, 2014, 9, e114263.	1.1	79
2632	Transcriptional Consequence and Impaired Gametogenesis with High-Grade Aneuploidy in Arabidopsis thaliana. PLoS ONE, 2014, 9, e114617.	1.1	6
2633	Comparative Genome Analyses Reveal Distinct Structure in the Saltwater Crocodile MHC. PLoS ONE, 2014, 9, e114631.	1.1	22
2634	BLAT-Based Comparative Analysis for Transposable Elements: BLATCAT. BioMed Research International, 2014, 2014, 1-7.	0.9	0
2635	Objective and Comprehensive Evaluation of Bisulfite Short Read Mapping Tools. Advances in Bioinformatics, 2014, 2014, 1-11.	5.7	52
2636	High-Performance Integrated Virtual Environment (HIVE) Tools and Applications for Big Data Analysis. Genes, 2014, 5, 957-981.	1.0	76
2637	Genome-wide mapping in a house mouse hybrid zone reveals hybrid sterility loci and Dobzhansky-Muller interactions. ELife, 2014, 3, .	2.8	107
2638	Suppression of cell wall-related genes associated with stunting of Oryza glaberrima infected with Rice tungro spherical virus. Frontiers in Microbiology, 2014, 5, 26.	1.5	26
2639	The role of photorespiration during the evolution of C4 photosynthesis in the genus Flaveria. ELife, 2014, 3, e02478.	2.8	182
2640	The Functional Potential of Microbial Communities in Hydraulic Fracturing Source Water and Produced Water from Natural Gas Extraction Characterized by Metagenomic Sequencing. PLoS ONE, 2014, 9, e107682.	1.1	51
2641	Four Generations of Sequencing- Is it Ready for the Clinic Yet?. Journal of Next Generation Sequencing & Applications, 2014, 01, .	0.3	5
2642	The early diverging ascomycetous budding yeast Saitoella complicata has three histone deacetylases belonging to the Clr6, Hos2, and Rpd3 lineages. Journal of General and Applied Microbiology, 2014, 60, 7-12.	0.4	5
2643	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0
2644	Algorithms for Mapping High-Throughput DNA Sequences**Jes Frellsen and Peter Menzel contributed equally.. , 2014, , 41-50.		5
2645	Gene and genome duplications and the origin of C4 photosynthesis: Birth of a trait in the Cleomaceae. Current Plant Biology, 2014, 1, 2-9.	2.3	46

#	ARTICLE	IF	CITATIONS
2646	Genome Sequence of <i>Fusarium graminearum</i> Isolate CS3005. <i>Genome Announcements</i> , 2014, 2, .	0.8	32
2647	A comprehensive survey of non-canonical splice sites in the human transcriptome. <i>Nucleic Acids Research</i> , 2014, 42, 10564-10578.	6.5	109
2649	Fungal Genomics. <i>Advances in Botanical Research</i> , 2014, , 1-52.	0.5	25
2650	Whole-Genome Sequencing for Rapid and Accurate Identification of Bacterial Transmission Pathways. <i>Methods in Microbiology</i> , 2014, 41, 123-152.	0.4	4
2651	Highly Variable Recombinational Landscape Modulates Efficacy of Natural Selection in Birds. <i>Genome Biology and Evolution</i> , 2014, 6, 2061-2075.	1.1	36
2652	The nuclear hormone receptor family member NR5A2 controls aspects of multipotent progenitor cell formation and acinar differentiation during pancreatic organogenesis. <i>Development (Cambridge)</i> , 2014, 141, 3123-3133.	1.2	92
2653	Transcriptome sequencing and analysis of <i>Plasmodium gallinaceum</i> reveals polymorphisms and selection on the apical membrane antigen-1. <i>Malaria Journal</i> , 2014, 13, 382.	0.8	25
2654	Dynamic evolution of the alpha ( $\hat{I}_\pm$ ) and beta ( $\hat{I}_2$ ) keratins has accompanied integument diversification and the adaptation of birds into novel lifestyles. <i>BMC Evolutionary Biology</i> , 2014, 14, 249.	3.2	84
2655	Tangram: a comprehensive toolbox for mobile element insertion detection. <i>BMC Genomics</i> , 2014, 15, 795.	1.2	54
2656	Unfixed Endogenous Retroviral Insertions in the Human Population. <i>Journal of Virology</i> , 2014, 88, 9529-9537.	1.5	118
2657	Estimating overannotation across prokaryotic genomes using BLAST+, UBLAST, LAST and BLAT. <i>BMC Research Notes</i> , 2014, 7, 651.	0.6	6
2658	Host and viral determinants for MxB restriction of HIV-1 infection. <i>Retrovirology</i> , 2014, 11, 90.	0.9	89
2659	Conserved syntenic clusters of protein coding genes are missing in birds. <i>Genome Biology</i> , 2014, 15, 565.	3.8	123
2660	Evaluation of de novo transcriptome assemblies from RNA-Seq data. <i>Genome Biology</i> , 2014, 15, 553.	3.8	256
2661	A PTCH1 Homolog Transcriptionally Activated by p53 Suppresses Hedgehog Signaling. <i>Journal of Biological Chemistry</i> , 2014, 289, 33020-33031.	1.6	29
2662	Efficient DNA Fingerprinting Based on the Targeted Sequencing of Active Retrotransposon Insertion Sites Using a Bench-Top High-Throughput Sequencing Platform. <i>DNA Research</i> , 2014, 21, 491-498.	1.5	20
2663	Definition of the Cattle Killer Cell Ig $\alpha$ -like Receptor Gene Family: Comparison with Aurochs and Human Counterparts. <i>Journal of Immunology</i> , 2014, 193, 6016-6030.	0.4	29
2664	Small RNAs as important regulators for the hybrid vigour of super-hybrid rice. <i>Journal of Experimental Botany</i> , 2014, 65, 5989-6002.	2.4	30

#	ARTICLE	IF	CITATIONS
2665	Clone Mapper: An Online Suite of Tools for RNAi Experiments in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2137-2145.	0.8	17
2666	Piecing the puzzle together: a revisit to transcript reconstruction problem in RNA-seq. <i>BMC Bioinformatics</i> , 2014, 15, S3.	1.2	1
2667	Population history and genomic signatures for high-altitude adaptation in Tibetan pigs. <i>BMC Genomics</i> , 2014, 15, 834.	1.2	140
2668	A naturally occurring, noncanonical GTP aptamer made of simple tandem repeats. <i>RNA Biology</i> , 2014, 11, 682-692.	1.5	9
2669	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. <i>Nucleic Acids Research</i> , 2014, 42, e73-e73.	6.5	445
2670	The Imprinted NPAP1 Gene in the Prader-Willi Syndrome Region Belongs to a POM121-Related Family of Retrogenes. <i>Genome Biology and Evolution</i> , 2014, 6, 344-351.	1.1	11
2671	Genomic Organization, Transcriptomic Analysis, and Functional Characterization of Avian $\beta$ - and $\beta$ -Keratins in Diverse Feather Forms. <i>Genome Biology and Evolution</i> , 2014, 6, 2258-2273.	1.1	67
2672	Diverse cell stresses induce unique patterns of tRNA up- and down-regulation: tRNA-seq for quantifying changes in tRNA copy number. <i>Nucleic Acids Research</i> , 2014, 42, e170-e170.	6.5	114
2673	Identification of Oncogenic Mutations and Gene Fusions in the Follicular Variant of Papillary Thyroid Carcinoma. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E2457-E2462.	1.8	55
2674	Postzygotic single-nucleotide mosaicisms in whole-genome sequences of clinically unremarkable individuals. <i>Cell Research</i> , 2014, 24, 1311-1327.	5.7	54
2675	Haploinsufficiency of <i>Sf3b1</i> leads to compromised stem cell function but not to myelodysplasia. <i>Leukemia</i> , 2014, 28, 1844-1850.	3.3	42
2676	Diversity in the preimmune immunoglobulin repertoire of SHR lines susceptible and resistant to end-organ injury. <i>Genes and Immunity</i> , 2014, 15, 528-533.	2.2	15
2677	Methods to Study Splicing from High-Throughput RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2014, 1126, 357-397.	0.4	68
2678	Gene-based SNP discovery and genetic mapping in pea. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2225-2241.	1.8	74
2679	Workload characterization for MG-RAST metagenomic data analytics service in the cloud. , 2014, , .		5
2680	The Genome of a Mongolian Individual Reveals the Genetic Imprints of Mongolians on Modern Human Populations. <i>Genome Biology and Evolution</i> , 2014, 6, 3122-3136.	1.1	24
2681	Genome-wide association study identifies QTLs for EBV of Backfat Thickness and average daily gain in Duroc pigs. <i>Russian Journal of Genetics</i> , 2014, 50, 1308-1315.	0.2	4
2682	Evolution of Gene Structural Complexity: An Alternative-Splicing-Based Model Accounts for Intron-Containing Retrogenes. <i>Plant Physiology</i> , 2014, 165, 412-423.	2.3	19

#	ARTICLE	IF	CITATIONS
2683	A Genome-Wide Analysis of Genetic Diversity in <i>Trypanosoma cruzi</i> Intergenic Regions. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2839.	1.3	8
2684	Functional Divergence and Evolutionary Turnover in Mammalian Phosphoproteomes. <i>PLoS Genetics</i> , 2014, 10, e1004062.	1.5	41
2685	Genomic Networks of Hybrid Sterility. <i>PLoS Genetics</i> , 2014, 10, e1004162.	1.5	84
2686	Assembly and characterization of novel <i>Alu</i> inserts detected from next-generation sequencing data. <i>Mobile Genetic Elements</i> , 2014, 4, 1-7.	1.8	6
2687	Identification of potential therapeutic targets in a model of neuropathic pain. <i>Frontiers in Genetics</i> , 2014, 5, 131.	1.1	15
2688	A high-throughput gene sequence alignment strategy using parallel computing. , 2014, , .		1
2689	Large Inverted Duplications in the Human Genome Form via a Fold-Back Mechanism. <i>PLoS Genetics</i> , 2014, 10, e1004139.	1.5	59
2690	Neutral nuclear variation in <i>Baboons</i> (genus <i>Papio</i> ) provides insights into their evolutionary and demographic histories. <i>American Journal of Physical Anthropology</i> , 2014, 155, 621-634.	2.1	20
2691	Bioinformatic exploration of RIO protein kinases of parasitic and free-living nematodes. <i>International Journal for Parasitology</i> , 2014, 44, 827-836.	1.3	13
2692	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. <i>Bioinformatics</i> , 2014, 30, 3302-3309.	1.8	23
2693	Transcription-Independent Functions of an RNA Polymerase II Subunit, Rpb2, During Genome Rearrangement in the Ciliate, <i>Oxytricha trifallax</i> . <i>Genetics</i> , 2014, 197, 839-849.	1.2	23
2694	Sequence Analysis of Industrially Important Genes from <i>Trichoderma</i> . , 2014, , 377-392.		11
2695	New MicroRNAs in <i>Drosophila</i> —Birth, Death and Cycles of Adaptive Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004096.	1.5	53
2696	NCYM, a Cis-Antisense Gene of MYCN, Encodes a De Novo Evolved Protein That Inhibits GSK3 $\beta$ Resulting in the Stabilization of MYCN in Human Neuroblastomas. <i>PLoS Genetics</i> , 2014, 10, e1003996.	1.5	83
2697	A comprehensive set of transcript sequences of the heavy metal hyperaccumulator <i>Noccaea caerulescens</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 261.	1.7	32
2698	P2Y <sub>12</sub> Receptor on the Verge of a Neuroinflammatory Breakdown. <i>Mediators of Inflammation</i> , 2014, 2014, 1-15.	1.4	65
2699	Toxoplasma Effector MAF1 Mediates Recruitment of Host Mitochondria and Impacts the Host Response. <i>PLoS Biology</i> , 2014, 12, e1001845.	2.6	148
2700	The Streamlined Genome of <i>Phytomonas</i> spp. Relative to Human Pathogenic Kinetoplastids Reveals a Parasite Tailored for Plants. <i>PLoS Genetics</i> , 2014, 10, e1004007.	1.5	66

#	ARTICLE	IF	CITATIONS
2701	CDKN2D-WDFY2 Is a Cancer-Specific Fusion Gene Recurrent in High-Grade Serous Ovarian Carcinoma. PLoS Genetics, 2014, 10, e1004216.	1.5	41
2702	Widespread Use of Non-productive Alternative Splice Sites in <i>Saccharomyces cerevisiae</i> . PLoS Genetics, 2014, 10, e1004249.	1.5	85
2703	Transcriptome interrogation of human myometrium identifies differentially expressed sense-antisense pairs of protein-coding and long non-coding RNA genes in spontaneous labor at term. Journal of Maternal-Fetal and Neonatal Medicine, 2014, 27, 1397-1408.	0.7	25
2704	Type I Interferon Regulates the Expression of Long Non-Coding RNAs. Frontiers in Immunology, 2014, 5, 548.	2.2	54
2705	A Practical Approach to a Viral Detection Pipeline Using Existing Viral and Non-Viral Sequence Resources. PDA Journal of Pharmaceutical Science and Technology, 2014, 68, 595-601.	0.3	1
2706	AlignGraph: algorithm for secondary <i>de novo</i> genome assembly guided by closely related references. Bioinformatics, 2014, 30, i319-i328.	1.8	61
2707	Lambda: the local aligner for massive biological data. Bioinformatics, 2014, 30, i349-i355.	1.8	60
2708	Comparative Metagenomic Analysis of Human Gut Microbiome Composition Using Two Different Bioinformatic Pipelines. BioMed Research International, 2014, 2014, 1-10.	0.9	68
2709	Shotgun metagenomics reveals a wide array of antibiotic resistance genes and mobile elements in a polluted lake in India. Frontiers in Microbiology, 2014, 5, 648.	1.5	193
2710	IDBA-MTP: A Hybrid MetaTranscriptomic Assembler Based on Protein Information. Lecture Notes in Computer Science, 2014, , 160-172.	1.0	8
2711	Analysis of the Genome and Transcriptome of <i>Cryptococcus neoformans</i> var. <i>grubii</i> Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. PLoS Genetics, 2014, 10, e1004261.	1.5	336
2712	Forty-Four Novel Protein-Coding Loci Discovered Using a Proteomics Informed by Transcriptomics (PIT) Approach in Rat Male Germ Cells. Biology of Reproduction, 2014, 91, 123.	1.2	20
2713	Commet: Comparing and combining multiple metagenomic datasets. , 2014, , .		24
2714	Data-Aware Resource Scheduling for Multicloud Workflows: A Fine-Grained Simulation Approach. , 2014, , .		13
2715	CAMDA 2014: Learning from differential expression in the Japanese Toxicogenomic Project. Systems Biomedicine (Austin, Tex ), 2014, 2, 41-46.	0.7	0
2716	Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. International Journal for Parasitology: Drugs and Drug Resistance, 2014, 4, 164-184.	1.4	149
2717	Complete genome assembly and characterization of an outbreak strain of the causative agent of swine erysipelas "Erysipelothrix rhusiopathiae SY1027. BMC Microbiology, 2014, 14, 176.	1.3	36
2718	AlgaePath: comprehensive analysis of metabolic pathways using transcript abundance data from next-generation sequencing in green algae. BMC Genomics, 2014, 15, 196.	1.2	36

#	ARTICLE	IF	CITATIONS
2719	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	1.2	262
2720	Towards computational improvement of DNA database indexing and short DNA query searching. <i>Biotechnology and Biotechnological Equipment</i> , 2014, 28, 958-967.	0.5	1
2721	The discrepancies in the results of bioinformatics tools for genomic structural annotation. <i>Proceedings of SPIE</i> , 2014, , .	0.8	0
2722	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for <i>PU.1</i> during haematopoietic specification. <i>Development (Cambridge)</i> , 2014, 141, 4018-4030.	1.2	26
2723	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	5.8	173
2724	Gene Prediction and Annotation in <i>Penstemon</i> (Plantaginaceae): A Workflow for Marker Development from Extremely Low-Coverage Genome Sequencing. <i>Applications in Plant Sciences</i> , 2014, 2, 1400044.	0.8	15
2725	Genome-wide eQTLs and heritability for gene expression traits in unrelated individuals. <i>BMC Genomics</i> , 2014, 15, 13.	1.2	43
2726	First Complete Genome Sequence of <i>Staphylococcus xylosus</i> , a Meat Starter Culture and a Host to Propagate <i>Staphylococcus aureus</i> Phages. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
2727	Complete Genome Sequences of IncI1 Plasmids Carrying Extended-Spectrum $\beta$ -Lactamase Genes. <i>Genome Announcements</i> , 2014, 2, .	0.8	19
2728	<i>Cryptococcus gattii</i> in North American Pacific Northwest: Whole-Population Genome Analysis Provides Insights into Species Evolution and Dispersal. <i>MBio</i> , 2014, 5, e01464-14.	1.8	126
2729	IRBIS: a systematic search for conserved complementarity. <i>Rna</i> , 2014, 20, 1519-1531.	1.6	16
2730	Differential Locus Expansion Distinguishes <i>Toxoplasmatinae</i> Species and Closely Related Strains of <i>Toxoplasma gondii</i> . <i>MBio</i> , 2014, 5, e01003-13.	1.8	22
2731	The <i>Cryptococcus neoformans</i> Transcriptome at the Site of Human Meningitis. <i>MBio</i> , 2014, 5, e01087-13.	1.8	113
2732	Accelerating the Next Generation Long Read Mapping with the FPGA-Based System. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 840-852.	1.9	43
2733	HiPGA: A High Performance Genome Assembler for Short Read Sequence Data. , 2014, , .		2
2734	Extragenic suppressor mutations in <i>ripA</i> disrupt stability and function of <i>LpxA</i> . <i>BMC Microbiology</i> , 2014, 14, 336.	1.3	6
2735	Genetic dysregulation in recurrent respiratory papillomatosis. <i>Laryngoscope</i> , 2014, 124, E320-5.	1.1	8
2736	HybSeq: Combining target enrichment and genome skimming for plant phylogenomics. <i>Applications in Plant Sciences</i> , 2014, 2, 1400042.	0.8	405

#	ARTICLE	IF	CITATIONS
2737	Anti-centrosome antibodies in breast cancer are the expression of autoimmunity. <i>Immunologic Research</i> , 2014, 60, 339-347.	1.3	11
2738	Approximate $k$ -Mer Matching Using Fuzzy Hash Maps. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 258-264.	1.9	8
2739	Identification of a recently active <i>Prunus</i> -specific non-autonomous Mutator element with considerable genome shaping force. <i>Plant Journal</i> , 2014, 79, 220-231.	2.8	18
2740	The <i>GATA</i> transcription factor/ <i>MTA</i> homolog <i>1</i> promotes longevity and stress resistance in <i>C. elegans</i> . <i>Aging Cell</i> , 2014, 13, 329-339.	3.0	11
2741	Diagnostic whole genome sequencing and split-read mapping for nucleotide resolution breakpoint identification in CNTNAP2 deficiency syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2014, 164, 2649-2655.	0.7	29
2742	Symbiotic adaptations in the fungal cultivar of leaf-cutting ants. <i>Nature Communications</i> , 2014, 5, 5675.	5.8	84
2743	Patterns of divergence of a large family of nodule cysteine-rich peptides in accessions of <i>Medicago truncatula</i> . <i>Plant Journal</i> , 2014, 78, 697-705.	2.8	38
2744	Haploinsufficiency of insulin gene enhancer protein 1 (ISL1) is associated with transposition of the great arteries. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2014, 2, 341-351.	0.6	14
2745	Range-wide multilocus phylogeography of the red fox reveals ancient continental divergence, minimal genomic exchange and distinct demographic histories. <i>Molecular Ecology</i> , 2014, 23, 4813-4830.	2.0	82
2746	Assessment and improvement of Indian-origin rhesus macaque and <i>M. auritian</i> -origin cynomolgus macaque genome annotations using deep transcriptome sequencing data. <i>Journal of Medical Primatology</i> , 2014, 43, 317-328.	0.3	4
2747	Transcriptome resources for the perennial sunflower <i>Helianthus maximiliani</i> obtained from ecologically divergent populations. <i>Molecular Ecology Resources</i> , 2014, 14, 812-819.	2.2	18
2748	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
2749	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
2750	A novel reannotation strategy for dissecting DNA methylation patterns of human long intergenic non-coding RNAs in cancers. <i>Nucleic Acids Research</i> , 2014, 42, 8258-8270.	6.5	40
2751	The expression profile of acid-sensing ion channel (ASIC) subunits ASIC1a, ASIC1b, ASIC2a, ASIC2b, and ASIC3 in the esophageal vagal afferent nerve subtypes. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 307, G922-G930.	1.6	33
2752	<i>Azolla</i> domestication towards a biobased economy?. <i>New Phytologist</i> , 2014, 202, 1069-1082.	3.5	53
2753	Evolutionary genetics and implications of small size and twinning in callitrichine primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1467-1472.	3.3	66
2754	In vitro Transcriptome Analysis of Two Chinese Isolates of <i>Streptococcus suis</i> Serotype 2. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 266-275.	3.0	4

#	ARTICLE	IF	CITATIONS
2755	Evidence for Soft Selective Sweeps in the Evolution of Pneumococcal Multidrug Resistance and Vaccine Escape. <i>Genome Biology and Evolution</i> , 2014, 6, 1589-1602.	1.1	112
2756	Detecting Noncoding RNA Expression: From Arrays to Next-Generation Sequencing. , 2014, , 25-44.		1
2757	Comparison of assembly algorithms for improving rate of metatranscriptomic functional annotation. <i>Microbiome</i> , 2014, 2, 39.	4.9	67
2758	Bayesian Estimation of Nonsynonymous/Synonymous Rate Ratios for Pairwise Sequence Comparisons. <i>Molecular Biology and Evolution</i> , 2014, 31, 1902-1913.	3.5	13
2759	Orione, a web-based framework for NGS analysis in microbiology. <i>Bioinformatics</i> , 2014, 30, 1928-1929.	1.8	139
2760	Genetic analysis of a consanguineous Pakistani family with Leber congenital amaurosis identifies a novel mutation in GUCY2D gene. <i>Journal of Genetics</i> , 2014, 93, 527-530.	0.4	2
2761	Global absolute quantification reveals tight regulation of protein expression in single <i>Xenopus</i> eggs. <i>Nucleic Acids Research</i> , 2014, 42, 9880-9891.	6.5	71
2762	Alignment-Annotator web server: rendering and annotating sequence alignments. <i>Nucleic Acids Research</i> , 2014, 42, W3-W6.	6.5	56
2763	Comparative genomics reveals molecular features unique to the songbird lineage. <i>BMC Genomics</i> , 2014, 15, 1082.	1.2	32
2764	Construction of a high-density genetic map based on large-scale markers developed by specific length amplified fragment sequencing (SLAF-seq) and its application to QTL analysis for isoflavone content in <i>Glycine max</i> . <i>BMC Genomics</i> , 2014, 15, 1086.	1.2	134
2765	Genome-wide analysis of alternative splicing in <i>Volvox carteri</i> . <i>BMC Genomics</i> , 2014, 15, 1117.	1.2	37
2766	Tissue-specific transcriptomics, chromosomal localization, and phylogeny of chemosensory and odorant binding proteins from the red flour beetle <i>Tribolium castaneum</i> reveal subgroup specificities for olfaction or more general functions. <i>BMC Genomics</i> , 2014, 15, 1141.	1.2	111
2767	Variable recombination dynamics during the emergence, transmission and "disarming" of a multidrug-resistant pneumococcal clone. <i>BMC Biology</i> , 2014, 12, 49.	1.7	75
2768	Mouse mammary tumor virus-based vector transduces non-dividing cells, enters the nucleus via a TNPO3-independent pathway and integrates in a less biased fashion than other retroviruses. <i>Retrovirology</i> , 2014, 11, 34.	0.9	22
2769	Complete genome sequence and comparative genome analysis of <i>Klebsiella oxytoca</i> HKOPL1 isolated from giant panda feces. <i>BMC Research Notes</i> , 2014, 7, 827.	0.6	14
2770	CLAST: CUDA implemented large-scale alignment search tool. <i>BMC Bioinformatics</i> , 2014, 15, 406.	1.2	13
2771	MitoCOGs: clusters of orthologous genes from mitochondria and implications for the evolution of eukaryotes. <i>BMC Evolutionary Biology</i> , 2014, 14, 237.	3.2	34
2772	Genes involved in floral meristem in tomato exhibit drastically reduced genetic diversity and signature of selection. <i>BMC Plant Biology</i> , 2014, 14, 279.	1.6	15

#	ARTICLE	IF	CITATIONS
2773	GWIPS-viz: development of a ribo-seq genome browser. <i>Nucleic Acids Research</i> , 2014, 42, D859-D864.	6.5	223
2774	Evolutionary Origins and Dynamics of Octoploid Strawberry Subgenomes Revealed by Dense Targeted Capture Linkage Maps. <i>Genome Biology and Evolution</i> , 2014, 6, 3295-3313.	1.1	197
2775	High-resolution mapping and new marker development for adult plant stripe rust resistance QTL in the wheat cultivar Kariega. <i>Molecular Breeding</i> , 2014, 34, 2005-2020.	1.0	22
2776	The Draft Assembly of the Radically Organized <i>Stylonychia lemnae</i> Macronuclear Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 1707-1723.	1.1	58
2777	Epstein-Barr Virus EBNA1 Protein Regulates Viral Latency through Effects on let-7 MicroRNA and Dicer. <i>Journal of Virology</i> , 2014, 88, 11166-11177.	1.5	67
2778	Assessing the State of Substitution Models Describing Noncoding RNA Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 65-75.	1.1	18
2779	Mirror Movement-Like Defects in Startle Behavior of Zebrafish Mutants Are Caused by Aberrant Midline Guidance of Identified Descending Hindbrain Neurons. <i>Journal of Neuroscience</i> , 2014, 34, 2898-2909.	1.7	15
2780	RBPmap: a web server for mapping binding sites of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2014, 42, W361-W367.	6.5	409
2781	Amplification and thrifty single-molecule sequencing of recurrent somatic structural variations. <i>Genome Research</i> , 2014, 24, 318-328.	2.4	21
2782	Apomictic and Sexual Germline Development Differ with Respect to Cell Cycle, Transcriptional, Hormonal and Epigenetic Regulation. <i>PLoS Genetics</i> , 2014, 10, e1004476.	1.5	68
2783	Gene Therapy for Wiskott-Aldrich Syndrome—Long-Term Efficacy and Genotoxicity. <i>Science Translational Medicine</i> , 2014, 6, 227ra33.	5.8	460
2784	Potential for genomic instability associated with retrotranspositionally-incompetent L1 loci. <i>Nucleic Acids Research</i> , 2014, 42, 10488-10502.	6.5	44
2785	A bioinformatician's guide to the forefront of suffix array construction algorithms. <i>Briefings in Bioinformatics</i> , 2014, 15, 138-154.	3.2	29
2786	Systematic design and functional analysis of artificial microRNAs. <i>Nucleic Acids Research</i> , 2014, 42, 6064-6077.	6.5	14
2787	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. <i>Genome Research</i> , 2014, 24, 310-317.	2.4	81
2788	Discovery of Invariant T Cells by Next-Generation Sequencing of the Human TCR $\beta$ -Chain Repertoire. <i>Journal of Immunology</i> , 2014, 193, 5338-5344.	0.4	23
2789	UnSplicer: mapping spliced RNA-seq reads in compact genomes and filtering noisy splicing. <i>Nucleic Acids Research</i> , 2014, 42, e25-e25.	6.5	3
2790	A genome-wide map of hyper-edited RNA reveals numerous new sites. <i>Nature Communications</i> , 2014, 5, 4726.	5.8	193

#	ARTICLE	IF	CITATIONS
2791	Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067.	1.1	153
2792	Characterization of Genetic Diversity in the Nematode <i>Pristionchus pacificus</i> from Population-Scale Resequencing Data. Genetics, 2014, 196, 1153-1165.	1.2	79
2793	Current Challenges in the Bioinformatics of Single Cell Genomics. Frontiers in Oncology, 2014, 4, 7.	1.3	40
2794	BambooGDB: a bamboo genome database with functional annotation and an analysis platform. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau006-bau006.	1.4	64
2795	MetaGeniE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing. PLoS ONE, 2014, 9, e110915.	1.1	14
2796	Single Nucleotide Polymorphisms (SNPs). , 2014, , 55-80.		2
2797	Parallel Evolution of Tetrodotoxin Resistance in Three Voltage-Gated Sodium Channel Genes in the Garter Snake <i>Thamnophis sirtalis</i> . Molecular Biology and Evolution, 2014, 31, 2836-2846.	3.5	60
2798	Improved search heuristics find 20 000 new alignments between human and mouse genomes. Nucleic Acids Research, 2014, 42, e59-e59.	6.5	33
2799	Plant vigour at establishment and following defoliation are both associated with responses to drought in perennial ryegrass ( <i>Lolium perenne</i> L.). Journal of Experimental Botany, 2014, 65, 5823-5834.	2.4	17
2800	Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. Genome Biology, 2014, 15, R48.	13.9	37
2801	Estimating differential expression from multiple indicators. Nucleic Acids Research, 2014, 42, e72-e72.	6.5	13
2802	MorusDB: a resource for mulberry genomics and genome biology. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau054-bau054.	1.4	40
2803	Comparative Genomics of <i>Taphrina</i> Fungi Causing Varying Degrees of Tumorous Deformity in Plants. Genome Biology and Evolution, 2014, 6, 861-872.	1.1	33
2804	Evolutionary Origin and Methylation Status of Human Intronic CpG Islands that Are Not Present in Mouse. Genome Biology and Evolution, 2014, 6, 1579-1588.	1.1	16
2805	Admixture mapping of prostate cancer in African Americans participating in the North Carolina-Louisiana Prostate Cancer Project (PCaP). Prostate, 2014, 74, 1-9.	1.2	24
2806	Detection of Gene Rearrangements in Targeted Clinical Next-Generation Sequencing. Journal of Molecular Diagnostics, 2014, 16, 405-417.	1.2	65
2807	Transcriptome de novo assembly sequencing and analysis of the toxic dinoflagellate <i>Alexandrium catenella</i> using the Illumina platform. Gene, 2014, 537, 285-293.	1.0	53
2808	A tool for mapping Single Nucleotide Polymorphisms using Graphics Processing Units. BMC Bioinformatics, 2014, 15, S10.	1.2	5

#	ARTICLE	IF	CITATIONS
2809	Structural organization, classification and phylogenetic relationship of cytochrome P450 genes in <i>Citrus clementina</i> and <i>Citrus sinensis</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 399-409.	0.6	11
2810	Assembly errors cause false tandem duplicate regions in the chicken ( <i>Gallus gallus</i> ) genome sequence. <i>Chromosoma</i> , 2014, 123, 165-168.	1.0	10
2811	Sequence capture using PCR-generated probes: a cost-effective method of targeted high-throughput sequencing for nonmodel organisms. <i>Molecular Ecology Resources</i> , 2014, 14, 1000-1010.	2.2	89
2812	Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , 2014, 24, 885-895.	2.4	200
2813	A whole-genome SNP array (RICE6K) for genomic breeding in rice. <i>Plant Biotechnology Journal</i> , 2014, 12, 28-37.	4.1	163
2814	<i>Thermococcus nautili</i> sp. nov., a hyperthermophilic archaeon isolated from a hydrothermal deep-sea vent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 1802-1810.	0.8	26
2815	Effect of growth rate and selection pressure on rates of transfer of an antibiotic resistance plasmid between <i>E. coli</i> strains. <i>Plasmid</i> , 2014, 72, 1-8.	0.4	50
2816	doublesex is a mimicry supergene. <i>Nature</i> , 2014, 507, 229-232.	13.7	320
2817	Identification of sex-specific molecular markers using restriction site-associated DNA sequencing. <i>Molecular Ecology Resources</i> , 2014, 14, 902-913.	2.2	124
2818	Analysis of the floral transcriptome of <i>Tarenaya hassleriana</i> (Cleomaceae), a member of the sister group to the Brassicaceae: towards understanding the base of morphological diversity in Brassicales. <i>BMC Genomics</i> , 2014, 15, 140.	1.2	12
2820	Evolution of primate $\beta$ and $\delta$ defensins revealed by analysis of genomes. <i>Molecular Biology Reports</i> , 2014, 41, 3859-3866.	1.0	22
2821	Molecular Evolution and Functional Divergence of the Metallothionein Gene Family in Vertebrates. <i>Journal of Molecular Evolution</i> , 2014, 78, 217-233.	0.8	17
2822	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
2823	Genotyping of BCL11A and HBS1L-MYB SNPs associated with fetal haemoglobin levels: a SNPshot minisequencing approach. <i>BMC Genomics</i> , 2014, 15, 108.	1.2	25
2824	Endogenous viral elements in algal genomes. <i>Acta Oceanologica Sinica</i> , 2014, 33, 102-107.	0.4	11
2825	Genome sequencing of high-penicillin producing industrial strain of <i>Penicillium chrysogenum</i> . <i>BMC Genomics</i> , 2014, 15, S11.	1.2	41
2826	Comparison of different assembly and annotation tools on analysis of simulated viral metagenomic communities in the gut. <i>BMC Genomics</i> , 2014, 15, 37.	1.2	73
2827	The role of pleiotropy and linkage in genes affecting a sexual ornament and bone allocation in the chicken. <i>Molecular Ecology</i> , 2014, 23, 2275-2286.	2.0	42

#	ARTICLE	IF	CITATIONS
2828	Describing Sequencing Results of Structural Chromosome Rearrangements with a Suggested Next-Generation Cytogenetic Nomenclature. <i>American Journal of Human Genetics</i> , 2014, 94, 695-709.	2.6	42
2829	The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates. <i>Nature Communications</i> , 2014, 5, 3657.	5.8	814
2830	Origins and functional evolution of Y chromosomes across mammals. <i>Nature</i> , 2014, 508, 488-493.	13.7	448
2831	The advantages of going large: genome-wide <i>scn</i> SNP <i>scn</i> s clarify the complex population history and systematics of the threatened western pond turtle. <i>Molecular Ecology</i> , 2014, 23, 2228-2241.	2.0	56
2832	Current impact and future directions of high throughput sequencing in plant virus diagnostics. <i>Virus Research</i> , 2014, 188, 90-96.	1.1	196
2833	Development of fluorescent double-strand probes labeled with 8-(p-CF <sub>3</sub> -cinnamyl)-adenosine for the detection of cyclin D1 breast cancer marker. <i>European Journal of Medicinal Chemistry</i> , 2014, 79, 77-88.	2.6	5
2834	The tobacco genome sequence and its comparison with those of tomato and potato. <i>Nature Communications</i> , 2014, 5, 3833.	5.8	503
2835	DICER1 is essential for survival of postmitotic rod photoreceptor cells in mice. <i>FASEB Journal</i> , 2014, 28, 3780-3791.	0.2	54
2836	Resources for systems biology in rice. <i>Journal of Plant Biology</i> , 2014, 57, 80-92.	0.9	34
2837	Detection and correction of assembly errors of rice <i>scn</i> N <i>scn</i> ipponbare reference sequence. <i>Plant Biology</i> , 2014, 16, 643-650.	1.8	11
2838	The ctenophore genome and the evolutionary origins of neural systems. <i>Nature</i> , 2014, 510, 109-114.	13.7	606
2839	Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913.	6.0	124
2840	GenomeVISTA“an integrated software package for whole-genome alignment and visualization. <i>Bioinformatics</i> , 2014, 30, 2654-2655.	1.8	27
2841	The three major types of <i>scn</i> CRISPR <i>scn</i> “ <i>scn</i> Cas <i>scn</i> systems function independently in <i>scn</i> CRISPR RNA <i>scn</i> biogenesis in <i>scn</i> <i>S</i> <i>scn</i> <i>scn</i> treptococcus thermophilus <i>scn</i> . <i>Molecular Microbiology</i> , 2014, 93, 98-112.	1.2	81
2842	Ensembl Genomes 2013: scaling up access to genome-wide data. <i>Nucleic Acids Research</i> , 2014, 42, D546-D552.	6.5	205
2843	Comparative <i>scn</i> BAC <i>scn</i> -based physical mapping of <i>scn</i> O <i>scn</i> ryza sativa <i>scn</i> ssp. <i>scn</i> indica <i>scn</i> var. 93“11 and evaluation of the two rice reference sequence assemblies. <i>Plant Journal</i> , 2014, 77, 795-805.	2.8	16
2844	Genomic adaptations of the halophilic Dead Sea filamentous fungus <i>Eurotium rubrum</i> . <i>Nature Communications</i> , 2014, 5, 3745.	5.8	62
2845	<i>Streptococcus pneumoniae</i> Arginine Synthesis Genes Promote Growth and Virulence in Pneumococcal Meningitis. <i>Journal of Infectious Diseases</i> , 2014, 209, 1781-1791.	1.9	23

#	ARTICLE	IF	CITATIONS
2846	Genome-wide analysis of HPV integration in human cancers reveals recurrent, focal genomic instability. <i>Genome Research</i> , 2014, 24, 185-199.	2.4	371
2847	Hidden diversity in the Andes: Comparison of species delimitation methods in montane marsupials. <i>Molecular Phylogenetics and Evolution</i> , 2014, 70, 137-151.	1.2	45
2848	Analysis of transcriptomes of three orb-weaver spider species reveals gene profiles involved in silk and toxin. <i>Insect Science</i> , 2014, 21, 687-698.	1.5	13
2849	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
2850	Alignment-free genetic sequence comparisons: a review of recent approaches by word analysis. <i>Briefings in Bioinformatics</i> , 2014, 15, 890-905.	3.2	110
2851	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. <i>Nature Genetics</i> , 2014, 46, 205-212.	9.4	417
2852	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 171-175.	9.4	542
2853	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 198-206.	3.6	565
2854	Fusion of TTYH1 with the C19MC microRNA cluster drives expression of a brain-specific DNMT3B isoform in the embryonal brain tumor ETMR. <i>Nature Genetics</i> , 2014, 46, 39-44.	9.4	167
2855	Comparative biology and expression of TENP, an egg protein related to the bacterial permeability-increasing family of proteins. <i>Gene</i> , 2014, 538, 99-108.	1.0	14
2856	Rhizosphere microbiome assemblage is affected by plant development. <i>ISME Journal</i> , 2014, 8, 790-803.	4.4	1,128
2857	Epigenetic Regulation of the DLK1-MEG3 MicroRNA Cluster in Human Type 2 Diabetic Islets. <i>Cell Metabolism</i> , 2014, 19, 135-145.	7.2	304
2858	Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014, 46, 88-92.	9.4	227
2859	An Automated Proteogenomic Method Uses Mass Spectrometry to Reveal Novel Genes in <i>Zea mays</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 157-167.	2.5	79
2860	De Novo Genome Assembly of the Economically Important Weed Horseweed Using Integrated Data from Multiple Sequencing Platforms. <i>Plant Physiology</i> , 2014, 166, 1241-1254.	2.3	101
2861	ABRA: improved coding indel detection via assembly-based realignment. <i>Bioinformatics</i> , 2014, 30, 2813-2815.	1.8	140
2862	Single-cell analyses of transcriptional heterogeneity during drug tolerance transition in cancer cells by RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4726-35.	3.3	164
2863	Integrative transcriptome sequencing identifies trans-splicing events with important roles in human embryonic stem cell pluripotency. <i>Genome Research</i> , 2014, 24, 25-36.	2.4	91

#	ARTICLE	IF	CITATIONS
2864	MEGANTE: A Web-Based System for Integrated Plant Genome Annotation. <i>Plant and Cell Physiology</i> , 2014, 55, e2-e2.	1.5	27
2865	Towards an integrative model of C4 photosynthetic subtypes: insights from comparative transcriptome analysis of NAD-ME, NADP-ME, and PEP-CK C4 species. <i>Journal of Experimental Botany</i> , 2014, 65, 3579-3593.	2.4	102
2866	Anchored multiplex PCR for targeted next-generation sequencing. <i>Nature Medicine</i> , 2014, 20, 1479-1484.	15.2	705
2867	Disease variants in genomes of 44 centenarians. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2014, 2, 438-450.	0.6	58
2868	<sc>exonsampler</sc>: a computer program for genome-wide and candidate gene exon sampling for targeted next-generation sequencing. <i>Molecular Ecology Resources</i> , 2014, 14, 1296-1301.	2.2	2
2869	Facilitating the use of large-scale biological data and tools in the era of translational bioinformatics. <i>Briefings in Bioinformatics</i> , 2014, 15, 942-952.	3.2	16
2870	Is the Alcohol Deprivation Effect Genetically Mediated? Studies with HXB/BXH Recombinant Inbred Rat Strains. <i>Alcoholism: Clinical and Experimental Research</i> , 2014, 38, 2148-2157.	1.4	11
2871	Fine-scale population epigenetic structure in relation to gastrointestinal parasite load in red grouse ( <i>Lagopus lagopus scotica</i> ). <i>Molecular Ecology</i> , 2014, 23, 4256-4273.	2.0	51
2872	Identification of candidate genes involved in the biosynthesis of carotenoids in <i>Brassica rapa</i> . <i>Horticulture Environment and Biotechnology</i> , 2014, 55, 342-351.	0.7	3
2873	Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. <i>Nature Communications</i> , 2014, 5, 4784.	5.8	118
2874	Preparation and Evaluation of <sup>99m</sup> Tc-Epidermal Growth Factor Receptor (EGFR)-Peptide Nucleic Acid for Visualization of EGFR Messenger RNA Expression in Malignant Tumors. <i>Journal of Nuclear Medicine</i> , 2014, 55, 1008-1016.	2.8	15
2875	Genomic resources and genetic diversity of captive lesser kudu ( <i>Tragelaphus imberbis</i> ). <i>Zoo Biology</i> , 2014, 33, 440-445.	0.5	4
2876	Endogenous Retrovirus Insertion in the <i>KIT</i> Oncogene Determines White and White spotting in Domestic Cats. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1881-1891.	0.8	66
2877	Data, Databases, Data Format, Database Search, Data Retrieval Systems, and Genome Browsers. , 2014, , 77-131.		0
2878	Identification and typing of <i>Brucella</i> spp. in stranded harbour porpoises ( <i>Phocoena phocoena</i> ) on the Dutch coast. <i>Veterinary Microbiology</i> , 2014, 173, 118-124.	0.8	21
2879	Merging of multi-string BWTs with applications. <i>Bioinformatics</i> , 2014, 30, 3524-3531.	1.8	36
2880	A Rapid Profiling Assay for Avian Leukosis Virus Subgroup E Proviruses in Chickens. <i>Avian Diseases</i> , 2014, 58, 34-38.	0.4	2
2881	RepARK: de novo creation of repeat libraries from whole-genome NGS reads. <i>Nucleic Acids Research</i> , 2014, 42, e80-e80.	6.5	67

#	ARTICLE	IF	CITATIONS
2882	Estimating the Population Mutation Rate from a <i>de novo</i> Assembled Bactrian Camel Genome and Cross-Species Comparison with Dromedary ESTs. <i>Journal of Heredity</i> , 2014, 105, 933-940.	1.0	19
2883	Comparative Transcriptome Atlases Reveal Altered Gene Expression Modules between Two Cleomaceae C3 and C4 Plant Species. <i>Plant Cell</i> , 2014, 26, 3243-3260.	3.1	106
2884	Identification of species-specific nuclear insertions of mitochondrial DNA (numts) in gorillas and their potential as population genetic markers. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 61-70.	1.2	12
2885	Phylogenetic signal detection from an ancient rapid radiation: Effects of noise reduction, long-branch attraction, and model selection in crown clade Apocynaceae. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 169-185.	1.2	63
2886	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014, 46, 701-706.	9.4	93
2887	Analysis Considerations for Utilizing RNA-Seq to Characterize the Brain Transcriptome. <i>International Review of Neurobiology</i> , 2014, 116, 21-54.	0.9	4
2888	Integrating genomics into the taxonomy and systematics of the Bacteria and Archaea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 316-324.	0.8	483
2889	Evidence for the persistence of an active endogenous retrovirus (ERVE) in humans. <i>Genetica</i> , 2014, 142, 451-460.	0.5	10
2890	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	6.0	520
2891	Transposable element dynamics and PIWI regulation impacts lncRNA and gene expression diversity in <i>Drosophila</i> ovarian cell cultures. <i>Genome Research</i> , 2014, 24, 1977-1990.	2.4	49
2892	Fungal Alternative Splicing is Associated with Multicellular Complexity and Virulence: A Genome-Wide Multi-Species Study. <i>DNA Research</i> , 2014, 21, 27-39.	1.5	106
2893	A survey of tools for variant analysis of next-generation genome sequencing data. <i>Briefings in Bioinformatics</i> , 2014, 15, 256-278.	3.2	480
2894	Alternative splicing of the sheep <i>MITF</i> gene: Novel transcripts detectable in skin. <i>Gene</i> , 2014, 552, 165-175.	1.0	21
2895	De novo assembly and characterization of the complete chloroplast genome of radish ( <i>Raphanus</i> ). <i>Journal of Overlooked Genomes</i> , 2014, 1, 1-14.	1.0	33
2896	Tools, resources and databases for SNPs and indels in sequences: a review. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 264.	0.1	14
2897	megaTALs: a rare-cleaving nuclease architecture for therapeutic genome engineering. <i>Nucleic Acids Research</i> , 2014, 42, 2591-2601.	6.5	151
2898	Evolution of the mir-181 microRNA family. <i>Computers in Biology and Medicine</i> , 2014, 52, 82-87.	3.9	31
2899	RNA-Seq for the identification of novel Mediator transcripts in endothelial progenitor cells. <i>Gene</i> , 2014, 547, 98-105.	1.0	10

#	ARTICLE	IF	CITATIONS
2900	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	9.4	225
2901	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251-1253.	6.0	348
2902	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
2903	Efficient de novo assembly of highly heterozygous genomes from whole-genome shotgun short reads. <i>Genome Research</i> , 2014, 24, 1384-1395.	2.4	1,000
2904	<i>CYP1B1</i> Gene Mutations Causing Primary Congenital Glaucoma in Tunisia. <i>Annals of Human Genetics</i> , 2014, 78, 255-263.	0.3	11
2905	Identification and Validation of Genetic Variants that Influence Transcription Factor and Cell Signaling Protein Levels. <i>American Journal of Human Genetics</i> , 2014, 95, 194-208.	2.6	54
2906	Proliferation of cells with HIV integrated into cancer genes contributes to persistent infection. <i>Science</i> , 2014, 345, 570-573.	6.0	573
2907	circBase: a database for circular RNAs. <i>Rna</i> , 2014, 20, 1666-1670.	1.6	1,417
2908	An integrated algorithm for local sequence alignment. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2014, 3, 1.	1.2	5
2909	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. <i>BMC Bioinformatics</i> , 2014, 15, 224.	1.2	284
2910	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. <i>BMC Bioinformatics</i> , 2014, 15, 262.	1.2	55
2911	Synthesis of 53 tissue and cell line expression QTL datasets reveals master eQTLs. <i>BMC Genomics</i> , 2014, 15, 532.	1.2	49
2912	A comprehensive analysis of piRNAs from adult human testis and their relationship with genes and mobile elements. <i>BMC Genomics</i> , 2014, 15, 545.	1.2	105
2913	An integrated genomic and metabolomic framework for cell wall biology in rice. <i>BMC Genomics</i> , 2014, 15, 596.	1.2	26
2914	A Bead-based Normalization for Uniform Sequencing depth (BeNUS) protocol for multi-samples sequencing exemplified by HLA-B. <i>BMC Genomics</i> , 2014, 15, 645.	1.2	29
2915	The <i>Babesia bovis</i> gene and promoter model: an update from full-length EST analysis. <i>BMC Genomics</i> , 2014, 15, 678.	1.2	8
2916	The American cranberry: first insights into the whole genome of a species adapted to bog habitat. <i>BMC Plant Biology</i> , 2014, 14, 165.	1.6	105
2917	Identification of G protein-coupled receptors in <i>Schistosoma haematobium</i> and <i>S. mansoni</i> by comparative genomics. <i>Parasites and Vectors</i> , 2014, 7, 242.	1.0	37

#	ARTICLE	IF	CITATIONS
2918	De novo transcriptome sequencing and sequence analysis of the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Parasites and Vectors</i> , 2014, 7, 314.	1.0	29
2919	Corset: enabling differential gene expression analysis for de novo assembled transcriptomes. <i>Genome Biology</i> , 2014, 15, 410.	3.8	427
2920	A genome-wide CNV analysis of schizophrenia reveals a potential role for a multiple-hit model. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2014, 165, 619-626.	1.1	25
2921	The Architecture of a Scrambled Genome Reveals Massive Levels of Genomic Rearrangement during Development. <i>Cell</i> , 2014, 158, 1187-1198.	13.5	152
2922	Genome-wide transcriptional changes of ramie ( <i>Boehmeria nivea</i> L. Gaud) in response to root-lesion nematode infection. <i>Gene</i> , 2014, 552, 67-74.	1.0	30
2923	Characterizing regions in the human genome unmappable by next-generation-sequencing at the read length of 1000 bases. <i>Computational Biology and Chemistry</i> , 2014, 53, 108-117.	1.1	16
2924	Heterochromatin Controls $\text{H}^3\text{H}2\text{A}$ Localization in <i>Neurospora crassa</i> . <i>Eukaryotic Cell</i> , 2014, 13, 990-1000.	3.4	26
2925	Multiple Groups of Endogenous Epsilon-Like Retroviruses Conserved across Primates. <i>Journal of Virology</i> , 2014, 88, 12464-12471.	1.5	15
2926	Hi-C Analysis in <i>Arabidopsis</i> Identifies the KNOT, a Structure with Similarities to the flamenco Locus of <i>Drosophila</i> . <i>Molecular Cell</i> , 2014, 55, 678-693.	4.5	264
2927	CEM-Designer: Design of custom expression microarrays in the post-ENCODE Era. <i>Journal of Biotechnology</i> , 2014, 189, 154-156.	1.9	2
2928	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. <i>Science</i> , 2014, 346, 251-256.	6.0	962
2929	Development and characterization of a new 12-plex ChrX miniSTR system. <i>International Journal of Legal Medicine</i> , 2014, 128, 595-598.	1.2	8
2930	Plant systems biology: insights, advances and challenges. <i>Planta</i> , 2014, 240, 33-54.	1.6	66
2931	IMP-HRM: an automated pipeline for high throughput SNP marker resource development for molecular breeding in orphan crops. <i>Euphytica</i> , 2014, 200, 197-206.	0.6	2
2932	A chromosome-based draft sequence of the hexaploid bread wheat ( <i>Triticum aestivum</i> ) genome. <i>Science</i> , 2014, 345, 1251-1288.	6.0	1,479
2933	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249-1251.	6.0	542
2934	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. <i>Genome Biology</i> , 2014, 15, R34.	13.9	242
2935	Multicilin drives centriole biogenesis via E2f proteins. <i>Genes and Development</i> , 2014, 28, 1461-1471.	2.7	130

#	ARTICLE	IF	CITATIONS
2936	Lacking alignments? The next-generation sequencing mapper segemehl revisited. <i>Bioinformatics</i> , 2014, 30, 1837-1843.	1.8	105
2937	Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539.	1.8	241
2938	The <i>Chlamydomonas</i> genome project: a decade on. <i>Trends in Plant Science</i> , 2014, 19, 672-680.	4.3	145
2939	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
2940	Genome editing assessment using CRISPR Genome Analyzer (CRISPR-GA). <i>Bioinformatics</i> , 2014, 30, 2968-2970.	1.8	136
2941	Evolutionary Origin and Human-Specific Expansion of a Cancer/Testis Antigen Gene Family. <i>Molecular Biology and Evolution</i> , 2014, 31, 2365-2375.	3.5	15
2942	Rewiring Host Lipid Metabolism by Large Viruses Determines the Fate of <i>Emiliania huxleyi</i> , a Bloom-Forming Alga in the Ocean. <i>Plant Cell</i> , 2014, 26, 2689-2707.	3.1	132
2943	The <i>Xenopus</i> alcohol dehydrogenase gene family: characterization and comparative analysis incorporating amphibian and reptilian genomes. <i>BMC Genomics</i> , 2014, 15, 216.	1.2	5
2944	RNA-seq analysis identifies an intricate regulatory network controlling cluster root development in white lupin. <i>BMC Genomics</i> , 2014, 15, 230.	1.2	43
2945	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. <i>BMC Genomics</i> , 2014, 15, 274.	1.2	12
2946	A house finch ( <i>Haemorrhous mexicanus</i> ) spleen transcriptome reveals intra- and interspecific patterns of gene expression, alternative splicing and genetic diversity in passerines. <i>BMC Genomics</i> , 2014, 15, 305.	1.2	12
2947	XSAnno: a framework for building ortholog models in cross-species transcriptome comparisons. <i>BMC Genomics</i> , 2014, 15, 343.	1.2	27
2948	GAP-Seq: a method for identification of DNA palindromes. <i>BMC Genomics</i> , 2014, 15, 394.	1.2	10
2949	Predicting the fungal CUG codon translation with Bagheera. <i>BMC Genomics</i> , 2014, 15, 411.	1.2	18
2950	A novel approach to identify driver genes involved in androgen-independent prostate cancer. <i>Molecular Cancer</i> , 2014, 13, 120.	7.9	53
2951	Novel principles of gamma-retroviral insertional transcription activation in murine leukemia virus-induced end-stage tumors. <i>Retrovirology</i> , 2014, 11, 36.	0.9	21
2952	Aptaligner: Automated Software for Aligning Pseudorandom DNA X-Aptamers from Next-Generation Sequencing Data. <i>Biochemistry</i> , 2014, 53, 3523-3525.	1.2	19
2953	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. <i>Environmental Microbiology Reports</i> , 2014, 6, 640-655.	1.0	36

#	ARTICLE	IF	CITATIONS
2954	Novel galanin receptors in teleost fish: Identification, expression and regulation by sex steroids. <i>General and Comparative Endocrinology</i> , 2014, 205, 109-120.	0.8	24
2955	Sequencing of the chloroplast genomes of cytoplasmic male-sterile and male-fertile lines of soybean and identification of polymorphic markers. <i>Plant Science</i> , 2014, 229, 208-214.	1.7	12
2956	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
2957	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. <i>DNA Research</i> , 2014, 21, 169-181.	1.5	201
2958	Loss of oncogenic Notch1 with resistance to a PI3K inhibitor in T-cell leukaemia. <i>Nature</i> , 2014, 513, 512-516.	13.7	60
2959	Get your high-quality low-cost genome sequence. <i>Trends in Plant Science</i> , 2014, 19, 288-291.	4.3	33
2960	The heterothallic sugarbeet pathogen <i>Cercospora beticola</i> contains exon fragments of both MAT genes that are homogenized by concerted evolution. <i>Fungal Genetics and Biology</i> , 2014, 62, 43-54.	0.9	15
2961	Molecular characterization and expression analysis of the small GTPase ROP members expressed in laticifers of the rubber tree ( <i>Hevea brasiliensis</i> ). <i>Plant Physiology and Biochemistry</i> , 2014, 74, 193-204.	2.8	4
2962	No evidence of clonal dominance after transplant of HOXB4-expanded cord blood cells in a nonhuman primate model. <i>Experimental Hematology</i> , 2014, 42, 497-504.	0.2	2
2963	Angiosperm Phylogeny Based on 18S/26S rDNA Sequence Data: Constructing a Large Data Set Using Next-Generation Sequence Data. <i>International Journal of Plant Sciences</i> , 2014, 175, 613-650.	0.6	24
2964	Genome-Wide Analysis of Heat-Sensitive Alternative Splicing in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2014, 165, 826-840.	2.3	119
2965	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	9.4	1,159
2966	Compressive biological sequence analysis and archival in the era of high-throughput sequencing technologies. <i>Briefings in Bioinformatics</i> , 2014, 15, 390-406.	3.2	51
2967	Unique Features of the Loblolly Pine ( <i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. <i>Genetics</i> , 2014, 196, 891-909.	1.2	207
2968	Improving transcriptome construction in non-model organisms: integrating manual and automated gene definition in <i>Emiliana huxleyi</i> . <i>BMC Genomics</i> , 2014, 15, 148.	1.2	31
2969	Sugarcane genome sequencing by methylation filtration provides tools for genomic research in the genus <i>Saccharum</i> . <i>Plant Journal</i> , 2014, 79, 162-172.	2.8	40
2970	The first set of expressed sequence tags (EST) from the medicinal mushroom <i>Agaricus subrufescens</i> delivers resource for gene discovery and marker development. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7879-7892.	1.7	13
2971	BIMA V3: an aligner customized for mate pair library sequencing. <i>Bioinformatics</i> , 2014, 30, 1627-1629.	1.8	80

#	ARTICLE	IF	CITATIONS
2972	The development of specific <sc>SNP</sc> markers for chromosome 14 in cotton using next-generation sequencing. <i>Plant Breeding</i> , 2014, 133, 256-261.	1.0	10
2973	Production, gene structure and characterization of two orthologs of leptin and a leptin receptor in tilapia. <i>General and Comparative Endocrinology</i> , 2014, 207, 74-85.	0.8	61
2974	Exploration of presence/absence variation and corresponding polymorphic markers in soybean genome. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 1009-1019.	4.1	21
2975	Gene duplication followed by exon structure divergence substitutes for alternative splicing in zebrafish. <i>Gene</i> , 2014, 546, 271-276.	1.0	7
2976	Hyb: A bioinformatics pipeline for the analysis of CLASH (crosslinking, ligation and sequencing of) Tj ETQq0 0 0 rgBT /Overlock, 10 Tf 50	1.9	77
2977	Comprehensive Transcriptome Assembly of Chickpea ( <i>Cicer arietinum</i> L.) Using Sanger and Next Generation Sequencing Platforms: Development and Applications. <i>PLoS ONE</i> , 2014, 9, e86039.	1.1	87
2978	Integrative workflows for metagenomic analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 70.	1.8	32
2979	Genome-wide Association Study of Integrated Meat Quality-related Traits of the Duroc Pig Breed. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014, 27, 303-309.	2.4	20
2980	On the optimal trimming of high-throughput mRNA sequence data. <i>Frontiers in Genetics</i> , 2014, 5, 13.	1.1	205
2981	Frequency-based re-sequencing tool for short reads on graphics processing units. <i>International Journal of Computational Science and Engineering</i> , 2014, 9, 3.	0.4	6
2982	De novo assembly of the dual transcriptomes of a polymorphic raptor species and its malarial parasite. <i>BMC Genomics</i> , 2015, 16, 1038.	1.2	15
2983	Jitterbug: somatic and germline transposon insertion detection at single-nucleotide resolution. <i>BMC Genomics</i> , 2015, 16, 768.	1.2	31
2984	High performance computing of a fusion gene detection pipeline on the K computer. , 2015, , .		3
2985	Linkage disequilibrium network analysis (<sc>LD</sc>na) gives a global view of chromosomal inversions, local adaptation and geographic structure. <i>Molecular Ecology Resources</i> , 2015, 15, 1031-1045.	2.2	85
2986	A fast and accurate parallel algorithm for genome mapping assembly aimed at massively parallel sequencers. , 2015, , .		2
2987	An Efficient Strategy Developed for Next-Generation Sequencing of Endosymbiont Genomes Performed Using Crude DNA Isolated from Host Tissues: A Case Study of &lt;i>Blattabacterium cuenoti</i> Inhabiting the Fat Bodies of Cockroaches. <i>Microbes and Environments</i> , 2015, 30, 208-220.	0.7	14
2988	ImmuSort, a database on gene plasticity and electronic sorting for immune cells. <i>Scientific Reports</i> , 2015, 5, 10370.	1.6	36
2989	Mutational spectrum of myeloid malignancies with inv(3)/t(3;3) reveals a predominant involvement of RAS/RTK signaling pathways. <i>Blood</i> , 2015, 125, 133-139.	0.6	86

#	ARTICLE	IF	CITATIONS
2990	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015, 1, 15007.	2.9	82
2991	Living without DAT: Loss and compensation of the dopamine transporter gene in sauropsids (birds and) Tj ETQq1 1,0,784314,rgBT /O	1.6	10
2992	Entropy-Scaling Search of Massive Biological Data. <i>Cell Systems</i> , 2015, 1, 130-140.	2.9	64
2993	<i>Lactococcus garvieae</i> : a small bacteria and a big data world. <i>Health Information Science and Systems</i> , 2015, 3, S5.	3.4	8
2994	The fate of recent duplicated genes following a fourth-round whole genome duplication in a tetraploid fish, common carp ( <i>Cyprinus carpio</i> ). <i>Scientific Reports</i> , 2015, 5, 8199.	1.6	60
2995	Phylogenetic and genomic diversity in isolates from the globally distributed <i>Acinetobacter baumannii</i> ST25 lineage. <i>Scientific Reports</i> , 2015, 5, 15188.	1.6	93
2996	Red clover ( <i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015, 5, 17394.	1.6	136
2997	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	2.4	67
2998	Southernâ€¦â€¦Sequencing: A Robust Screening Approach for Molecular Characterization of Genetically Modified Crops. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.08.0037.	1.6	65
2999	RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <i>Scientific Reports</i> , 2015, 5, 8365.	1.6	2,080
3000	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, <i>Hypothenemus hampei</i> . <i>Scientific Reports</i> , 2015, 5, 12525.	1.6	60
3001	Generation and Analysis of Microbial Metatranscriptomes. , 2015, , 2.4.5-1-2.4.5-19.		1
3002	Defining the <i>Schistosoma haematobium</i> kinome enables the prediction of essential kinases as anti-schistosome drug targets. <i>Scientific Reports</i> , 2015, 5, 17759.	1.6	37
3003	Sequencing of plant genomes â€œ a review. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 361-376.	0.8	20
3004	Comprehensive assembly of novel transcripts from unmapped human RNAâ€¦Seq data and their association with cancer. <i>Molecular Systems Biology</i> , 2015, 11, 826.	3.2	18
3005	TRUFA: A User-Friendly Web Server for <i>de novo</i> RNA-seq Analysis Using Cluster Computing. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S23873.	0.6	37
3006	Transcriptome Analysis in Domesticated Species: Challenges and Strategies. <i>Bioinformatics and Biology Insights</i> , 2015, 9S4, BBI.S29334.	1.0	17
3007	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178

#	ARTICLE	IF	CITATIONS
3008	Resequencing of the common marmoset genome improves genome assemblies and gene-coding sequence analysis. <i>Scientific Reports</i> , 2015, 5, 16894.	1.6	32
3009	No association between HPV positive breast cancer and expression of human papilloma viral transcripts. <i>Scientific Reports</i> , 2015, 5, 18081.	1.6	21
3010	Data in support of genome-wide identification of lineage-specific genes within <i>Caenorhabditis elegans</i> . <i>Data in Brief</i> , 2015, 4, 595-601.	0.5	3
3011	Evolutionary conservation and function of the human embryonic stem cell specific miR-302/367 cluster. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 16, 83-98.	0.4	20
3012	Transcriptional profiling of predator-induced phenotypic plasticity in <i>Daphnia pulex</i> . <i>Frontiers in Zoology</i> , 2015, 12, 18.	0.9	32
3013	The <i>Haemonchus contortus</i> kinome - a resource for fundamental molecular investigations and drug discovery. <i>Parasites and Vectors</i> , 2015, 8, 623.	1.0	14
3014	Discovery and characterization of <i>Alu</i> repeat sequences via precise local read assembly. <i>Nucleic Acids Research</i> , 2015, 43, gkv1089.	6.5	31
3015	Sequence Analysis and Characterization of Active Human <i>Alu</i> subfamilies Based on the 1000 Genomes Pilot Project. <i>Genome Biology and Evolution</i> , 2015, 7, evv167.	1.1	60
3016	Fusion transcript loci share many genomic features with non-fusion loci. <i>BMC Genomics</i> , 2015, 16, 1021.	1.2	16
3017	A human 3'UTR clone collection to study post-transcriptional gene regulation. <i>BMC Genomics</i> , 2015, 16, 1036.	1.2	7
3018	LOTUS-DB: an integrative and interactive database for <i>Nelumbo nucifera</i> study. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav023.	1.4	18
3019	dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav052-bav052.	1.4	13
3020	Human endogenous retrovirus HERV-K(HML-2) activity in prostate cancer is dominated by a few loci. <i>Prostate</i> , 2015, 75, 1958-1971.	1.2	43
3021	Identification of disrupted <i>AUTS2</i> and <i>EPHA6</i> genes by array painting in a patient carrying a de novo balanced translocation t(3;7) with intellectual disability and neurodevelopment disorder. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 3031-3037.	0.7	11
3022	Negligible nuclear introgression despite complete mitochondrial capture between two species of chipmunks. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1961-1972.	1.1	88
3023	Eco-genomic analysis of the poleward range expansion of the wasp spider <i>A. rigoie bruennichi</i> shows rapid adaptation and genomic admixture. <i>Global Change Biology</i> , 2015, 21, 4320-4332.	4.2	54
3024	Genome-wide association and genome partitioning reveal novel genomic regions underlying variation in gastrointestinal nematode burden in a wild bird. <i>Molecular Ecology</i> , 2015, 24, 4175-4192.	2.0	20
3025	Regulation of flowering time by the histone deacetylase <i>HDA5</i> in <i>A. rabidopsis</i> . <i>Plant Journal</i> , 2015, 82, 925-936.	2.8	94

#	ARTICLE	IF	CITATIONS
3026	A host plant genome ( <i>Zizania latifolia</i> ) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609.	2.8	67
3027	Exploring the tertiary gene pool of bread wheat: sequence assembly and analysis of chromosome 5M <sup>g</sup> of <i>Aegilops geniculata</i> . <i>Plant Journal</i> , 2015, 84, 733-746.	2.8	48
3028	IRcall and IRclassifier: two methods for flexible detection of intron retention events from RNA-Seq data. <i>BMC Genomics</i> , 2015, 16, S9.	1.2	11
3029	misFinder: identify mis-assemblies in an unbiased manner using reference and paired-end reads. <i>BMC Bioinformatics</i> , 2015, 16, 386.	1.2	14
3030	Genome-wide evolutionary and functional analysis of the Equine Repetitive Element 1: an insertion in the myostatin promoter affects gene expression. <i>BMC Genetics</i> , 2015, 16, 126.	2.7	25
3031	Draft genome of a commonly misdiagnosed multidrug resistant pathogen <i>Candida auris</i> . <i>BMC Genomics</i> , 2015, 16, 686.	1.2	206
3032	Generation of a de novo transcriptome from equine lamellar tissue. <i>BMC Genomics</i> , 2015, 16, 739.	1.2	14
3033	Characterization and fine mapping of a novel barley Stage Green-Revertible Albino Gene (HvSGRA) by Bulked Segregant Analysis based on SSR assay and Specific Length Amplified Fragment Sequencing. <i>BMC Genomics</i> , 2015, 16, 838.	1.2	44
3034	Functionally conserved enhancers with divergent sequences in distant vertebrates. <i>BMC Genomics</i> , 2015, 16, 882.	1.2	18
3035	High-density genetic map construction and gene mapping of pericarp color in wax gourd using specific-locus amplified fragment (SLAF) sequencing. <i>BMC Genomics</i> , 2015, 16, 1035.	1.2	84
3036	Global expression differences and tissue specific expression differences in rice evolution result in two contrasting types of differentially expressed genes. <i>BMC Genomics</i> , 2015, 16, 1099.	1.2	5
3037	Construction of a dense genetic linkage map and mapping quantitative trait loci for economic traits of a doubled haploid population of <i>Pyropia haitanensis</i> (Bangiales, Rhodophyta). <i>BMC Plant Biology</i> , 2015, 15, 228.	1.6	51
3038	Differential expression analysis of human endogenous retroviruses based on ENCODE RNA-seq data. <i>BMC Medical Genomics</i> , 2015, 8, 71.	0.7	20
3039	Gene activity in primary T cells infected with HIV89.6: intron retention and induction of genomic repeats. <i>Retrovirology</i> , 2015, 12, 79.	0.9	40
3040	Comparative genomics of <i>Steinernema</i> reveals deeply conserved gene regulatory networks. <i>Genome Biology</i> , 2015, 16, 200.	3.8	77
3041	The first draft genome of the aquatic model plant <i>Lemna minor</i> opens the route for future stress physiology research and biotechnological applications. <i>Biotechnology for Biofuels</i> , 2015, 8, 188.	6.2	112
3042	A comprehensive epigenome map of <i>Plasmodium falciparum</i> reveals unique mechanisms of transcriptional regulation and identifies H3K36me2 as a global mark of gene suppression. <i>Epigenetics and Chromatin</i> , 2015, 8, 32.	1.8	55
3043	JAFFA: High sensitivity transcriptome-focused fusion gene detection. <i>Genome Medicine</i> , 2015, 7, 43.	3.6	132

#	ARTICLE	IF	CITATIONS
3044	Dp412: a novel human embryonic dystrophin isoform induced by BMP4 in early differentiated cells. <i>Skeletal Muscle</i> , 2015, 5, 40.	1.9	28
3045	Strong spurious transcription likely contributes to DNA insert bias in typical metagenomic clone libraries. <i>Microbiome</i> , 2015, 3, 22.	4.9	25
3046	Draft Genome Sequence of <i>Mycobacterium neworleansense</i> Strain ATCC 49404 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
3047	High-throughput monitoring of integration site clonality in preclinical and clinical gene therapy studies. <i>Molecular Therapy - Methods and Clinical Development</i> , 2015, 2, 14061.	1.8	8
3048	Discovering All Transcriptome Single-Nucleotide Polymorphisms and Scanning for Selection Signatures in Ducks ( <i>Anas platyrhynchos</i> ). <i>Evolutionary Bioinformatics</i> , 2015, 11s1, EBO.S21545.	0.6	5
3049	Identification and Expression Analysis of Ribosome Biogenesis Factor Co-orthologs in <i>Solanum lycopersicum</i> . <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S20751.	1.0	62
3050	The sequenced rat brain transcriptome – its use in identifying networks predisposing alcohol consumption. <i>FEBS Journal</i> , 2015, 282, 3556-3578.	2.2	52
3051	Acid sensitivity of the spinal dorsal root ganglia C-fiber nociceptors innervating the guinea pig esophagus. <i>Neurogastroenterology and Motility</i> , 2015, 27, 865-874.	1.6	15
3052	GraP: platform for functional genomics analysis of <i>Gossypium raimondii</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav047.	1.4	14
3053	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
3054	Co-expression of <i>march5b</i> and <i>tlr7</i> in large yellow croaker <i>Larimichthys crocea</i> in response to <i>Cryptocaryon irritans</i> infection. <i>Journal of Fish Biology</i> , 2015, 87, 360-370.	0.7	15
3055	FARE-CAFE: a database of functional and regulatory elements of cancer-associated fusion events. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav086.	1.4	11
3056	A synteny-based draft genome sequence of the forage grass <i>Lolium perenne</i> . <i>Plant Journal</i> , 2015, 84, 816-826.	2.8	166
3057	Draft Genome Sequence of <i>Mycobacterium lentiflavum</i> CSUR P1491. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
3058	Kiwifruit Information Resource (KIR): a comparative platform for kiwifruit genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav113.	1.4	14
3059	An Introduction to Genome Annotation. <i>Current Protocols in Bioinformatics</i> , 2015, 52, 4.1.1-4.1.17.	25.8	4
3060	Meta-Analysis of DNA Tumor-Viral Integration Site Selection Indicates a Role for Repeats, Gene Expression and Epigenetics. <i>Cancers</i> , 2015, 7, 2217-2235.	1.7	27
3061	Transcriptome Sequencing of Lima Bean ( <i>Phaseolus lunatus</i> ) to Identify Putative Positive Selection in <i>Phaseolus</i> and Legumes. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15172-15187.	1.8	13

#	ARTICLE	IF	CITATIONS
3062	Analysis of pollen-specific alternative splicing in <i>Arabidopsis thaliana</i> via semi-quantitative PCR. PeerJ, 2015, 3, e919.	0.9	11
3063	Identification of long non-coding RNA involved in osteogenic differentiation from mesenchymal stem cells using RNA-Seq data. Genetics and Molecular Research, 2015, 14, 18268-18279.	0.3	41
3064	Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. Plant Genome, 2015, 8, eplantgenome2015.06.0045.	1.6	10
3065	Identification of Ramie Genes in Response to <i>Pratylenchus coffeae</i> Infection Challenge by Digital Gene Expression Analysis. International Journal of Molecular Sciences, 2015, 16, 21989-22007.	1.8	26
3066	Diversity of acid stress resistant variants of <i>Listeria monocytogenes</i> and the potential role of ribosomal protein S21 encoded by rpsU. Frontiers in Microbiology, 2015, 6, 422.	1.5	35
3067	Spatial and temporal dynamics of virus occurrence in two freshwater lakes captured through metagenomic analysis. Frontiers in Microbiology, 2015, 6, 960.	1.5	69
3068	The role of biofilms as environmental reservoirs of antibiotic resistance. Frontiers in Microbiology, 2015, 6, 1216.	1.5	321
3069	Integrated Omics™, Targeted Metabolite and Single-cell Analyses of Arctic Snow Algae Functionality and Adaptability. Frontiers in Microbiology, 2015, 6, 1323.	1.5	59
3070	Toward the Understanding of the Human Virome. , 2015, , 135-143.		1
3071	Survey of Programs Used to Detect Alternative Splicing Isoforms from Deep Sequencing Data In Silico. BioMed Research International, 2015, 2015, 1-9.	0.9	6
3072	Novel Exons and Splice Variants in the Human Antibody Heavy Chain Identified by Single Cell and Single Molecule Sequencing. PLoS ONE, 2015, 10, e0117050.	1.1	19
3073	Developmental Genetic Mechanisms of C4 Syndrome Based on Transcriptome Analysis of C3 Cotyledons and C4 Assimilating Shoots in <i>Haloxylon ammodendron</i> . PLoS ONE, 2015, 10, e0117175.	1.1	38
3074	De Novo Origin of VCY2 from Autosome to Y-Transposed Amplicon. PLoS ONE, 2015, 10, e0119651.	1.1	5
3075	Transcriptome Assembly, Gene Annotation and Tissue Gene Expression Atlas of the Rainbow Trout. PLoS ONE, 2015, 10, e0121778.	1.1	53
3076	Genome-Wide Identification, Characterization and Evolutionary Analysis of Long Intergenic Noncoding RNAs in Cucumber. PLoS ONE, 2015, 10, e0121800.	1.1	98
3077	Identification and Functional Analysis of Genome Mutations in a Fluoride-Resistant <i>Streptococcus mutans</i> Strain. PLoS ONE, 2015, 10, e0122630.	1.1	52
3078	Influence of a Non-Hospital Medical Care Facility on Antimicrobial Resistance in Wastewater. PLoS ONE, 2015, 10, e0122635.	1.1	36
3079	Comparative Genome Analyses of <i>Serratia marcescens</i> FS14 Reveals Its High Antagonistic Potential. PLoS ONE, 2015, 10, e0123061.	1.1	51

#	ARTICLE	IF	CITATIONS
3080	ALDB: A Domestic-Animal Long Noncoding RNA Database. PLoS ONE, 2015, 10, e0124003.	1.1	90
3081	Annotation of the Protein Coding Regions of the Equine Genome. PLoS ONE, 2015, 10, e0124375.	1.1	29
3082	Genome-Wide Transcriptional Profiling of <i>Clostridium perfringens</i> SM101 during Sporulation Extends the Core of Putative Sporulation Genes and Genes Determining Spore Properties and Germination Characteristics. PLoS ONE, 2015, 10, e0127036.	1.1	13
3083	Whole Transcriptome Analysis Using Next-Generation Sequencing of Sterile-Cultured <i>Eisenia andrei</i> for Immune System Research. PLoS ONE, 2015, 10, e0118587.	1.1	6
3084	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.5	83
3085	Nmf9 Encodes a Highly Conserved Protein Important to Neurological Function in Mice and Flies. PLoS Genetics, 2015, 11, e1005344.	1.5	11
3086	Genus-Wide Comparative Genomics of <i>Malassezia</i> Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. PLoS Genetics, 2015, 11, e1005614.	1.5	198
3087	ApiAP2 Factors as Candidate Regulators of Stochastic Commitment to Merozoite Production in <i>Theileria annulata</i> . PLoS Neglected Tropical Diseases, 2015, 9, e0003933.	1.3	29
3088	<i>Schistosoma mansoni</i> Egg, Adult Male and Female Comparative Gene Expression Analysis and Identification of Novel Genes by RNA-Seq. PLoS Neglected Tropical Diseases, 2015, 9, e0004334.	1.3	90
3089	Large-Scale SNP Discovery and Genotyping for Constructing a High-Density Genetic Map of Tea Plant Using Specific-Locus Amplified Fragment Sequencing (SLAF-seq). PLoS ONE, 2015, 10, e0128798.	1.1	68
3090	Analysis of Multiple <i>Brachyspira hyodysenteriae</i> Genomes Confirms That the Species Is Relatively Conserved but Has Potentially Important Strain Variation. PLoS ONE, 2015, 10, e0131050.	1.1	36
3091	BGD: A Database of Bat Genomes. PLoS ONE, 2015, 10, e0131296.	1.1	2
3092	<i>Salix purpurea</i> Stimulates the Expression of Specific Bacterial Xenobiotic Degradation Genes in a Soil Contaminated with Hydrocarbons. PLoS ONE, 2015, 10, e0132062.	1.1	75
3093	Functional Analysis of Chicken IRF7 in Response to dsRNA Analog Poly(I:C) by Integrating Overexpression and Knockdown. PLoS ONE, 2015, 10, e0133450.	1.1	45
3094	Improving the Annotation of <i>Arabidopsis lyrata</i> Using RNA-Seq Data. PLoS ONE, 2015, 10, e0137391.	1.1	82
3095	Whole Blood Gene Expression Profiles of Patients with a Past Aneurysmal Subarachnoid Hemorrhage. PLoS ONE, 2015, 10, e0139352.	1.1	11
3096	Small RNA Sequencing Uncovers New miRNAs and moRNAs Differentially Expressed in Normal and Primary Myelofibrosis CD34+ Cells. PLoS ONE, 2015, 10, e0140445.	1.1	20
3097	A catalogue of novel bovine long noncoding RNA across 18 tissues. PLoS ONE, 2015, 10, e0141225.	1.1	130

#	ARTICLE	IF	CITATIONS
3098	Identification of Genetic Variation between Obligate Plant Pathogens <i>Pseudoperonospora cubensis</i> and <i>P. humuli</i> Using RNA Sequencing and Genotyping-By-Sequencing. <i>PLoS ONE</i> , 2015, 10, e0143665.	1.1	29
3099	Using Next Generation Sequencing for Multiplexed Trait-Linked Markers in <i>Wheat</i> . <i>PLoS ONE</i> , 2015, 10, e0143890.	1.1	28
3100	Investigation of a Quadruplex-Forming Repeat Sequence Highly Enriched in <i>Xanthomonas</i> and <i>Nostoc</i> sp.. <i>PLoS ONE</i> , 2015, 10, e0144275.	1.1	12
3101	Transcript Quantification by RNA-Seq Reveals Differentially Expressed Genes in the Red and Yellow Fruits of <i>Fragaria vesca</i> . <i>PLoS ONE</i> , 2015, 10, e0144356.	1.1	46
3102	Application of a Novel "Pan-Genome"-Based Strategy for Assigning RNAseq Transcript Reads to <i>Staphylococcus aureus</i> Strains. <i>PLoS ONE</i> , 2015, 10, e0145861.	1.1	9
3103	Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy. <i>PLoS ONE</i> , 2015, 10, e0145176.	1.1	26
3104	Re-analysis of RNA-seq transcriptome data reveals new aspects of gene activity in <i>Arabidopsis</i> root hairs. <i>Frontiers in Plant Science</i> , 2015, 6, 421.	1.7	16
3105	Identification of heat-responsive genes in carnation ( <i>Dianthus caryophyllus</i> L.) by RNA-seq. <i>Frontiers in Plant Science</i> , 2015, 6, 519.	1.7	36
3106	RNA-Seq analysis identifies key genes associated with haustorial development in the root hemiparasite <i>Santalum album</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 661.	1.7	49
3107	Differential gene expression in pre-laying and laying period ovaries of Sichuan White geese ( <i>Anser</i> ) Tj ETQq1 1 0.784314 rgBT / Overlook 0.3 15		
3108	Long Read Alignment with Parallel MapReduce Cloud Platform. <i>BioMed Research International</i> , 2015, 2015, 1-13.	0.9	8
3109	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
3110	Evaluation and Application of the Strand-Specific Protocol for Next-Generation Sequencing. <i>BioMed Research International</i> , 2015, 2015, 1-8.	0.9	11
3111	<i>De Novo</i> Transcriptome Sequencing of the Orange-Fleshed Sweet Potato and Analysis of Differentially Expressed Genes Related to Carotenoid Biosynthesis. <i>International Journal of Genomics</i> , 2015, 2015, 1-10.	0.8	27
3112	A Complex Genome-MicroRNA Interplay in Human Mitochondria. <i>BioMed Research International</i> , 2015, 2015, 1-13.	0.9	37
3113	Novel RNA variants in colorectal cancers. <i>Oncotarget</i> , 2015, 6, 36587-36602.	0.8	15
3114	Identification of an AVP-NP11 mutation within the AVP moiety in a family with neurohypophyseal diabetes insipidus: review of the literature. <i>Hormones</i> , 2015, 14, 442-6.	0.9	2
3115	A Unified Single Nucleotide Polymorphism Map of Sunflower ( <i>Helianthus annuus</i> L.) Derived from Current Genomic Resources. <i>Crop Science</i> , 2015, 55, 1696-1702.	0.8	16

#	ARTICLE	IF	CITATIONS
3116	Structural variation discovery in the cancer genome using next generation sequencing: Computational solutions and perspectives. <i>Oncotarget</i> , 2015, 6, 5477-5489.	0.8	33
3117	Comprehensive analyses of genomes, transcriptomes and metabolites of neem tree. <i>PeerJ</i> , 2015, 3, e1066.	0.9	35
3118	The exonuclease Nibbler regulates age-associated traits and modulates piRNA length in <i>Drosophila</i> . <i>Aging Cell</i> , 2015, 14, 443-452.	3.0	58
3119	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. <i>MBio</i> , 2015, 6, e00306-15.	1.8	380
3120	TUT7 controls the fate of precursor microRNAs by using three different uridylation mechanisms. <i>EMBO Journal</i> , 2015, 34, 1801-1815.	3.5	97
3121	Development of a high-resolution NGS-based HLA-typing and analysis pipeline. <i>Nucleic Acids Research</i> , 2015, 43, e70-e70.	6.5	77
3122	Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12462.	1.0	317
3123	Structural basis for retroviral integration into nucleosomes. <i>Nature</i> , 2015, 523, 366-369.	13.7	133
3124	A Comprehensive Transcriptomic and Proteomic Analysis of Hydra Head Regeneration. <i>Molecular Biology and Evolution</i> , 2015, 32, 1928-1947.	3.5	106
3125	Recurrent somatic mutations in regulatory regions of human cancer genomes. <i>Nature Genetics</i> , 2015, 47, 710-716.	9.4	225
3126	Secondary structure-based analysis of mouse brain small RNA sequences obtained by using next-generation sequencing. <i>Genomics</i> , 2015, 106, 122-128.	1.3	5
3127	Oxytocin receptor gene sequences in owl monkeys and other primates show remarkable interspecific regulatory and protein coding variation. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 160-177.	1.2	11
3128	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. <i>Nature Communications</i> , 2015, 6, 7256.	5.8	77
3129	Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. <i>Molecular Biology and Evolution</i> , 2015, 32, 2367-2382.	3.5	66
3130	The First High-Density Genetic Map Construction in Tree Peony ( <i>Paeonia Sect. Moutan</i> ) using Genotyping by Specific-Locus Amplified Fragment Sequencing. <i>PLoS ONE</i> , 2015, 10, e0128584.	1.1	49
3131	Inferring bona fide transfrags in RNA-Seq derived-transcriptome assemblies of non-model organisms. <i>BMC Bioinformatics</i> , 2015, 16, 58.	1.2	7
3132	Lineage specific evolution of the VNTR composite retrotransposon central domain and its role in retrotransposition of gibbon LAVA elements. <i>BMC Genomics</i> , 2015, 16, 389.	1.2	12
3133	Genome-wide amplification of proviral sequences reveals new polymorphic HERV-K(HML-2) proviruses in humans and chimpanzees that are absent from genome assemblies. <i>Retrovirology</i> , 2015, 12, 35.	0.9	26

#	ARTICLE	IF	CITATIONS
3134	A Python package for parsing, validating, mapping and formatting sequence variants using HGVS nomenclature. <i>Bioinformatics</i> , 2015, 31, 268-270.	1.8	74
3135	Selecting Specific PCR Primers with MFEprimer. <i>Methods in Molecular Biology</i> , 2015, 1275, 201-213.	0.4	20
3136	RNA-Seq: Improving Our Understanding of Retinal Biology and Disease. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a017152.	2.9	23
3137	Disentangling the Relationship of the Australian Marsupial Orders Using Retrotransposon and Evolutionary Network Analyses. <i>Genome Biology and Evolution</i> , 2015, 7, 985-992.	1.1	38
3138	Implementation of Amplicon Parallel Sequencing Leads to Improvement of Diagnosis and Therapy of Lung Cancer Patients. <i>Journal of Thoracic Oncology</i> , 2015, 10, 1049-1057.	0.5	85
3139	BatAlign: an incremental method for accurate alignment of sequencing reads. <i>Nucleic Acids Research</i> , 2015, 43, e107-e107.	6.5	9
3140	Transposable element detection from whole genome sequence data. <i>Mobile DNA</i> , 2015, 6, 24.	1.3	139
3141	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. <i>Genome Biology and Evolution</i> , 2015, 7, evv172.	1.1	22
3142	The molecular evolution of spiggin nesting glue in sticklebacks. <i>Molecular Ecology</i> , 2015, 24, 4474-4488.	2.0	9
3143	The Genome of the <i>Great Speckled Wood</i> Provides Insights into Bird Diversification. <i>Genome Biology and Evolution</i> , 2015, 7, 2680-2691.	1.1	55
3144	SuRankCo: supervised ranking of contigs in de novo assemblies. <i>BMC Bioinformatics</i> , 2015, 16, 240.	1.2	13
3145	Scrutinizing the immune defence inventory of <i>Camponotus floridanus</i> applying total transcriptome sequencing. <i>BMC Genomics</i> , 2015, 16, 540.	1.2	33
3146	The complete mitochondrial genome sequence of the green microalga <i>Lobosphaera (Parietochloris) incisa</i> reveals a new type of palindromic repetitive repeat. <i>BMC Genomics</i> , 2015, 16, 580.	1.2	9
3147	Construction of a high-density genetic map using specific length amplified fragment markers and identification of a quantitative trait locus for anthracnose resistance in walnut ( <i>Juglans regia</i> L.). <i>BMC Genomics</i> , 2015, 16, 614.	1.2	72
3148	Genome sequencing of herb Tulsi ( <i>Ocimum tenuiflorum</i> ) unravels key genes behind its strong medicinal properties. <i>BMC Plant Biology</i> , 2015, 15, 212.	1.6	80
3149	Exploiting single-molecule transcript sequencing for eukaryotic gene prediction. <i>Genome Biology</i> , 2015, 16, 184.	3.8	148
3150	Spatio-temporal regulation of circular RNA expression during porcine embryonic brain development. <i>Genome Biology</i> , 2015, 16, 245.	3.8	422
3151	Global Diversity Lines: A Five-Continent Reference Panel of Sequenced <i>Drosophila melanogaster</i> Strains. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 593-603.	0.8	124

#	ARTICLE	IF	CITATIONS
3152	Endogenous Small RNA Mediates Meiotic Silencing of a Novel DNA Transposon. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1949-1960.	0.8	34
3153	Unique transposon landscapes are pervasive across <i>Drosophila melanogaster</i> genomes. <i>Nucleic Acids Research</i> , 2015, 43, 10655-10672.	6.5	114
3154	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14936-14941.	3.3	329
3155	A thesaurus of genetic variation for interrogation of repetitive genomic regions. <i>Nucleic Acids Research</i> , 2015, 43, e68-e68.	6.5	5
3156	The ReproGenomics Viewer: an integrative cross-species toolbox for the reproductive science community. <i>Nucleic Acids Research</i> , 2015, 43, W109-W116.	6.5	46
3157	High speed BLASTN: an accelerated MegaBLAST search tool. <i>Nucleic Acids Research</i> , 2015, 43, 7762-7768.	6.5	322
3158	A Novel Algorithm for Classifying Protein Structure Familiar by Using the Graph Mining Approach. <i>Lecture Notes in Computer Science</i> , 2015, , 723-729.	1.0	1
3159	Draft Genome Sequence of the Archiascomycetous Yeast <i>Saitoella complicata</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	1
3160	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain UV74 Reveals Extensive Variability within Its Genomic Group. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
3161	Draft Genome Sequence of <i>Mycobacterium bohemicum</i> Strain DSM 44277 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
3162	Analysis of paired end Pol II ChIP-seq and short capped RNA-seq in MCF-7 cells. <i>Genomics Data</i> , 2015, 5, 263-267.	1.3	3
3163	The X Chromosome of Hemipteran Insects: Conservation, Dosage Compensation and Sex-Biased Expression. <i>Genome Biology and Evolution</i> , 2015, 7, 3259-3268.	1.1	45
3164	ScanIndel: a hybrid framework for indel detection via gapped alignment, split reads and de novo assembly. <i>Genome Medicine</i> , 2015, 7, 127.	3.6	50
3165	A draft genome sequence of an invasive mosquito: an Italian <i>Aedes albopictus</i> . <i>Pathogens and Global Health</i> , 2015, 109, 207-220.	1.0	35
3166	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. , 2015, , 563-612.		8
3167	Comprehensive Transcriptome Analysis Reveals Accelerated Genic Evolution in a Tibet Fish, <i>Gymnodiptychus pachycheilus</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 251-261.	1.1	112
3168	Development of a novel method to create double-strand break repair fingerprints using next-generation sequencing. <i>DNA Repair</i> , 2015, 26, 44-53.	1.3	14
3169	Characterization of E3 ubiquitin ligase neuregulin receptor degradation protein-1 (Nrdp1) in the large yellow croaker ( <i>Larimichthys crocea</i> ) and its immune responses to Cryptocaryon irritans. <i>Gene</i> , 2015, 556, 98-105.	1.0	20

#	ARTICLE	IF	CITATIONS
3170	Uncapped 5' ends of mRNAs targeted by cytoplasmic capping map to the vicinity of downstream CAGE tags. <i>FEBS Letters</i> , 2015, 589, 279-284.	1.3	22
3171	Genome assembly and annotation of a <i>Drosophila simulans</i> strain from Madagascar. <i>Molecular Ecology Resources</i> , 2015, 15, 372-381.	2.2	46
3172	Whole-genome sequencing reveals absence of recent gene flow and separate demographic histories for <i>Anopheles punctulatus</i> mosquitoes in Papua New Guinea. <i>Molecular Ecology</i> , 2015, 24, 1263-1274.	2.0	13
3173	Online Resources for Genomic Analysis Using High-Throughput Sequencing. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.top083667.	0.2	6
3174	Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of <i>Fistulina hepatica</i> and <i>Cylindrobasidium torrendii</i> . <i>Fungal Genetics and Biology</i> , 2015, 76, 78-92.	0.9	141
3175	Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2015, 9, 1928-1940.	4.4	155
3176	Smoking-Associated Site-Specific Differential Methylation in Buccal Mucosa in the COPD Gene Study. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 53, 246-254.	1.4	49
3177	Chaperone network composition in <i>Solanum lycopersicum</i> explored by transcriptome profiling and microarray meta-analysis. <i>Plant, Cell and Environment</i> , 2015, 38, 693-709.	2.8	71
3178	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. <i>Nature Communications</i> , 2015, 6, 6120.	5.8	178
3179	HIV-1 Integration Landscape during Latent and Active Infection. <i>Cell</i> , 2015, 160, 420-432.	13.5	393
3180	Next-Generation Sequencing of Duplication CNVs Reveals that Most Are Tandem and Some Create Fusion Genes at Breakpoints. <i>American Journal of Human Genetics</i> , 2015, 96, 208-220.	2.6	123
3181	Long-Term Balancing Selection in LAD1 Maintains a Missense Trans-Species Polymorphism in Humans, Chimpanzees, and Bonobos. <i>Molecular Biology and Evolution</i> , 2015, 32, 1186-1196.	3.5	70
3182	Three CCT domain-containing genes were identified to regulate heading date by candidate gene-based association mapping and transformation in rice. <i>Scientific Reports</i> , 2015, 5, 7663.	1.6	61
3183	The draft genome of Tibetan hulless barley reveals adaptive patterns to the high stressful Tibetan Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1095-1100.	3.3	147
3184	Studying Genome Heterogeneity within the Arbuscular Mycorrhizal Fungal Cytoplasm. <i>Genome Biology and Evolution</i> , 2015, 7, 505-521.	1.1	30
3185	First insights into the giant panda ( <i>Ailuropoda melanoleuca</i> ) blood transcriptome: a resource for novel gene loci and immunogenetics. <i>Molecular Ecology Resources</i> , 2015, 15, 1001-1013.	2.2	25
3186	Genetic mapping of the nulliplex-branch gene ( <i>gb_nb1</i> ) in cotton using next-generation sequencing. <i>Theoretical and Applied Genetics</i> , 2015, 128, 539-547.	1.8	63
3187	Integrated genome sequence and linkage map of physic nut ( <i>Jatropha curcas</i> L.), a biodiesel plant. <i>Plant Journal</i> , 2015, 81, 810-821.	2.8	149

#	ARTICLE	IF	CITATIONS
3188	Polymerase chain reaction-based serotyping of pathogenic bacteria in food. <i>Journal of Microbiological Methods</i> , 2015, 110, 18-26.	0.7	25
3189	Sustained Heterozygosity Across a Self-Incompatibility Locus in an Inbred Ascidian. <i>Molecular Biology and Evolution</i> , 2015, 32, 81-90.	3.5	6
3190	Multicolor CRISPR labeling of chromosomal loci in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3002-3007.	3.3	363
3191	AmpliVar: Mutation Detection in High-Throughput Sequence from Amplicon-Based Libraries. <i>Human Mutation</i> , 2015, 36, 411-418.	1.1	7
3192	Nicotinic receptors in non-human primates: Analysis of genetic and functional conservation with humans. <i>Neuropharmacology</i> , 2015, 96, 263-273.	2.0	14
3193	A CRISPR/Cas9 Vector System for Tissue-Specific Gene Disruption in Zebrafish. <i>Developmental Cell</i> , 2015, 32, 756-764.	3.1	325
3194	TCR sequences and tissue distribution discriminate the subsets of naïve and activated/memory Treg cells in mice. <i>European Journal of Immunology</i> , 2015, 45, 1524-1534.	1.6	25
3195	Expression and regulation of long noncoding RNAs in TLR4 signaling in mouse macrophages. <i>BMC Genomics</i> , 2015, 16, 45.	1.2	76
3196	In silico identification and characterisation of 17 polymorphic anonymous non-coding sequence markers (ANMs) for red grouse ( <i>Lagopus lagopus scotica</i> ). <i>Conservation Genetics Resources</i> , 2015, 7, 319-323.	0.4	2
3197	Single-nucleotide polymorphism identification and genotyping in <i>Camelina sativa</i> . <i>Molecular Breeding</i> , 2015, 35, 35.	1.0	36
3198	The genome and transcriptome of the zoonotic hookworm <i>Ancylostoma ceylanicum</i> identify infection-specific gene families. <i>Nature Genetics</i> , 2015, 47, 416-422.	9.4	91
3199	Identification of Functional Variants for Cleft Lip with or without Cleft Palate in or near PAX7, FGFR2, and NOG by Targeted Sequencing of GWAS Loci. <i>American Journal of Human Genetics</i> , 2015, 96, 397-411.	2.6	150
3200	Genome-wide characterization of developmental stage- and tissue-specific transcription factors in wheat. <i>BMC Genomics</i> , 2015, 16, 125.	1.2	19
3201	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528.	5.8	1,062
3202	Bridger: a new framework for de novo transcriptome assembly using RNA-seq data. <i>Genome Biology</i> , 2015, 16, 30.	3.8	258
3203	New cryptic karyotypic differences between cattle ( <i>Bos taurus</i> ) and goat ( <i>Capra hircus</i> ). <i>Chromosome Research</i> , 2015, 23, 225-235.	1.0	8
3204	PAIDB v2.0: exploration and analysis of pathogenicity and resistance islands. <i>Nucleic Acids Research</i> , 2015, 43, D624-D630.	6.5	139
3205	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. <i>PLoS Genetics</i> , 2015, 11, e1004850.	1.5	76

#	ARTICLE	IF	CITATIONS
3206	Sex-Biased Expression of Young Genes in <i>Xenopus tropicalis</i> . Cytogenetic and Genome Research, 2015, 145, 265-277.	0.6	4
3207	Design and bioinformatics analysis of genome-wide CLIP experiments. Nucleic Acids Research, 2015, 43, 5263-5274.	6.5	65
3208	Loss of function of OsMADS3 via the insertion of a novel retrotransposon leads to recessive male sterility in rice ( <i>Oryza sativa</i> ). Plant Science, 2015, 238, 188-197.	1.7	14
3210	Genetic Regulation of Bone Metabolism in the Chicken: Similarities and Differences to Mammalian Systems. PLoS Genetics, 2015, 11, e1005250.	1.5	47
3211	Quantitative Measurement of Immunoglobulins and Free Light Chains Using Mass Spectrometry. Analytical Chemistry, 2015, 87, 8268-8274.	3.2	27
3212	Single-cell RNA-seq transcriptome analysis of linear and circular RNAs in mouse preimplantation embryos. Genome Biology, 2015, 16, 148.	13.9	369
3213	The barber's pole worm CAP protein superfamily – A basis for fundamental discovery and biotechnology advances. Biotechnology Advances, 2015, 33, 1744-1754.	6.0	16
3214	Cypiripi: exact genotyping of <i>CYP2D6</i> using high-throughput sequencing data. Bioinformatics, 2015, 31, i27-i34.	1.8	37
3215	A high-density genetic map for P genome of <i>Agropyron Gaertn.</i> based on specific-locus amplified fragment sequencing (SLAF-seq). Planta, 2015, 242, 1335-1347.	1.6	41
3216	A genome survey sequencing of the Java mouse deer ( <i>Tragulus javanicus</i> ) adds new aspects to the evolution of lineage specific retrotransposons in Ruminantia ( <i>Cetartiodactyla</i> ). Gene, 2015, 571, 271-278.	1.0	8
3217	Incl shufflons: Assembly issues in the next-generation sequencing era. Plasmid, 2015, 80, 111-117.	0.4	30
3218	A Revised Genome Assembly of the Region 5q22 to Canine <i>SOX9</i> Includes the <i>RevSex</i> Orthologous Region. Sexual Development, 2015, 9, 155-161.	1.1	10
3219	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. Nature Medicine, 2015, 21, 895-905.	15.2	1,306
3220	A piRNA-like small RNA interacts with and modulates p-ERM proteins in human somatic cells. Nature Communications, 2015, 6, 7316.	5.8	88
3222	Can We Identify Genes with Increased Phylogenetic Reliability?. Systematic Biology, 2015, 64, 824-837.	2.7	80
3223	Chromosome-Specific Painting in <i>Cucumis</i> Species Using Bulked Oligonucleotides. Genetics, 2015, 200, 771-779.	1.2	192
3224	Long Noncoding RNAs and Cancer. , 2015, , 91-114.		4
3225	Np9, a cellular protein of retroviral ancestry restricted to human, chimpanzee and gorilla, binds and regulates ubiquitin ligase MDM2. Cell Cycle, 2015, 14, 2619-2633.	1.3	16

#	ARTICLE	IF	CITATIONS
3226	Transposable Elements and DNA Methylation Create in Embryonic Stem Cells Human-Specific Regulatory Sequences Associated with Distal Enhancers and Noncoding RNAs. <i>Genome Biology and Evolution</i> , 2015, 7, 1432-1454.	1.1	67
3227	Natural variation of the expression pattern of the segmentation gene <i>even-skipped</i> in <i>melanogaster</i> . <i>Developmental Biology</i> , 2015, 405, 173-181.	0.9	23
3228	A review: FPGA based word matching stage of BLASTN. , 2015, , .		4
3229	Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005011.	1.5	29
3230	Identification of agonists for a group of human odorant receptors. <i>Frontiers in Pharmacology</i> , 2015, 6, 35.	1.6	37
3231	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	1.2	177
3232	Effects of low temperature on mRNA and small RNA transcriptomes in <i>Solanum lycopersicoides</i> leaf revealed by RNA-Seq. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 768-773.	1.0	22
3233	Genome-wide identification of lineage-specific genes within <i>Caenorhabditis elegans</i> . <i>Genomics</i> , 2015, 106, 242-248.	1.3	19
3234	Whole transcriptome analysis reveals changes in expression of immune-related genes during and after bleaching in a reef-building coral. <i>Royal Society Open Science</i> , 2015, 2, 140214.	1.1	189
3235	Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. <i>Scientific Reports</i> , 2015, 5, 11534.	1.6	42
3236	Construction of a linkage map based on retrotransposon insertion polymorphisms in sweetpotato via high-throughput sequencing. <i>Breeding Science</i> , 2015, 65, 145-153.	0.9	32
3237	The radish genome and comprehensive gene expression profile of tuberous root formation and development. <i>Scientific Reports</i> , 2015, 5, 10835.	1.6	154
3238	Numerous Transitions of Sex Chromosomes in Diptera. <i>PLoS Biology</i> , 2015, 13, e1002078.	2.6	279
3239	Biosequence Time-Frequency Processing: Pathogen Detection and Identification. <i>Applied and Numerical Harmonic Analysis</i> , 2015, , 65-85.	0.1	0
3240	A RESTful API for Accessing Microbial Community Data for MG-RAST. <i>PLoS Computational Biology</i> , 2015, 11, e1004008.	1.5	83
3241	Novel Transcription Factor Variants through RNA-Sequencing: The Importance of Being "Alternative". <i>International Journal of Molecular Sciences</i> , 2015, 16, 1755-1771.	1.8	8
3242	G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. <i>Nature Methods</i> , 2015, 12, 519-522.	9.0	633
3243	A single nucleotide polymorphism associated with isolated cleft lip and palate, thyroid cancer and hypothyroidism alters the activity of an oral epithelium and thyroid enhancer near FOXE1. <i>Human Molecular Genetics</i> , 2015, 24, 3895-3907.	1.4	36

#	ARTICLE	IF	CITATIONS
3244	Haploinsufficiency of the miR-873/miR-876 microRNA cluster is associated with craniofacial abnormalities. <i>Gene</i> , 2015, 561, 95-100.	1.0	15
3245	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
3246	Proteogenomic Analysis of <i>Trichophyton rubrum</i> Aided by RNA Sequencing. <i>Journal of Proteome Research</i> , 2015, 14, 2207-2218.	1.8	7
3247	Genome sequence of cultivated Upland cotton ( <i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	9.4	1,064
3248	Comparative transcriptome of rhizome and leaf in <i>Ligusticum Chuanxiong</i> . <i>Plant Systematics and Evolution</i> , 2015, 301, 2073-2085.	0.3	9
3249	Potassium stress growth characteristics and energetics in the haloarchaeon <i>Haloarcula marismortui</i> . <i>Extremophiles</i> , 2015, 19, 315-325.	0.9	13
3250	Whole-genome sequencing of <i>Bacillus subtilis</i> XF-1 reveals mechanisms for biological control and multiple beneficial properties in plants. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 925-937.	1.4	44
3251	DRESS: dimensionality reduction for efficient sequence search. <i>Data Mining and Knowledge Discovery</i> , 2015, 29, 1280-1311.	2.4	0
3252	De novo assembly, gene annotation, and marker development of mulberry ( <i>Morus atropurpurea</i> ) transcriptome. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	19
3253	Identification and characterisation of 17 polymorphic candidate genes for response to parasitic nematode ( <i>Trichostrongylus tenuis</i> ) infection in red grouse ( <i>Lagopus lagopus scotica</i> ). <i>Conservation Genetics Resources</i> , 2015, 7, 23-28.	0.4	3
3254	Cigarette smoke mediates epigenetic repression of miR-217 during esophageal adenocarcinogenesis. <i>Oncogene</i> , 2015, 34, 5548-5559.	2.6	32
3255	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	13.5	482
3256	Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <i>Salvia miltiorrhiza</i> and tanshinone biosynthesis. <i>Plant Journal</i> , 2015, 82, 951-961.	2.8	337
3257	RIEMS: a software pipeline for sensitive and comprehensive taxonomic classification of reads from metagenomics datasets. <i>BMC Bioinformatics</i> , 2015, 16, 69.	1.2	73
3258	The distribution and mutagenesis of short coding INDELS from 1,128 whole exomes. <i>BMC Genomics</i> , 2015, 16, 143.	1.2	9
3259	Transcriptome characterization of three wild Chinese <i>Vitis</i> uncovers a large number of distinct disease related genes. <i>BMC Genomics</i> , 2015, 16, 223.	1.2	23
3260	Identification of novel fusion genes in lung cancer using breakpoint assembly of transcriptome sequencing data. <i>Genome Biology</i> , 2015, 16, 7.	3.8	44
3261	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. <i>Genome Biology</i> , 2015, 16, 48.	3.8	216

#	ARTICLE	IF	CITATIONS
3262	Evaluating the performance of anchored hybrid enrichment at the tips of the tree of life: a phylogenetic analysis of Australian Eugongylus group scincid lizards. <i>BMC Evolutionary Biology</i> , 2015, 15, 62.	3.2	57
3263	BAP1 mutation is a frequent somatic event in peritoneal malignant mesothelioma. <i>Journal of Translational Medicine</i> , 2015, 13, 122.	1.8	69
3264	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357
3265	Dynamics of gene expression patterns during early development of the European seabass ( <i>Dicentrarchus labrax</i> ). <i>Physiological Genomics</i> , 2015, 47, 158-169.	1.0	23
3266	Genome sequence-independent identification of RNA editing sites. <i>Nature Methods</i> , 2015, 12, 347-350.	9.0	102
3267	Scrimmer: designing primers from transcriptome data. <i>Molecular Ecology Resources</i> , 2015, 15, 1415-1420.	2.2	6
3268	<i>Drosophila</i> Muller F Elements Maintain a Distinct Set of Genomic Properties Over 40 Million Years of Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 719-740.	0.8	84
3269	Implications of <i>miR166</i> and <i>miR159</i> induction to the basal response mechanisms of an andigena potato ( <i>Solanum tuberosum</i> subsp. <i>andigena</i> ) to salinity stress, predicted from network models in <i>Arabidopsis</i> . <i>Genome</i> , 2015, 58, 13-24.	0.9	38
3270	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. <i>Genome Research</i> , 2015, 25, 814-824.	2.4	69
3271	Elucidating the composition and conservation of the autophagy pathway in photosynthetic eukaryotes. <i>Autophagy</i> , 2015, 11, 701-715.	4.3	79
3272	Gender-specific postnatal demethylation and establishment of epigenetic memory. <i>Genes and Development</i> , 2015, 29, 923-933.	2.7	83
3273	Identification of a gene controlling variation in the salt tolerance of rapeseed ( <i>Brassica napus</i> L.). <i>Planta</i> , 2015, 242, 313-326.	1.6	45
3274	Faster sequence homology searches by clustering subsequences. <i>Bioinformatics</i> , 2015, 31, 1183-1190.	1.8	64
3275	Breakmer: detection of structural variation in targeted massively parallel sequencing data using kmers. <i>Nucleic Acids Research</i> , 2015, 43, e19-e19.	6.5	161
3276	CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. <i>BMC Genomics</i> , 2015, 16, 236.	1.2	514
3277	Diverse chitinases are invoked during the activity-dormancy transition in spruce. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	16
3278	The variation game: Cracking complex genetic disorders with NGS and omics data. <i>Methods</i> , 2015, 79-80, 18-31.	1.9	22
3279	HAlign: Fast multiple similar DNA/RNA sequence alignment based on the centre star strategy. <i>Bioinformatics</i> , 2015, 31, 2475-2481.	1.8	136

#	ARTICLE	IF	CITATIONS
3280	T-lex2: genotyping, frequency estimation and re-annotation of transposable elements using single or pooled next-generation sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, e22-e22.	6.5	61
3281	Triticeae Resources in Ensembl Plants. <i>Plant and Cell Physiology</i> , 2015, 56, e3-e3.	1.5	59
3282	SNPfisher: tools for probing genetic variation in laboratory-reared zebrafish. <i>Development (Cambridge)</i> , 2015, 142, 1542-52.	1.2	39
3283	The BRAF Pseudogene Functions as a Competitive Endogenous RNA and Induces Lymphoma In Vivo. <i>Cell</i> , 2015, 161, 319-332.	13.5	293
3284	An Rtf2 Domain-Containing Protein Influences Pre-mRNA Splicing and Is Essential for Embryonic Development in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2015, 200, 523-535.	1.2	36
3285	16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 4119-4129.	1.7	79
3286	Transcriptome-wide identification of adenosine-to-inosine editing using the ICE-seq method. <i>Nature Protocols</i> , 2015, 10, 715-732.	5.5	67
3287	IDBA-MTP: A Hybrid Metatranscriptomic Assembler Based on Protein Information. <i>Journal of Computational Biology</i> , 2015, 22, 367-376.	0.8	19
3288	Woods: A fast and accurate functional annotator and classifier of genomic and metagenomic sequences. <i>Genomics</i> , 2015, 106, 1-6.	1.3	34
3289	Germline and somatic imprinting in the nonhuman primate highlights species differences in oocyte methylation. <i>Genome Research</i> , 2015, 25, 611-623.	2.4	25
3290	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
3291	Identification of a Recently Active Mammalian SINE Derived from Ribosomal RNA. <i>Genome Biology and Evolution</i> , 2015, 7, 775-788.	1.1	12
3292	Improving the gene structure annotation of the apicomplexan parasite <i>Neospora caninum</i> fulfils a vital requirement towards an in silico-derived vaccine. <i>International Journal for Parasitology</i> , 2015, 45, 305-318.	1.3	11
3293	A novel locus of resistance to severe malaria in a region of ancient balancing selection. <i>Nature</i> , 2015, 526, 253-257.	13.7	182
3294	Viral metagenomics in drug-naïve, first-onset schizophrenia patients with prominent negative symptoms. <i>Psychiatry Research</i> , 2015, 229, 678-684.	1.7	2
3295	Gene panels and primers for next generation sequencing studies on neurodegenerative disorders. <i>Molecular and Cellular Toxicology</i> , 2015, 11, 89-143.	0.8	32
3296	Human Mpn1 promotes post-transcriptional processing and stability of U6atac. <i>FEBS Letters</i> , 2015, 589, 2417-2423.	1.3	16
3297	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	9.4	422

#	ARTICLE	IF	CITATIONS
3298	VISA - Vector Integration Site Analysis server: a web-based server to rapidly identify retroviral integration sites from next-generation sequencing. BMC Bioinformatics, 2015, 16, 212.	1.2	37
3299	The distribution and evolution of Arabidopsis thaliana cis natural antisense transcripts. BMC Genomics, 2015, 16, 444.	1.2	8
3300	MG-RAST, a Metagenomics Service for the Analysis of Microbial Community Structure and Function. Springer Protocols, 2015, , 69-87.	0.1	4
3301	Genetic mapping uncovers cis-regulatory landscape of RNA editing. Nature Communications, 2015, 6, 8194.	5.8	76
3302	microDuMIP: target-enrichment technique for microarray-based duplex molecular inversion probes. Nucleic Acids Research, 2015, 43, e28-e28.	6.5	11
3303	Discovering new biology through RNA-Seq. Plant Physiology, 2015, 169, pp.01081.2015.	2.3	28
3304	Rapid evolution of chemosensory receptor genes in a pair of sibling species of orchid bees (Apidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.2	56
3305	Unravelling the genome of Holy basil: an "incomparable" "elixir of life" of traditional Indian medicine. BMC Genomics, 2015, 16, 413.	1.2	60
3306	The Evolution of Bony Vertebrate Enhancers at Odds with Their Coding Sequence Landscape. Genome Biology and Evolution, 2015, 7, 2333-2343.	1.1	9
3307	The essential gene set of a photosynthetic organism. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6634-43.	3.3	166
3308	Comparative genome analysis of Mycoplasma pneumoniae. BMC Genomics, 2015, 16, 610.	1.2	59
3309	Metagenomic analysis of planktonic microbial consortia from a non-tidal urban-impacted segment of James River. Standards in Genomic Sciences, 2015, 10, 65.	1.5	24
3310	GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. Conservation Genetics Resources, 2015, 7, 851-857.	0.4	5
3311	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. Science, 2015, 350, 691-694.	6.0	430
3312	Characterization of fossilized relatives of the White Spot Syndrome Virus in genomes of decapod crustaceans. BMC Evolutionary Biology, 2015, 15, 142.	3.2	14
3313	Reference genome of wild goat (capra aegagrus) and sequencing of goat breeds provide insight into genic basis of goat domestication. BMC Genomics, 2015, 16, 431.	1.2	103
3314	Transcriptional profiling provides insights into metronomic cyclophosphamide-activated, innate immune-dependent regression of brain tumor xenografts. BMC Cancer, 2015, 15, 375.	1.1	18
3315	Structural basis of head to head polyketide fusion by CorB. Chemical Science, 2015, 6, 6525-6536.	3.7	20

#	ARTICLE	IF	CITATIONS
3316	BSPAT: a fast online tool for DNA methylation co-occurrence pattern analysis based on high-throughput bisulfite sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, 220.	1.2	28
3317	Transcriptome sequencing and annotation of the polychaete <i>Hermodice carunculata</i> (Annelida). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 10 23	1.2	23
3318	Cell periphery-related proteins as major genomic targets behind the adaptive evolution of an industrial <i>Saccharomyces cerevisiae</i> strain to combined heat and hydrolysate stress. <i>BMC Genomics</i> , 2015, 16, 514.	1.2	36
3319	Identification and analysis of retrogenes in the East Asian nematode <i>Caenorhabditis sp. 5</i> genome. <i>Genome</i> , 2015, 58, 349-355.	0.9	2
3320	Spider Transcriptomes Identify Ancient Large-Scale Gene Duplication Event Potentially Important in Silk Gland Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 1856-1870.	1.1	74
3321	Mapping a Type 1 FHB resistance on chromosome 4AS of <i>Triticum macha</i> and deployment in combination with two Type 2 resistances. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1725-1738.	1.8	10
3322	Read count-based method for high-throughput allelic genotyping of transposable elements and structural variants. <i>BMC Genomics</i> , 2015, 16, 508.	1.2	0
3323	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12628-12640.	4.6	72
3324	SANSparallel: interactive homology search against Uniprot. <i>Nucleic Acids Research</i> , 2015, 43, W24-W29.	6.5	38
3325	Complete Genome Sequence of <i>Streptococcus thermophilus</i> SMQ-301, a Model Strain for Phage-Host Interactions. <i>Genome Announcements</i> , 2015, 3, .	0.8	33
3326	RNA-Seq based phylogeny recapitulates previous phylogeny of the genus <i>Flaveria</i> (Asteraceae) with some modifications. <i>BMC Evolutionary Biology</i> , 2015, 15, 116.	3.2	46
3327	Assessing Recent Selection and Functionality at Long Noncoding RNA Loci in the Mouse Genome. <i>Genome Biology and Evolution</i> , 2015, 7, 2432-2444.	1.1	12
3328	GESPA: classifying nsSNPs to predict disease association. <i>BMC Bioinformatics</i> , 2015, 16, 228.	1.2	6
3329	A large genomic deletion leads to enhancer adoption by the lamin B1 gene: a second path to autosomal dominant adult-onset demyelinating leukodystrophy (ADLD). <i>Human Molecular Genetics</i> , 2015, 24, 3143-3154.	1.4	117
3330	Local sequence assembly reveals a high-resolution profile of somatic structural variations in 97 cancer genomes. <i>Nucleic Acids Research</i> , 2015, 43, 8146-8156.	6.5	22
3331	Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10967-10972.	3.3	1,023
3332	Identification and Characterization of Androgen-Responsive Genes in Zebrafish Embryos. <i>Environmental Science &amp; Technology</i> , 2015, 49, 11789-11798.	4.6	42
3333	Tentacle: distributed quantification of genes in metagenomes. <i>GigaScience</i> , 2015, 4, 40.	3.3	10

#	ARTICLE	IF	CITATIONS
3334	The genome of the vervet ( <i>Chlorocebus aethiops sabaeus</i> ). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114
3335	High-resolution analysis of the human T-cell receptor repertoire. <i>Nature Communications</i> , 2015, 6, 8081.	5.8	123
3336	RASER: reads aligner for SNPs and editing sites of RNA. <i>Bioinformatics</i> , 2015, 31, 3906-3913.	1.8	21
3337	Identification, Phylogeny, and Function of fabp2 Paralogs in Two Non-Model Teleost Fish Species. <i>Marine Biotechnology</i> , 2015, 17, 663-677.	1.1	7
3338	Accelerated rates of protein evolution in barley grain and pistil biased genes might be legacy of domestication. <i>Plant Molecular Biology</i> , 2015, 89, 253-261.	2.0	6
3339	Genome wide polymorphisms and yield heterosis in rice ( <i>Oryza sativa</i> subsp. indica). <i>Tropical Plant Biology</i> , 2015, 8, 117-125.	1.0	2
3340	Detecting protein complexes using connectivity among nodes in a PPI Network. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1.	1.2	2
3341	Rare k-mer DNA: Identification of sequence motifs and prediction of CpG island and promoter. <i>Journal of Theoretical Biology</i> , 2015, 387, 88-100.	0.8	13
3342	ICRmax: An optimized approach to detect tumor-specific interchromosomal rearrangements for clinical application. <i>Genomics</i> , 2015, 105, 265-272.	1.3	4
3343	Stable recombination hotspots in birds. <i>Science</i> , 2015, 350, 928-932.	6.0	280
3344	Comparative genomics of grass EST libraries reveals previously uncharacterized splicing events in crop plants. <i>BMC Plant Biology</i> , 2015, 15, 39.	1.6	3
3345	piRNA-like small RNAs mark extended 3' UTRs present in germ and somatic cells. <i>BMC Genomics</i> , 2015, 16, 462.	1.2	14
3346	Genetic signatures of adaptation revealed from transcriptome sequencing of Arctic and red foxes. <i>BMC Genomics</i> , 2015, 16, 585.	1.2	22
3347	Prokaryotic Metatranscriptomics. <i>Springer Protocols</i> , 2015, , 69-98.	0.1	1
3348	E-MEM: efficient computation of maximal exact matches for very large genomes. <i>Bioinformatics</i> , 2015, 31, 509-514.	1.8	26
3349	Identification of a new maize inflorescence meristem mutant and association analysis using SLAF-seq method. <i>Euphytica</i> , 2015, 202, 35-44.	0.6	33
3350	Profiling the RNA editomes of wild-type <i>C. elegans</i> and ADAR mutants. <i>Genome Research</i> , 2015, 25, 66-75.	2.4	70
3351	Chemokine receptors in Atlantic salmon. <i>Developmental and Comparative Immunology</i> , 2015, 49, 79-95.	1.0	37

#	ARTICLE	IF	CITATIONS
3352	Comparing the effectiveness of metagenomics and metabarcoding for diet analysis of a leaf-feeding monkey ( <i>Ptygathrix nemaeus</i> ). <i>Molecular Ecology Resources</i> , 2015, 15, 250-261.	2.2	119
3353	Intron evolution in <i>Neurospora</i> : the role of mutational bias and selection. <i>Genome Research</i> , 2015, 25, 100-110.	2.4	9
3354	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	9.4	413
3355	The Mutational Landscape in Pediatric Acute Lymphoblastic Leukemia Deciphered by Whole Genome Sequencing. <i>Human Mutation</i> , 2015, 36, 118-128.	1.1	38
3356	RNA-seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 613-624.	4.1	202
3357	A phylogenomic analysis of turtles. <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 250-257.	1.2	244
3358	Off-target assessment of CRISPR-Cas9 guiding RNAs in human PS and mouse ES cells. <i>Genesis</i> , 2015, 53, 225-236.	0.8	55
3359	High-resolution genetic maps of <i>Eucalyptus</i> improve <i>Eucalyptus grandis</i> genome assembly. <i>New Phytologist</i> , 2015, 206, 1283-1296.	3.5	90
3360	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015, 43, D662-D669.	6.5	1,145
3361	Performance evaluation of Warshall algorithm and dynamic programming for Markov chain in local sequence alignment. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, 7, 78-81.	2.2	4
3362	Fast and sensitive protein alignment using DIAMOND. <i>Nature Methods</i> , 2015, 12, 59-60.	9.0	8,761
3363	Species-Specific Exon Loss in Human Transcriptomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 481-494.	3.5	7
3364	Thiamine Pyrophosphate Riboswitch in Some Representative Plant Species: A Bioinformatics Study. <i>Journal of Computational Biology</i> , 2015, 22, 1-9.	0.8	13
3365	Improved rat genome gene prediction by integration of ESTs with RNA-Seq information. <i>Bioinformatics</i> , 2015, 31, 25-32.	1.8	6
3366	A near complete snapshot of the <i>Zea mays</i> seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519.	1.6	28
3367	Classification of cytochrome P450s in common bean ( <i>Phaseolus vulgaris</i> L.). <i>Plant Systematics and Evolution</i> , 2015, 301, 211-216.	0.3	8
3368	Preliminary genomic survey and sequence analysis of the complement system in non-eutherian mammals. <i>Australian Mammalogy</i> , 2016, 38, 80.	0.7	6
3369	Freshwater Metaviromics and Bacteriophages: A Current Assessment of the State of the Art in Relation to Bioinformatic Challenges. <i>Evolutionary Bioinformatics</i> , 2016, 12s1, EBO.S38549.	0.6	20

#	ARTICLE	IF	CITATIONS
3370	Genomics Study of <i>Mycobacterium tuberculosis</i> Strains from Different Ethnic Populations in Taiwan. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S40152.	0.6	2
3371	[Letter to the Editor] Many commercial hot-start polymerases demonstrate activity prior to thermal activation. <i>BioTechniques</i> , 2016, 61, 293-296.	0.8	6
3372	Sixteen kiwi ( <i>Apteryx</i> spp) transcriptomes provide a wealth of genetic markers and insight into sex chromosome evolution in birds. <i>BMC Genomics</i> , 2016, 17, 410.	1.2	16
3373	PeanutBase and Other Bioinformatic Resources for Peanut. , 2016, , 241-252.		46
3374	Differences in molecular evolutionary rates among microRNAs in the human and chimpanzee genomes. <i>BMC Genomics</i> , 2016, 17, 528.	1.2	13
3375	In-Silico Prediction and Functional Analysis of Salt Stress Responsive Genes in Rice ( <i>Oryza sativa</i> ). <i>Rice Research Open Access</i> , 2016, 4, .	0.4	7
3376	Postnatal regulation of <i>MAMDC4</i> in the porcine intestinal epithelium is influenced by bacterial colonization. <i>Physiological Reports</i> , 2016, 4, e13018.	0.7	18
3377	Genome Sequence and Analysis of <i>Peptoclostridium difficile</i> Strain ZJCDC-S82. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S32476.	0.6	9
3378	Comparative Analysis of Human B Cell Epitopes Based on BCG Genomes. <i>BioMed Research International</i> , 2016, 2016, 1-5.	0.9	2
3379	Identifying Cancer Driver Genes Using Replication-Incompetent Retroviral Vectors. <i>Cancers</i> , 2016, 8, 99.	1.7	4
3380	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. <i>Frontiers in Genetics</i> , 2016, 7, 5.	1.1	4
3381	Bacterioplankton Dynamics within a Large Anthropogenically Impacted Urban Estuary. <i>Frontiers in Microbiology</i> , 2015, 6, 1438.	1.5	98
3382	Tricking <i>Arthrinium malaysianum</i> into Producing Industrially Important Enzymes Under 2-Deoxy D-Glucose Treatment. <i>Frontiers in Microbiology</i> , 2016, 7, 596.	1.5	10
3383	Metagenomic Reconstruction of Key Anaerobic Digestion Pathways in Municipal Sludge and Industrial Wastewater Biogas-Producing Systems. <i>Frontiers in Microbiology</i> , 2016, 7, 778.	1.5	103
3384	Expression of a Novel D4 Dopamine Receptor in the Lamprey Brain. <i>Evolutionary Considerations about Dopamine Receptors</i> . <i>Frontiers in Neuroanatomy</i> , 2016, 9, 165.	0.9	11
3385	BBBomics-Human Blood Brain Barrier Transcriptomics Hub. <i>Frontiers in Neuroscience</i> , 2016, 10, 71.	1.4	31
3386	Prediction of Toxin Genes from Chinese Yellow Catfish Based on Transcriptomic and Proteomic Sequencing. <i>International Journal of Molecular Sciences</i> , 2016, 17, 556.	1.8	14
3387	Expression Patterns and Functional Novelty of Ribonuclease 1 in Herbivorous <i>Megalobrama amblycephala</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 786.	1.8	5

#	ARTICLE	IF	CITATIONS
3388	Endogenous Multiple Exon Skipping and Back-Splicing at the DMD Mutation Hotspot. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1722.	1.8	35
3389	Digital Gene Expression Profiling to Explore Differentially Expressed Genes Associated with Terpenoid Biosynthesis during Fruit Development in <i>Litsea cubeba</i> . <i>Molecules</i> , 2016, 21, 1251.	1.7	9
3390	BinPacker: Packing-Based De Novo Transcriptome Assembly from RNA-seq Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004772.	1.5	116
3391	H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. <i>PLoS Genetics</i> , 2016, 12, e1005796.	1.5	25
3392	Mitochondrial Genome and Nuclear Markers Provide New Insight into the Evolutionary History of Macaques. <i>PLoS ONE</i> , 2016, 11, e0154665.	1.1	25
3393	Hotair Is Dispensable for Mouse Development. <i>PLoS Genetics</i> , 2016, 12, e1006232.	1.5	93
3394	A Point Mutation in a lincRNA Upstream of GDNF Is Associated to a Canine Insensitivity to Pain: A Spontaneous Model for Human Sensory Neuropathies. <i>PLoS Genetics</i> , 2016, 12, e1006482.	1.5	31
3395	Sex-Biased Transcriptome of <i>Schistosoma mansoni</i> : Host-Parasite Interaction, Genetic Determinants and Epigenetic Regulators Are Associated with Sexual Differentiation. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004930.	1.3	57
3396	The Mouse Solitary Odorant Receptor Gene Promoters as Models for the Study of Odorant Receptor Gene Choice. <i>PLoS ONE</i> , 2016, 11, e0144698.	1.1	3
3397	Rapid Identification of Candidate Genes for Seed Weight Using the SLAF-Seq Method in <i>Brassica napus</i> . <i>PLoS ONE</i> , 2016, 11, e0147580.	1.1	70
3398	Sp1 and Sp3 Are the Transcription Activators of Human ek1 Promoter in TSA-Treated Human Colon Carcinoma Cells. <i>PLoS ONE</i> , 2016, 11, e0147886.	1.1	12
3399	A Phylogenomic Approach Based on PCR Target Enrichment and High Throughput Sequencing: Resolving the Diversity within the South American Species of <i>Bartsia L.</i> (Orobanchaceae). <i>PLoS ONE</i> , 2016, 11, e0148203.	1.1	70
3400	TOPORS, a Dual E3 Ubiquitin and Sumo1 Ligase, Interacts with 26 S Protease Regulatory Subunit 4, Encoded by the PSMC1 Gene. <i>PLoS ONE</i> , 2016, 11, e0148678.	1.1	10
3401	Identification of Targets of CUG-BP, Elav-Like Family Member 1 (CELFL1) Regulation in Embryonic Heart Muscle. <i>PLoS ONE</i> , 2016, 11, e0149061.	1.1	30
3402	Population Structure and Antimicrobial Resistance Profiles of <i>Streptococcus suis</i> Serotype 2 Sequence Type 25 Strains. <i>PLoS ONE</i> , 2016, 11, e0150908.	1.1	32
3403	Mapping of a Novel Race Specific Resistance Gene to <i>Phytophthora</i> Root Rot of Pepper ( <i>Capsicum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl... Sequencing Strategy. <i>PLoS ONE</i> , 2016, 11, e0151401.	1.1	49
3404	Using Synthetic Mouse Spike-In Transcripts to Evaluate RNA-Seq Analysis Tools. <i>PLoS ONE</i> , 2016, 11, e0153782.	1.1	13
3405	Characterisation of <i>Candida</i> within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients. <i>PLoS ONE</i> , 2016, 11, e0155033.	1.1	45

#	ARTICLE	IF	CITATIONS
3406	BLAT2DOLite: An Online System for Identifying Significant Relationships between Genetic Sequences and Diseases. PLoS ONE, 2016, 11, e0157274.	1.1	2
3407	Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks ( <i>Quercus</i> L. sect. <i>Quercus</i> ). PLoS ONE, 2016, 11, e0158221.	1.1	34
3408	The Genomic Scrapheap Challenge; Extracting Relevant Data from Unmapped Whole Genome Sequencing Reads, Including Strain Specific Genomic Segments, in Rats. PLoS ONE, 2016, 11, e0160036.	1.1	5
3409	Differing Alterations of Two Esca Associated Fungi, <i>Phaeoacremonium aleophilum</i> and <i>Phaeoconiella chlamydospora</i> on Transcriptomic Level, to Co-Cultured <i>Vitis vinifera</i> L. calli. PLoS ONE, 2016, 11, e0163344.	1.1	7
3410	The Phenotypic and Genetic Underpinnings of Flower Size in Polemoniaceae. <i>Frontiers in Plant Science</i> , 2015, 6, 1144.	1.7	21
3411	High-Density Genetic Mapping Identifies New Major Loci for Tolerance to Low-Phosphorus Stress in Soybean. <i>Frontiers in Plant Science</i> , 2016, 7, 372.	1.7	57
3412	Targeted Capture Sequencing in Whitebark Pine Reveals Range-Wide Demographic and Adaptive Patterns Despite Challenges of a Large, Repetitive Genome. <i>Frontiers in Plant Science</i> , 2016, 7, 484.	1.7	38
3413	Natural Allelic Variations in Highly Polyploidy <i>Saccharum</i> Complex. <i>Frontiers in Plant Science</i> , 2016, 7, 804.	1.7	40
3414	Transcriptome Profiling of Huanglongbing (HLB) Tolerant and Susceptible Citrus Plants Reveals the Role of Basal Resistance in HLB Tolerance. <i>Frontiers in Plant Science</i> , 2016, 7, 933.	1.7	75
3415	Cloning and Characterization of TaTGW-7A Gene Associated with Grain Weight in Wheat via SLAF-seq-BSA. <i>Frontiers in Plant Science</i> , 2016, 7, 1902.	1.7	75
3416	&lt;em>TRPM8&/em>&nbsp;genetic variations associated with COPD risk in the Chinese Han population. <i>International Journal of COPD</i> , 2016, Volume 11, 2563-2571.	0.9	18
3417	An Analysis of Adenovirus Genomes Using Whole Genome Software Tools. <i>Bioinformatics</i> , 2016, 12, 301-310.	0.2	3
3418	Circular RNAs and their associations with breast cancer subtypes. <i>Oncotarget</i> , 2016, 7, 80967-80979.	0.8	140
3419	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016, 5, .	2.8	237
3420	An evaluation of transcriptome-based exon capture for frog phylogenomics across multiple scales of divergence (Class: Amphibia, Order: Anura). <i>Molecular Ecology Resources</i> , 2016, 16, 1069-1083.	2.2	92
3421	Para-allopatry in hybridizing fire-bellied toads ( <i>Bombina bombina</i> and <i>B. variegata</i> ): Inference from transcriptome-wide coalescence analyses. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1803-1818.	1.1	25
3422	CrisprVariants charts the mutation spectrum of genome engineering experiments. <i>Nature Biotechnology</i> , 2016, 34, 701-702.	9.4	149
3423	Structure and evolution of the gorilla and orangutan growth hormone loci. <i>Mammalian Genome</i> , 2016, 27, 511-523.	1.0	3

#	ARTICLE	IF	CITATIONS
3424	Lentiviral vectorâ€mediated insertional mutagenesis screen identifies genes that influence androgen independent prostate cancer progression and predict clinical outcome. <i>Molecular Carcinogenesis</i> , 2016, 55, 1761-1771.	1.3	37
3425	The complete genome of a viable archaeum isolated from 123â€millionâ€yearâ€old rock salt. <i>Environmental Microbiology</i> , 2016, 18, 565-579.	1.8	31
3426	Identification of Multiple Forms of RNA Transcripts Associated with Human-Specific Retrotransposed Gene Copies. <i>Genome Biology and Evolution</i> , 2016, 8, 2288-2296.	1.1	3
3427	Clinical and Genetic Features of Patients With <i>TNFRSF1A</i> Variants in Japan: Findings of a Nationwide Survey. <i>Arthritis and Rheumatology</i> , 2016, 68, 2760-2771.	2.9	21
3428	The Genetic Linkage Map of the Medicinal Mushroom <i>Agaricus subrufescens</i> Reveals Highly Conserved Macrosynteny with the Congeneric Species <i>Agaricus bisporus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1217-1226.	0.8	13
3429	A high-density SNP genotyping array for <i>Brassica napus</i> and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1887-1899.	1.8	205
3430	Study of the long-distance migration of small brown planthoppers <i>Laodelphax striatellus</i> in China using next-generation sequencing. <i>Pest Management Science</i> , 2016, 72, 298-305.	1.7	12
3431	A local alignment approach to similarity analysis of industrial alarm flood sequences. <i>Control Engineering Practice</i> , 2016, 55, 13-25.	3.2	51
3432	Phylogenetic marker development for target enrichment from transcriptome and genome skim data: the pipeline and its application in southern African <i>Oxalis</i> (Oxalidaceae). <i>Molecular Ecology Resources</i> , 2016, 16, 1124-1135.	2.2	101
3433	Identification of <i>CR</i> 1 retroposons in <i>Arborophila rufipectus</i> and their application to <i>P</i> hasianidae phylogeny. <i>Molecular Ecology Resources</i> , 2016, 16, 1037-1049.	2.2	1
3434	Highâ€throughput RNA sequencing reveals structural differences of orthologous brainâ€expressed genes between western lowland gorillas and humans. <i>Journal of Comparative Neurology</i> , 2016, 524, 288-308.	0.9	2
3435	Anthropogenic effects on bacterial diversity and function along a riverâ€toâ€estuary gradient in Northwest Greece revealed by metagenomics. <i>Environmental Microbiology</i> , 2016, 18, 4640-4652.	1.8	58
3436	Genomeâ€wide identification of differential methylation between primary and recurrent hepatocellular carcinomas. <i>Molecular Carcinogenesis</i> , 2016, 55, 1163-1174.	1.3	15
3437	Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. <i>Poultry Science</i> , 2016, 95, 2250-2258.	1.5	11
3438	Studying RNA Homology and Conservation with Infernal: From Single Sequences to RNA Families. <i>Current Protocols in Bioinformatics</i> , 2016, 54, 12.13.1-12.13.25.	25.8	21
3439	<i>SCR</i> 96, a small cysteineâ€rich secretory protein of <i>P</i> <i>hytophthora cactorum</i> , can trigger cell death in the Solanaceae and is important for pathogenicity and oxidative stress tolerance. <i>Molecular Plant Pathology</i> , 2016, 17, 577-587.	2.0	42
3440	Curation of the genome annotation of <i>Pichia pastoris</i> ( <i>Komagataella phaffii</i> ) CBS7435 from gene level to protein function. <i>FEMS Yeast Research</i> , 2016, 16, fow051.	1.1	69
3441	A Distinct Class of Chromoanagenesis Events Characterized by Focal Copy Number Gains. <i>Human Mutation</i> , 2016, 37, 661-668.	1.1	30

#	ARTICLE	IF	CITATIONS
3442	Molecular analysis of complex cases of alpha <sup>0</sup> and beta <sup>+</sup> thalassemia in Mexican mestizo patients with microcytosis and hypochromia reveals two novel alpha <sup>0</sup> thalassemia deletions $\alpha^{\text{Mex1}}$ and $\alpha^{\text{Mex2}}$ . International Journal of Laboratory Hematology, 2016, 38, 535-542.	0.7	6
3443	A genetic delineation of Patchouli ( <i>Pogostemon cablin</i> ) revealed by specific locus amplified fragment sequencing. Journal of Systematics and Evolution, 2016, 54, 491-501.	1.6	16
3444	Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096.	1.4	344
3445	Distinct interacting core taxa in co-occurrence networks enable discrimination of polymicrobial oral diseases with similar symptoms. Scientific Reports, 2016, 6, 30997.	1.6	70
3446	Improvement of genome assembly completeness and identification of novel full-length protein-coding genes by RNA-seq in the giant panda genome. Scientific Reports, 2016, 5, 18019.	1.6	12
3447	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. Nature Communications, 2016, 7, 12797.	5.8	190
3448	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D626-D634.	6.5	308
3449	The mitochondrial genome map of <i>Nelumbo nucifera</i> reveals ancient evolutionary features. Scientific Reports, 2016, 6, 30158.	1.6	40
3450	Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: <i>Phaffia rhodozyma</i> . BMC Genomics, 2016, 17, 901.	1.2	35
3451	New insights into the <i>Plasmodium vivax</i> transcriptome using RNA-Seq. Scientific Reports, 2016, 6, 20498.	1.6	65
3452	Roar: detecting alternative polyadenylation with standard mRNA sequencing libraries. BMC Bioinformatics, 2016, 17, 423.	1.2	64
3453	Computational workflow for the fine-grained analysis of metagenomic samples. BMC Genomics, 2016, 17, 802.	1.2	6
3454	A chromosome-level genome assembly of the Asian arowana, <i>Scleropages formosus</i> . Scientific Data, 2016, 3, 160105.	2.4	13
3455	Kmerind. , 2016, , .		11
3456	Genome-Wide Analysis of Transposon and Retroviral Insertions Reveals Preferential Integrations in Regions of DNA Flexibility. G3: Genes, Genomes, Genetics, 2016, 6, 805-817.	0.8	19
3457	Genetic architecture of the maize kernel row number revealed by combining QTL mapping using a high-density genetic map and bulked segregant RNA sequencing. BMC Genomics, 2016, 17, 915.	1.2	63
3458	SARVAVID. , 2016, , .		14
3459	Possible mechanisms of acquisition of herpesvirus virokines. Biochemistry (Moscow), 2016, 81, 1350-1357.	0.7	1

#	ARTICLE	IF	CITATIONS
3460	Acquired RAS or EGFR mutations and duration of response to EGFR blockade in colorectal cancer. <i>Nature Communications</i> , 2016, 7, 13665.	5.8	170
3461	SNP-Seek II: A resource for allele mining and analysis of big genomic data in <i>Oryza sativa</i> . <i>Current Plant Biology</i> , 2016, 7-8, 16-25.	2.3	48
3462	A pipeline for local assembly of minisatellite alleles from single-molecule sequencing data. <i>Bioinformatics</i> , 2017, 33, 650-653.	1.8	2
3463	SeqLib: a C++ API for rapid BAM manipulation, sequence alignment and sequence assembly. <i>Bioinformatics</i> , 2017, 33, 751-753.	1.8	12
3464	Genome-wide characterization of microsatellites in Triticeae species: abundance, distribution and evolution. <i>Scientific Reports</i> , 2016, 6, 32224.	1.6	30
3465	The intron-enriched HERV-K(HML-10) family suppresses apoptosis, an indicator of malignant transformation. <i>Mobile DNA</i> , 2016, 7, 25.	1.3	23
3466	Draft genome sequence of <i>Cicer reticulatum</i> L., the wild progenitor of chickpea provides a resource for agronomic trait improvement. <i>DNA Research</i> , 2017, 24, dsw042.	1.5	73
3467	Comparative metagenomics reveals taxonomically idiosyncratic yet functionally congruent communities in periodontitis. <i>Scientific Reports</i> , 2016, 6, 38993.	1.6	89
3468	The seahorse genome and the evolution of its specialized morphology. <i>Nature</i> , 2016, 540, 395-399.	13.7	186
3469	DNA Methylation Identifies Loci Distinguishing Hereditary Nonpolyposis Colorectal Cancer Without Germ-Line MLH1/MSH2 Mutation from Sporadic Colorectal Cancer. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e208.	1.3	14
3470	The Asian arowana ( <i>Scleropages formosus</i> ) genome provides new insights into the evolution of an early lineage of teleosts. <i>Scientific Reports</i> , 2016, 6, 24501.	1.6	89
3471	Analyses of Compact <i>Trichinella</i> Kinomes Reveal a MOS-Like Protein Kinase with a Unique N-Terminal Domain. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2847-2856.	0.8	6
3472	A comprehensive benchmark of RNA-RNA interaction prediction tools for all domains of life. <i>Bioinformatics</i> , 2017, 33, 988-996.	1.8	54
3473	Is the Evolution of <i>Salmonella enterica</i> subsp. <i>enterica</i> Linked to Restriction-Modification Systems?. <i>MSystems</i> , 2016, 1, .	1.7	74
3474	Hybrid error correction approach and de novo assembly for minion sequencing long reads. , 2016, , .		0
3475	Fast Construction of an Index Tree for Large Non-ordered Discrete Datasets Using Multi-way Top-Down Split and MapReduce. , 2016, , .		1
3476	CAP protein superfamily members in <i>Toxocara canis</i> . <i>Parasites and Vectors</i> , 2016, 9, 360.	1.0	6
3477	De novo transcriptome assembly and analysis of differentially expressed genes of two barley genotypes reveal root-zone-specific responses to salt exposure. <i>Scientific Reports</i> , 2016, 6, 31558.	1.6	33

#	ARTICLE	IF	CITATIONS
3478	Efficient Hybrid De Novo Error Correction and Assembly for Long Reads. , 2016, , .		2
3479	Viral deep sequencing needs an adaptive approach: IRMA, the iterative refinement meta-assembler. BMC Genomics, 2016, 17, 708.	1.2	134
3480	The Next Generation Sequencing and Applications in Clinical Research. Translational Bioinformatics, 2016, , 83-113.	0.0	0
3481	Genome wide identification and functional prediction of long non-coding RNAs in Brassica rapa. Genes and Genomics, 2016, 38, 547-555.	0.5	5
3482	Identification of a novel fusion transcript between human relaxin-1 (RLN1) and human relaxin-2 (RLN2) in prostate cancer. Molecular and Cellular Endocrinology, 2016, 420, 159-168.	1.6	18
3483	Germline Chromothripsis Driven by L1-Mediated Retrotransposition and Alu/Alu Homologous Recombination. Human Mutation, 2016, 37, 385-395.	1.1	50
3484	Long-read sequence assembly of the gorilla genome. Science, 2016, 352, aae0344.	6.0	368
3485	JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. Journal of Proteome Research, 2016, 15, 2309-2320.	1.8	76
3486	Navigating highly homologous genes in a molecular diagnostic setting: a resource for clinical next-generation sequencing. Genetics in Medicine, 2016, 18, 1282-1289.	1.1	170
3487	Identification of polymorphic and off-target probe binding sites on the Illumina Infinium MethylationEPIC BeadChip. Genomics Data, 2016, 9, 22-24.	1.3	264
3488	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. Marine Genomics, 2016, 30, 3-13.	0.4	164
3489	Identification of human RNA editing sites: A historical perspective. Methods, 2016, 107, 42-47.	1.9	66
3490	Aberrant PD-L1 expression through 3' UTR disruption in multiple cancers. Nature, 2016, 534, 402-406.	18.7	536
3491	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. BMC Genomics, 2016, 17, 267.	1.2	74
3492	A time- and cost-effective strategy to sequence mammalian Y Chromosomes: an application to the de novo assembly of gorilla Y. Genome Research, 2016, 26, 530-540.	2.4	99
3493	Stress-induced gene expression and behavior are controlled by DNA methylation and methyl donor availability in the dentate gyrus. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4830-4835.	3.3	100
3494	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. Tree Genetics and Genomes, 2016, 12, 1.	0.6	25
3495	A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. Nature Genetics, 2016, 48, 657-666.	9.4	432

#	ARTICLE	IF	CITATIONS
3496	Bacterial Genomic Data Analysis in the Next-Generation Sequencing Era. <i>Methods in Molecular Biology</i> , 2016, 1415, 407-422.	0.4	5
3497	Reversible Burst of Transcriptional Changes during Induction of Crassulacean Acid Metabolism in <i>Talinum triangulare</i> . <i>Plant Physiology</i> , 2016, 170, 102-122.	2.3	93
3498	Evaluation of Descriptor Algorithms of Biological Sequences and Distance Measures for the Intelligent Cluster Index (IClx). <i>Communications in Computer and Information Science</i> , 2016, , 434-448.	0.4	0
3499	Redundans: an assembly pipeline for highly heterozygous genomes. <i>Nucleic Acids Research</i> , 2016, 44, e113-e113.	6.5	429
3500	Impact of Hypocaloric Hyperproteic Diet on Gut Microbiota in Overweight or Obese Patients with Nonalcoholic Fatty Liver Disease: A Pilot Study. <i>Digestive Diseases and Sciences</i> , 2016, 61, 2721-2731.	1.1	56
3501	Application of whole genome shotgun sequencing for detection and characterization of genetically modified organisms and derived products. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 4595-4614.	1.9	43
3502	HsfA2 Controls the Activity of Developmentally and Stress-Regulated Heat Stress Protection Mechanisms in Tomato Male Reproductive Tissues. <i>Plant Physiology</i> , 2016, 170, 2461-2477.	2.3	148
3503	DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. <i>Genome Biology</i> , 2016, 17, 92.	3.8	14
3504	Development of new PCR multiplex system by the simultaneous detection of 10 miniSTRs, SE33, Penta E, Penta D, and four Y-STRs. <i>International Journal of Legal Medicine</i> , 2016, 130, 1409-1419.	1.2	4
3505	An automated approach for global identification of sRNA-encoding regions in RNA-Seq data from <i>Mycobacterium tuberculosis</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2016, 48, 544-553.	0.9	18
3506	The genome of the largest bony fish, ocean sunfish ( <i>Mola mola</i> ), provides insights into its fast growth rate. <i>GigaScience</i> , 2016, 5, 36.	3.3	32
3507	SNP calling from RNA-seq data without a reference genome: identification, quantification, differential analysis and impact on the protein sequence. <i>Nucleic Acids Research</i> , 2016, 44, gkw655.	6.5	66
3508	Indel detection from RNA-seq data: tool evaluation and strategies for accurate detection of actionable mutations. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw069.	3.2	44
3509	Comparative genomic analysis between newly sequenced <i>Brucella suis</i> Vaccine Strain S2 and the Virulent <i>Brucella suis</i> Strain 1330. <i>BMC Genomics</i> , 2016, 17, 741.	1.2	12
3510	Four novel polymorphisms of buffalo INSIG2 gene are associated with milk production traits in Chinese buffaloes. <i>Molecular and Cellular Probes</i> , 2016, 30, 294-299.	0.9	15
3511	Targeted next-generation sequencing for TP53, RAS, BRAF, ALK and NF1 mutations in anaplastic thyroid cancer. <i>Endocrine</i> , 2016, 54, 733-741.	1.1	41
3512	A <i>Bacillus anthracis</i> Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. <i>MBio</i> , 2016, 7, .	1.8	52
3513	<i>Butyricimonas phoceensis</i> sp. nov., a new anaerobic species isolated from the human gut microbiota of a French morbidly obese patient. <i>New Microbes and New Infections</i> , 2016, 14, 38-48.	0.8	9

#	ARTICLE	IF	CITATIONS
3514	Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. <i>Genome Biology</i> , 2016, 17, 208.	3.8	912
3515	Deciphering the Wient Demographic and Adaptive Histories from Individual Whole-Genome Sequences. <i>Molecular Biology and Evolution</i> , 2016, 33, 2801-2814.	3.5	41
3516	Comprehensive analysis of microRNA signature of mouse pancreatic acini: overexpression of miR-21-3p in acute pancreatitis. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, G974-G980.	1.6	35
3517	Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. <i>Bioinformatics</i> , 2016, 32, 3058-3064.	1.8	22
3518	Meiotic pairing and gene expression disturbance in germ cells from an infertile boar with a balanced reciprocal autosome-autosome translocation. <i>Chromosome Research</i> , 2016, 24, 511-527.	1.0	8
3519	Proline coordination with fatty acid synthesis and redox metabolism of chloroplast and mitochondria. <i>Plant Physiology</i> , 2016, 172, pp.01097.2016.	2.3	60
3520	Identification and Correction of Erroneous Protein Sequences in Public Databases. <i>Methods in Molecular Biology</i> , 2016, 1415, 179-192.	0.4	1
3521	Norovirus Whole-Genome Sequencing by SureSelect Target Enrichment: a Robust and Sensitive Method. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2530-2537.	1.8	67
3522	Single cell genomics reveals activation signatures of endogenous SCAR's networks in aneuploid human embryos and clinically intractable malignant tumors. <i>Cancer Letters</i> , 2016, 381, 176-193.	3.2	23
3523	Non-human primates avoid the detrimental effects of prenatal androgen exposure in mixed-sex litters: combined demographic, behavioral, and genetic analyses. <i>American Journal of Primatology</i> , 2016, 78, 1304-1315.	0.8	7
3524	Discovery and characterization of single nucleotide polymorphisms in coho salmon, <i>Oncorhynchus kisutch</i> . <i>Molecular Ecology Resources</i> , 2016, 16, 277-287.	2.2	13
3525	Variant in the <i>RFWD3</i> gene associated with <i>PATN1</i> , a modifier of leopard complex spotting. <i>Animal Genetics</i> , 2016, 47, 91-101.	0.6	31
3526	Utility of next-generation RNA sequencing in identifying chimeric transcription involving human endogenous retroviruses. <i>Apmis</i> , 2016, 124, 127-139.	0.9	10
3527	Characterization of the cell receptor beta chain repertoire in tumor-infiltrating lymphocytes. <i>Cancer Medicine</i> , 2016, 5, 2513-2521.	1.3	17
3528	TALEN-Mediated Mutagenesis and Genome Editing. <i>Methods in Molecular Biology</i> , 2016, 1451, 17-30.	0.4	22
3529	Identification of Coilin Mutants in a Screen for Enhanced Expression of an Alternatively Spliced GFP Reporter Gene in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2016, 203, 1709-1720.	1.2	15
3530	Genomics Resources for Plants. , 2016, , 29-57.		2
3531	Visualizing Genomic Annotations with the UCSC Genome Browser. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot093062.	0.2	14

#	ARTICLE	IF	CITATIONS
3532	Comparative Analysis of Genome and Epigenome in Closely Related Medaka Species Identifies Conserved Sequence Preferences for DNA Hypomethylated Domains. <i>Zoological Science</i> , 2016, 33, 358.	0.3	2
3533	Polymorphic Malware Detection Using Sequence Classification Methods. , 2016, , .		33
3534	Identification of new branch points and unconventional introns in <i>Saccharomyces cerevisiae</i> Rna, 2016, 22, 1522-1534.	1.6	32
3535	Uncovering Earth's virome. <i>Nature</i> , 2016, 536, 425-430.	13.7	880
3536	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	3.3	211
3537	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	6.0	241
3538	AnnoLnc: a web server for systematically annotating novel human lncRNAs. <i>BMC Genomics</i> , 2016, 17, 931.	1.2	51
3539	Prevalence and Abundance of Florfenicol and Linezolid Resistance Genes in Soils Adjacent to Swine Feedlots. <i>Scientific Reports</i> , 2016, 6, 32192.	1.6	70
3540	Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. <i>Nature Communications</i> , 2016, 7, 12233.	5.8	106
3541	Draft genome of the living fossil <i>Ginkgo biloba</i> . <i>GigaScience</i> , 2016, 5, 49.	3.3	232
3543	The cancer-associated CTCFL/BORIS protein targets multiple classes of genomic repeats, with a distinct binding and functional preference for humanoid-specific SVA transposable elements. <i>Epigenetics and Chromatin</i> , 2016, 9, 35.	1.8	33
3544	Genome Analysis of Plants. , 2016, , 1-27.		0
3545	A novel <i>TP53-KPNA3</i> translocation defines a de novo treatment-resistant clone in osteosarcoma. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000992.	0.5	13
3546	Experiences of testing bioinformatics programs for detecting subtle faults. , 2016, , .		7
3547	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9111-9116.	3.3	260
3548	Pleiotropic effect of thyroid hormones on gene expression in fish as exemplified from the blue bream <i>Ballerus ballerus</i> (Cyprinidae): Results of transcriptomic analysis. <i>Doklady Biochemistry and Biophysics</i> , 2016, 467, 124-127.	0.3	10
3549	Variant discovery and breakpoint region prediction for studying the human 22q11.2 deletion using BAC clone and whole genome sequencing analysis. <i>Human Molecular Genetics</i> , 2016, 25, 3754-3767.	1.4	20
3550	Overexpression of CHOP in Myelinating Cells Does Not Confer a Significant Phenotype under Normal or Metabolic Stress Conditions. <i>Journal of Neuroscience</i> , 2016, 36, 6803-6819.	1.7	21

#	ARTICLE	IF	CITATIONS
3551	Transcriptome analysis of woodland strawberry ( <i>Fragaria vesca</i> ) response to the infection by Strawberry vein banding virus (SVBV). <i>Virology Journal</i> , 2016, 13, 128.	1.4	24
3552	Microbiota Dysbiosis Controls the Neuroinflammatory Response after Stroke. <i>Journal of Neuroscience</i> , 2016, 36, 7428-7440.	1.7	530
3553	<i>Tessaracoccus massiliensis</i> sp. nov., a new bacterial species isolated from the human gut. <i>New Microbes and New Infections</i> , 2016, 13, 3-12.	0.8	8
3554	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). <i>Nature Communications</i> , 2016, 7, 12339.	5.8	69
3555	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	5.9	416
3556	Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. <i>Scientific Reports</i> , 2016, 6, 22525.	1.6	143
3557	High expression of new genes in trochophore enlightening the ontogeny and evolution of trochozoans. <i>Scientific Reports</i> , 2016, 6, 34664.	1.6	32
3558	An evaluation of the accuracy and speed of metagenome analysis tools. <i>Scientific Reports</i> , 2016, 6, 19233.	1.6	278
3559	A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232.	3.8	12
3560	LSCplus: a fast solution for improving long read accuracy by short read alignment. <i>BMC Bioinformatics</i> , 2016, 17, 451.	1.2	19
3561	The next generation of target capture technologies - large DNA fragment enrichment and sequencing determines regional genomic variation of high complexity. <i>BMC Genomics</i> , 2016, 17, 486.	1.2	61
3562	The genome of the miyu croaker reveals well-developed innate immune and sensory systems. <i>Scientific Reports</i> , 2016, 6, 21902.	1.6	67
3563	Exploring the transcriptome of <i>Staphylococcus aureus</i> in its natural niche. <i>Scientific Reports</i> , 2016, 6, 33174.	1.6	52
3564	Feralisation targets different genomic loci to domestication in the chicken. <i>Nature Communications</i> , 2016, 7, 12950.	5.8	60
3565	The endotracheal tube microbiome associated with <i>Pseudomonas aeruginosa</i> or <i>Staphylococcus epidermidis</i> . <i>Scientific Reports</i> , 2016, 6, 36507.	1.6	51
3566	Regulation of amino-acid metabolism controls flux to lipid accumulation in <i>Yarrowia lipolytica</i> . <i>Npj Systems Biology and Applications</i> , 2016, 2, 16005.	1.4	141
3567	Systems-wide analysis of manganese deficiency-induced changes in gene activity of <i>Arabidopsis</i> roots. <i>Scientific Reports</i> , 2016, 6, 35846.	1.6	17
3568	RNA editing generates cellular subsets with diverse sequence within populations. <i>Nature Communications</i> , 2016, 7, 12145.	5.8	48

#	ARTICLE	IF	CITATIONS
3569	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	5.9	207
3570	Comparative assessment of methods for the fusion transcripts detection from RNA-Seq data. <i>Scientific Reports</i> , 2016, 6, 21597.	1.6	123
3571	Morphological and Transcriptomic Analysis of a Beetle Chemosensory System Reveals a Gnathal Olfactory Center. <i>BMC Biology</i> , 2016, 14, 90.	1.7	73
3572	Association of variations in HLA class II and other loci with susceptibility to EGFR-mutated lung adenocarcinoma. <i>Nature Communications</i> , 2016, 7, 12451.	5.8	49
3573	Expansion and stress responses of AP2/EREBP superfamily in <i>Brachypodium distachyon</i> . <i>Scientific Reports</i> , 2016, 6, 21623.	1.6	82
3574	Identification of a novel 15.5 kb SHOX deletion associated with marked intrafamilial phenotypic variability and analysis of its molecular origin. <i>Journal of Genetics</i> , 2016, 95, 839-845.	0.4	3
3575	Mechanical cell competition kills cells via induction of lethal p53 levels. <i>Nature Communications</i> , 2016, 7, 11373.	5.8	162
3576	Transcriptomic Resources and Marker Validation for Diploid and Polyploid <i>Veronica</i> (Plantaginaceae) from New Zealand and Europe. <i>Applications in Plant Sciences</i> , 2016, 4, 1600091.	0.8	2
3577	Improving Re-annotation of Annotated Eukaryotic Genomes. , 2016, , 171-195.		2
3578	Natural variation in non-coding regions underlying phenotypic diversity in budding yeast. <i>Scientific Reports</i> , 2016, 6, 21849.	1.6	100
3579	LTR-mediated retroposition as a mechanism of RNA-based duplication in metazoans. <i>Genome Research</i> , 2016, 26, 1663-1675.	2.4	42
3580	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	1.8	49
3581	RES-Scanner: a software package for genome-wide identification of RNA-editing sites. <i>GigaScience</i> , 2016, 5, 37.	3.3	55
3582	The Simple Chordate <i>Ciona intestinalis</i> Has a Reduced Complement of Genes Associated with Fanconi Anemia. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S37920.	0.6	6
3583	Draft Genome Sequence of <i>Mycobacterium houstonense</i> Strain ATCC 49403 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
3584	Draft Genome Sequence of <i>Mycobacterium interjectum</i> Strain ATCC 51457 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
3585	The multicellularity genes of dictyostelid social amoebas. <i>Nature Communications</i> , 2016, 7, 12085.	5.8	63
3586	LINE-1-like retrotransposons contribute to RNA-based gene duplication in dicots. <i>Scientific Reports</i> , 2016, 6, 24755.	1.6	13

#	ARTICLE	IF	CITATIONS
3587	Assembling the <i>Setaria italica</i> L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. <i>Scientific Reports</i> , 2016, 6, 35076.	1.6	10
3588	Amplification, Next-generation Sequencing, and Genomic DNA Mapping of Retroviral Integration Sites. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	36
3589	Contribution of type W human endogenous retroviruses to the human genome: characterization of HERV-W proviral insertions and processed pseudogenes. <i>Retrovirology</i> , 2016, 13, 67.	0.9	62
3590	Complete genome sequence of thermophilic <i>Bacillus smithii</i> type strain DSM 4216T. <i>Standards in Genomic Sciences</i> , 2016, 11, 52.	1.5	13
3591	RNA-Sequencing for profiling goat milk transcriptome in colostrum and mature milk. <i>BMC Veterinary Research</i> , 2016, 12, 264.	0.7	71
3592	Retrozymes are a unique family of non-autonomous retrotransposons with hammerhead ribozymes that propagate in plants through circular RNAs. <i>Genome Biology</i> , 2016, 17, 135.	3.8	39
3593	High-quality genome assembly of channel catfish, <i>Ictalurus punctatus</i> . <i>GigaScience</i> , 2016, 5, 39.	3.3	45
3594	Complete plastid genome of <i>Eriobotrya japonica</i> (Thunb.) Lindl and comparative analysis in Rosaceae. <i>SpringerPlus</i> , 2016, 5, 2036.	1.2	13
3595	Pinpointing the vesper bat transposon revolution using the <i>Miniopterus natalensis</i> genome. <i>Mobile DNA</i> , 2016, 7, 12.	1.3	23
3596	Evidence for L1-associated DNA rearrangements and negligible L1 retrotransposition in glioblastoma multiforme. <i>Mobile DNA</i> , 2016, 7, 21.	1.3	32
3597	Molecular analysis of the Sydney rock oyster ( <i>Saccostrea glomerata</i> ) CO <sub>2</sub> stress response. <i>Climate Change Responses</i> , 2016, 3, .	2.6	9
3599	PGD: a pangolin genome hub for the research community. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw063.	1.4	5
3600	gEVE: a genome-based endogenous viral element database provides comprehensive viral protein-coding sequences in mammalian genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw087.	1.4	56
3601	Unlocking the genetic diversity of Creole wheats. <i>Scientific Reports</i> , 2016, 6, 23092.	1.6	75
3602	Mitogenome assembly from genomic multiplex libraries: comparison of strategies and novel mitogenomes for five species of frogs. <i>Molecular Ecology Resources</i> , 2016, 16, 686-693.	2.2	21
3603	Characterization of the teosinte transcriptome reveals adaptive sequence divergence during maize domestication. <i>Molecular Ecology Resources</i> , 2016, 16, 1465-1477.	2.2	7
3604	Novel mutations in the genes <i>TGM1</i> and <i>ALOXE3</i> underlying autosomal recessive congenital ichthyosis. <i>International Journal of Dermatology</i> , 2016, 55, 524-530.	0.5	6
3605	Whole genome duplication in coast redwood ( <i>Sequoia sempervirens</i> ) and its implications for explaining the rarity of polyploidy in conifers. <i>New Phytologist</i> , 2016, 211, 186-193.	3.5	49

#	ARTICLE	IF	CITATIONS
3606	PTESFinder: a computational method to identify post-transcriptional exon shuffling (PTES) events. BMC Bioinformatics, 2016, 17, 31.	1.2	45
3607	UNDR ROVER - a fast and accurate variant caller for targeted DNA sequencing. BMC Bioinformatics, 2016, 17, 165.	1.2	3
3608	Multivariate models from RNA-Seq SNVs yield candidate molecular targets for biomarker discovery: SNV-DA. BMC Genomics, 2016, 17, 263.	1.2	7
3609	Promoter methylation and mRNA expression of HLA-G in relation to HLA-G protein expression in colorectal cancer. Human Immunology, 2016, 77, 764-772.	1.2	9
3610	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. BMC Genomics, 2016, 17, 180.	1.2	71
3611	Next-generation sequencing-based detection of germline L1-mediated transductions. BMC Genomics, 2016, 17, 342.	1.2	7
3612	Homozygosity mapping identified a novel protein truncating mutation (p.Ser100Leufs*24) of the BBS9 gene in a consanguineous Pakistani family with Bardet Biedl syndrome. BMC Medical Genetics, 2016, 17, 10.	2.1	13
3613	Evaluation of microRNA alignment techniques. Rna, 2016, 22, 1120-1138.	1.6	56
3614	A High-Resolution SNP Array-Based Linkage Map Anchors a New Domestic Cat Draft Genome Assembly and Provides Detailed Patterns of Recombination. G3: Genes, Genomes, Genetics, 2016, 6, 1607-1616.	0.8	41
3615	Informed k-mer selection for de novo transcriptome assembly. Bioinformatics, 2016, 32, 1670-1677.	1.8	25
3616	Effects of Gene Duplication, Positive Selection, and Shifts in Gene Expression on the Evolution of the Venom Gland Transcriptome in Widow Spiders. Genome Biology and Evolution, 2016, 8, 228-242.	1.1	54
3617	The MG-RAST metagenomics database and portal in 2015. Nucleic Acids Research, 2016, 44, D590-D594.	6.5	187
3618	TBR1 regulates autism risk genes in the developing neocortex. Genome Research, 2016, 26, 1013-1022.	2.4	71
3619	RapMap: a rapid, sensitive and accurate tool for mapping RNA-seq reads to transcriptomes. Bioinformatics, 2016, 32, i192-i200.	1.8	99
3620	Evolutionary direction of processed pseudogenes. Science China Life Sciences, 2016, 59, 839-849.	2.3	5
3621	Human C-terminally truncated ER $\alpha$ variants resulting from the use of alternative exons in the ligand-binding domain. Molecular and Cellular Endocrinology, 2016, 425, 111-122.	1.6	16
3622	Noncontiguous finished genome sequence and description of Paenibacillus ihumii sp. nov. strain AT5. New Microbes and New Infections, 2016, 10, 142-150.	0.8	17
3623	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. Epigenetics, 2016, 11, 501-516.	1.3	65

#	ARTICLE	IF	CITATIONS
3624	Sequence and partial functional analysis of canine Bcl-2 family proteins. <i>Research in Veterinary Science</i> , 2016, 104, 126-135.	0.9	1
3625	CDROM: Classification of Duplicate gene RetentiOn Mechanisms. <i>BMC Evolutionary Biology</i> , 2016, 16, 82.	3.2	11
3626	Statistical evaluation of methods for identification of differentially abundant genes in comparative metagenomics. <i>BMC Genomics</i> , 2016, 17, 78.	1.2	114
3627	Identification of mRNA isoform switching in breast cancer. <i>BMC Genomics</i> , 2016, 17, 181.	1.2	27
3628	Genomic and transcriptomic comparison of nucleotide variations for insights into bruchid resistance of mungbean ( <i>Vigna radiata</i> [L.] R. Wilczek). <i>BMC Plant Biology</i> , 2016, 16, 46.	1.6	36
3629	Bitpacking techniques for indexing genomes: I. Hash tables. <i>Algorithms for Molecular Biology</i> , 2016, 11, 5.	0.3	3
3630	Landscape and evolutionary dynamics of terminal repeat retrotransposons in miniature in plant genomes. <i>Genome Biology</i> , 2016, 17, 7.	3.8	50
3631	Reconstruction of the insulin-like signalling pathway of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2016, 9, 64.	1.0	12
3632	Genome ARTIST: a robust, high-accuracy aligner tool for mapping transposon insertions and self-insertions. <i>Mobile DNA</i> , 2016, 7, 3.	1.3	11
3633	Genomic analysis of mouse VL30 retrotransposons. <i>Mobile DNA</i> , 2016, 7, 10.	1.3	21
3634	Metatranscriptomic analysis of diverse microbial communities reveals core metabolic pathways and microbiome-specific functionality. <i>Microbiome</i> , 2016, 4, 2.	4.9	118
3635	Timing and Scope of Genomic Expansion within Annelida: Evidence from Homeoboxes in the Genome of the Earthworm <i>Eisenia fetida</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 271-281.	1.1	45
3636	Microsatellite markers used for genome-wide association mapping of partial resistance to <i>Sclerotinia sclerotiorum</i> in a world collection of <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2016, 36, 72.	1.0	64
3637	Enhanced diagnostic yield in Meckel-Gruber and Joubert syndrome through exome sequencing supplemented with split-read mapping. <i>BMC Medical Genetics</i> , 2016, 17, 1.	2.1	67
3638	Rapid identification of rice blast resistance gene by specific length amplified fragment sequencing. <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 462-468.	0.5	8
3639	Transcriptome asymmetry in synthetic and natural allotetraploid wheats, revealed by RNA-seq. <i>New Phytologist</i> , 2016, 209, 1264-1277.	3.5	63
3640	Genome-wide association study of 8 carcass traits in Jinghai Yellow chickens using specific-locus amplified fragment sequencing technology. <i>Poultry Science</i> , 2016, 95, 500-506.	1.5	25
3641	Genome-Wide Survey of Gut Fungi (Harpellales) Reveals the First Horizontally Transferred Ubiquitin Gene from a Mosquito Host. <i>Molecular Biology and Evolution</i> , 2016, 33, 2544-2554.	3.5	28

#	ARTICLE	IF	CITATIONS
3642	Complete chloroplast genomes of <i>Saccharum spontaneum</i> , <i>Saccharum officinarum</i> and <i>Miscanthus floridulus</i> (Panicoideae: Andropogoneae) reveal the plastid view on sugarcane origins. <i>Systematics and Biodiversity</i> , 2016, 14, 548-571.	0.5	34
3643	PEP_scaffolder: using (homologous) proteins to scaffold genomes. <i>Bioinformatics</i> , 2016, 32, 3193-3195.	1.8	14
3644	Crystallins of the chicken lens: remnants of an ancient vertebrate gene family in birds. <i>FEBS Journal</i> , 2016, 283, 1516-1530.	2.2	14
3645	Activating ERBB2/HER2 mutations indicate susceptibility to pan-HER inhibitors in Lynch and Lynch-like colorectal cancer. <i>Gut</i> , 2016, 65, 1296-1305.	6.1	65
3646	Abundant and broad expression of transcription-induced chimeras and protein products in mammalian genomes. <i>Biochemical and Biophysical Research Communications</i> , 2016, 470, 759-765.	1.0	8
3647	SIENA: Efficient Compilation of Selective Protein Binding Site Ensembles. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 248-259.	2.5	39
3648	Improving microRNA target prediction by modeling with unambiguously identified microRNA-target pairs from CLIP-ligation studies. <i>Bioinformatics</i> , 2016, 32, 1316-1322.	1.8	203
3649	MG-RAST, a Metagenomics Service for Analysis of Microbial Community Structure and Function. <i>Methods in Molecular Biology</i> , 2016, 1399, 207-233.	0.4	371
3650	MEPD: medaka expression pattern database, genes and more. <i>Nucleic Acids Research</i> , 2016, 44, D819-D821.	6.5	11
3651	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , 2016, 6, 166-175.	7.7	282
3652	TMO: time and memory optimized algorithm applicable for more accurate alignment of trinucleotide repeat disorders associated genes. <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 388-403.	0.5	1
3653	Legume information system (LegumeInfo.org): a key component of a set of federated data resources for the legume family. <i>Nucleic Acids Research</i> , 2016, 44, D1181-D1188.	6.5	152
3654	RiboFR-Seq: a novel approach to linking 16S rRNA amplicon profiles to metagenomes. <i>Nucleic Acids Research</i> , 2016, 44, e99-e99.	6.5	24
3655	Minimap and miniasm: fast mapping and de novo assembly for noisy long sequences. <i>Bioinformatics</i> , 2016, 32, 2103-2110.	1.8	1,082
3656	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	6.5	376
3657	Learning to cope with stress modulates anterior cingulate cortex stargazin expression in monkeys and mice. <i>Neurobiology of Learning and Memory</i> , 2016, 131, 95-100.	1.0	7
3658	Efficient privacy-preserving string search and an application in genomics. <i>Bioinformatics</i> , 2016, 32, 1652-1661.	1.8	46
3659	The real cost of sequencing: scaling computation to keep pace with data generation. <i>Genome Biology</i> , 2016, 17, 53.	3.8	264

#	ARTICLE	IF	CITATIONS
3660	GMAP and GSNAP for Genomic Sequence Alignment: Enhancements to Speed, Accuracy, and Functionality. <i>Methods in Molecular Biology</i> , 2016, 1418, 283-334.	0.4	354
3661	<i>Microvirga massiliensis</i> sp. nov., the human commensal with the largest genome. <i>MicrobiologyOpen</i> , 2016, 5, 307-322.	1.2	27
3662	An Exon-Capture System for the Entire Class Ophiuroidea. <i>Molecular Biology and Evolution</i> , 2016, 33, 281-294.	3.5	90
3663	Organellar Genomes of White Spruce ( <i>Picea glauca</i> ): Assembly and Annotation. <i>Genome Biology and Evolution</i> , 2016, 8, 29-41.	1.1	46
3664	Genetic mapping and molecular marker development for Pi65(t), a novel broad-spectrum resistance gene to rice blast using next-generation sequencing. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1035-1044.	1.8	82
3665	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
3666	Next-Generation Sequencing-Assisted DNA-Based Digital PCR for a Personalized Approach to the Detection and Quantification of Residual Disease in Chronic Myeloid Leukemia Patients. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 176-189.	1.2	34
3667	Haplotyping germline and cancer genomes with high-throughput linked-read sequencing. <i>Nature Biotechnology</i> , 2016, 34, 303-311.	9.4	617
3668	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	5.8	189
3669	Discovery of a new repeat family in the <i>Callithrix jacchus</i> genome. <i>Genome Research</i> , 2016, 26, 649-659.	2.4	11
3670	Genetic features of <i>Mycobacterium tuberculosis</i> modern Beijing sublineage. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	35
3671	Organizational Heterogeneity of the Human Genome: Significant Variation of Recombination Rate of 100 kbp Sequences within GC Ranges. , 2016, , .		0
3672	Sequence Diversity, Intersubgroup Relationships, and Origins of the Mouse Leukemia Gammaretroviruses of Laboratory and Wild Mice. <i>Journal of Virology</i> , 2016, 90, 4186-4198.	1.5	13
3673	Host Mitochondrial Association Evolved in the Human Parasite <i>Toxoplasma gondii</i> via Neofunctionalization of a Gene Duplicate. <i>Genetics</i> , 2016, 203, 283-298.	1.2	27
3674	Comparative transcriptome analysis reveals a potential photosynthate partitioning mechanism between lipid and starch biosynthetic pathways in green microalgae. <i>Algal Research</i> , 2016, 16, 54-62.	2.4	44
3675	TheVignaGenome Server, "VigGS": A Genomic Knowledge Base of the GenusVignaBased on High-Quality, Annotated Genome Sequence of the Azuki Bean, <i>Vigna angularis</i> (Willd.) Ohwi & Ohashi. <i>Plant and Cell Physiology</i> , 2016, 57, e2-e2.	1.5	49
3676	TauCstF-64 Mediates Correct mRNA Polyadenylation and Splicing of Activator and Repressor Isoforms of the Cyclic AMP-Responsive Element Modulator (CREM) in Mouse Testis1. <i>Biology of Reproduction</i> , 2016, 94, 34.	1.2	16
3677	Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016, 13, 177-183.	9.0	274

#	ARTICLE	IF	CITATIONS
3678	Genome-wide identification and characterization of transcription start sites and promoters in the tunicate <i>Ciona intestinalis</i> . <i>Genome Research</i> , 2016, 26, 140-150.	2.4	13
3679	Genetical Genomics of Behavior: A Novel Chicken Genomic Model for Anxiety Behavior. <i>Genetics</i> , 2016, 202, 327-340.	1.2	51
3680	Characterization of <i>Ambra1</i> in asexual cycle of a non-vertebrate chordate, the colonial tunicate <i>Botryllus schlosseri</i> , and phylogenetic analysis of the protein group in Bilateria. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 46-57.	1.2	5
3681	Comprehensive evaluation of fusion transcript detection algorithms and a meta-caller to combine top performing methods in paired-end RNA-seq data. <i>Nucleic Acids Research</i> , 2016, 44, e47-e47.	6.5	141
3682	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. <i>Nucleic Acids Research</i> , 2016, 44, D604-D609.	6.5	60
3683	Comparative genomics analysis of decapod shrimps in the Pancrustacea clade. <i>Biochemical Systematics and Ecology</i> , 2016, 64, 111-121.	0.6	5
3684	The <i>Physarum polycephalum</i> Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. <i>Genome Biology and Evolution</i> , 2016, 8, 109-125.	1.1	87
3685	Hypomorphic mutations in <i>TRNT1</i> cause retinitis pigmentosa with erythrocytic microcytosis. <i>Human Molecular Genetics</i> , 2016, 25, 44-56.	1.4	64
3686	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomics Data. <i>Methods in Molecular Biology</i> , 2016, 1374, 115-140.	0.4	216
3687	A new amino acid substitution (Ala-205-Phe) in acetolactate synthase (ALS) confers broad spectrum resistance to ALS-inhibiting herbicides. <i>Planta</i> , 2016, 243, 149-159.	1.6	49
3688	The complement of family M1 aminopeptidases of <i>Haemonchus contortus</i> – Biotechnological implications. <i>Biotechnology Advances</i> , 2016, 34, 65-76.	6.0	8
3689	Rapid Short-Read Sequencing and Aneuploidy Detection Using MinION Nanopore Technology. <i>Genetics</i> , 2016, 202, 37-44.	1.2	32
3690	Fecal Recovery of Ingested Cellular DNA: Implications for Noninvasive Detection of Upper Gastrointestinal Neoplasms. <i>Digestive Diseases and Sciences</i> , 2016, 61, 117-125.	1.1	5
3691	Transposition burst of mariner-like elements in the sequenced genome of <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 69, 14-24.	1.2	11
3692	SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. <i>Bioinformatics</i> , 2016, 32, 354-361.	1.8	161
3693	NCLscan: accurate identification of non-co-linear transcripts (fusion, trans-splicing and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T e29-e29.	6.5	98
3694	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 157-166.	1.4	73
3695	Will solid-state drives accelerate your bioinformatics? In-depth profiling, performance analysis and beyond. <i>Briefings in Bioinformatics</i> , 2016, 17, 713-727.	3.2	12

#	ARTICLE	IF	CITATIONS
3696	Transcriptional dynamics of <i>Phytophthora infestans</i> during sequential stages of hemibiotrophic infection of tomato. <i>Molecular Plant Pathology</i> , 2016, 17, 29-41.	2.0	77
3697	Analysis of the tomato leaf transcriptome during successive hemibiotrophic stages of a compatible interaction with the oomycete pathogen <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 42-54.	2.0	55
3698	cuBLASTP: Fine-Grained Parallelization of Protein Sequence Search on CPU+GPU. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 830-843.	1.9	19
3699	Short Read Mapping: An Algorithmic Tour. <i>Proceedings of the IEEE</i> , 2017, 105, 436-458.	16.4	63
3700	Characterizing and annotating the genome using RNA-seq data. <i>Science China Life Sciences</i> , 2017, 60, 116-125.	2.3	35
3701	Identification of misexpressed genetic elements in hybrids between <i>Drosophila</i> -related species. <i>Scientific Reports</i> , 2017, 7, 40618.	1.6	49
3702	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124
3703	GENE-IS: Time-Efficient and Accurate Analysis of Viral Integration Events in Large-Scale Gene Therapy Data. <i>Molecular Therapy - Nucleic Acids</i> , 2017, 6, 133-139.	2.3	21
3704	A second generation SNP and SSR integrated linkage map and QTL mapping for the Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Scientific Reports</i> , 2017, 7, 39826.	1.6	38
3705	Cytosine methylation at CpCpG sites triggers accumulation of non-CpG methylation in gene bodies. <i>Nucleic Acids Research</i> , 2017, 45, gkw1330.	6.5	26
3706	Integrating genomic resources of flatfish (Pleuronectiformes) to boost aquaculture production. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 21, 41-55.	0.4	21
3707	Accurate clinical genetic testing for autoinflammatory diseases using the next-generation sequencing platform MiSeq. <i>Biochemistry and Biophysics Reports</i> , 2017, 9, 146-152.	0.7	17
3708	Detection of splicing variants in the leaf and spike transcripts of wild diploid wheat <i>Aegilops tauschii</i> and transmission of the splicing patterns to synthetic hexaploid wheat. <i>Plant Gene</i> , 2017, 9, 6-12.	1.4	1
3709	Transcriptome profiles reveal gene regulation of peanut ( <i>Arachis hypogaea</i> L.) nodulation. <i>Scientific Reports</i> , 2017, 7, 40066.	1.6	42
3710	A molecular genetic toolbox for <i>Yarrowia lipolytica</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 2.	6.2	62
3711	RPAN: rice pan-genome browser for ~3000 rice genomes. <i>Nucleic Acids Research</i> , 2017, 45, 597-605.	6.5	156
3712	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
3713	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332

#	ARTICLE	IF	CITATIONS
3714	Association mapping of morphological traits in wild and captive zebra finches: reliable within, but not between populations. <i>Molecular Ecology</i> , 2017, 26, 1285-1305.	2.0	18
3715	PEMapper and PECaller provide a simplified approach to whole-genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1923-E1932.	3.3	31
3716	A user guide to the Brassica 60K Illumina Infinium <sup>®</sup> SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2017, 130, 621-633.	1.8	90
3717	A novel archaeal species belonging to <i>Methanoculleus</i> genus identified via de-novo assembly and metagenomic binning process in biogas reactors. <i>Anaerobe</i> , 2017, 46, 23-32.	1.0	63
3718	Convergent Evolution of the Osmoregulation System in Decapod Shrimps. <i>Marine Biotechnology</i> , 2017, 19, 76-88.	1.1	13
3719	The evolution and population diversity of human-specific segmental duplications. <i>Nature Ecology and Evolution</i> , 2017, 1, 69.	3.4	123
3720	ETS Proto-oncogene 1 Transcriptionally Up-regulates the Cholangiocyte Senescence-associated Protein Cyclin-dependent Kinase Inhibitor 2A. <i>Journal of Biological Chemistry</i> , 2017, 292, 4833-4846.	1.6	26
3721	Defining the diverse spectrum of inversions, complex structural variation, and chromothripsis in the morbid human genome. <i>Genome Biology</i> , 2017, 18, 36.	3.8	159
3722	Aboriginal mitogenomes reveal 50,000 years of regionalism in Australia. <i>Nature</i> , 2017, 544, 180-184.	13.7	195
3723	Chromatin states shape insertion profiles of the piggyBac, Tol2 and Sleeping Beauty transposons and murine leukemia virus. <i>Scientific Reports</i> , 2017, 7, 43613.	1.6	46
3724	An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. <i>BMC Genomics</i> , 2017, 18, 95.	1.2	153
3725	Mutational landscape reflects the biological continuum of plasma cell dyscrasias. <i>Blood Cancer Journal</i> , 2017, 7, e537-e537.	2.8	32
3726	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
3727	MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580.	6.5	328
3728	Comparative study of viromes from freshwater samples of the Ile-Balkhash region of Kazakhstan captured through metagenomic analysis. <i>VirusDisease</i> , 2017, 28, 18-25.	1.0	28
3729	Reduced representation genome sequencing reveals patterns of genetic diversity and selection in apple. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 190-204.	4.1	30
3730	Genomic Rearrangements in <i>Arabidopsis</i> Considered as Quantitative Traits. <i>Genetics</i> , 2017, 205, 1425-1441.	1.2	21
3733	Identification of some main <i>Streptococcus iniae</i> associated proteins: relationship. <i>Veterinary Research Communications</i> , 2017, 41, 85-95.	0.6	1

#	ARTICLE	IF	CITATIONS
3734	Evolutionary mechanism and biological functions of 8-mers containing CG dinucleotide in yeast. <i>Chromosome Research</i> , 2017, 25, 173-189.	1.0	6
3735	Molecular characteristics of two new waxy mutations in China waxy maize. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	28
3736	Genetic and functional analysis of the bovine uterine microbiota. Part II: Purulent vaginal discharge versus healthy cows. <i>Journal of Dairy Science</i> , 2017, 100, 3863-3874.	1.4	45
3737	SAG-QC: quality control of single amplified genome information by subtracting non-target sequences based on sequence compositions. <i>BMC Bioinformatics</i> , 2017, 18, 152.	1.2	4
3738	Polymorphic malware detection using sequence classification methods and ensembles. <i>Eurasip Journal on Information Security</i> , 2017, 2017, .	2.2	39
3739	Comparative genomics of canine hemoglobin genes reveals primacy of beta subunit delta in adult carnivores. <i>BMC Genomics</i> , 2017, 18, 141.	1.2	9
3740	Small genomic insertions form enhancers that misregulate oncogenes. <i>Nature Communications</i> , 2017, 8, 14385.	5.8	76
3741	Transcriptome analysis around the onset of strawberry fruit ripening uncovers an important role of oxidative phosphorylation in ripening. <i>Scientific Reports</i> , 2017, 7, 41477.	1.6	58
3742	Functional preservation and variation in the cone opsin genes of nocturnal tarsiers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160075.	1.8	51
3743	Genomics and evolution of protein phosphatases. <i>Science Signaling</i> , 2017, 10, .	1.6	206
3744	A genetic screen implicates a CWC16/Yju2/CCDC130 protein and SMU1 in alternative splicing in <i>Arabidopsis thaliana</i> . <i>Rna</i> , 2017, 23, 1068-1079.	1.6	20
3745	Typing and Characterization of Bacteria Using Bottom-up Tandem Mass Spectrometry Proteomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1052-1063.	2.5	66
3746	Large-scale collection of full-length cDNA and transcriptome analysis in <i>Hevea brasiliensis</i> . <i>DNA Research</i> , 2017, 24, dsw056.	1.5	18
3747	Comparative studies of vertebrate iduronate 2-sulfatase (IDS) genes and proteins: evolution of A mammalian X-linked gene. <i>3 Biotech</i> , 2017, 7, 22.	1.1	12
3748	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. <i>Nature Genetics</i> , 2017, 49, 913-924.	9.4	340
3749	Squamate Conserved Loci (Sq<sc>CL</sc>): A unified set of conserved loci for phylogenomics and population genetics of squamate reptiles. <i>Molecular Ecology Resources</i> , 2017, 17, e12-e24.	2.2	36
3750	Pneumococcal prophages are diverse, but not without structure or history. <i>Scientific Reports</i> , 2017, 7, 42976.	1.6	62
3751	GeSeq: versatile and accurate annotation of organelle genomes. <i>Nucleic Acids Research</i> , 2017, 45, W6-W11.	6.5	1,964

#	ARTICLE	IF	CITATIONS
3752	High-density genetic map construction and QTLs identification for plant height in white jute ( <i>Corchorus capsularis</i> L.) using specific locus amplified fragment (SLAF) sequencing. <i>BMC Genomics</i> , 2017, 18, 355.	1.2	46
3753	Expansion of the redox-sensitive proteome coincides with the plastid endosymbiosis. <i>Nature Plants</i> , 2017, 3, 17066.	4.7	26
3754	Transposable Element Misregulation Is Linked to the Divergence between Parental piRNA Pathways in <i>Drosophila</i> Hybrids. <i>Genome Biology and Evolution</i> , 2017, 9, 1450-1470.	1.1	26
3755	From data to knowledge: The future of multi-omics data analysis for the rhizosphere. <i>Rhizosphere</i> , 2017, 3, 222-229.	1.4	30
3756	Draft genome sequence of the Tibetan medicinal herb <i>Rhodiola crenulata</i> . <i>GigaScience</i> , 2017, 6, 1-5.	3.3	33
3757	Targeted Enrichment for Pathogen Detection and Characterization in Three Felid Species. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1658-1670.	1.8	25
3758	Detection of viromes of RNA viruses using the next generation sequencing libraries prepared by three methods. <i>Virus Research</i> , 2017, 237, 22-26.	1.1	8
3759	Chromosome-level genome assembly and transcriptome of the green alga <i>Chromochloris zofingiensis</i> illuminates astaxanthin production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4296-E4305.	3.3	131
3760	Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes. <i>Briefings in Bioinformatics</i> , 2018, 19, 1415-1429.	3.2	34
3761	Heritable L1 retrotransposition in the mouse primordial germline and early embryo. <i>Genome Research</i> , 2017, 27, 1395-1405.	2.4	90
3762	Target enrichment sequencing in cultivated peanut ( <i>Arachis hypogaea</i> L.) using probes designed from transcript sequences. <i>Molecular Genetics and Genomics</i> , 2017, 292, 955-965.	1.0	17
3763	Overexpression of hsa-miR-939 follows by NGFR down-regulation and apoptosis reduction. <i>Journal of Biosciences</i> , 2017, 42, 23-30.	0.5	5
3764	Integrated high-density consensus genetic map of <i>Pyrus</i> and anchoring of the 'Bartlett' v1.0 ( <i>Pyrus communis</i> ) genome. <i>DNA Research</i> , 2017, 24, dsw063.	1.5	28
3765	An Agile Functional Analysis of Metagenomic Data Using SUPER-FOCUS. <i>Methods in Molecular Biology</i> , 2017, 1611, 35-44.	0.4	2
3766	A-to-I RNA Editing in the Earliest-Diverging Eumetazoan Phyla. <i>Molecular Biology and Evolution</i> , 2017, 34, 1890-1901.	3.5	45
3767	Mutational screening of SLC39A5, LEPREL1 and LRPAP1 in a cohort of 187 high myopia patients. <i>Scientific Reports</i> , 2017, 7, 1120.	1.6	21
3768	Simultaneous speciation in the European high mountain flowering plant genus <i>Facchinia</i> ( <i>Minuartia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 2017, 112, 23-35.	1.2	13
3769	Whole genome sequencing predicts novel human disease models in rhesus macaques. <i>Genomics</i> , 2017, 109, 214-220.	1.3	28

#	ARTICLE	IF	CITATIONS
3770	Whole exome association of rare deletions in multiplex oral cleft families. <i>Genetic Epidemiology</i> , 2017, 41, 61-69.	0.6	10
3771	Inferring Function from Homology. <i>Methods in Molecular Biology</i> , 2017, 1526, 23-40.	0.4	5
3772	A human microprotein that interacts with the mRNA decapping complex. <i>Nature Chemical Biology</i> , 2017, 13, 174-180.	3.9	212
3774	Genomic Database Searching. <i>Methods in Molecular Biology</i> , 2017, 1525, 225-269.	0.4	2
3775	Large-Scale Sequence Comparison. <i>Methods in Molecular Biology</i> , 2017, 1525, 191-224.	0.4	3
3776	CRISPR-STOP: gene silencing through base-editing-induced nonsense mutations. <i>Nature Methods</i> , 2017, 14, 710-712.	9.0	290
3777	Application of the cghRA framework to the genomic characterization of Diffuse Large B-Cell Lymphoma. <i>Bioinformatics</i> , 2017, 33, 2977-2985.	1.8	3
3778	Sexual Dimorphism and Retinal Mosaic Diversification following the Evolution of a Violet Receptor in Butterflies. <i>Molecular Biology and Evolution</i> , 2017, 34, 2271-2284.	3.5	46
3779	HALC: High throughput algorithm for long read error correction. <i>BMC Bioinformatics</i> , 2017, 18, 204.	1.2	55
3780	High-throughput sequencing of transposable element insertions suggests adaptive evolution of the invasive Asian tiger mosquito towards temperate environments. <i>Molecular Ecology</i> , 2017, 26, 3968-3981.	2.0	34
3781	Identification of Sex-determining Loci in Pacific White Shrimp <i>Litopenaeus vannamei</i> Using Linkage and Association Analysis. <i>Marine Biotechnology</i> , 2017, 19, 277-286.	1.1	60
3782	Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5671-5676.	3.3	49
3783	Bioinformatics Tools for Genome-Wide Epigenetic Research. <i>Advances in Experimental Medicine and Biology</i> , 2017, 978, 489-512.	0.8	43
3784	A Secure-Ware System for Web Server: Ensuring Platform Interoperability, Security, Privacy, Usability and Functionality. <i>The National Academy of Sciences, India</i> , 2017, 40, 157-160.	0.8	4
3785	<i>MET</i> Exon 14 Mutation Encodes an Actionable Therapeutic Target in Lung Adenocarcinoma. <i>Cancer Research</i> , 2017, 77, 4498-4505.	0.4	57
3786	Reading <sc>LINE</sc>s within the cocaine addicted brain. <i>Brain and Behavior</i> , 2017, 7, e00678.	1.0	11
3787	Playing hide and seek with repeats in local and global de novo transcriptome assembly of short RNA-seq reads. <i>Algorithms for Molecular Biology</i> , 2017, 12, 2.	0.3	18
3788	InÂVivo Murine-Matured Human CD3 + Cells as a Preclinical Model for T Cell-Based Immunotherapies. <i>Molecular Therapy - Methods and Clinical Development</i> , 2017, 6, 17-30.	1.8	13

#	ARTICLE	IF	CITATIONS
3789	The genome sequence of <i>Barbarea vulgaris</i> facilitates the study of ecological biochemistry. <i>Scientific Reports</i> , 2017, 7, 40728.	1.6	33
3790	Gene-enriched draft genome of the cattle tick <i>Rhipicephalus microplus</i> : assembly by the hybrid Pacific Biosciences/Illumina approach enabled analysis of the highly repetitive genome. <i>International Journal for Parasitology</i> , 2017, 47, 569-583.	1.3	48
3791	Crop wild relative populations of <i>Beta vulgaris</i> allow direct mapping of agronomically important genes. <i>Nature Communications</i> , 2017, 8, 15708.	5.8	58
3792	Analysis of LINE-1 Elements in DNA from Postmortem Brains of Individuals with Schizophrenia. <i>Neuropsychopharmacology</i> , 2017, 42, 2602-2611.	2.8	60
3793	Analysis of Copy Number Variation in the <i>Abp</i> Gene Regions of Two House Mouse Subspecies Suggests Divergence during the Gene Family Expansions. <i>Genome Biology and Evolution</i> , 2017, 9, .	1.1	5
3794	Sequencing, de novo assembling, and annotating the genome of the endangered Chinese crocodile lizard <i>Shinisaurus crocodilurus</i> . <i>GigaScience</i> , 2017, 6, 1-6.	3.3	23
3795	History cleans up messes: The impact of time in driving divergence and introgression in a tropical suture zone. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1888-1899.	1.1	17
3796	Association Mapping of Yield and Yield-related Traits Under Reproductive Stage Drought Stress in Rice ( <i>Oryza sativa</i> L.). <i>Rice</i> , 2017, 10, 21.	1.7	75
3797	Androgen receptor and miR-206 regulation in prostate cancer. <i>Transcription</i> , 2017, 8, 313-327.	1.7	15
3798	Repeated divergent selection on pigmentation genes in a rapid finch radiation. <i>Science Advances</i> , 2017, 3, e1602404.	4.7	148
3799	The Genome of Medicinal Plant <i>Macleaya cordata</i> Provides New Insights into Benzylisoquinoline Alkaloids Metabolism. <i>Molecular Plant</i> , 2017, 10, 975-989.	3.9	116
3800	RNA-Sequencing data supports the existence of novel VEGFA splicing events but not of VEGFAxxx isoforms. <i>Scientific Reports</i> , 2017, 7, 58.	1.6	16
3801	An episomal vector-based CRISPR/Cas9 system for highly efficient gene knockout in human pluripotent stem cells. <i>Scientific Reports</i> , 2017, 7, 2320.	1.6	91
3802	An Engineered Virus Library as a Resource for the Spectrum-wide Exploration of Virus and Vector Diversity. <i>Cell Reports</i> , 2017, 19, 1698-1709.	2.9	49
3803	The Limitations of Existing Approaches in Improving MicroRNA Target Prediction Accuracy. <i>Methods in Molecular Biology</i> , 2017, 1617, 133-158.	0.4	16
3804	Exploring structural variation and gene family architecture with De Novo assemblies of 15 <i>Medicago</i> genomes. <i>BMC Genomics</i> , 2017, 18, 261.	1.2	87
3805	Whipworm kinomes reflect a unique biology and adaptation to the host animal. <i>International Journal for Parasitology</i> , 2017, 47, 857-866.	1.3	10
3806	In silico analysis of the sequence features responsible for alternatively spliced introns in the model green alga <i>Chlamydomonas reinhardtii</i> . <i>Plant Molecular Biology</i> , 2017, 94, 253-265.	2.0	16

#	ARTICLE	IF	CITATIONS
3807	Live birth derived from oocyte spindle transfer to prevent mitochondrial disease. <i>Reproductive BioMedicine Online</i> , 2017, 34, 361-368.	1.1	255
3808	Generation of mature T cells from human hematopoietic stem and progenitor cells in artificial thymic organoids. <i>Nature Methods</i> , 2017, 14, 521-530.	9.0	165
3809	Different expression patterns of sperm motility-related genes in testis of diploid and tetraploid cyprinid fish. <i>Biology of Reproduction</i> , 2017, 96, 907-920.	1.2	21
3810	The emergence of the hyperinvasive vine, <i>Mikania micrantha</i> (Asteraceae), via admixture and founder events inferred from population transcriptomics. <i>Molecular Ecology</i> , 2017, 26, 3405-3423.	2.0	16
3811	Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017, 1, 120.	3.4	353
3812	Tracking aCAD-ALK gene rearrangement in urine and blood of a colorectal cancer patient treated with an ALK inhibitor. <i>Annals of Oncology</i> , 2017, 28, 1302-1308.	0.6	32
3813	Genome-wide sequencing of longan ( <i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	103
3814	Deep reticulation and incomplete lineage sorting obscure the diploid phylogeny of rain-lilies and allies (Amaryllidaceae tribe Hippeastreae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 231-247.	1.2	88
3815	Monitoring of childhood ALL using BCR-ABL1 genomic breakpoints identifies a subgroup with CML-like biology. <i>Blood</i> , 2017, 129, 2771-2781.	0.6	84
3816	Loss of AXIN1 drives acquired resistance to WNT pathway blockade in colorectal cancer cells carrying RSPO 3 fusions. <i>EMBO Molecular Medicine</i> , 2017, 9, 293-303.	3.3	54
3817	Time-course expression QTL atlas of the global transcriptional response of wheat to <i>Fusarium graminearum</i> . <i>Plant Biotechnology Journal</i> , 2017, 15, 1453-1464.	4.1	32
3818	Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. <i>Nature Communications</i> , 2017, 8, 14742.	5.8	96
3819	Kart: a divide-and-conquer algorithm for NGS read alignment. <i>Bioinformatics</i> , 2017, 33, 2281-2287.	1.8	39
3820	Efficient CNV breakpoint analysis reveals unexpected structural complexity and correlation of dosage-sensitive genes with clinical severity in genomic disorders. <i>Human Molecular Genetics</i> , 2017, 26, 1927-1941.	1.4	20
3821	Construction of a high-density genetic map and the X/Y sex-determining gene mapping in spinach based on large-scale markers developed by specific-locus amplified fragment sequencing (SLAF-seq). <i>BMC Genomics</i> , 2017, 18, 276.	1.2	49
3822	A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 109-117.	0.8	228
3823	Clinical Next-Generation Sequencing. , 2017, , 35-54.		1
3825	Copy number increases of transposable elements and protein-coding genes in an invasive fish of hybrid origin. <i>Molecular Ecology</i> , 2017, 26, 4712-4724.	2.0	28

#	ARTICLE	IF	CITATIONS
3826	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. <i>BMC Genomics</i> , 2017, 18, 225.	1.2	342
3827	The birth of a human-specific neural gene by incomplete duplication and gene fusion. <i>Genome Biology</i> , 2017, 18, 49.	3.8	39
3828	Evaluation and assessment of read-mapping by multiple next-generation sequencing aligners based on genome-wide characteristics. <i>Genomics</i> , 2017, 109, 186-191.	1.3	68
3829	Hyper-methylation of the upstream CpG island shore is a likely mechanism of GPER1 silencing in breast cancer cells. <i>Gene</i> , 2017, 614, 65-73.	1.0	28
3830	Detecting alternatively spliced transcript isoforms from single-molecule long-read sequences without a reference genome. <i>Molecular Ecology Resources</i> , 2017, 17, 1243-1256.	2.2	126
3831	Alterations in Gastric Microbiota After H. Pylori Eradication and in Different Histological Stages of Gastric Carcinogenesis. <i>Scientific Reports</i> , 2017, 7, 44935.	1.6	156
3832	Bioinformatic tools for analysis of CLIP ribonucleoprotein data. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1404.	3.2	9
3833	<i>Candidatus Dichloromethanomonas elyunquensis</i> gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the Peptococcaceae family. <i>Systematic and Applied Microbiology</i> , 2017, 40, 150-159.	1.2	50
3834	Evolution of transcript modification by N <sup>6</sup> -methyladenosine in primates. <i>Genome Research</i> , 2017, 27, 385-392.	2.4	49
3835	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. <i>Methods in Molecular Biology</i> , 2017, 1533, 1-31.	0.4	189
3836	Bioinformatics strategies for taxonomy independent binning and visualization of sequences in shotgun metagenomics. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 48-55.	1.9	106
3837	Identification and characterization of protein coding genes in monsonia ( <i>Monsonia burkeana</i> Planch.) Tj ETQq1 1 0,784314 rgBT /Over	0.5	4
3838	Level of genetic differentiation affects relative performances of expressed sequence tag and genomic SSRs. <i>Molecular Ecology Resources</i> , 2017, 17, 893-903.	2.2	11
3839	The genome draft of coconut ( <i>Cocos nucifera</i> ). <i>GigaScience</i> , 2017, 6, 1-11.	3.3	96
3840	Spontaneous circadian rhythms in a cold-adapted natural isolate of <i>Aureobasidium pullulans</i> . <i>Scientific Reports</i> , 2017, 7, 13837.	1.6	15
3841	sRNAAnalyzer—a flexible and customizable small RNA sequencing data analysis pipeline. <i>Nucleic Acids Research</i> , 2017, 45, 12140-12151.	6.5	76
3842	Keeping it complicated: Mitochondrial genome plasticity across diplomonads. <i>Scientific Reports</i> , 2017, 7, 14166.	1.6	18
3843	A new version of the grapevine reference genome assembly (12X.v2) and of its annotation (VCost.v3). <i>Genomics Data</i> , 2017, 14, 56-62.	1.3	248

#	ARTICLE	IF	CITATIONS
3844	A Genetic Screen for Pre-mRNA Splicing Mutants of <i>Arabidopsis thaliana</i> Identifies Putative U1 snRNP Components RBM25 and PRP39a. <i>Genetics</i> , 2017, 207, 1347-1359.	1.2	28
3845	A distinct hematopoietic stem cell population for rapid multilineage engraftment in nonhuman primates. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	97
3846	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	13.5	973
3847	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
3848	High-throughput analysis unveils a highly shared satellite DNA library among three species of fish genus <i>Astyanax</i> . <i>Scientific Reports</i> , 2017, 7, 12726.	1.6	40
3849	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	13.7	495
3850	DNA sequencing at 40: past, present and future. <i>Nature</i> , 2017, 550, 345-353.	13.7	729
3851	SoyBase: A Comprehensive Database for Soybean Genetic and Genomic Data. <i>Compendium of Plant Genomes</i> , 2017, , 193-211.	0.3	2
3852	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	3.4	121
3853	High rate of translocation-based gene birth on the <i>Drosophila</i> Y chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11721-11726.	3.3	35
3854	Metatranscriptomic and metagenomic description of the bacterial nitrogen metabolism in waste water wet oxidation effluents. <i>Heliyon</i> , 2017, 3, e00427.	1.4	12
3855	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
3856	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	1.9	84
3857	Regulation of the activity of the promoter of RNA-induced silencing, C3PO. <i>Protein Science</i> , 2017, 26, 1807-1818.	3.1	12
3858	The high-quality genome of <i>Brassica napus</i> cultivar 'ZS11' reveals the introgression history in semi-winter morphotype. <i>Plant Journal</i> , 2017, 92, 452-468.	2.8	233
3859	The draft genome assembly of <i>Rhododendron delavayi</i> Franch. var. <i>delavayi</i> . <i>GigaScience</i> , 2017, 6, 1-11.	3.3	64
3860	Genomic structure and evolution of the mating type locus in the green seaweed <i>Ulva partita</i> . <i>Scientific Reports</i> , 2017, 7, 11679.	1.6	25
3861	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356

#	ARTICLE	IF	CITATIONS
3862	Comprehensive analysis of lncRNAs and mRNAs in skeletal muscle of rainbow trout ( <i>Oncorhynchus</i> ) Tj ETQq0 0 0 rgBT /Overlgck 10 Tf 5	1.6	10
3863	Evaluation of single-cell genomics to address evolutionary questions using three SAGs of the choanoflagellate <i>Monosiga brevicollis</i> . <i>Scientific Reports</i> , 2017, 7, 11025.	1.6	19
3864	Acidophilic green algal genome provides insights into adaptation to an acidic environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8304-E8313.	3.3	93
3865	Identification and functional prediction of stress responsive AP2/ERF transcription factors in <i>Brassica napus</i> by genome-wide analysis. <i>Computational Biology and Chemistry</i> , 2017, 71, 32-56.	1.1	24
3866	On the application of reverse vaccinology to parasitic diseases: a perspective on feature selection and ranking of vaccine candidates. <i>International Journal for Parasitology</i> , 2017, 47, 779-790.	1.3	13
3867	Assessment of T-cell receptor repertoire and clonal expansion in peripheral T-cell lymphoma using RNA-seq data. <i>Scientific Reports</i> , 2017, 7, 11301.	1.6	27
3868	Single nucleotide polymorphisms for <sc>DNA</sc> typing in the domestic horse. <i>Animal Genetics</i> , 2017, 48, 669-676.	0.6	20
3869	Metagenomics for Monitoring Environmental Biodiversity: Challenges, Progress, and Opportunities. <i>Health Information Science</i> , 2017, , 73-87.	0.3	2
3870	Molecular analysis of three <i>Clostridium difficile</i> strain genomes isolated from pig farm-related samples. <i>Anaerobe</i> , 2017, 48, 224-231.	1.0	4
3871	Probabilistic Models for Error Correction of Nonuniform Sequencing Data. , 2017, , 131-145.		0
3872	A transcriptome atlas of rabbit revealed by PacBio single-molecule long-read sequencing. <i>Scientific Reports</i> , 2017, 7, 7648.	1.6	125
3873	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. <i>Scientific Reports</i> , 2017, 7, 8859.	1.6	50
3874	Multi-omics Analyses of Starvation Responses Reveal a Central Role for Lipoprotein Metabolism in Acute Starvation Survival in <i>C.Ælegans</i> . <i>Cell Systems</i> , 2017, 5, 38-52.e4.	2.9	52
3875	Nanopore long-read RNAseq reveals widespread transcriptional variation among the surface receptors of individual B cells. <i>Nature Communications</i> , 2017, 8, 16027.	5.8	329
3876	Genome-wide identification, functional prediction, and evolutionary analysis of the R2R3-MYB superfamily in <i>Brassica napus</i> . <i>Genome</i> , 2017, 60, 797-814.	0.9	48
3877	Improvement of the Threespine Stickleback Genome Using a Hi-C-Based Proximity-Guided Assembly. <i>Journal of Heredity</i> , 2017, 108, 693-700.	1.0	62
3878	Differentiating <i>Botulinum Neurotoxin</i> -Producing <i>Clostridia</i> with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	18
3879	Comparative genomic analysis of <i>Mycobacterium tuberculosis</i> Beijing-like strains revealed specific genetic variations associated with virulence and drug resistance. <i>Infection, Genetics and Evolution</i> , 2017, 54, 314-323.	1.0	30

#	ARTICLE	IF	CITATIONS
3880	<i><sc>KIT</sc> </i> mutations and <sc>CD</sc> 117 overexpression are markers of better progressionâ€free survival in vulvar melanomas. British Journal of Dermatology, 2017, 177, 1376-1384.	1.4	16
3881	Splicing Activation by Rbfox Requires Self-Aggregation through Its Tyrosine-Rich Domain. Cell, 2017, 170, 312-323.e10.	13.5	102
3882	Development of Insertion and Deletion Markers for Bottle Gourd Based on Restriction Site-associated DNA Sequencing Data. Horticultural Plant Journal, 2017, 3, 13-16.	2.3	9
3883	Whole-Genome Sequencing and Concordance Between Antimicrobial Susceptibility Genotypes and Phenotypes of Bacterial Isolates Associated with Bovine Respiratory Disease. G3: Genes, Genomes, Genetics, 2017, 7, 3059-3071.	0.8	19
3884	GCN2 phosphorylates HIV-1 integrase and decreases HIV-1 replication by limiting viral integration. Scientific Reports, 2017, 7, 2283.	1.6	17
3885	High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. Scientific Reports, 2017, 7, 7106.	1.6	56
3886	A systems approach to a spatio-temporal understanding of the drought stress response in maize. Scientific Reports, 2017, 7, 6590.	1.6	68
3887	Quantitative metagenomics reveals unique gut microbiome biomarkers in ankylosing spondylitis. Genome Biology, 2017, 18, 142.	3.8	268
3888	A review of existing whole genome data suggests lichen mycelia may be haploid or diploid. Bryologist, 2017, 120, 302-310.	0.1	14
3889	Elevated auxin biosynthesis and transport underlie high vein density in C <sub>4</sub> leaves. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6884-E6891.	3.3	34
3890	Presence of a Shared 5â€2-Leader Sequence in Ancestral Human and Mammalian Retroviruses and Its Transduction into Feline Leukemia Virus. Journal of Virology, 2017, 91, .	1.5	9
3891	Transcriptome Association Identifies Regulators of Wheat Spike Architecture. Plant Physiology, 2017, 175, 746-757.	2.3	94
3892	Recombinant Origins of Pathogenic and Nonpathogenic Mouse Gammaretroviruses with Polytopic Host Range. Journal of Virology, 2017, 91, .	1.5	14
3893	Age, estrogen, and immune response in breast adenocarcinoma and adjacent normal tissue. Oncolmmunology, 2017, 6, e1356142.	2.1	34
3894	MinIONâ„¢ nanopore sequencing of environmental metagenomes: a synthetic approach. GigaScience, 2017, 6, 1-10.	3.3	111
3895	Oncogenic Role of THOR, a Conserved Cancer/Testis Long Non-coding RNA. Cell, 2017, 171, 1559-1572.e20.	13.5	200
3896	Efficient transgenesis and annotated genome sequence of the regenerative flatworm model Macrostomum lignano. Nature Communications, 2017, 8, 2120.	5.8	60
3897	Genome Analysis. Compendium of Plant Genomes, 2017, , 3-19.	0.3	0

#	ARTICLE	IF	CITATIONS
3898	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017, 171, 1437-1452.e17.	13.5	2,281
3899	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. <i>Nature Communications</i> , 2017, 8, 1433.	5.8	86
3900	The deep conservation of the Lepidoptera Z chromosome suggests a non-canonical origin of the W. <i>Nature Communications</i> , 2017, 8, 1486.	5.8	87
3901	Convergent evolution of Y chromosome gene content in flies. <i>Nature Communications</i> , 2017, 8, 785.	5.8	59
3902	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
3903	Variant Review with the Integrative Genomics Viewer. <i>Cancer Research</i> , 2017, 77, e31-e34.	0.4	798
3904	Finding Similar Nucleotide Sequences Using Network BLAST Searches. <i>Current Protocols in Bioinformatics</i> , 2017, 58, 3.3.1-3.3.25.	25.8	12
3905	Automated tools for comparative sequence analysis of genic regions using the GenePalette application. <i>Developmental Biology</i> , 2017, 429, 158-164.	0.9	22
3906	Indoleacrylic Acid Produced by Commensal Peptostreptococcus Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	5.1	523
3907	Soft Sweeps Are the Dominant Mode of Adaptation in the Human Genome. <i>Molecular Biology and Evolution</i> , 2017, 34, 1863-1877.	3.5	164
3908	Expression of a SOX1 overlapping transcript in neural differentiation and cancer models. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 4245-4258.	2.4	24
3909	Personalized RNA mutanome vaccines mobilize poly-specific therapeutic immunity against cancer. <i>Nature</i> , 2017, 547, 222-226.	13.7	1,806
3910	Customized workflow development and data modularization concepts for RNA-Sequencing and metatranscriptome experiments. <i>Journal of Biotechnology</i> , 2017, 261, 85-96.	1.9	16
3911	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	9.4	693
3912	A massively parallel strategy for STR marker development, capture, and genotyping. <i>Nucleic Acids Research</i> , 2017, 45, e142-e142.	6.5	8
3913	The pomegranate ( <i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. <i>Plant Journal</i> , 2017, 91, 1108-1128.	2.8	109
3914	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. <i>BMC Genomics</i> , 2017, 18, 7.	1.2	30
3915	Improved annotation with de novo transcriptome assembly in four social amoeba species. <i>BMC Genomics</i> , 2017, 18, 120.	1.2	7

#	ARTICLE	IF	CITATIONS
3916	Comparative genomic identification and validation of $\beta$ -defensin genes in the <i>Ovis aries</i> genome. <i>BMC Genomics</i> , 2017, 18, 278.	1.2	14
3917	A comprehensive hybridization model allows whole HERV transcriptome profiling using high density microarray. <i>BMC Genomics</i> , 2017, 18, 286.	1.2	29
3918	HirBin: high-resolution identification of differentially abundant functions in metagenomes. <i>BMC Genomics</i> , 2017, 18, 316.	1.2	12
3919	Evolutionary history of glucose-6-phosphatase encoding genes in vertebrate lineages: towards a better understanding of the functions of multiple duplicates. <i>BMC Genomics</i> , 2017, 18, 342.	1.2	29
3920	A simple and economical method for improving whole genome alignment. <i>BMC Genomics</i> , 2017, 18, 362.	1.2	3
3921	CottonFGD: an integrated functional genomics database for cotton. <i>BMC Plant Biology</i> , 2017, 17, 101.	1.6	271
3922	Whole genome sequencing of an ExPEC that caused fatal pneumonia at a pig farm in Changchun, China. <i>BMC Veterinary Research</i> , 2017, 13, 169.	0.7	10
3923	Geno- and phenotypic characteristics of a transfected <i>Babesia bovis</i> 6-Cys-E knockout clonal line. <i>Parasites and Vectors</i> , 2017, 10, 214.	1.0	12
3924	Gene silencing by RNA interference in <i>Sarcoptes scabiei</i> : a molecular tool to identify novel therapeutic targets. <i>Parasites and Vectors</i> , 2017, 10, 289.	1.0	22
3925	New insights into global biogeography, population structure and natural selection from the genome of the epipelagic copepod <i>Oithona</i> . <i>Molecular Ecology</i> , 2017, 26, 4467-4482.	2.0	37
3926	McClintock: An Integrated Pipeline for Detecting Transposable Element Insertions in Whole-Genome Shotgun Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2763-2778.	0.8	81
3927	Genomic organization and evolution of olfactory receptors and trace amine-associated receptors in channel catfish, <i>Ictalurus punctatus</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 644-651.	1.1	15
3928	Distinct biogeographical patterns of marine bacterial taxonomy and functional genes. <i>Global Ecology and Biogeography</i> , 2017, 26, 177-190.	2.7	65
3929	Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. <i>Indian Journal of Microbiology</i> , 2017, 57, 23-38.	1.5	21
3930	Whole-Genome Sequencing of Cytogenetically Balanced Chromosome Translocations Identifies Potentially Pathological Gene Disruptions and Highlights the Importance of Microhomology in the Mechanism of Formation. <i>Human Mutation</i> , 2017, 38, 180-192.	1.1	58
3931	Identification of new TRIP12 variants and detailed clinical evaluation of individuals with non-syndromic intellectual disability with or without autism. <i>Human Genetics</i> , 2017, 136, 179-192.	1.8	43
3932	Draft genome of the American Eel ( <i>Anguilla rostrata</i> ). <i>Molecular Ecology Resources</i> , 2017, 17, 806-811.	2.2	21
3933	Genomic Basis of Adaptive Evolution: The Survival of <i>Amur Ide</i> ( <i>Leuciscus waleckii</i> ) in an Extremely Alkaline Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 145-159.	3.5	66

#	ARTICLE	IF	CITATIONS
3934	Satellite DNA content illuminates the ancestry of a supernumerary (B) chromosome. <i>Chromosoma</i> , 2017, 126, 487-500.	1.0	36
3935	Functional Diversification of the Four MARCKS Family Members in Zebrafish Neural Development. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 119-138.	0.6	14
3936	Identification of a New Rice Low-Tiller Mutant and Association Analyses Based on the SLAF-seq Method. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 72-82.	1.0	19
3937	A Bloom filter based semi-index on <i>q</i> -grams. <i>Software - Practice and Experience</i> , 2017, 47, 799-811.	2.5	0
3938	Genome assembly and annotation of <i>Arabidopsis halleri</i> , a model for heavy metal hyperaccumulation and evolutionary ecology. <i>Molecular Ecology Resources</i> , 2017, 17, 1025-1036.	2.2	98
3939	Metagenomics of Two Severe Foodborne Outbreaks Provides Diagnostic Signatures and Signs of Coinfection Not Attainable by Traditional Methods. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	54
3940	A Bayesian Hidden Markov Mixture Model to Detect Overexpressed Chromosome Regions. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2017, 66, 387-412.	0.5	1
3941	Draft genome of the sea cucumber <i>Apostichopus japonicus</i> and genetic polymorphism among color variants. <i>GigaScience</i> , 2017, 6, 1-6.	3.3	26
3942	Whole-genome sequencing and SNV genotyping of "Nebbiolo"™ ( <i>Vitis vinifera</i> L.) clones. <i>Scientific Reports</i> , 2017, 7, 17294.	1.6	72
3943	De novo assembling and primary analysis of genome and transcriptome of gray whale <i>Eschrichtius robustus</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 258.	3.2	11
3944	Sequencing the Chickpea Genome. <i>Compendium of Plant Genomes</i> , 2017, , 117-123.	0.3	0
3945	Long-read sequence assembly of the firefly <i>Pyrocoelia pectoralis</i> genome. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	32
3946	Draft genome of the lined seahorse, <i>Hippocampus erectus</i> . <i>GigaScience</i> , 2017, 6, 1-6.	3.3	38
3947	CNVcaller: highly efficient and widely applicable software for detecting copy number variations in large populations. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	101
3948	Root transcriptomic responses of grafted grapevines to heterogeneous nitrogen availability depend on rootstock genotype. <i>Journal of Experimental Botany</i> , 2017, 68, 4339-4355.	2.4	42
3949	Genome-wide analysis of SSR and ILP markers in trees: diversity profiling, alternate distribution, and applications in duplication. <i>Scientific Reports</i> , 2017, 7, 17902.	1.6	20
3950	Genomics Resources for Peanut Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 69-91.	0.3	7
3951	A SNP-enabled assessment of genetic diversity, evolutionary relationships and the identification of candidate genes in chrysanthemum. <i>Genome Biology and Evolution</i> , 2017, 8, evw270.	1.1	38

#	ARTICLE	IF	CITATIONS
3952	Transcriptome assembly in <i>Suaeda aralocaspica</i> to reveal the distinct temporal gene/miRNA alterations between the dimorphic seeds during germination. <i>BMC Genomics</i> , 2017, 18, 806.	1.2	11
3953	Differences in the genetic control of early egg development and reproduction between <i>C. elegans</i> and its parthenogenetic relative <i>D. coronatus</i> . <i>EvoDevo</i> , 2017, 8, 16.	1.3	4
3954	Scaling bioinformatics applications on HPC. <i>BMC Bioinformatics</i> , 2017, 18, 501.	1.2	9
3955	Accelerating Smith-Waterman Alignment Workload with Scalable Vector Computing. , 2017, , .		3
3956	Transcription through the eye of a needle: daily and annual cyclic gene expression variation in Douglas-fir needles. <i>BMC Genomics</i> , 2017, 18, 558.	1.2	35
3957	The draft genome of <i>Ruellia speciosa</i> (Beautiful Wild Petunia: Acanthaceae). <i>DNA Research</i> , 2017, 24, dsw054.	1.5	31
3958	Evolution of Alu Subfamily Structure in the Saimiri Lineage of New World Monkeys. <i>Genome Biology and Evolution</i> , 2017, 9, 2365-2376.	1.1	16
3959	An Annotated Draft Genome for <i>Radix auricularia</i> (Gastropoda, Mollusca). <i>Genome Biology and Evolution</i> , 2017, 9, 585-592.	1.1	57
3960	Detecting large deletions at base pair level by combining split read and paired read data. <i>BMC Bioinformatics</i> , 2017, 18, 413.	1.2	2
3961	Gapless genome assembly of <i>Colletotrichum higginsianum</i> reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. <i>BMC Genomics</i> , 2017, 18, 667.	1.2	111
3962	The coding and noncoding transcriptome of <i>Neurospora crassa</i> . <i>BMC Genomics</i> , 2017, 18, 978.	1.2	26
3963	Establishment of a genome-wide and quantitative protocol for assessment of transcriptional activity at human retrotransposon L1 antisense promoters. <i>Genes and Genetic Systems</i> , 2017, 92, 243-249.	0.2	1
3964	Global transcriptional landscape and promoter mapping of the gut commensal <i>Bifidobacterium breve</i> UCC2003. <i>BMC Genomics</i> , 2017, 18, 991.	1.2	24
3965	Photosynthesis in <i>C<sub>3</sub></i> and <i>C<sub>4</sub></i> intermediate <i>Moricandia</i> species. <i>Journal of Experimental Botany</i> , 2017, 68, 191-206.	2.4	58
3966	Age-related gene expression changes, and transcriptome wide association study of physical and cognitive aging traits, in the Lothian Birth Cohort 1936. <i>Aging</i> , 2017, 9, 2489-2503.	1.4	33
3967	Optimal choice of word length when comparing two Markov sequences using a $\chi^2$ -statistic. <i>BMC Genomics</i> , 2017, 18, 732.	1.2	8
3968	High Level of Nonsynonymous Changes in Common Bean Suggests That Selection under Domestication Increased Functional Diversity at Target Traits. <i>Frontiers in Plant Science</i> , 2016, 7, 2005.	1.7	19
3969	High-Density Genetic Map Construction and Gene Mapping of Basal Branching Habit and Flowers per Leaf Axil in Sesame. <i>Frontiers in Plant Science</i> , 2017, 8, 636.	1.7	65

#	ARTICLE	IF	CITATIONS
3970	Genome-Wide SNP Markers Based on SLAF-Seq Uncover Breeding Traces in Rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 648.	1.7	68
3971	Mapping and Preliminary Analysis of ABORTED MICROSPORES (AMS) as the Candidate Gene Underlying the Male Sterility (MS-5) Mutant in Melon ( <i>Cucumis melo</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 902.	1.7	27
3972	A Highly Dense Genetic Map for <i>Ginkgo biloba</i> Constructed Using Sequence-Based Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1041.	1.7	45
3973	The First Genetic Map in Sweet Osmanthus ( <i>Osmanthus fragrans</i> Lour.) Using Specific Locus Amplified Fragment Sequencing. <i>Frontiers in Plant Science</i> , 2017, 8, 1621.	1.7	46
3974	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2017, 18, 578.	1.2	54
3975	Reliable Detection of Herpes Simplex Virus Sequence Variation by High-Throughput Resequencing. <i>Viruses</i> , 2017, 9, 226.	1.5	9
3976	Interpreting whole genome and exome sequencing data of individual gastric cancer samples. <i>BMC Genomics</i> , 2017, 18, 517.	1.2	11
3977	Complete mitochondrial genome sequences of the northern spotted owl ( <i>Strix occidentalis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 of a duplicated control region. <i>PeerJ</i> , 2017, 5, e3901.	0.9	19
3978	A Massively Parallel Sequence Similarity Search for Metagenomic Sequencing Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2124.	1.8	4
3979	Genome Sequences of Marine Shrimp <i>Exopalaemon carinicauda</i> Holthuis Provide Insights into Genome Size Evolution of Caridea. <i>Marine Drugs</i> , 2017, 15, 213.	2.2	52
3980	Transcriptomic Complexity of <i>Aspergillus terreus</i> Velvet Gene Family under the Influence of Butyrolactone I. <i>Microorganisms</i> , 2017, 5, 12.	1.6	30
3981	Insights into the Function of Long Noncoding RNAs in Sepsis Revealed by Gene Co-Expression Network Analysis. <i>Non-coding RNA</i> , 2017, 3, 5.	1.3	30
3982	LTR-Retrotransposons from Bdelloid Rotifers Capture Additional ORFs Shared between Highly Diverse Retroelement Types. <i>Viruses</i> , 2017, 9, 78.	1.5	10
3983	Contrasting patterns of evolutionary constraint and novelty revealed by comparative sperm proteomic analysis in Lepidoptera. <i>BMC Genomics</i> , 2017, 18, 931.	1.2	18
3984	A Frameshift Mutation in KIT is Associated with White Spotting in the Arabian Camel. <i>Genes</i> , 2017, 8, 1020		33
3985	Dynamics of genomic innovation in the unicellular ancestry of animals. <i>ELife</i> , 2017, 6, .	2.8	121
3986	A Glimpse into the Satellite DNA Library in Characidae Fish (Teleostei, Characiformes). <i>Frontiers in Genetics</i> , 2017, 8, 103.	1.1	27
3987	Computational Model Reveals Limited Correlation between Germinal Center B-Cell Subclone Abundance and Affinity: Implications for Repertoire Sequencing. <i>Frontiers in Immunology</i> , 2017, 8, 221.	2.2	20

#	ARTICLE	IF	CITATIONS
3988	Metagenomic Analysis of Hot Springs in Central India Reveals Hydrocarbon Degrading Thermophiles and Pathways Essential for Survival in Extreme Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 2123.	1.5	96
3989	Genome Plasticity and Polymorphisms in Critical Genes Correlate with Increased Virulence of Dutch Outbreak-Related <i>Coxiella burnetii</i> Strains. <i>Frontiers in Microbiology</i> , 2017, 8, 1526.	1.5	26
3990	Specific-Locus Amplified Fragment Sequencing Reveals Spontaneous Single-Nucleotide Mutations in Rice OsMsh6 Mutants. <i>BioMed Research International</i> , 2017, 2017, 1-7.	0.9	3
3991	PALADIN: protein alignment for functional profiling whole metagenome shotgun data. <i>Bioinformatics</i> , 2017, 33, 1473-1478.	1.8	38
3992	A Review on Recent Computational Methods for Predicting Noncoding RNAs. <i>BioMed Research International</i> , 2017, 2017, 1-14.	0.9	25
3993	Describing Genomic and Epigenomic Traits Underpinning Emerging Fungal Pathogens. <i>Advances in Genetics</i> , 2017, 100, 73-140.	0.8	17
3994	HLA genotyping by next-generation sequencing of complementary DNA. <i>BMC Genomics</i> , 2017, 18, 914.	1.2	19
3995	The mouse genome displays highly dynamic populations of KRAB-zinc finger protein genes and related genetic units. <i>PLoS ONE</i> , 2017, 12, e0173746.	1.1	39
3996	MIPE: A metagenome-based community structure explorer and SSU primer evaluation tool. <i>PLoS ONE</i> , 2017, 12, e0174609.	1.1	7
3997	The Agassizâ€™s desert tortoise genome provides a resource for the conservation of a threatened species. <i>PLoS ONE</i> , 2017, 12, e0177708.	1.1	33
3998	The effects of sampling on the efficiency and accuracy of kâ€™mer indexes: Theoretical and empirical comparisons using the human genome. <i>PLoS ONE</i> , 2017, 12, e0179046.	1.1	1
3999	Microbiome overview in swine lungs. <i>PLoS ONE</i> , 2017, 12, e0181503.	1.1	33
4000	Comprehensive benchmarking of SNV callers for highly admixed tumor data. <i>PLoS ONE</i> , 2017, 12, e0186175.	1.1	12
4001	Construction of an SNP-based high-density linkage map for flax ( <i>Linum usitatissimum</i> L.) using specific length amplified fragment sequencing (SLAF-seq) technology. <i>PLoS ONE</i> , 2017, 12, e0189785.	1.1	25
4002	Allelic variants of OsHKT1;1 underlie the divergence between indica and japonica subspecies of rice ( <i>Oryza sativa</i> ) for root sodium content. <i>PLoS Genetics</i> , 2017, 13, e1006823.	1.5	118
4003	A comprehensive overview and evaluation of circular RNA detection tools. <i>PLoS Computational Biology</i> , 2017, 13, e1005420.	1.5	313
4004	An independent component analysis confounding factor correction framework for identifying broad impact expression quantitative trait loci. <i>PLoS Computational Biology</i> , 2017, 13, e1005537.	1.5	12
4005	Rfx2 Stabilizes Foxj1 Binding at Chromatin Loops to Enable Multiciliated Cell Gene Expression. <i>PLoS Genetics</i> , 2017, 13, e1006538.	1.5	68

#	ARTICLE	IF	CITATIONS
4006	Genomic introgression mapping of field-derived multiple-anthelmintic resistance in <i>Teladorsagia circumcincta</i> . <i>PLoS Genetics</i> , 2017, 13, e1006857.	1.5	67
4007	Flavivirus and Filovirus EvoPrinters: New alignment tools for the comparative analysis of viral evolution. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005673.	1.3	3
4008	A miRNA catalogue and ncRNA annotation of the short-living fish <i>Nothobranchius furzeri</i> . <i>BMC Genomics</i> , 2017, 18, 693.	1.2	18
4009	Evaluating allopolyploid origins in strawberries ( <i>Fragaria</i> ) using haplotypes generated from target capture sequencing. <i>BMC Evolutionary Biology</i> , 2017, 17, 180.	3.2	69
4010	The complete chloroplast genome of <i>Primulina</i> and two novel strategies for development of high polymorphic loci for population genetic and phylogenetic studies. <i>BMC Evolutionary Biology</i> , 2017, 17, 224.	3.2	18
4011	Gene expression patterns of chicken neuregulin 3 in association with copy number variation and frameshift deletion. <i>BMC Genetics</i> , 2017, 18, 69.	2.7	3
4012	An integrated and comparative approach towards identification, characterization and functional annotation of candidate genes for drought tolerance in sorghum ( <i>Sorghum bicolor</i> (L.) Moench). <i>BMC Genetics</i> , 2017, 18, 119.	2.7	27
4013	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017, 15, 62.	1.7	286
4014	Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur ( <i>Microcebus murinus</i> ). <i>BMC Biology</i> , 2017, 15, 110.	1.7	53
4015	De novo assembly and characterization of breast cancer transcriptomes identifies large numbers of novel fusion-gene transcripts of potential functional significance. <i>BMC Medical Genomics</i> , 2017, 10, 53.	0.7	10
4016	HAlign-II: efficient ultra-large multiple sequence alignment and phylogenetic tree reconstruction with distributed and parallel computing. <i>Algorithms for Molecular Biology</i> , 2017, 12, 25.	0.3	30
4017	SuperTranscripts: a data driven reference for analysis and visualisation of transcriptomes. <i>Genome Biology</i> , 2017, 18, 148.	3.8	79
4018	Consideration of non-canonical splice sites improves gene prediction on the <i>Arabidopsis thaliana</i> Niederzenz-1 genome sequence. <i>BMC Research Notes</i> , 2017, 10, 667.	0.6	24
4019	Stress amplifies sex differences in primate prefrontal profiles of gene expression. <i>Biology of Sex Differences</i> , 2017, 8, 36.	1.8	7
4020	Perilipin-2 modulates dietary fat-induced microbial global gene expression profiles in the mouse intestine. <i>Microbiome</i> , 2017, 5, 117.	4.9	17
4021	Comparative Transcriptome and DNA methylation analyses of the molecular mechanisms underlying skin color variations in Crucian carp ( <i>Carassius carassius</i> L.). <i>BMC Genetics</i> , 2017, 18, 95.	2.7	43
4022	K-mer clustering algorithm using a MapReduce framework: application to the parallelization of the Inchworm module of Trinity. <i>BMC Bioinformatics</i> , 2017, 18, 467.	1.2	17
4023	Similarity Projection: A Geometric Measure for Comparison of Biological Sequences. , 2017, , .		0

#	ARTICLE	IF	CITATIONS
4024	Transcriptome analysis reveals the host selection fitness mechanisms of the <i>Rhizoctonia solani</i> AG11A pathogen. <i>Scientific Reports</i> , 2017, 7, 10120.	1.6	43
4025	MPD: multiplex primer design for next-generation targeted sequencing. <i>BMC Bioinformatics</i> , 2017, 18, 14.	1.2	23
4026	Detection and quantification of mitochondrial DNA deletions from next-generation sequence data. <i>BMC Bioinformatics</i> , 2017, 18, 407.	1.2	29
4027	VISMapper: ultra-fast exhaustive cartography of viral insertion sites for gene therapy. <i>BMC Bioinformatics</i> , 2017, 18, 421.	1.2	1
4028	An optimized approach for annotation of large eukaryotic genomic sequences using genetic algorithm. <i>BMC Bioinformatics</i> , 2017, 18, 460.	1.2	2
4029	Fast batch searching for protein homology based on compression and clustering. <i>BMC Bioinformatics</i> , 2017, 18, 508.	1.2	6
4030	Overexpressed HSF1 cancer signature genes cluster in human chromosome 8q. <i>Human Genomics</i> , 2017, 11, 35.	1.4	17
4031	Draft de novo transcriptome assembly and proteome characterization of the electric lobe of <i>Tetronarce californica</i> : a molecular tool for the study of cholinergic neurotransmission in the electric organ. <i>BMC Genomics</i> , 2017, 18, 611.	1.2	7
4032	C <sup>3</sup> cotyledons are followed by C <sup>4</sup> leaves: intra-individual transcriptome analysis of <i>Salsola soda</i> (Chenopodiaceae). <i>Journal of Experimental Botany</i> , 2017, 68, 161-176.	2.4	29
4033	Transcriptome Analysis for Non-Model Organism: Current Status and Best-Practices. , 0, , .		10
4034	RetrogeneDB—a database of plant and animal retrocopies. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	30
4035	Identification of Proteases and Protease Inhibitors in Allergenic and Non-Allergenic Pollen. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1199.	1.8	19
4036	Large scale genomic analysis shows no evidence for pathogen adaptation between the blood and cerebrospinal fluid niches during bacterial meningitis. <i>Microbial Genomics</i> , 2017, 3, e000103.	1.0	53
4037	Efficient Genome-wide Association in Biobanks Using Topic Modeling Identifies Multiple Novel Disease Loci. <i>Molecular Medicine</i> , 2017, 23, 285-294.	1.9	19
4038	Approaches for in silico finishing of microbial genome sequences. <i>Genetics and Molecular Biology</i> , 2017, 40, 553-576.	0.6	17
4039	Cooption of heat shock regulatory system for anhydrobiosis in the sleeping chironomid <i>Polypedilum vanderplanki</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2477-E2486.	3.3	25
4040	Site-specificity of serine integrase demonstrated by the <i>attB</i> sequence preference of $\Phi$ BT1 integrase. <i>FEBS Letters</i> , 2018, 592, 1389-1399.	1.3	3
4041	Analysis of RNA Editing Sites from RNA-Seq Data Using GIREMI. <i>Methods in Molecular Biology</i> , 2018, 1751, 101-108.	0.4	7

#	ARTICLE	IF	CITATIONS
4042	Homo sapiens-Specific Binding Site Variants within Brain Exclusive Enhancers Are Subject to Accelerated Divergence across Human Population. <i>Genome Biology and Evolution</i> , 2018, 10, 956-966.	1.1	10
4044	A translational silencing function of MCP1P1/Regnase-1 specified by the target site context. <i>Nucleic Acids Research</i> , 2018, 46, 4256-4270.	6.5	20
4045	Evolution of pyrrolizidine alkaloid biosynthesis in Apocynaceae: revisiting the defence de-escalation hypothesis. <i>New Phytologist</i> , 2018, 218, 762-773.	3.5	21
4046	Whole-Genome Analysis Illustrates Global Clonal Population Structure of the Ubiquitous Dermatophyte Pathogen <i>Trichophyton rubrum</i> . <i>Genetics</i> , 2018, 208, 1657-1669.	1.2	48
4047	Gene Space and Transcriptome Assemblies of Leafy Spurge ( <i>Euphorbia esula</i> ) Identify Promoter Sequences, Repetitive Elements, High-Quality Markers, and a Full-Length Chloroplast Genome. <i>Weed Science</i> , 2018, 66, 355-367.	0.8	11
4048	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. <i>Nature</i> , 2018, 555, 371-376.	13.7	649
4049	Discovery of coding regions in the human genome by integrated proteogenomics analysis workflow. <i>Nature Communications</i> , 2018, 9, 903.	5.8	108
4050	Landscape of the spliced leader trans-splicing mechanism in <i>Schistosoma mansoni</i> . <i>Scientific Reports</i> , 2018, 8, 3877.	1.6	20
4051	Gene arrangement and sequence of mitochondrial genomes yield insights into the phylogeny and evolution of bees and sphecid wasps (Hymenoptera: Apoidea). <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 1-9.	1.2	49
4052	Gain-of-function analysis of cis-acting diversification elements in <i>DT</i> 40 cells. <i>Immunology and Cell Biology</i> , 2018, 96, 948-957.	1.0	1
4053	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	6.0	461
4054	Parallel evolution of Batesian mimicry supergene in two <i>Papilio</i> butterflies, <i>P. polytes</i> and <i>P. memnon</i> . <i>Science Advances</i> , 2018, 4, eaao5416.	4.7	48
4055	A Blast implementation in Hadoop MapReduce using low cost commodity hardware. <i>Procedia Computer Science</i> , 2018, 127, 69-75.	1.2	5
4056	Chromosome-scale assembly of the <i>Monopterus</i> genome. <i>GigaScience</i> , 2018, 7, .	3.3	30
4057	A Framework for Resolving Cryptic Species: A Case Study from the Lizards of the Australian Wet Tropics. <i>Systematic Biology</i> , 2018, 67, 1061-1075.	2.7	71
4058	De novo draft assembly of the <i>Botrylloides leachii</i> genome provides further insight into tunicate evolution. <i>Scientific Reports</i> , 2018, 8, 5518.	1.6	36
4059	Comparison of closely related, uncultivated <i>Coxiella</i> tick endosymbiont population genomes reveals clues about the mechanisms of symbiosis. <i>Environmental Microbiology</i> , 2018, 20, 1751-1764.	1.8	33
4060	Improved de novo genomic assembly for the domestic donkey. <i>Science Advances</i> , 2018, 4, eaaq0392.	4.7	46

#	ARTICLE	IF	CITATIONS
4061	G-Anchor: a novel approach for whole-genome comparative mapping utilizing evolutionary conserved DNA sequences. <i>GigaScience</i> , 2018, 7, .	3.3	3
4062	Detection and genotyping of human papillomavirus (HPV) in HIV-infected women and its relationship with HPV/HIV co-infection. <i>Medicine (United States)</i> , 2018, 97, e9545.	0.4	39
4063	Draft genome of the Peruvian scallop <i>Argopecten purpuratus</i> . <i>GigaScience</i> , 2018, 7, .	3.3	60
4064	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. <i>Cancer Cell</i> , 2018, 33, 607-619.e15.	7.7	88
4065	L1 retrotransposition is a common feature of mammalian hepatocarcinogenesis. <i>Genome Research</i> , 2018, 28, 639-653.	2.4	79
4066	HNRNPA1 promotes recognition of splice site decoys by U2AF2 in vivo. <i>Genome Research</i> , 2018, 28, 689-698.	2.4	28
4067	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	3.4	124
4068	Genomic Analyses Yield Markers for Identifying Agronomically Important Genes in Potato. <i>Molecular Plant</i> , 2018, 11, 473-484.	3.9	73
4069	Filtering of target sequence capture individuals facilitates species tree construction in the plant subtribe <i>Lochrominae</i> (Solanaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 123, 26-34.	1.2	9
4070	Evolution of the Quorum network and the mobilome (plasmids and bacteriophages) in clinical strains of <i>Acinetobacter baumannii</i> during a decade. <i>Scientific Reports</i> , 2018, 8, 2523.	1.6	28
4071	Databases for Rice Omics Studies. , 2018, , 541-554.		1
4072	Identification of piRNA Binding Sites Reveals the Argonaute Regulatory Landscape of the <i>C.Âelegans</i> Germline. <i>Cell</i> , 2018, 172, 937-951.e18.	13.5	189
4073	Whole-genome assembly of the coral reef Pearlscale Pygmy Angelfish ( <i>Centropyge vrolikii</i> ). <i>Scientific Reports</i> , 2018, 8, 1498.	1.6	13
4074	Contribution of transposable elements and distal enhancers to evolution of human-specific features of interphase chromatin architecture in embryonic stem cells. <i>Chromosome Research</i> , 2018, 26, 61-84.	1.0	28
4075	Identification of an (AC) <sub>n</sub> microsatellite in the <i>Six1</i> gene promoter and its effect on production traits in Pietrain $\times$ Duroc $\times$ Landrace $\times$ Yorkshire pigs <sup>1</sup> . <i>Journal of Animal Science</i> , 2018, 96, 17-26.	0.2	3
4076	5-Azacytidine prevents relapse and produces long-term complete remissions in leukemia xenografts treated with Moxetumomab pasudotox. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1867-E1875.	3.3	12
4077	ZNF462 and KLF12 are disrupted by a de novo translocation in a patient with syndromic intellectual disability and autism spectrum disorder. <i>European Journal of Medical Genetics</i> , 2018, 61, 376-383.	0.7	13
4078	Novel FR-900493 Analogues That Inhibit the Outgrowth of <i>Clostridium difficile</i> Spores. <i>ACS Omega</i> , 2018, 3, 1726-1739.	1.6	21

#	ARTICLE	IF	CITATIONS
4079	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
4080	Genome sequence and description of <i>Haloferax massiliense</i> sp. nov., a new halophilic archaeon isolated from the human gut. <i>Extremophiles</i> , 2018, 22, 485-498.	0.9	14
4081	SLAF-based high-density genetic map construction and QTL mapping for major economic traits in sea urchin <i>Strongylocentrotus intermedius</i> . <i>Scientific Reports</i> , 2018, 8, 820.	1.6	33
4082	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. <i>Nucleic Acids Research</i> , 2018, 46, e38-e38.	6.5	116
4083	Draft genome and reference transcriptomic resources for the urticating pine defoliator <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). <i>Molecular Ecology Resources</i> , 2018, 18, 602-619.	2.2	23
4084	Genome assembly of the Pink Ipê <sup>a</sup> ( <i>Handroanthus impetiginosus</i> , Bignoniaceae), a highly valued, ecologically keystone Neotropical timber forest tree. <i>GigaScience</i> , 2018, 7, 1-16.	3.3	23
4085	Uncovering Genomic Regions Associated with <i>Trypanosoma</i> Infections in Wild Populations of the Tsetse Fly <i>Glossina fuscipes</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 887-897.	0.8	8
4086	Assembly of the <i>Lactuca sativa</i> , L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. <i>Journal of Biotechnology</i> , 2018, 267, 12-18.	1.9	13
4087	<i>MYRF</i> is associated with encephalopathy with reversible myelin vacuolization. <i>Annals of Neurology</i> , 2018, 83, 98-106.	2.8	35
4088	Detection of de novo single nucleotide variants in offspring of atomic-bomb survivors close to the hypocenter by whole-genome sequencing. <i>Journal of Human Genetics</i> , 2018, 63, 357-363.	1.1	20
4089	The Hidden Genomic and Transcriptomic Plasticity of Giant Marker Chromosomes in Cancer. <i>Genetics</i> , 2018, 208, 951-961.	1.2	13
4090	Duplicated membrane estrogen receptors in the European sea bass ( <i>Dicentrarchus labrax</i> ): Phylogeny, expression and regulation throughout the reproductive cycle. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2018, 178, 234-242.	1.2	16
4091	Transcription profiling and identification of infection-related genes in <i>Phytophthora cactorum</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 541-555.	1.0	23
4092	Computational Strategies for Exploring Circular RNAs. <i>Trends in Genetics</i> , 2018, 34, 389-400.	2.9	113
4093	Analysis of DNA Methylation in Young People: Limited Evidence for an Association Between Victimization Stress and Epigenetic Variation in Blood. <i>American Journal of Psychiatry</i> , 2018, 175, 517-529.	4.0	114
4094	Analysis of the <i>Aedes albopictus</i> C6/36 genome provides insight into cell line utility for viral propagation. <i>GigaScience</i> , 2018, 7, 1-13.	3.3	51
4095	A New Standard for Crustacean Genomes: The Highly Contiguous, Annotated Genome Assembly of the Clam Shrimp <i>Eulimnadia texana</i> Reveals HOX Gene Order and Identifies the Sex Chromosome. <i>Genome Biology and Evolution</i> , 2018, 10, 143-156.	1.1	33
4096	POU6f1 Mediates Neuropeptide-Dependent Plasticity in the Adult Brain. <i>Journal of Neuroscience</i> , 2018, 38, 1443-1461.	1.7	20

#	ARTICLE	IF	CITATIONS
4097	DNAAF1 links heart laterality with the AAA+ ATPase RUVBL1 and ciliary intraflagellar transport. <i>Human Molecular Genetics</i> , 2018, 27, 529-545.	1.4	45
4098	Human Accelerated Regions and Other Human-Specific Sequence Variations in the Context of Evolution and Their Relevance for Brain Development. <i>Genome Biology and Evolution</i> , 2018, 10, 166-188.	1.1	61
4099	Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. <i>Science</i> , 2018, 359, 55-61.	6.0	102
4100	Multiplexed gene synthesis in emulsions for exploring protein functional landscapes. <i>Science</i> , 2018, 359, 343-347.	6.0	102
4101	Unexpected conservation of the RNA splicing apparatus in the highly streamlined genome of <i>Galdieria sulphuraria</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 41.	3.2	14
4102	The constitutive differential transcriptome of a brain circuit for vocal learning. <i>BMC Genomics</i> , 2018, 19, 231.	1.2	25
4103	A manually annotated <i>Actinidia chinensis</i> var. <i>chinensis</i> (kiwifruit) genome highlights the challenges associated with draft genomes and gene prediction in plants. <i>BMC Genomics</i> , 2018, 19, 257.	1.2	167
4104	Comparative genomics of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> reveals chromosomal variations and genome plasticity. <i>BMC Genomics</i> , 2018, 19, 279.	1.2	56
4105	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. <i>Genome Biology</i> , 2018, 19, 38.	3.8	46
4106	Analysis of lineage-specific Alu subfamilies in the genome of the olive baboon, <i>Papio anubis</i> . <i>Mobile DNA</i> , 2018, 9, 10.	1.3	10
4107	Successful application of human-based methyl capture sequencing for methylome analysis in non-human primate models. <i>BMC Genomics</i> , 2018, 19, 267.	1.2	10
4108	Alignment-Free Sequence Analysis and Applications. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 93-114.	2.8	78
4109	A new strategy to infer circularity applied to four new complete frog mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 4011-4018.	0.8	15
4110	Partially Local Multi-way Alignments. <i>Mathematics in Computer Science</i> , 2018, 12, 207-234.	0.2	4
4111	Necklace: combining reference and assembled transcriptomes for more comprehensive RNA-Seq analysis. <i>GigaScience</i> , 2018, 7, .	3.3	9
4112	Targeting legume loci: A comparison of three methods for target enrichment bait design in Leguminosae phylogenomics. <i>Applications in Plant Sciences</i> , 2018, 6, e1036.	0.8	64
4113	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018, 9, 1702.	5.8	73
4114	Piercing the dark matter: bioinformatics of long-range sequencing and mapping. <i>Nature Reviews Genetics</i> , 2018, 19, 329-346.	7.7	395

#	ARTICLE	IF	CITATIONS
4115	DNA Conformation Induces Adaptable Binding by Tandem Zinc Finger Proteins. <i>Cell</i> , 2018, 173, 221-233.e12.	13.5	52
4116	HybPhyloMaker: Target Enrichment Data Analysis From Raw Reads to Species Trees. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431774261.	0.6	34
4117	A Genetic Screen Identifies PRP18a, a Putative Second Step Splicing Factor Important for Alternative Splicing and a Normal Phenotype in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1367-1377.	0.8	15
4118	Genomic insight into the taxonomy of <i>Rhizobium</i> genospecies that nodulate <i>Phaseolus vulgaris</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 300-310.	1.2	44
4119	High-density genetic map construction and comparative genome analysis in asparagus bean. <i>Scientific Reports</i> , 2018, 8, 4836.	1.6	16
4120	Deep learning improves antimicrobial peptide recognition. <i>Bioinformatics</i> , 2018, 34, 2740-2747.	1.8	282
4121	HOXB7 overexpression in lung cancer is a hallmark of acquired stem-like phenotype. <i>Oncogene</i> , 2018, 37, 3575-3588.	2.6	29
4122	Darwin. , 2018, , .		66
4123	Rapid Multiplex Small DNA Sequencing on the MinION Nanopore Sequencing Platform. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1649-1657.	0.8	25
4124	High-throughput analysis of satellite DNA in the grasshopper <i>Pyrgomorpha conica</i> reveals abundance of homologous and heterologous higher-order repeats. <i>Chromosoma</i> , 2018, 127, 323-340.	1.0	29
4125	Phylogenomic evidence for a recent and rapid radiation of lizards in the Patagonian <i>Liolaemus fitzingerii</i> species group. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 243-254.	1.2	25
4126	Genome-wide association identifies a novel locus for delirium risk. <i>Neurobiology of Aging</i> , 2018, 68, 160.e9-160.e14.	1.5	14
4127	Identification and characterization of evolutionarily conserved alternative splicing events in a mangrove genus <i>Sonneratia</i> . <i>Scientific Reports</i> , 2018, 8, 4425.	1.6	5
4128	EumicrobeDBLite: a lightweight genomic resource and analytic platform for draft oomycete genomes. <i>Molecular Plant Pathology</i> , 2018, 19, 227-237.	2.0	24
4129	NGS-FC: A Next-Generation Sequencing Data Format Converter. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1-1.	1.9	1
4130	LINE-1 Hypermethylation in Serum Cell-Free DNA of Relapsing Remitting Multiple Sclerosis Patients. <i>Molecular Neurobiology</i> , 2018, 55, 4681-4688.	1.9	24
4131	Genome structure of <i>Rosa multiflora</i> , a wild ancestor of cultivated roses. <i>DNA Research</i> , 2018, 25, 113-121.	1.5	70
4132	Genome-wide Mapping of Off-Target Events in Single-Stranded Oligodeoxynucleotide-Mediated Gene Repair Experiments. <i>Molecular Therapy</i> , 2018, 26, 115-131.	3.7	1

#	ARTICLE	IF	CITATIONS
4133	Using RNA-seq to determine patterns of sex-bias in gene expression in the brain of the sex-role reversed Gulf Pipefish ( <i>Syngnathus scovelli</i> ). <i>Marine Genomics</i> , 2018, 37, 120-127.	0.4	10
4134	Accurate Profiling and Quantification of tRNA Fragments from RNA-Seq Data: A Vade Mecum for MINTmap. <i>Methods in Molecular Biology</i> , 2018, 1680, 237-255.	0.4	21
4135	Intelligent mining of large-scale bio-data: Bioinformatics applications. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 10-29.	0.5	29
4136	Quantitative sequence characterization for repetitive DNA content in the supernumerary chromosome of the migratory locust. <i>Chromosoma</i> , 2018, 127, 45-57.	1.0	25
4137	qPrimerDB: a thermodynamics-based gene-specific qPCR primer database for 147 organisms. <i>Nucleic Acids Research</i> , 2018, 46, D1229-D1236.	6.5	115
4138	<i>ABCA4</i> midigenes reveal the full splice spectrum of all reported noncanonical splice site variants in Stargardt disease. <i>Genome Research</i> , 2018, 28, 100-110.	2.4	134
4139	3C-PCR: a novel proximity ligation-based approach to phase chromosomal rearrangement breakpoints with distal allelic variants. <i>Human Genetics</i> , 2018, 137, 55-62.	1.8	5
4140	Integration of Comparative Genomics with Genome-Scale Metabolic Modeling to Investigate Strain-Specific Phenotypical Differences. <i>Methods in Molecular Biology</i> , 2018, 1716, 151-175.	0.4	4
4141	The Hardy Rubber Tree Genome Provides Insights into the Evolution of Polyisoprene Biosynthesis. <i>Molecular Plant</i> , 2018, 11, 429-442.	3.9	62
4142	The landscape of miRNA editing in animals and its impact on miRNA biogenesis and targeting. <i>Genome Research</i> , 2018, 28, 132-143.	2.4	81
4143	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	2.8	406
4144	Assembly and analysis of a <i>qingke</i> reference genome demonstrate its close genetic relation to modern cultivated barley. <i>Plant Biotechnology Journal</i> , 2018, 16, 760-770.	4.1	50
4145	Voluntary exposure to a toxin: the genetic influence on ethanol consumption. <i>Mammalian Genome</i> , 2018, 29, 128-140.	1.0	9
4146	Comparative transcriptome analysis provides insights of anti-insect molecular mechanism of <i>Cassia obtusifolia</i> trypsin inhibitor against <i>Pieris rapae</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2018, 97, e21427.	0.6	7
4147	Conservation analysis of long non-coding RNAs in plants. <i>Science China Life Sciences</i> , 2018, 61, 190-198.	2.3	83
4148	Stable Core Gut Microbiota across the Freshwater-to-Saltwater Transition for Farmed Atlantic Salmon. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	90
4149	Microhaplotypes provide increased power from short-read DNA sequences for relationship inference. <i>Molecular Ecology Resources</i> , 2018, 18, 296-305.	2.2	101
4150	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. <i>New Phytologist</i> , 2018, 217, 1292-1306.	3.5	92

#	ARTICLE	IF	CITATIONS
4151	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. <i>Systematic and Applied Microbiology</i> , 2018, 41, 1-12.	1.2	24
4152	Universal target-enrichment baits for anthozoan (Cnidaria) phylogenomics: New approaches to long-standing problems. <i>Molecular Ecology Resources</i> , 2018, 18, 281-295.	2.2	114
4153	Clear cell sarcomas of the kidney are characterised by <i>BCOR</i> gene abnormalities, including exon 15 internal tandem duplications and <i>BCOR</i> - <i>CCNB3</i> gene fusion. <i>Histopathology</i> , 2018, 72, 320-329.	1.6	60
4154	BLAST Using Big Data Technologies: A Survey. , 2018, , .		1
4155	Seasonality Drives Microbial Community Structure, Shaping both Eukaryotic and Prokaryotic Host-Viral Relationships in an Arctic Marine Ecosystem. <i>Viruses</i> , 2018, 10, 715.	1.5	26
4156	Tissue-specific alternative splicing of pentatricopeptide repeat (PPR) family genes in <i>Arabidopsis thaliana</i> . <i>BioScience Trends</i> , 2018, 12, 569-579.	1.1	4
4157	Splice-Aware Multiple Sequence Alignment of Protein Isoforms. , 2018, 2018, 200-210.		5
4158	Potential of <i>Oryza officinalis</i> to augment the cold tolerance genetic mechanisms of <i>Oryza sativa</i> by network complementation. <i>Scientific Reports</i> , 2018, 8, 16346.	1.6	32
4159	Potent HIV-1-Specific CD8 T Cell Responses Induced in Mice after Priming with a Multiepitopic DNA-TMEP and Boosting with the HIV Vaccine MVA-B. <i>Viruses</i> , 2018, 10, 424.	1.5	9
4160	A benchmark study of sequence alignment methods for protein clustering. <i>BMC Bioinformatics</i> , 2018, 19, 529.	1.2	26
4161	Replication-incompetent gammaretroviral and lentiviral vector-based insertional mutagenesis screens identify prostate cancer progression genes. <i>Oncotarget</i> , 2018, 9, 15451-15463.	0.8	18
4162	Inference of Sequence Homology by BLAST visualization of Influenza Genome set. , 2018, , .		0
4163	Protein database search using compressed k-mer vocabularies. , 2018, , .		0
4164	Identification of Arbuscular Mycorrhiza Fungi Responsive microRNAs and Their Regulatory Network in Maize. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3201.	1.8	29
4165	Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. <i>Cell Reports</i> , 2018, 25, 2617-2633.	2.9	74
4166	Predicting Genes in Single Genomes with AUGUSTUS. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e57.	25.8	225
4167	Whole genome sequencing of <i>Trypanosoma cruzi</i> field isolates reveals extensive genomic variability and complex aneuploidy patterns within TcII DTU. <i>BMC Genomics</i> , 2018, 19, 816.	1.2	45
4168	Wingless promotes EGFR signaling in follicle stem cells to maintain self-renewal. <i>Development (Cambridge)</i> , 2018, 145, dev168716.	1.2	26

#	ARTICLE	IF	CITATIONS
4169	Mobile elements contribute to the uniqueness of human genome with 15,000 human-specific insertions and 14ÂMbp sequence increase. <i>DNA Research</i> , 2018, 25, 521-533.	1.5	45
4170	Regulatory processes that control haploid expression of salmon sperm mRNAs. <i>BMC Research Notes</i> , 2018, 11, 639.	0.6	1
4171	Transcriptome reprogramming during severe dehydration contributes to physiological and metabolic changes in the resurrection plant <i>Haberlea rhodopensis</i> . <i>BMC Plant Biology</i> , 2018, 18, 351.	1.6	40
4172	Comparative genetic and genomic analysis of the novel fusellovirus <i>Sulfolobus</i> spindle-shaped virus 10. <i>Virus Evolution</i> , 2018, 4, vey022.	2.2	20
4173	A Method for RNA Structure Prediction Shows Evidence for Structure in lncRNAs. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 111.	1.6	16
4174	RGAAT: A Reference-based Genome Assembly and Annotation Tool for New Genomes and Upgrade of Known Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 373-381.	3.0	15
4175	Assessing the impact of exact reads on reducing the error rate of read mapping. <i>BMC Bioinformatics</i> , 2018, 19, 406.	1.2	2
4176	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	5.8	101
4177	Comparative genomics of 84 <i>Pectobacterium</i> genomes reveals the variations related to a pathogenic lifestyle. <i>BMC Genomics</i> , 2018, 19, 889.	1.2	53
4178	Full Shotgun DNA Metagenomics. <i>Learning Materials in Biosciences</i> , 2018, , 163-175.	0.2	1
4179	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , 2018, 9, 5114.	5.8	2,816
4180	The transcriptomic landscape of yaks reveals molecular pathways for high altitude adaptation. <i>Genome Biology and Evolution</i> , 2019, 11, 72-85.	1.1	41
4181	QTL Mapping Combined With Bulk Segregant Analysis Identify SNP Markers Linked to Leaf Shape Traits in <i>Pisum sativum</i> Using SLAF Sequencing. <i>Frontiers in Genetics</i> , 2018, 9, 615.	1.1	25
4182	Virus detection in high-throughput sequencing data without a reference genome of the host. <i>Infection, Genetics and Evolution</i> , 2018, 66, 180-187.	1.0	9
4183	Opaque-2 Regulates a Complex Gene Network Associated with Cell Differentiation and Storage Functions of Maize Endosperm. <i>Plant Cell</i> , 2018, 30, 2425-2446.	3.1	83
4184	Genetic mapping of anthocyanin accumulation-related genes in pepper fruits using a combination of SLAF-seq and BSA. <i>PLoS ONE</i> , 2018, 13, e0204690.	1.1	17
4185	Progress of analytical tools and techniques for human gut microbiome research. <i>Journal of Microbiology</i> , 2018, 56, 693-705.	1.3	49
4186	High-Throughput Genotyping of CRISPR/Cas Edited Cells in 96-Well Plates. <i>Methods and Protocols</i> , 2018, 1, 29.	0.9	6

#	ARTICLE	IF	CITATIONS
4187	Roquin targets mRNAs in a 3' UTR-specific manner by different modes of regulation. <i>Nature Communications</i> , 2018, 9, 3810.	5.8	40
4188	The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. <i>Genome Biology and Evolution</i> , 2018, 10, 2785-2800.	1.1	42
4189	Fine mapping and candidate gene screening of the downy mildew resistance gene RPF1 in Spinach. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2529-2541.	1.8	35
4190	Considerations for Optimization of High-Throughput Sequencing Bioinformatics Pipelines for Virus Detection. <i>Viruses</i> , 2018, 10, 528.	1.5	21
4191	High-density genetic map of <i>Populus deltoides</i> constructed by using specific length amplified fragment sequencing. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	13
4192	MetaPCN: a pipeline for construction and graphical visualization of annotated pangenome networks. <i>GigaScience</i> , 2018, 7, .	3.3	6
4193	Genomic Characterization and Probiotic Potency of <i>Bacillus</i> sp. DU-106, a Highly Effective Producer of L-Lactic Acid Isolated From Fermented Yogurt. <i>Frontiers in Microbiology</i> , 2018, 9, 2216.	1.5	34
4194	Repurposing of promoters and enhancers during mammalian evolution. <i>Nature Communications</i> , 2018, 9, 4066.	5.8	51
4195	Whole-genome comparison of endogenous retrovirus segregation across wild and domestic host species populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11012-11017.	3.3	18
4196	Genome-wide Surveillance of Transcription Errors in Eukaryotic Organisms. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	5
4197	Rapid preimplantation genetic screening using a handheld, nanopore-based DNA sequencer. <i>Fertility and Sterility</i> , 2018, 110, 910-916.e2.	0.5	18
4198	Single-step Precision Genome Editing in Yeast Using CRISPR-Cas9. <i>Bio-protocol</i> , 2018, 8, .	0.2	45
4199	Unicellular Origin of the Animal MicroRNA Machinery. <i>Current Biology</i> , 2018, 28, 3288-3295.e5.	1.8	42
4200	Whole genome shotgun sequencing revealed highly polymorphic genome regions and genes in <i>Escherichia coli</i> O157:H7 isolates collected from a single feedlot. <i>PLoS ONE</i> , 2018, 13, e0202775.	1.1	1
4201	Deciphering Genome Organization of the Polyploid <i>Brassica napus</i> . <i>Compendium of Plant Genomes</i> , 2018, , 87-97.	0.3	0
4202	Fine Mapping of Lobe Leaf Genes in Two <i>Brassica napus</i> Lines Using SLAF Sequencing. <i>Crop Science</i> , 2018, 58, 1684-1692.	0.8	1
4203	Genomic distribution of a novel <i>Pyrenophora tritici-repentis</i> ToxA insertion element. <i>PLoS ONE</i> , 2018, 13, e0206586.	1.1	16
4204	Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. <i>Nature Plants</i> , 2018, 4, 879-887.	4.7	316

#	ARTICLE	IF	CITATIONS
4205	Firefly genomes illuminate parallel origins of bioluminescence in beetles. <i>ELife</i> , 2018, 7, .	2.8	108
4206	UM-HACC-2A: MYB-NFIB fusion-positive human adenoid cystic carcinoma cell line. <i>Oral Oncology</i> , 2018, 87, 21-28.	0.8	23
4207	Structural and Comparative Analysis of the Complete Chloroplast Genome of <i>Pyrus hopeiensis</i> Wild Plants with a Tiny Population and Three Other <i>Pyrus</i> Species. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3262.	1.8	27
4208	Classifying Protein Specific Residue Structures Based on Graph Mining. <i>IEEE Access</i> , 2018, 6, 55828-55837.	2.6	3
4209	The somatic piRNA pathway controls germline transposition over generations. <i>Nucleic Acids Research</i> , 2018, 46, 9524-9536.	6.5	34
4210	Out of the Can: A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, <i>Sardina pilchardus</i> . <i>Genes</i> , 2018, 9, 485.	1.0	30
4211	A Comparative Assessment of Human and Chimpanzee iPSC-derived Cardiomyocytes with Primary Heart Tissues. <i>Scientific Reports</i> , 2018, 8, 15312.	1.6	57
4212	Non-invasive genotyping with a massively parallel sequencing panel for the detection of SNPs in HPA-axis genes. <i>Scientific Reports</i> , 2018, 8, 15944.	1.6	0
4213	Homology Search and Multiple Alignment. <i>Computational Biology</i> , 2018, , 325-360.	0.1	0
4214	Cis-regulated alternative splicing divergence and its potential contribution to environmental responses in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 97, 555-570.	2.8	33
4215	Phenotypic characterization and whole genome analysis of extended-spectrum beta-lactamase-producing bacteria isolated from dogs in Germany. <i>PLoS ONE</i> , 2018, 13, e0206252.	1.1	27
4216	Xenotropic Mouse Gammaretroviruses Isolated from Pre-Leukemic Tissues Include a Recombinant. <i>Viruses</i> , 2018, 10, 418.	1.5	1
4217	Evolutionary conservation of Y Chromosome ampliconic gene families despite extensive structural variation. <i>Genome Research</i> , 2018, 28, 1841-1851.	2.4	33
4218	High-resolution chromosome painting with repetitive and single-copy oligonucleotides in <i>Arachis</i> species identifies structural rearrangements and genome differentiation. <i>BMC Plant Biology</i> , 2018, 18, 240.	1.6	10
4219	Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy and Tools. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	14
4220	A novel panel of short mononucleotide repeats linked to informative polymorphisms enabling effective high volume low cost discrimination between mismatch repair deficient and proficient tumours. <i>PLoS ONE</i> , 2018, 13, e0203052.	1.1	14
4221	Pairs of Adjacent Conserved Noncoding Elements Separated by Conserved Genomic Distances Act as Cis-Regulatory Units. <i>Genome Biology and Evolution</i> , 2018, 10, 2535-2550.	1.1	1
4222	Development of Species-Specific InDel Markers in Citrus. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 653-662.	1.0	9

#	ARTICLE	IF	CITATIONS
4223	Genome Annotation of a Model Diatom <i>Phaeodactylum tricornutum</i> Using an Integrated Proteogenomic Pipeline. <i>Molecular Plant</i> , 2018, 11, 1292-1307.	3.9	44
4224	Factors Influencing Gene Family Size Variation Among Related Species in a Plant Family, Solanaceae. <i>Genome Biology and Evolution</i> , 2018, 10, 2596-2613.	1.1	54
4225	Comparison of Healthy and Dandruff Scalp Microbiome Reveals the Role of Commensals in Scalp Health. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 346.	1.8	63
4226	Rare variants in the splicing regulatory elements of EXOC3L4 are associated with brain glucose metabolism in Alzheimer's disease. <i>BMC Medical Genomics</i> , 2018, 11, 76.	0.7	12
4227	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018, 562, 373-379.	13.7	236
4228	Improving nanopore read accuracy with the R2C2 method enables the sequencing of highly multiplexed full-length single-cell cDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9726-9731.	3.3	180
4229	Comparative genomics and transcriptomics of <i>Chrysolophus</i> provide insights into the evolution of complex plumage colouration. <i>GigaScience</i> , 2018, 7, .	3.3	14
4230	From Short Reads to Chromosome-Scale Genome Assemblies. <i>Methods in Molecular Biology</i> , 2018, 1848, 151-197.	0.4	7
4231	Repeated translocation of a gene cassette drives sex-chromosome turnover in strawberries. <i>PLoS Biology</i> , 2018, 16, e2006062.	2.6	85
4232	Metagenomic Approaches Highlight the Organization and Dynamics of Plankton at the Species Level. , 2018, , 239-273.		1
4233	Complete sequence of kenaf ( <i>Hibiscus cannabinus</i> ) mitochondrial genome and comparative analysis with the mitochondrial genomes of other plants. <i>Scientific Reports</i> , 2018, 8, 12714.	1.6	43
4234	Draft genome of <i>Dugesia japonica</i> provides insights into conserved regulatory elements of the brain restriction gene <i>nou-darake</i> in planarians. <i>Zoological Letters</i> , 2018, 4, 24.	0.7	38
4235	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	6.5	476
4236	Chromosome Y-encoded antigens associate with acute graft-versus-host disease in sex-mismatched stem cell transplant. <i>Blood Advances</i> , 2018, 2, 2419-2429.	2.5	11
4237	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018, 9, 2054.	5.8	68
4238	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	13.7	433
4239	The Eukaryotic Proteome Is Shaped by E3 Ubiquitin Ligases Targeting C-Terminal Degrons. <i>Cell</i> , 2018, 173, 1622-1635.e14.	13.5	198
4240	Association of Polygenic Risk Scores for Multiple Cancers in a Phenome-wide Study: Results from The Michigan Genomics Initiative. <i>American Journal of Human Genetics</i> , 2018, 102, 1048-1061.	2.6	147

#	ARTICLE	IF	CITATIONS
4241	Using WormBase: A Genome Biology Resource for <i>Caenorhabditis elegans</i> and Related Nematodes. <i>Methods in Molecular Biology</i> , 2018, 1757, 399-470.	0.4	28
4242	Methylation guide RNA evolution in archaea: structure, function and genomic organization of 110 C/D box sRNA families across six <i>Pyrobaculum</i> species. <i>Nucleic Acids Research</i> , 2018, 46, 5678-5691.	6.5	7
4243	Bidirectional regulation of adenosine-to-inosine (A-to-I) RNA editing by DEAH box helicase 9 (DHX9) in cancer. <i>Nucleic Acids Research</i> , 2018, 46, 7953-7969.	6.5	41
4244	SMARTIV: combined sequence and structure de-novo motif discovery for in-vivo RNA binding data. <i>Nucleic Acids Research</i> , 2018, 46, W221-W228.	6.5	7
4245	Description of <i>Mediterraneibacter massiliensis</i> , gen. nov., sp. nov., a new genus isolated from the gut microbiota of an obese patient and reclassification of <i>Ruminococcus faecis</i> , <i>Ruminococcus lactaris</i> , <i>Ruminococcus torques</i> , <i>Ruminococcus gnavus</i> and <i>Clostridium glycyrrhizinilyticum</i> as <i>Mediterraneibacter faecis</i> comb. nov., <i>Mediterraneibacter lactaris</i> comb. nov., <i>Mediterraneibacter torques</i> comb. nov., <i>Mediterraneibacter gnavus</i> comb. nov. and <i>Mediterraneibacter glycyrrhizinilyticus</i> comb. nov.. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2107-2128.	0.7	87
4246	The Ensembl Genome Browser: Strategies for Accessing Eukaryotic Genome Data. <i>Methods in Molecular Biology</i> , 2018, 1757, 115-139.	0.4	13
4247	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, .	3.3	38
4248	Metagenomics reveal triclosan-induced changes in the antibiotic resistome of anaerobic digesters. <i>Environmental Pollution</i> , 2018, 241, 1182-1190.	3.7	28
4249	De Novo Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. <i>Neuron</i> , 2018, 99, 302-314.e4.	3.8	112
4250	Efficient and precise editing of endogenous transcripts with SNAP-tagged ADARs. <i>Nature Methods</i> , 2018, 15, 535-538.	9.0	113
4251	Association mapping from sequencing reads using k-mers. <i>ELife</i> , 2018, 7, .	2.8	88
4252	Comparative genomics of bdelloid rotifers: Insights from desiccating and nondesiccating species. <i>PLoS Biology</i> , 2018, 16, e2004830.	2.6	78
4254	Molecular Cytogenetics Guides Massively Parallel Sequencing of a Radiation-Induced Chromosome Translocation in Human Cells. <i>Radiation Research</i> , 2018, 190, 88.	0.7	11
4255	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, .	2.8	149
4256	The genetic architecture of genome-wide recombination rate variation in allopolyploid wheat revealed by nested association mapping. <i>Plant Journal</i> , 2018, 95, 1039-1054.	2.8	97
4257	Efficacy and safety of a clinically relevant foamy vector design in human hematopoietic repopulating cells. <i>Journal of Gene Medicine</i> , 2018, 20, e3028.	1.4	2
4258	High-quality assembly of the reference genome for scarlet sage, <i>Salvia splendens</i> , an economically important ornamental plant. <i>GigaScience</i> , 2018, 7, .	3.3	49
4259	Resolving the rapid plant radiation of early diverging lineages in the tropical Zingiberales: Pushing the limits of genomic data. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 55-68.	1.2	53

#	ARTICLE	IF	CITATIONS
4260	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	9.4	335
4261	Development of Target Sequence Capture and Estimation of Genomic Relatedness in a Mixed Oak Stand. <i>Frontiers in Plant Science</i> , 2018, 9, 996.	1.7	18
4262	Expanding the Mutation Spectrum in ABCA4: Sixty Novel Disease Causing Variants and Their Associated Phenotype in a Large French Stargardt Cohort. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2196.	1.8	22
4263	No Evidence for Recent Selection at FOXP2 among Diverse Human Populations. <i>Cell</i> , 2018, 174, 1424-1435.e15.	13.5	99
4264	Naked mole-rat transcriptome signatures of socially suppressed sexual maturation and links of reproduction to aging. <i>BMC Biology</i> , 2018, 16, 77.	1.7	26
4265	Blazing Signature Filter: a library for fast pairwise similarity comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 221.	1.2	6
4266	The genome of <i>Rhizophagus clarus</i> HR1 reveals a common genetic basis for auxotrophy among arbuscular mycorrhizal fungi. <i>BMC Genomics</i> , 2018, 19, 465.	1.2	91
4267	Discovery of Novel Genes and Other Lineage-Specific Features Through Comparative Genomics. , 2018, , 225-241.		2
4268	Curation of microarray oligonucleotides and corresponding ESTs/cDNAs used for gene expression analysis in zebra finches. <i>BMC Research Notes</i> , 2018, 11, 309.	0.6	4
4269	Genome Sequencing and Analysis of the Peanut B-Genome Progenitor ( <i>Arachis ipaensis</i> ). <i>Frontiers in Plant Science</i> , 2018, 9, 604.	1.7	38
4270	The habu genome reveals accelerated evolution of venom protein genes. <i>Scientific Reports</i> , 2018, 8, 11300.	1.6	58
4271	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. <i>Forensic Science International: Genetics</i> , 2018, 36, 213-224.	1.6	35
4272	Comparative transcriptome analysis of the invasive weed <i>Mikania micrantha</i> with its native congeners provides insights into genetic basis underlying successful invasion. <i>BMC Genomics</i> , 2018, 19, 392.	1.2	19
4273	Coinfections identified from metagenomic analysis of cervical lymph nodes from tularemia patients. <i>BMC Infectious Diseases</i> , 2018, 18, 319.	1.3	8
4274	Combining RNA-seq data and homology-based gene prediction for plants, animals and fungi. <i>BMC Bioinformatics</i> , 2018, 19, 189.	1.2	192
4275	Comparative Genomics of <i>Escherichia coli</i> Sequence Type 219 Clones From the Same Patient: Evolution of the IncI1 blaCMY-Carrying Plasmid in Vivo. <i>Frontiers in Microbiology</i> , 2018, 9, 1518.	1.5	12
4276	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. <i>Nature Communications</i> , 2018, 9, 2905.	5.8	56
4277	Identification of SNPs associated with residual feed intake from the muscle of <i>Litopenaeus vannamei</i> using bulk segregant RNA-seq. <i>Aquaculture</i> , 2018, 497, 56-63.	1.7	9

#	ARTICLE	IF	CITATIONS
4278	Transcriptional profiling of HERV-K(HML-2) in amyotrophic lateral sclerosis and potential implications for expression of HML-2 proteins. <i>Molecular Neurodegeneration</i> , 2018, 13, 39.	4.4	47
4279	SNP hot-spots in the clam parasite QPX. <i>BMC Genomics</i> , 2018, 19, 486.	1.2	2
4280	Metatranscriptome Sequencing Reveals Insights into the Gene Expression and Functional Potential of Rumen Wall Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 43.	1.5	54
4281	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680.	1.5	36
4282	Genomic Variations in Probiotic <i>Lactobacillus plantarum</i> P-8 in the Human and Rat Gut. <i>Frontiers in Microbiology</i> , 2018, 9, 893.	1.5	21
4283	Hydrogen-Fueled Microbial Pathways in Biogas Upgrading Systems Revealed by Genome-Centric Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1079.	1.5	66
4284	Relationship Between Sequence Homology, Genome Architecture, and Meiotic Behavior of the Sex Chromosomes in North American Voles. <i>Genetics</i> , 2018, 210, 83-97.	1.2	4
4285	Size and Content of the Sex-Determining Region of the Y Chromosome in Dioecious <i>Mercurialis annua</i> , a Plant with Homomorphic Sex Chromosomes. <i>Genes</i> , 2018, 9, 277.	1.0	23
4286	Investigating the Molecular Genetic Basis of Cytoplasmic Sex Determination Caused by <i>Wolbachia</i> Endosymbionts in Terrestrial Isopods. <i>Genes</i> , 2018, 9, 290.	1.0	17
4287	Transcriptional analyses provide new insight into the late-stage immune response of a diseased Caribbean coral. <i>Royal Society Open Science</i> , 2018, 5, 172062.	1.1	30
4288	REXTAL: Regional Extension of Assemblies Using Linked-Reads. <i>Lecture Notes in Computer Science</i> , 2018, 10847, 63-78.	1.0	2
4289	Identification of candidate genes for gelatinization temperature, gel consistency and pericarp color by GWAS in rice based on SLAF-sequencing. <i>PLoS ONE</i> , 2018, 13, e0196690.	1.1	25
4290	Long Non-Coding RNAs Responsive to Salt and Boron Stress in the Hyper-Arid <i>Lluteo</i> Maize from Atacama Desert. <i>Genes</i> , 2018, 9, 170.	1.0	53
4291	miR-196b target screen reveals mechanisms maintaining leukemia stemness with therapeutic potential. <i>Journal of Experimental Medicine</i> , 2018, 215, 2115-2136.	4.2	20
4292	Epigenome: The Guide to Genomic Expression. , 2018, , 89-103.		0
4293	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	13.5	420
4294	Genomic analysis of MHC-based mate choice in the monogamous California mouse. <i>Behavioral Ecology</i> , 2018, 29, 1167-1180.	1.0	9
4295	Analysis of the canid Y-chromosome phylogeny using short-read sequencing data reveals the presence of distinct haplogroups among Neolithic European dogs. <i>BMC Genomics</i> , 2018, 19, 350.	1.2	24

#	ARTICLE	IF	CITATIONS
4296	P_RNA_scaffolder: a fast and accurate genome scaffolder using paired-end RNA-sequencing reads. BMC Genomics, 2018, 19, 175.	1.2	49
4297	Bioinformatics analyses and in vitro evidence for five and six stacked G-quadruplex forming sequences. Biochimie, 2018, 150, 70-75.	1.3	17
4298	Cigarette smoke and chewing tobacco alter expression of different sets of miRNAs in oral keratinocytes. Scientific Reports, 2018, 8, 7040.	1.6	34
4299	Population size may shape the accumulation of functional mutations following domestication. BMC Evolutionary Biology, 2018, 18, 4.	3.2	15
4300	HERV-W group evolutionary history in non-human primates: characterization of ERV-W orthologs in Catarrhini and related ERV groups in Platyrrhini. BMC Evolutionary Biology, 2018, 18, 6.	3.2	26
4301	Reconstruction of a replication-competent ancestral murine endogenous retrovirus-L. Retrovirology, 2018, 15, 34.	0.9	11
4302	seq-seq-pan: building a computational pan-genome data structure on whole genome alignment. BMC Genomics, 2018, 19, 47.	1.2	25
4303	CAS-viewer: web-based tool for splicing-guided integrative analysis of multi-omics cancer data. BMC Medical Genomics, 2018, 11, 25.	0.7	17
4304	Recently integrated Alu insertions in the squirrel monkey (Saimiri) lineage and application for population analyses. Mobile DNA, 2018, 9, 9.	1.3	6
4305	Sequencing Plant Genomes. Progress in Botany Fortschritte Der Botanik, 2018, , 109-193.	0.1	4
4306	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
4307	Improved strategy for the curation and classification of kinases, with broad applicability to other eukaryotic protein groups. Scientific Reports, 2018, 8, 6808.	1.6	10
4309	Unsupervised, Statistically Based Systems Biology Approach for Unraveling the Genetics of Complex Traits: A Demonstration with Ethanol Metabolism. Alcoholism: Clinical and Experimental Research, 2018, 42, 1177-1191.	1.4	7
4310	NvERTx: A gene expression database to compare embryogenesis and regeneration in the sea anemone <i>Nematostella vectensis</i> . Development (Cambridge), 2018, 145, .	1.2	47
4311	Genome sequence of the progenitor of wheat A subgenome Triticum urartu. Nature, 2018, 557, 424-428.	13.7	354
4312	Applications and efficiencies of the first cat 63K DNA array. Scientific Reports, 2018, 8, 7024.	1.6	38
4313	Contrasting duplication patterns reflect functional diversities of ubiquitin and ubiquitin-like protein modifiers in plants. Plant Journal, 2018, 95, 296-311.	2.8	11
4314	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. BMC Genomics, 2018, 19, 588.	1.2	64

#	ARTICLE	IF	CITATIONS
4315	Genome Plasticity in Cultured <i>Leishmania donovani</i> : Comparison of Early and Late Passages. <i>Frontiers in Microbiology</i> , 2018, 9, 1279.	1.5	43
4316	A Review of Tools to Automatically Infer Chromosomal Positions From dbSNP and HGVS Genetic Variants. , 2018, , 133-156.		1
4317	BPSL1626: Reverse and Structural Vaccinology Reveal a Novel Candidate for Vaccine Design Against <i>Burkholderia pseudomallei</i> . <i>Antibodies</i> , 2018, 7, 26.	1.2	11
4318	Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. <i>Forensic Science International: Genetics</i> , 2018, 37, 162-171.	1.6	13
4319	QTL Mapping and Marker Identification for Sex-Determining: Indicating XY Sex Determination System in the Swimming Crab ( <i>Portunus trituberculatus</i> ). <i>Frontiers in Genetics</i> , 2018, 9, 337.	1.1	31
4320	Genetical genomics of growth in a chicken model. <i>BMC Genomics</i> , 2018, 19, 72.	1.2	31
4321	The chromosome-level genome assemblies of two rattans ( <i>Calamus simplicifolius</i> and <i>Daemonorops</i> ) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	3.3	28
4322	The genome sequence of the commercially cultivated mushroom <i>Agrocybe aegerita</i> reveals a conserved repertoire of fruiting-related genes and a versatile suite of biopolymer-degrading enzymes. <i>BMC Genomics</i> , 2018, 19, 48.	1.2	39
4323	The landscape of the A-to-I RNA editome from 462 human genomes. <i>Scientific Reports</i> , 2018, 8, 12069.	1.6	15
4324	Draft genome of <i>Glyptosternon maculatum</i> , an endemic fish from Tibet Plateau. <i>GigaScience</i> , 2018, 7, .	3.3	18
4325	The Genetics of a Behavioral Speciation Phenotype in an Island System. <i>Genes</i> , 2018, 9, 346.	1.0	16
4326	phylotaR: An Automated Pipeline for Retrieving Orthologous DNA Sequences from GenBank in R. <i>Life</i> , 2018, 8, 20.	1.1	26
4327	Whole body transcriptomes and new insights into the biology of the tick <i>Ixodes ricinus</i> . <i>Parasites and Vectors</i> , 2018, 11, 364.	1.0	27
4328	The small RNA complement of adult <i>Schistosoma haematobium</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006535.	1.3	17
4329	Ancient convergent losses of <i>Paraoxonase 1</i> yield potential risks for modern marine mammals. <i>Science</i> , 2018, 361, 591-594.	6.0	79
4330	Developmental barcoding of whole mouse via homing CRISPR. <i>Science</i> , 2018, 361, .	6.0	263
4331	Evolutionary stability of topologically associating domains is associated with conserved gene regulation. <i>BMC Biology</i> , 2018, 16, 87.	1.7	119
4332	Characterization of <i>Haemophilus parasuis</i> Serovar 2 CL120103, a Moderately Virulent Strain in China. <i>Open Life Sciences</i> , 2018, 13, 217-226.	0.6	0

#	ARTICLE	IF	CITATIONS
4333	Characterization of the $\beta$ -defensin genes in giant panda. <i>Scientific Reports</i> , 2018, 8, 12308.	1.6	7
4334	Trichoplax genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. <i>Scientific Reports</i> , 2018, 8, 11168.	1.6	36
4335	Genome-wide mapping of large deletions and their population-genetic properties in dairy cattle. <i>DNA Research</i> , 2018, 25, 49-59.	1.5	18
4337	Identification and expression analysis of long noncoding RNAs in embryogenesis and larval metamorphosis of <i>Ciona savignyi</i> . <i>Marine Genomics</i> , 2018, 40, 64-72.	0.4	3
4338	Population resequencing reveals candidate genes associated with salinity adaptation of the Pacific oyster <i>Crassostrea gigas</i> . <i>Scientific Reports</i> , 2018, 8, 8683.	1.6	13
4339	A High Quality Genome for <i>Mus spicilegus</i> , a Close Relative of House Mice with Unique Social and Ecological Adaptations. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2145-2152.	0.8	8
4340	Genome-wide identification, functional prediction and expression profiling of long non-coding RNAs in <i>Camelina sativa</i> . <i>Plant Growth Regulation</i> , 2018, 86, 49-63.	1.8	10
4341	Computational and Statistical Considerations in the Analysis of Metagenomic Data. , 2018, , 81-102.		10
4343	Massive NGS data analysis reveals hundreds of potential novel gene fusions in human cell lines. <i>GigaScience</i> , 2018, 7, .	3.3	6
4344	Comparing fixed sampling with minimizer sampling when using k-mer indexes to find maximal exact matches. <i>PLoS ONE</i> , 2018, 13, e0189960.	1.1	10
4345	Preferential use of unmutated immunoglobulin heavy variable region genes in Boxer dogs with chronic lymphocytic leukemia. <i>PLoS ONE</i> , 2018, 13, e0191205.	1.1	6
4346	Fungal Genome Annotation. <i>Methods in Molecular Biology</i> , 2018, 1775, 171-184.	0.4	14
4347	The Genomic Architecture of a Rapid Island Radiation: Recombination Rate Variation, Chromosome Structure, and Genome Assembly of the Hawaiian Cricket <i>Laupala</i> . <i>Genetics</i> , 2018, 209, 1329-1344.	1.2	32
4348	A survey of microRNA single nucleotide polymorphisms identifies novel breast cancer susceptibility loci in a case-control, population-based study of African-American women. <i>Breast Cancer Research</i> , 2018, 20, 45.	2.2	15
4349	A high-quality genome sequence of <i>Rosa chinensis</i> to elucidate ornamental traits. <i>Nature Plants</i> , 2018, 4, 473-484.	4.7	224
4350	Detecting de Novo Homoeologous Recombination Events in Cultivated <i>Brassica napus</i> Using a Genome-Wide SNP Array. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2673-2683.	0.8	33
4351	Long-lived rodents reveal signatures of positive selection in genes associated with lifespan. <i>PLoS Genetics</i> , 2018, 14, e1007272.	1.5	39
4352	Genome-wide identification and analysis of A-to-I RNA editing events in bovine by transcriptome sequencing. <i>PLoS ONE</i> , 2018, 13, e0193316.	1.1	27

#	ARTICLE	IF	CITATIONS
4353	Urinary cell-free DNA is a versatile analyte for monitoring infections of the urinary tract. <i>Nature Communications</i> , 2018, 9, 2412.	5.8	121
4354	<i>In silico</i> read normalization using set multi-cover optimization. <i>Bioinformatics</i> , 2018, 34, 3273-3280.	1.8	8
4355	Long-read sequencing and de novo genome assembly of <i>Ammopiptanthus nanus</i> , a desert shrub. <i>GigaScience</i> , 2018, 7, .	3.3	22
4356	Cloning and functional analysis of five TERMINAL FLOWER 1/CENTRORADIALIS-like genes from <i>Hevea brasiliensis</i> . <i>Physiologia Plantarum</i> , 2019, 166, 612-627.	2.6	10
4357	Genome sequence of <i>Jatropha curcas</i> L., a non-edible biodiesel plant, provides a resource to improve seed-related traits. <i>Plant Biotechnology Journal</i> , 2019, 17, 517-530.	4.1	56
4358	Genome Alignment. , 2019, , 268-283.		0
4359	Bioinformatics Approaches for Studying Alternative Splicing. , 2019, , 221-234.		6
4360	Sequence Analysis. , 2019, , 292-322.		8
4361	Genome Informatics. , 2019, , 178-194.		0
4362	Novel gene fusions in secretory carcinoma of the salivary glands: enlarging the ETV6 family. <i>Human Pathology</i> , 2019, 83, 50-58.	1.1	70
4363	Transcriptomic Analysis With the Progress of Symbiosis in "Crack-Entry" Legume <i>Arachis hypogaea</i> Highlights Its Contrast With "Infection Thread" Adapted Legumes. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 271-285.	1.4	59
4364	Prediction of Coding and Non-Coding RNA. , 2019, , 230-240.		4
4365	Vaccine Target Discovery. , 2019, , 241-251.		10
4366	Bioinformatic analysis of the complete genome sequence of <i>Pectobacterium carotovorum</i> subsp. <i>brasiliense</i> BZA12 and candidate effector screening. <i>Journal of Plant Pathology</i> , 2019, 101, 39-49.	0.6	8
4367	The complete chloroplast genome sequence of <i>Aesculus Chinensis</i> Bunge, a major street tree. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1686-1687.	0.2	1
4368	Uncovering missed indels by leveraging unmapped reads. <i>Scientific Reports</i> , 2019, 9, 11093.	1.6	8
4369	Transposable elements contribute to dynamic genome content in maize. <i>Plant Journal</i> , 2019, 100, 1052-1065.	2.8	76
4370	Development of molecular markers associated with resistance to <i>Meloidogyne incognita</i> by performing quantitative trait locus analysis and genome-wide association study in sweetpotato. <i>DNA Research</i> , 2019, 26, 399-409.	1.5	17

#	ARTICLE	IF	CITATIONS
4371	BART-Seq: cost-effective massively parallelized targeted sequencing for genomics, transcriptomics, and single-cell analysis. <i>Genome Biology</i> , 2019, 20, 155.	3.8	19
4372	Dicyemid Mesozoans: A Unique Parasitic Lifestyle and a Reduced Genome. <i>Genome Biology and Evolution</i> , 2019, 11, 2232-2243.	1.1	15
4373	Genetic Diversity, Virulence, Race Profiling, and Comparative Genomic Analysis of the <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> Strains Infecting Cabbages in China. <i>Frontiers in Microbiology</i> , 2019, 10, 1373.	1.5	16
4374	Performance of gene expression analyses using <i>de novo</i> assembled transcripts in polyploid species. <i>Bioinformatics</i> , 2019, 35, 4314-4320.	1.8	10
4375	Draft Genome of the Rice Coral <i>Montipora capitata</i> Obtained from Linked-Read Sequencing. <i>Genome Biology and Evolution</i> , 2019, 11, 2045-2054.	1.1	30
4376	Weighted Gene Co-expression Network Analysis (WGCNA) Reveals the Hub Role of Protein Ubiquitination in the Acquisition of Desiccation Tolerance in <i>Boea hygrometrica</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 2707-2719.	1.5	26
4377	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. <i>Scientific Reports</i> , 2019, 9, 11769.	1.6	179
4378	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
4379	The complete chloroplast genome sequences of <i>Pistacia chinensis</i> Bunge, a potential bioenergy tree. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1774-1775.	0.2	4
4380	Endogenous Retrovirus-Derived Long Noncoding RNA Enhances Innate Immune Responses via Derepressing RELA Expression. <i>MBio</i> , 2019, 10, .	1.8	39
4381	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. <i>Nature Biotechnology</i> , 2019, 37, 907-915.	9.4	6,567
4382	Metagenomics analysis of cocoa bean fermentation microbiome identifying species diversity and putative functional capabilities. <i>Heliyon</i> , 2019, 5, e02170.	1.4	56
4383	Exploring the molecular basis of neuronal excitability in a vocal learner. <i>BMC Genomics</i> , 2019, 20, 629.	1.2	12
4384	Conserved Pseudoknots in lncRNA MEG3 Are Essential for Stimulation of the p53 Pathway. <i>Molecular Cell</i> , 2019, 75, 982-995.e9.	4.5	138
4385	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
4386	The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data. <i>Scientific Data</i> , 2019, 6, 122.	2.4	29
4387	Whole-Genome Alignment. <i>Methods in Molecular Biology</i> , 2019, 1910, 121-147.	0.4	5
4388	A high-quality genome of <i>Eragrostis curvula</i> grass provides insights into Poaceae evolution and supports new strategies to enhance forage quality. <i>Scientific Reports</i> , 2019, 9, 10250.	1.6	27

#	ARTICLE	IF	CITATIONS
4389	Centromere Satellite Repeats Have Undergone Rapid Changes in Polyploid Wheat Subgenomes. <i>Plant Cell</i> , 2019, 31, 2035-2051.	3.1	56
4390	Instability of the Pseudoautosomal Boundary in House Mice. <i>Genetics</i> , 2019, 212, 469-487.	1.2	15
4391	Arctic charr brain transcriptome strongly affected by summer seasonal growth but only subtly by feed deprivation. <i>BMC Genomics</i> , 2019, 20, 529.	1.2	6
4392	Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. <i>BMC Medical Genomics</i> , 2019, 12, 104.	0.7	10
4393	Closing target trimming and CTTdocker programs for discovering hidden superfamily loci in genomes. <i>PLoS ONE</i> , 2019, 14, e0209468.	1.1	7
4394	Stress, novel sex genes, and epigenetic reprogramming orchestrate socially controlled sex change. <i>Science Advances</i> , 2019, 5, eaaw7006.	4.7	99
4395	MRE11A Isoform Expression Associated with Outcome Following Radiotherapy in Muscle-Invasive Bladder Cancer does not Alter Cell Survival and DNA Double-Strand Break Repair Following Ionising Radiation. <i>Bladder Cancer</i> , 2019, 5, 147-157.	0.2	2
4396	Ecological speciation in sympatric palms: 3. Genetic map reveals genomic islands underlying species divergence in <i>Howea</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1986-1995.	1.1	13
4397	<i>Musa balbisiana</i> genome reveals subgenome evolution and functional divergence. <i>Nature Plants</i> , 2019, 5, 810-821.	4.7	132
4398	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
4399	De novo genome assembly of the endangered <i>Acer yangbiense</i> , a plant species with extremely small populations endemic to Yunnan Province, China. <i>GigaScience</i> , 2019, 8, .	3.3	42
4400	Transposable Elements: Classification, Identification, and Their Use As a Tool For Comparative Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 177-207.	0.4	74
4401	Curing cytoplasmic male sterility via TALEN-mediated mitochondrial genome editing. <i>Nature Plants</i> , 2019, 5, 722-730.	4.7	126
4402	The Methodology Behind Network Thinking: Graphs to Analyze Microbial Complexity and Evolution. <i>Methods in Molecular Biology</i> , 2019, 1910, 271-308.	0.4	4
4403	The genome assembly of asparagus bean, <i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i> . <i>Scientific Data</i> , 2019, 6, 124.	2.4	18
4404	Genome and transcriptome characterization of the glycoengineered <i>Nicotiana benthamiana</i> line $\hat{\Gamma}$ XT/FT. <i>BMC Genomics</i> , 2019, 20, 594.	1.2	20
4405	Noncoding CGG repeat expansions in neuronal intranuclear inclusion disease, oculopharyngodistal myopathy and an overlapping disease. <i>Nature Genetics</i> , 2019, 51, 1222-1232.	9.4	265
4406	Impact of sequencing depth and technology on de novo RNA-Seq assembly. <i>BMC Genomics</i> , 2019, 20, 604.	1.2	40

#	ARTICLE	IF	CITATIONS
4407	Distribution of endogenous gammaretroviruses and variants of the Fv1 restriction gene in individual mouse strains and strain subgroups. <i>PLoS ONE</i> , 2019, 14, e0219576.	1.1	4
4408	Large-scale potential <i>scp</i> RNA editing profiling in different adult chicken tissues. <i>Animal Genetics</i> , 2019, 50, 460-474.	0.6	12
4409	The genome of <i>Peromyscus leucopus</i> , natural host for Lyme disease and other emerging infections. <i>Science Advances</i> , 2019, 5, eaaw6441.	4.7	41
4410	The genome assembly and annotation of yellowhorn ( <i>Xanthoceras sorbifolium</i> Bunge). <i>GigaScience</i> , 2019, 8, .	3.3	37
4411	HLA alleles and haplotypes observed in 263 US families. <i>Human Immunology</i> , 2019, 80, 644-660.	1.2	18
4412	Major natural genetic variation contributes to waterlogging tolerance in maize seedlings. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	6
4413	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2019, 10, 2789.	5.8	14
4414	Improved detection of influenza A virus from blue-winged teals by sequencing directly from swab material. <i>Ecology and Evolution</i> , 2019, 9, 6534-6546.	0.8	18
4415	Box, stalked, and upside-down? Draft genomes from diverse jellyfish (Cnidaria, Acraspeda) lineages: <i>Alatina alata</i> (Cubozoa), <i>Calvadosia cruxmelitensis</i> (Staurozoa), and <i>Cassiopea xamachana</i> (Scyphozoa). <i>GigaScience</i> , 2019, 8, .	3.3	53
4416	Prevalence of viral photosynthesis genes along a freshwater to saltwater transect in Southeast USA. <i>Environmental Microbiology Reports</i> , 2019, 11, 672-689.	1.0	24
4417	Extensive intraspecific gene order and gene structural variations in upland cotton cultivars. <i>Nature Communications</i> , 2019, 10, 2989.	5.8	144
4418	Chromosome-level genome assembly of golden pompano ( <i>Trachinotus ovatus</i> ) in the family Carangidae. <i>Scientific Data</i> , 2019, 6, 216.	2.4	42
4419	Exploring the basis of 2-propenyl and 3-butenyl glucosinolate synthesis by QTL mapping and RNA-sequencing in <i>Brassica juncea</i> . <i>PLoS ONE</i> , 2019, 14, e0220597.	1.1	9
4420	A new species in the major malaria vector complex sheds light on reticulated species evolution. <i>Scientific Reports</i> , 2019, 9, 14753.	1.6	56
4421	Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019, 10, 4680.	5.8	75
4422	Profiling the Functional Diversity of Termite Mound Soil Bacteria as Revealed by Shotgun Sequencing. <i>Genes</i> , 2019, 10, 637.	1.0	24
4423	The Structure, Evolution, and Gene Expression Within the Caprine Leukocyte Receptor Complex. <i>Frontiers in Immunology</i> , 2019, 10, 2302.	2.2	17
4424	Analysis of Tissue-specific RNA Editing Events of Genes Involved in RNA Editing in <i>Arabidopsis thaliana</i> . <i>Journal of Plant Biology</i> , 2019, 62, 351-358.	0.9	12

#	ARTICLE	IF	CITATIONS
4425	Mutation analysis of LRP10 in Japanese patients with familial Parkinson's disease, progressive supranuclear palsy, and frontotemporal dementia. <i>Neurobiology of Aging</i> , 2019, 84, 235.e11-235.e16.	1.5	10
4426	Genome Assembly of the A-Group <i>Wolbachia</i> in <i>Nasonia oneida</i> Using Linked-Reads Technology. <i>Genome Biology and Evolution</i> , 2019, 11, 3008-3013.	1.1	10
4427	Alternative mRNA Splicing in Three Venom Families Underlying a Possible Production of Divergent Venom Proteins of the Habu Snake, <i>Protobothrops flavoviridis</i> . <i>Toxins</i> , 2019, 11, 581.	1.5	22
4428	Genome-Wide Identification and Transcriptomic Analysis of MicroRNAs Across Various <i>Amphioxus</i> Organs Using Deep Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 877.	1.1	1
4429	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	18
4430	pblat: a multithread blat algorithm speeding up aligning sequences to genomes. <i>BMC Bioinformatics</i> , 2019, 20, 28.	1.2	65
4431	Structural variation of the complete chloroplast genome and plastid phylogenomics of the genus <i>Asteropyrum</i> (Ranunculaceae). <i>Scientific Reports</i> , 2019, 9, 15285.	1.6	38
4432	BBcancer: an expression atlas of blood-based biomarkers in the early diagnosis of cancers. <i>Nucleic Acids Research</i> , 2020, 48, D789-D796.	6.5	29
4433	In-silico prediction of novel genes responsive to drought and salinity stress tolerance in bread wheat ( <i>Triticum aestivum</i> ). <i>PLoS ONE</i> , 2019, 14, e0223962.	1.1	7
4434	From cytogenetics to cytogenomics: whole-genome sequencing as a first-line test comprehensively captures the diverse spectrum of disease-causing genetic variation underlying intellectual disability. <i>Genome Medicine</i> , 2019, 11, 68.	3.6	88
4435	Multi-Tissue Transcriptomes Yield Information on High-Altitude Adaptation and Sex-Determination in <i>Scutigera cf. sikimensis</i> . <i>Genes</i> , 2019, 10, 873.	1.0	1
4436	Genetic Variations of Ultraconserved Elements in the Human Genome. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 549-559.	1.0	13
4437	UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761.	6.5	138
4438	Exploration of intermediate-sized INDELs by next-generation multigene panel testing in Han Chinese patients with breast cancer. <i>Human Genome Variation</i> , 2019, 6, 51.	0.4	3
4439	A New Chloroplast DNA Extraction Protocol Significantly Improves the Chloroplast Genome Sequence Quality of Foxtail Millet ( <i>Setaria italica</i> (L.) P. Beauv.). <i>Scientific Reports</i> , 2019, 9, 16227.	1.6	4
4440	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019, 179, 1057-1067.e14.	13.5	320
4441	Adaptive Radiation Genomics of Two Ecologically Divergent Hawaiian Honeycreepers: The <i>ÂkaiapÂu</i> and the <i>Hawai'i</i> <i>Âamakihi</i> . <i>Journal of Heredity</i> , 2020, 111, 21-32.	1.0	6
4442	MitoMut. , 2019, , .		0

#	ARTICLE	IF	CITATIONS
4443	Optimized sequencing depth and de novo assembler for deeply reconstructing the transcriptome of the tea plant, an economically important plant species. <i>BMC Bioinformatics</i> , 2019, 20, 553.	1.2	7
4444	SwiftOrtho: A fast, memory-efficient, multiple genome orthology classifier. <i>GigaScience</i> , 2019, 8, .	3.3	26
4445	Identification of Single Nucleotide Polymorphism in Red Clover ( <i>Trifolium pratense</i> L.) Using Targeted Genomic Amplicon Sequencing and RNA-seq. <i>Frontiers in Plant Science</i> , 2019, 10, 1257.	1.7	8
4446	A Nearly Complete Genome of <i>Ciona intestinalis</i> Type A ( <i>C. robusta</i> ) Reveals the Contribution of Inversion to Chromosomal Evolution in the Genus <i>Ciona</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 3144-3157.	1.1	81
4447	Comparative Genomics Analysis Reveals High Levels of Differential Retrotransposition among Primates from the Hominidae and the Cercopithecidae Families. <i>Genome Biology and Evolution</i> , 2019, 11, 3309-3325.	1.1	12
4448	The transcription factor ETS1 promotes apoptosis resistance of senescent cholangiocytes by epigenetically up-regulating the apoptosis suppressor BCL2L1. <i>Journal of Biological Chemistry</i> , 2019, 294, 18698-18713.	1.6	22
4449	Toward Deep Learning Approaches for Learning Structure Motifs and Classifying Biological Sequences From RNA A-to-I Editing Events. <i>IEEE Access</i> , 2019, 7, 127464-127474.	2.6	4
4450	NCLcomparator: systematically post-screening non-co-linear transcripts (circular, trans-spliced, or Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	19
4451	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. <i>Genome Biology</i> , 2019, 20, 213.	3.8	379
4452	Butterfly Mimicry Polymorphisms Highlight Phylogenetic Limits of Gene Reuse in the Evolution of Diverse Adaptations. <i>Molecular Biology and Evolution</i> , 2019, 36, 2842-2853.	3.5	30
4453	An expanded landscape of human long noncoding RNA. <i>Nucleic Acids Research</i> , 2019, 47, 7842-7856.	6.5	92
4454	A comparison of immunoglobulin <scp>IGHV</scp>, <scp> IGHD</scp> and <scp>IGHJ</scp> genes in wild-derived and classical inbred mouse strains. <i>Immunology and Cell Biology</i> , 2019, 97, 888-901.	1.0	25
4455	Rapidly evolving protointrons in <i>Saccharomyces</i> genomes revealed by a hungry spliceosome. <i>PLoS Genetics</i> , 2019, 15, e1008249.	1.5	16
4456	Hi-Plex2: a simple and robust approach to targeted sequencing-based genetic screening. <i>BioTechniques</i> , 2019, 67, 118-122.	0.8	11
4457	Chinese Fir Breeding in the High-Throughput Sequencing Era: Insights from SNPs. <i>Forests</i> , 2019, 10, 681.	0.9	10
4458	A high-quality genome assembly for the endangered golden snub-nosed monkey ( <i>Rhinopithecus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	3.3	22
4459	A SNP-Based High-Density Genetic Map of Leaf and Fruit Related Quantitative Trait Loci in Wolfberry ( <i>Lycium</i> Linn.). <i>Frontiers in Plant Science</i> , 2019, 10, 977.	1.7	16
4460	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. <i>Forensic Science International: Genetics</i> , 2019, 43, 102146.	1.6	15

#	ARTICLE	IF	CITATIONS
4461	CNER: A toolkit for exploring extreme noncoding conservation. PLoS Computational Biology, 2019, 15, e1006940.	1.5	17
4462	Novel Locus Associated with Symmetrical Lupoid Onychodystrophy in the Bearded Collie. Genes, 2019, 10, 635.	1.0	1
4463	BREAK, MAKE and TAKE: an information retrieval approach. Sadhana - Academy Proceedings in Engineering Sciences, 2019, 44, 1.	0.8	0
4464	Burkholderia pseudomallei, the causative agent of melioidosis, is rare but ecologically established and widely dispersed in the environment in Puerto Rico. PLoS Neglected Tropical Diseases, 2019, 13, e0007727.	1.3	26
4465	Dietary Energy Level Promotes Rumen Microbial Protein Synthesis by Improving the Energy Productivity of the Ruminal Microbiome. Frontiers in Microbiology, 2019, 10, 847.	1.5	43
4466	The evolution study on Oryza rufipogon. dw by whole-genome sequencing. Journal of Genetics, 2019, 98, 1.	0.4	3
4467	Srrm234, but not canonical SR and hnRNP proteins, drive inclusion of <i>Dscam</i> exon 9 variable exons. Rna, 2019, 25, 1353-1365.	1.6	16
4468	Long noncoding RNAs are involved in multiple immunological pathways in response to vaccination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17121-17126.	3.3	58
4469	Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. Clinica Chimica Acta, 2019, 498, 38-46.	0.5	38
4470	The Tannat genome: Unravelling its unique characteristics. BIO Web of Conferences, 2019, 12, 01016.	0.1	1
4471	The population genetics of structural variants in grapevine domestication. Nature Plants, 2019, 5, 965-979.	4.7	229
4472	Horizontally transmitted symbiont populations in deep-sea mussels are genetically isolated. ISME Journal, 2019, 13, 2954-2968.	4.4	42
4473	Gene expression vs. sequence divergence: comparative transcriptome sequencing among natural <i>Rhinolophus ferrumequinum</i> populations with different acoustic phenotypes. Frontiers in Zoology, 2019, 16, 37.	0.9	13
4474	Dosage regulation, and variation in gene expression and copy number of human Y chromosome ampliconic genes. PLoS Genetics, 2019, 15, e1008369.	1.5	19
4475	Transcriptome profiling reveals insights into the molecular mechanism of drought tolerance in sweetpotato. Journal of Integrative Agriculture, 2019, 18, 9-23.	1.7	33
4476	The statistical power of k-mer based aggregative statistics for alignment-free detection of horizontal gene transfer. Synthetic and Systems Biotechnology, 2019, 4, 150-156.	1.8	5
4477	DNA Sequencing Technologies. ACM Computing Surveys, 2020, 52, 1-30.	16.1	8
4478	Transcription analysis of the response of the porcine adrenal cortex to a single subclinical dose of lipopolysaccharide from <i>Salmonella</i> Enteritidis. International Journal of Biological Macromolecules, 2019, 141, 1228-1245.	3.6	5

#	ARTICLE	IF	CITATIONS
4479	A purely bioinformatic pipeline for the prediction of mammalian odorant receptor gene enhancers. <i>BMC Bioinformatics</i> , 2019, 20, 474.	1.2	6
4480	The Epigenetic Signature of Colonizing New Environments in Anolis Lizards. <i>Molecular Biology and Evolution</i> , 2019, 36, 2165-2170.	3.5	31
4481	Molecular characterization of the ERF family in susceptible poplar infected by virulent <i>Melampsora larici-populina</i> . <i>Physiological and Molecular Plant Pathology</i> , 2019, 108, 101437.	1.3	7
4482	The sequencing and de novo assembly of the <i>Larimichthys crocea</i> genome using PacBio and Hi-C technologies. <i>Scientific Data</i> , 2019, 6, 188.	2.4	50
4483	Pedigree-based estimation of human mobile element retrotransposition rates. <i>Genome Research</i> , 2019, 29, 1567-1577.	2.4	75
4484	The sequence and de novo assembly of <i>Takifugu bimaculatus</i> genome using PacBio and Hi-C technologies. <i>Scientific Data</i> , 2019, 6, 187.	2.4	29
4485	Comparative Transcriptomics Provides Insights into Reticulate and Adaptive Evolution of a Butterfly Radiation. <i>Genome Biology and Evolution</i> , 2019, 11, 2963-2975.	1.1	7
4486	Evaluation of bottom-up and top-down mass spectrum identifications with different customized protein sequences databases. <i>Bioinformatics</i> , 2020, 36, 1030-1036.	1.8	4
4487	The Biodiversity and Geochemistry of Cryoconite Holes in Queen Maud Land, East Antarctica. <i>Microorganisms</i> , 2019, 7, 160.	1.6	21
4488	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
4489	de novo 3.8-Mb inversion affecting the EDA and XIST genes in a heterozygous female calf with generalized hypohidrotic ectodermal dysplasia. <i>BMC Genomics</i> , 2019, 20, 715.	1.2	8
4490	Rapid Detection of Genetic Engineering, Structural Variation, and Antimicrobial Resistance Markers in Bacterial Biothreat Pathogens by Nanopore Sequencing. <i>Scientific Reports</i> , 2019, 9, 13501.	1.6	23
4491	Long-read sequencing and haplotype linkage analysis enabled preimplantation genetic testing for patients carrying pathogenic inversions. <i>Journal of Medical Genetics</i> , 2019, 56, 741-749.	1.5	25
4492	A Sequence-Based Novel Approach for Quality Evaluation of Third-Generation Sequencing Reads. <i>Genes</i> , 2019, 10, 44.	1.0	3
4493	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54.	1.0	8
4494	Inflammation in Traumatic Brain Injury: Roles for Toxic A1 Astrocytes and Microglial-Astrocytic Crosstalk. <i>Neurochemical Research</i> , 2019, 44, 1410-1424.	1.6	82
4495	Defective Epstein-Barr virus in chronic active infection and haematological malignancy. <i>Nature Microbiology</i> , 2019, 4, 404-413.	5.9	152
4496	Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, .	3.3	36

#	ARTICLE	IF	CITATIONS
4497	Genome structure and evolution of <i>Antirrhinum majus</i> L. <i>Nature Plants</i> , 2019, 5, 174-183.	4.7	85
4498	Precise RNA editing by recruiting endogenous ADARs with antisense oligonucleotides. <i>Nature Biotechnology</i> , 2019, 37, 133-138.	9.4	186
4499	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. <i>Cell</i> , 2019, 176, 1222-1237.e22.	13.5	347
4500	Aligning optical maps to de Bruijn graphs. <i>Bioinformatics</i> , 2019, 35, 3250-3256.	1.8	4
4501	The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. <i>GigaScience</i> , 2019, 8, .	3.3	143
4502	Complete Chloroplast Genome Sequences of <i>Kaempferia Galanga</i> and <i>Kaempferia Elegans</i> : Molecular Structures and Comparative Analysis. <i>Molecules</i> , 2019, 24, 474.	1.7	59
4503	Dynamic Interactions Between the Genome and an Endogenous Retrovirus: <i>Tirant</i> in <i>Drosophila simulans</i> Wild-Type Strains. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 855-865.	0.8	5
4504	The Network of Cancer Genes (NCG): a comprehensive catalogue of known and candidate cancer genes from cancer sequencing screens. <i>Genome Biology</i> , 2019, 20, 1.	3.8	938
4505	The Genome of <i>Armadillidium vulgare</i> (Crustacea, Isopoda) Provides Insights into Sex Chromosome Evolution in the Context of Cytoplasmic Sex Determination. <i>Molecular Biology and Evolution</i> , 2019, 36, 727-741.	3.5	43
4506	Prediction of functional microRNA targets by integrative modeling of microRNA binding and target expression data. <i>Genome Biology</i> , 2019, 20, 18.	3.8	556
4507	Taxonomic profiling and populational patterns of bacterial bile salt hydrolase (BSH) genes based on worldwide human gut microbiome. <i>Microbiome</i> , 2019, 7, 9.	4.9	261
4508	Alternative splicing coupled to nonsense-mediated mRNA decay contributes to the high-altitude adaptation of maca ( <i>Lepidium meyenii</i> ). <i>Gene</i> , 2019, 694, 7-18.	1.0	10
4509	Environmental filtering of bacterial functional diversity along an aridity gradient. <i>Scientific Reports</i> , 2019, 9, 866.	1.6	33
4510	Gene editing of the multi-copy H2A.B gene and its importance for fertility. <i>Genome Biology</i> , 2019, 20, 23.	3.8	29
4511	De novo assembly of white poplar genome and genetic diversity of white poplar population in Irtys River basin in China. <i>Science China Life Sciences</i> , 2019, 62, 609-618.	2.3	55
4512	Stress-Free Evolution: The Nrf-Coordinated Oxidative Stress Response in Early Diverging Metazoans. <i>Integrative and Comparative Biology</i> , 2019, 59, 799-810.	0.9	9
4513	<i>Stenotrophomonas maltophilia</i> Differential Gene Expression in Synthetic Cystic Fibrosis Sputum Reveals Shared and Cystic Fibrosis Strain-Specific Responses to the Sputum Environment. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	8
4514	Pairwise alignment of nucleotide sequences using maximal exact matches. <i>BMC Bioinformatics</i> , 2019, 20, 261.	1.2	4

#	ARTICLE	IF	CITATIONS
4515	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	1.2	23
4516	Parallel Molecular Evolution in Pathways, Genes, and Sites in High-Elevation Hummingbirds Revealed by Comparative Transcriptomics. <i>Genome Biology and Evolution</i> , 2019, 11, 1573-1585.	1.1	49
4517	Variable Baseline <i>Papio cynocephalus</i> Endogenous Retrovirus (PcEV) Expression Is Upregulated in Acutely SIV-Infected Macaques and Correlated to STAT1 Expression in the Spleen. <i>Frontiers in Immunology</i> , 2019, 10, 901.	2.2	1
4518	Transcriptome Changes during Major Developmental Transitions Accompanied with Little Alteration of DNA Methylome in Two <i>Pleurotus</i> Species. <i>Genes</i> , 2019, 10, 465.	1.0	8
4519	Long-read based de novo assembly of low-complexity metagenome samples results in finished genomes and reveals insights into strain diversity and an active phage system. <i>BMC Microbiology</i> , 2019, 19, 143.	1.3	104
4520	MammaPrint and BluePrint Molecular Diagnostics Using Targeted RNA Next-Generation Sequencing Technology. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 808-823.	1.2	15
4521	Factors other than hTau overexpression that contribute to tauopathy-like phenotype in rTg4510 mice. <i>Nature Communications</i> , 2019, 10, 2479.	5.8	117
4522	Genome sequencing provides insights into the evolution and antioxidant activity of Chinese bayberry. <i>BMC Genomics</i> , 2019, 20, 458.	1.2	31
4523	Different methylation levels in the KLF4, ATF3 and DLEC1 genes in the myometrium and in corpus uteri mesenchymal tumours as assessed by MS-HRM. <i>Pathology Research and Practice</i> , 2019, 215, 152465.	1.0	5
4524	Vulnerability of seagrass blue carbon to microbial attack following exposure to warming and oxygen. <i>Science of the Total Environment</i> , 2019, 686, 264-275.	3.9	42
4525	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean ( <i>Glycine max</i> L.). <i>Heredity</i> , 2019, 123, 579-592.	1.2	41
4526	A new reference genome for <i>Sorghum bicolor</i> reveals high levels of sequence similarity between sweet and grain genotypes: implications for the genetics of sugar metabolism. <i>BMC Genomics</i> , 2019, 20, 420.	1.2	73
4527	Microhomologies are prevalent at Cas9-induced larger deletions. <i>Nucleic Acids Research</i> , 2019, 47, 7402-7417.	6.5	100
4528	Chromosomal and Genomic Dynamics of Satellite DNAs in Characidae (Characiformes, Teleostei) Species. <i>Zebrafish</i> , 2019, 16, 408-414.	0.5	2
4529	Phylogenomic Approaches to DNA Barcoding of Herbal Medicines: Developing Clade-Specific Diagnostic Characters for <i>Berberis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 586.	1.7	28
4530	Leaf Transcriptome Assembly of <i>Protium copal</i> (Burseraceae) and Annotation of Terpene Biosynthetic Genes. <i>Genes</i> , 2019, 10, 392.	1.0	6
4531	Genome assembly of a tropical maize inbred line provides insights into structural variation and crop improvement. <i>Nature Genetics</i> , 2019, 51, 1052-1059.	9.4	202
4532	Darwin-WGA: A Co-processor Provides Increased Sensitivity in Whole Genome Alignments with High Speedup. , 2019, , .		17

#	ARTICLE	IF	CITATIONS
4533	Genomic metrics made easy: what to do and where to go in the new era of bacterial taxonomy. <i>Critical Reviews in Microbiology</i> , 2019, 45, 182-200.	2.7	65
4534	Altered microRNA expression profiles in large offspring syndrome and Beckwith-Wiedemann syndrome. <i>Epigenetics</i> , 2019, 14, 850-876.	1.3	32
4535	Comment on "A comprehensive overview and evaluation of circular RNA detection tools". <i>PLoS Computational Biology</i> , 2019, 15, e1006158.	1.5	15
4536	HNCDB: An Integrated Gene and Drug Database for Head and Neck Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 371.	1.3	7
4537	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	1.0	25
4538	Draft genome of the big-headed turtle <i>Platysternon megacephalum</i> . <i>Scientific Data</i> , 2019, 6, 60.	2.4	26
4539	Transcript and metabolite changes during the early phase of abscisic acid-mediated induction of crassulacean acid metabolism in <i>Talinum triangulare</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6581-6596.	2.4	19
4540	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. <i>Genome Biology</i> , 2019, 20, 97.	3.8	122
4541	Retrotransposons evolution and impact on lncRNA and protein coding genes in pigs. <i>Mobile DNA</i> , 2019, 10, 19.	1.3	22
4542	Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. <i>PLoS Genetics</i> , 2019, 15, e1008119.	1.5	70
4543	Mitochondrial autoimmunity and MNRR1 in breast carcinogenesis. <i>BMC Cancer</i> , 2019, 19, 411.	1.1	20
4544	Slow Delivery Immunization Enhances HIV Neutralizing Antibody and Germinal Center Responses via Modulation of Immunodominance. <i>Cell</i> , 2019, 177, 1153-1171.e28.	13.5	293
4545	How dynamic could be the 45S rDNA cistron? An intriguing variability in a grasshopper species revealed by integration of chromosomal and genomic data. <i>Chromosoma</i> , 2019, 128, 165-175.	1.0	14
4546	Genomes of the wild beets <i>Beta patula</i> and <i>Beta vulgaris</i> ssp. <i>maritima</i> . <i>Plant Journal</i> , 2019, 99, 1242-1253.	2.8	28
4547	New Era in Plant Alternative Splicing Analysis Enabled by Advances in High-Throughput Sequencing (HTS) Technologies. <i>Frontiers in Plant Science</i> , 2019, 10, 740.	1.7	9
4548	Functional adaptations in the cecal and colonic metagenomes associated with the consumption of transglycosylated starch in a pig model. <i>BMC Microbiology</i> , 2019, 19, 87.	1.3	13
4549	A high-density genetic map developed by specific-locus amplified fragment (SLAF) sequencing and identification of a locus controlling anthocyanin pigmentation in stalk of Zicaitai ( <i>Brassica rapa</i> L.) <i>Tj ETQq0 0 0 rgBL2 Overlock 10 Tf 00</i>		
4550	Computational Methods for Mapping, Assembly and Quantification for Coding and Non-coding Transcripts. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 628-637.	1.9	25

#	ARTICLE	IF	CITATIONS
4551	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. <i>Current Biology</i> , 2019, 29, 1712-1720.e7.	1.8	27
4552	A brief overview of the concepts, methods and computational tools used in phylogenetic tree construction and gene prediction. <i>Meta Gene</i> , 2019, 21, 100586.	0.3	8
4553	Sex-Biased Gene Expression and Dosage Compensation on the <i>Artemia franciscana</i> Z-Chromosome. <i>Genome Biology and Evolution</i> , 2019, 11, 1033-1044.	1.1	25
4554	Phylogenomic analyses reveal an exceptionally high number of evolutionary shifts in a florally diverse clade of African legumes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 156-167.	1.2	17
4555	A chromosome-level genome of black rockfish, <i>Sebastes schlegelii</i> , provides insights into the evolution of live birth. <i>Molecular Ecology Resources</i> , 2019, 19, 1309-1321.	2.2	44
4556	Genomic changes in the biological control agent <i>Cryptolaemus montrouzieri</i> associated with introduction. <i>Evolutionary Applications</i> , 2019, 12, 989-1000.	1.5	9
4557	Local protein synthesis is a ubiquitous feature of neuronal pre- and postsynaptic compartments. <i>Science</i> , 2019, 364, .	6.0	285
4558	Islands of retroelements are major components of <i>Drosophila</i> centromeres. <i>PLoS Biology</i> , 2019, 17, e3000241.	2.6	124
4559	CiliaCarta: An integrated and validated compendium of ciliary genes. <i>PLoS ONE</i> , 2019, 14, e0216705.	1.1	104
4560	Visualizing flow in an intact CSF network using optical coherence tomography: implications for human congenital hydrocephalus. <i>Scientific Reports</i> , 2019, 9, 6196.	1.6	27
4561	The complete chloroplast genome sequence of <i>Pyrus phaeocarpa</i> Rehd.. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1370-1371.	0.2	2
4562	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. <i>Genome Biology</i> , 2019, 20, 79.	3.8	81
4563	Diversity, Virulence, and Antimicrobial Resistance in Isolates From the Newly Emerging <i>Klebsiella pneumoniae</i> ST101 Lineage. <i>Frontiers in Microbiology</i> , 2019, 10, 542.	1.5	69
4564	BHap: a novel approach for bacterial haplotype reconstruction. <i>Bioinformatics</i> , 2019, 35, 4624-4631.	1.8	18
4565	Dauer signalling pathway model for <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2019, 12, 187.	1.0	25
4566	Exploiting selection at linked sites to infer the rate and strength of adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 977-984.	3.4	43
4567	SeqTailor: a user-friendly webserver for the extraction of DNA or protein sequences from next-generation sequencing data. <i>Nucleic Acids Research</i> , 2019, 47, W623-W631.	6.5	15
4568	The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, .	3.3	88

#	ARTICLE	IF	CITATIONS
4569	Insertion of a chimeric retrotransposon sequence in mouse Axin1 locus causes metastable kinky tail phenotype. <i>Mobile DNA</i> , 2019, 10, 17.	1.3	11
4570	Analysis of Subtelomeric REXTAL Assemblies Using QUASt. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	1.9	3
4571	Genus-wide <i>Leptospira</i> core genome multilocus sequence typing for strain taxonomy and global surveillance. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007374.	1.3	98
4572	Germline-restricted chromosome (GRC) is widespread among songbirds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11845-11850.	3.3	68
4573	Methanethiol and Dimethylsulfide Cycling in Stiffkey Saltmarsh. <i>Frontiers in Microbiology</i> , 2019, 10, 1040.	1.5	23
4574	Linkage-based genome assembly improvement of oil palm ( <i>Elaeis guineensis</i> ). <i>Scientific Reports</i> , 2019, 9, 6619.	1.6	16
4575	A Transmissible RNA Pathway in Honey Bees. <i>Cell Reports</i> , 2019, 27, 1949-1959.e6.	2.9	44
4576	Amplification Dynamics of Platy-1 Retrotransposons in the Cebidae Platyrrhine Lineage. <i>Genome Biology and Evolution</i> , 2019, 11, 1105-1116.	1.1	3
4577	On the critical evaluation and confirmation of germline sequence variants identified using massively parallel sequencing. <i>Journal of Biotechnology</i> , 2019, 298, 64-75.	1.9	8
4578	A Modifying Autoantigen in Graves' Disease. <i>Endocrinology</i> , 2019, 160, 1008-1020.	1.4	11
4579	Subtype classification and functional annotation of L1Md retrotransposon promoters. <i>Mobile DNA</i> , 2019, 10, 14.	1.3	18
4580	TransLiG: a de novo transcriptome assembler that uses line graph iteration. <i>Genome Biology</i> , 2019, 20, 81.	3.8	30
4581	Details in the evaluation of circular RNA detection tools: Reply to Chen and Chuang. <i>PLoS Computational Biology</i> , 2019, 15, e1006916.	1.5	8
4582	Chromosome-Level Assembly of the Chinese Seabass ( <i>Lateolabrax maculatus</i> ) Genome. <i>Frontiers in Genetics</i> , 2019, 10, 275.	1.1	33
4583	Shedding Light on a Secretive Tertiary Urodelean Relict: Hynobiid Salamanders ( <i>Paradactylodon</i> ). <i>Trends in Ecology and Evolution</i> , 2019, 34, 1000-1008.	1.0	4
4584	Predicting Genes in Closely Related Species with Scipio and WebScipio. <i>Methods in Molecular Biology</i> , 2019, 1962, 193-206.	0.4	0
4585	Structural and Functional Annotation of Eukaryotic Genomes with GenSAS. <i>Methods in Molecular Biology</i> , 2019, 1962, 29-51.	0.4	66
4586	Accurate high throughput alignment via line sweep-based seed processing. <i>Nature Communications</i> , 2019, 10, 1939.	5.8	11

#	ARTICLE	IF	CITATIONS
4587	Divergent Fine-Scale Recombination Landscapes between a Freshwater and Marine Population of Threespine Stickleback Fish. <i>Genome Biology and Evolution</i> , 2019, 11, 1552-1572.	1.1	44
4588	Agricultural Origins of a Highly Persistent Lineage of Vancomycin-Resistant <i>Enterococcus faecalis</i> in New Zealand. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
4589	Long-read based assembly and synteny analysis of a reference <i>Drosophila subobscura</i> genome reveals signatures of structural evolution driven by inversions recombination-suppression effects. <i>BMC Genomics</i> , 2019, 20, 223.	1.2	15
4590	Cryo-EM structure of a light chain-derived amyloid fibril from a patient with systemic AL amyloidosis. <i>Nature Communications</i> , 2019, 10, 1103.	5.8	120
4591	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. <i>Nature Communications</i> , 2019, 10, 1338.	5.8	38
4592	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. <i>Nature Genetics</i> , 2019, 51, 739-748.	9.4	568
4593	Molecular spectrum of somaclonal variation in PLB-regenerated <i>Oncidium</i> revealed by SLAF-seq. <i>Plant Cell, Tissue and Organ Culture</i> , 2019, 137, 541-552.	1.2	8
4594	Evolution-guided evaluation of the inverted terminal repeats of the synthetic transposon Sleeping Beauty. <i>Scientific Reports</i> , 2019, 9, 1171.	1.6	5
4595	Genome-wide analysis reveals the genomic features of the turkey vulture ( <i>Cathartes aura</i> ) as a scavenger. <i>Molecular Genetics and Genomics</i> , 2019, 294, 679-692.	1.0	10
4596	The transcriptome of the veiled chameleon ( <i>Chamaeleo calytratus</i> ): A resource for studying the evolution and development of vertebrates. <i>Developmental Dynamics</i> , 2019, 248, 702-708.	0.8	26
4597	Dicer1 is required for pigment cell and craniofacial development in zebrafish. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 472-485.	0.9	12
4598	A Genomic Analysis Workflow for Colorectal Cancer Precision Oncology. <i>Clinical Colorectal Cancer</i> , 2019, 18, 91-101.e3.	1.0	29
4599	RNA sequencing discloses the genome-wide profile of long noncoding RNAs in dilated cardiomyopathy. <i>Molecular Medicine Reports</i> , 2019, 19, 2569-2580.	1.1	8
4600	Does the human placenta delivered at term have a microbiota? Results of cultivation, quantitative real-time PCR, 16S rRNA gene sequencing, and metagenomics. <i>American Journal of Obstetrics and Gynecology</i> , 2019, 220, 267.e1-267.e39.	0.7	196
4601	Genome Sequence of Flavor-Producing Yeast <i>Saprochaete suaveolens</i> NRRL Y-17571. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
4602	Origination and evolution of orphan genes and de novo genes in the genome of <i>Caenorhabditis elegans</i> . <i>Science China Life Sciences</i> , 2019, 62, 579-593.	2.3	21
4603	Deep-learning augmented RNA-seq analysis of transcript splicing. <i>Nature Methods</i> , 2019, 16, 307-310.	9.0	74
4604	Improving in-silico normalization using read weights. <i>Scientific Reports</i> , 2019, 9, 5133.	1.6	9

#	ARTICLE	IF	CITATIONS
4605	Canine Parvovirus-2c (CPV-2c) Infection in Wild Asian Palm Civets ( <i>Paradoxurus hermaphroditus</i> ) in Singapore. <i>Journal of Wildlife Diseases</i> , 2019, 55, 965.	0.3	5
4606	ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline. <i>Bioinformatics</i> , 2019, 35, 4156-4158.	1.8	24
4607	The genome-wide landscape of small insertion and deletion mutations in <i>Monopterus albus</i> . <i>Journal of Genetics and Genomics</i> , 2019, 46, 75-86.	1.7	2
4608	A Novel Chimeric Mitochondrial Gene Confers Cytoplasmic Effects on Seed Oil Content in Polyploid Rapeseed ( <i>Brassica napus</i> ). <i>Molecular Plant</i> , 2019, 12, 582-596.	3.9	26
4609	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	3.4	121
4610	AtFusionDB: a database of fusion transcripts in <i>Arabidopsis thaliana</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	8
4611	Genetic variation and population genetic structure of <i>Laodelphax striatellus</i> via genome-wide single nucleotide polymorphisms from specific locus amplified fragment sequencing. <i>Journal of Applied Entomology</i> , 2019, 143, 315-327.	0.8	8
4612	Magic roundabout is an endothelial-specific ohnolog of ROBO1 which neo-functionalized to an essential new role in angiogenesis. <i>PLoS ONE</i> , 2019, 14, e0208952.	1.1	7
4613	Identifying integration sites of the HIV-1 genome with intact and aberrant ends through deep sequencing. <i>Journal of Virological Methods</i> , 2019, 267, 59-65.	1.0	3
4614	<i>Anaerotruncus massiliensis</i> sp. nov., a succinate-producing bacterium isolated from human stool from an obese patient after bariatric surgery. <i>New Microbes and New Infections</i> , 2019, 29, 100508.	0.8	18
4615	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	5.8	183
4616	Characterization of mammalian Lipocalin UTRs in silico: Predictions for their role in post-transcriptional regulation. <i>PLoS ONE</i> , 2019, 14, e0213206.	1.1	2
4617	Memory and relatedness of transcriptional activity in mammalian cell lineages. <i>Nature Communications</i> , 2019, 10, 1208.	5.8	34
4618	Chromothripsis during telomere crisis is independent of NHEJ, and consistent with a replicative origin. <i>Genome Research</i> , 2019, 29, 737-749.	2.4	47
4619	Circular RNAs in human and vertebrate neural retinas. <i>RNA Biology</i> , 2019, 16, 821-829.	1.5	26
4620	Genomic analysis of marker-associated fiber development genes in upland cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq1 1,0.784314 rgBT /Ove 0,6	1.0	5
4621	Carbapenem-Susceptible OXA-23-Producing <i>Proteus mirabilis</i> in the French Community. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	10
4622	A quick guide for student-driven community genome annotation. <i>PLoS Computational Biology</i> , 2019, 15, e1006682.	1.5	33

#	ARTICLE	IF	CITATIONS
4623	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. Nature Communications, 2019, 10, 1636.	5.8	41
4624	The Genome and mRNA Transcriptome of the Cosmopolitan Calanoid Copepod <i>Acartia tonsa</i> Dana Improve the Understanding of Copepod Genome Size Evolution. Genome Biology and Evolution, 2019, 11, 1440-1450.	1.1	26
4625	Genome Sequence of an Arthroconidial Yeast, <i>Saprochaete fungicola</i> CBS 625.85. Microbiology Resource Announcements, 2019, 8, .	0.3	1
4626	SplicedFamAlign: CDS-to-gene spliced alignment and identification of transcript orthology groups. BMC Bioinformatics, 2019, 20, 133.	1.2	8
4627	MGS-Fast: Metagenomic shotgun data fast annotation using microbial gene catalogs. GigaScience, 2019, 8, .	3.3	15
4628	Whole genome sequencing reveals complexity in both HPV sequences present and HPV integrations in HPV-positive oropharyngeal squamous cell carcinomas. BMC Cancer, 2019, 19, 352.	1.1	26
4629	Analysis of 100 high-coverage genomes from a pedigreed captive baboon colony. Genome Research, 2019, 29, 848-856.	2.4	27
4630	Placenta Transcriptome Profiling in Intrauterine Growth Restriction (IUGR). International Journal of Molecular Sciences, 2019, 20, 1510.	1.8	53
4631	Tools and Methods in the Analysis of Simple Sequences. , 2019, , 127-153.		0
4632	High-throughput methods in aptamer discovery and analysis. Methods in Enzymology, 2019, 621, 329-346.	0.4	8
4633	Low-cost assembly of a cacao crop genome is able to resolve complex heterozygous bubbles. Horticulture Research, 2019, 6, 44.	2.9	5
4634	Chromosomal inversions in the Atlantic cod genome: Implications for management of Canada's Northern cod stock. Fisheries Research, 2019, 216, 29-40.	0.9	12
4635	Dynamic evolutionary history and gene content of sex chromosomes across diverse songbirds. Nature Ecology and Evolution, 2019, 3, 834-844.	3.4	68
4636	Genome-wide de novo L1 Retrotransposition Connects Endonuclease Activity with Replication. Cell, 2019, 177, 837-851.e28.	13.5	88
4637	scRNAseq: a single-cell RNA-seq assembler via imputing dropouts and combing junctions. Bioinformatics, 2019, 35, 4264-4271.	1.8	7
4638	Evolutionary Implications of the microRNA- and piRNA Complement of <i>Lepidodermella squamata</i> (Gastrotricha). Non-coding RNA, 2019, 5, 19.	1.3	5
4639	Widespread and Functional RNA Circularization in Localized Prostate Cancer. Cell, 2019, 176, 831-843.e22.	13.5	317
4640	Genomic content of a novel yeast species <i>Hanseniaspora gamundiae</i> sp. nov. from fungal stromata (Cyttaria) associated with a unique fermented beverage in Andean Patagonia, Argentina. PLoS ONE, 2019, 14, e0210792.	1.1	37

#	ARTICLE	IF	CITATIONS
4641	Resolving the backbone of the Brassicaceae phylogeny for investigating trait diversity. <i>New Phytologist</i> , 2019, 222, 1638-1651.	3.5	123
4642	Land-plant Phylogenomic and Pomegranate Transcriptomic Analyses Reveal an Evolutionary Scenario of CYP75 Genes Subsequent to Whole Genome Duplications. <i>Journal of Plant Biology</i> , 2019, 62, 48-60.	0.9	14
4643	Comprehensive structural variation genome map of individuals carrying complex chromosomal rearrangements. <i>PLoS Genetics</i> , 2019, 15, e1007858.	1.5	36
4644	Development of High-Density SNP Markers and Their Application in Evaluating Genetic Diversity and Population Structure in <i>Elaeis guineensis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 130.	1.7	49
4645	Biochemical composition of green microalgae <i>Pseudoneochloris marina</i> grown under different temperature and light conditions. <i>Biocatalysis and Agricultural Biotechnology</i> , 2019, 18, 101032.	1.5	29
4646	Genomewide Association Study of Fracture Nonunion Using Electronic Health Records. <i>JBMR Plus</i> , 2019, 3, 23-28.	1.3	9
4647	Ipa1 Is an RNA Polymerase II Elongation Factor that Facilitates Termination by Maintaining Levels of the Poly(A) Site Endonuclease Ysh1. <i>Cell Reports</i> , 2019, 26, 1919-1933.e5.	2.9	8
4648	Draft genome of the river water buffalo. <i>Ecology and Evolution</i> , 2019, 9, 3378-3388.	0.8	32
4649	The <i>Galleria mellonella</i> Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. <i>Cell Reports</i> , 2019, 26, 2451-2464.e5.	2.9	103
4650	Unraveling the complex genome of <i>Saccharum spontaneum</i> using Polyploid Gene Assembler. <i>DNA Research</i> , 2019, 26, 205-216.	1.5	8
4651	Computational Biology and Genomics Tools for Biohydrogen Research. , 2019, , 435-444.		1
4652	A cell cycle-coordinated Polymerase II transcription compartment encompasses gene expression before global genome activation. <i>Nature Communications</i> , 2019, 10, 691.	5.8	42
4653	Ribosomal DNA harbors an evolutionarily conserved clock of biological aging. <i>Genome Research</i> , 2019, 29, 325-333.	2.4	98
4654	Heterogeneous Nuclear Ribonucleoprotein H1 Coordinates with Phytochrome and the U1 snRNP Complex to Regulate Alternative Splicing in <i>Physcomitrella patens</i> . <i>Plant Cell</i> , 2019, 31, 2510-2524.	3.1	33
4655	Monoallelic, antisense, and total RNA transcription in an <i>in vitro</i> neural differentiation system based on F1-hybrid mice. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	1
4656	A computational model based on long short-term memory for predicting organellar genes in plastid genomes. , 2019, , .		0
4657	Molecular Dating of the Emergence of Anaerobic Rumen Fungi and the Impact of Laterally Acquired Genes. <i>MSystems</i> , 2019, 4, .	1.7	28
4658	Predisposition to childhood acute lymphoblastic leukemia caused by a constitutional translocation disrupting ETV6. <i>Blood Advances</i> , 2019, 3, 2722-2731.	2.5	10

#	ARTICLE	IF	CITATIONS
4659	Complete Fix-Free Codes for the Statistical Dictionary-Based String Matching Problem. , 2019, , .		0
4660	Genome Sequencing and Transcriptome Analysis Reveal Recent Species-Specific Gene Duplications in the Plastic Gilthead Sea Bream ( <i>Sparus aurata</i> ). <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	26
4661	Genome-Wide Variant Identification and High-Density Genetic Map Construction Using RADseq for <i>Platycladus orientalis</i> (Cupressaceae). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3663-3672.	0.8	5
4662	RNA ligation precedes the retrotransposition of U6/LINE-1 chimeric RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20612-20622.	3.3	23
4663	Utilization of Tissue Ploidy Level Variation in <i>de Novo</i> Transcriptome Assembly of <i>Pinus sylvestris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3409-3421.	0.8	16
4664	An empirical assessment of a single family-wide hybrid capture locus set at multiple evolutionary timescales in Asteraceae. <i>Applications in Plant Sciences</i> , 2019, 7, e11295.	0.8	28
4665	Sex matters: Otolith shape and genomic variation in deacon rockfish ( <i>Sebastes diaconus</i> ). <i>Ecology and Evolution</i> , 2019, 9, 13153-13173.	0.8	17
4666	Evidence for adaptive introgression of exons across a hybrid swarm in deer. <i>BMC Evolutionary Biology</i> , 2019, 19, 199.	3.2	12
4667	A Puzzling Anomaly in the 4-Mer Composition of the Giant Pandoravirus Genomes Reveals a Stringent New Evolutionary Selection Process. <i>Journal of Virology</i> , 2019, 93, .	1.5	9
4668	Integrative transcriptome analysis discloses the molecular basis of a heterogeneous fungal phytopathogen complex, <i>Rhizoctonia solani</i> AG-1 subgroups. <i>Scientific Reports</i> , 2019, 9, 19626.	1.6	20
4669	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	1.2	59
4670	deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. <i>Genome Biology</i> , 2019, 20, 274.	3.8	41
4671	Pseudo-chromosome-length genome assembly of a double haploid <i>Bartlett</i> pear ( <i>Pyrus communis</i> L.). <i>GigaScience</i> , 2019, 8, .	3.3	76
4672	Atypical chromosome 22q11.2 deletions are complex rearrangements and have different mechanistic origins. <i>Human Molecular Genetics</i> , 2019, 28, 3724-3733.	1.4	7
4673	Annotated Draft Genomes of Two Caddisfly Species <i>Plectrocnemia conspersa</i> CURTIS and <i>Hydropsyche tenuis</i> NAVAS (Insecta: Trichoptera). <i>Genome Biology and Evolution</i> , 2019, 11, 3445-3451.	1.1	21
4674	Programmed DNA elimination of germline development genes in songbirds. <i>Nature Communications</i> , 2019, 10, 5468.	5.8	66
4675	Retroelement Insertion in a CRISPR/Cas9 Editing Site in the Early Embryo Intensifies Genetic Mosaicism. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 273.	1.8	8
4676	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	3.3	106

#	ARTICLE	IF	CITATIONS
4677	Comparative genomics of <i>Mycoplasma pneumoniae</i> isolated from children with pneumonia: South Korea, 2010–2016. <i>BMC Genomics</i> , 2019, 20, 910.	1.2	7
4678	Environmental transcriptomes of invasive <i>dreissena</i> , a model species in ecotoxicology and invasion biology. <i>Scientific Data</i> , 2019, 6, 234.	2.4	6
4679	Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . <i>Communications Biology</i> , 2019, 2, 428.	2.0	19
4680	Minimal <i>in vivo</i> requirements for developmentally regulated cardiac long intergenic non-coding RNAs. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	19
4681	Towards Improved Molecular Identification Tools in Fine Fescue ( <i>Festuca L.</i> , Poaceae) Turfgrasses: Nuclear Genome Size, Ploidy, and Chloroplast Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 1223.	1.1	14
4682	Discovery of genomic variations by whole-genome resequencing of the North American Araucana chicken. <i>PLoS ONE</i> , 2019, 14, e0225834.	1.1	8
4683	SGID: a comprehensive and interactive database of the silkworm. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	12
4684	ReVac: a reverse vaccinology computational pipeline for prioritization of prokaryotic protein vaccine candidates. <i>BMC Genomics</i> , 2019, 20, 981.	1.2	18
4685	Alu insertion polymorphisms shared by <i>Papio baboons</i> and <i>Theropithecus gelada</i> reveal an intertwined common ancestry. <i>Mobile DNA</i> , 2019, 10, 46.	1.3	11
4686	Evolution of the new head by gradual acquisition of neural crest regulatory circuits. <i>Nature</i> , 2019, 574, 675-678.	13.7	74
4687	QTL identification for seed weight and size based on a high-density SLAF-seq genetic map in peanut ( <i>Arachis hypogaea L.</i> ). <i>BMC Plant Biology</i> , 2019, 19, 537.	1.6	54
4688	Genetic Diversity and Signatures of Selection in 15 Chinese Indigenous Dog Breeds Revealed by Genome-Wide SNPs. <i>Frontiers in Genetics</i> , 2019, 10, 1174.	1.1	12
4689	Functional metagenomics: a tool to gain knowledge for agronomic and veterinary sciences. <i>Biotechnology and Genetic Engineering Reviews</i> , 2019, 35, 69-91.	2.4	6
4690	Multiple forms of selection shape reproductive isolation in a primate hybrid zone. <i>Molecular Ecology</i> , 2019, 28, 1056-1069.	2.0	24
4691	The variations of TRBV genes usages in the peripheral blood of a healthy population are associated with their evolution and single nucleotide polymorphisms. <i>Human Immunology</i> , 2019, 80, 195-203.	1.2	2
4692	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648.	6.5	70
4693	Actively personalized vaccination trial for newly diagnosed glioblastoma. <i>Nature</i> , 2019, 565, 240-245.	13.7	637
4694	Ecdysis triggering hormone receptors regulate male courtship behavior via antennal lobe interneurons in <i>Drosophila</i> . <i>General and Comparative Endocrinology</i> , 2019, 278, 79-88.	0.8	11

#	ARTICLE	IF	CITATIONS
4695	Analysis of chromosome microstructures in products of conception associated with recurrent miscarriage. <i>Reproductive BioMedicine Online</i> , 2019, 38, 787-795.	1.1	12
4696	Chromosomal level reference genome of <i>Tachypleus tridentatus</i> provides insights into evolution and adaptation of horseshoe crabs. <i>Molecular Ecology Resources</i> , 2019, 19, 744-756.	2.2	25
4697	Gorillas have been infected with the HERV-K (HML-2) endogenous retrovirus much more recently than humans and chimpanzees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1337-1346.	3.3	27
4698	Differential alternative polyadenylation contributes to the developmental divergence between two rice subspecies, <i>japonica</i> and <i>indica</i> . <i>Plant Journal</i> , 2019, 98, 260-276.	2.8	26
4699	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
4700	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 12-31.	4.1	25
4701	Modelling of zero-inflation improves inference of metagenomic gene count data. <i>Statistical Methods in Medical Research</i> , 2019, 28, 3712-3728.	0.7	10
4702	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	6.5	699
4703	Defining TP53 pioneering capabilities with competitive nucleosome binding assays. <i>Genome Research</i> , 2019, 29, 107-115.	2.4	41
4704	A physical and genetic map of <i>Cannabis sativa</i> identifies extensive rearrangements at the <i>THC/CBD acid synthase</i> loci. <i>Genome Research</i> , 2019, 29, 146-156.	2.4	160
4705	Heterochromatin-Enriched Assemblies Reveal the Sequence and Organization of the <i>Drosophila melanogaster</i> Y Chromosome. <i>Genetics</i> , 2019, 211, 333-348.	1.2	98
4706	Profiling microRNA expression in Atlantic killifish ( <i>Fundulus heteroclitus</i> ) gill and responses to arsenic and hyperosmotic stress. <i>Aquatic Toxicology</i> , 2019, 206, 142-153.	1.9	13
4707	De novo assembly and comparative transcriptome analysis: novel insights into terpenoid biosynthesis in <i>Chamaemelum nobile</i> L.. <i>Plant Cell Reports</i> , 2019, 38, 101-116.	2.8	20
4708	DNA Methylation as a Biomarker in Environmental Epidemiology. , 2019, , 173-189.		1
4709	SQURE reveals locus-specific regulation of interspersed repeat expression. <i>Nucleic Acids Research</i> , 2019, 47, e27-e27.	6.5	115
4710	Understanding antimicrobial discovery and resistance from a metagenomic and metatranscriptomic perspective: advances and applications. <i>Environmental Microbiology Reports</i> , 2019, 11, 62-86.	1.0	34
4711	Evaluation and application of RNA-Seq by MinION. <i>DNA Research</i> , 2019, 26, 55-65.	1.5	49
4712	Comparative bioinformatic analysis suggests that specific dauer-like signalling pathway components regulate <i>Toxocara canis</i> development and migration in the mammalian host. <i>Parasites and Vectors</i> , 2019, 12, 32.	1.0	15

#	ARTICLE	IF	CITATIONS
4713	Improved Genome Sequence of Wild Emmer Wheat Zavitan with the Aid of Optical Maps. G3: Genes, Genomes, Genetics, 2019, 9, 619-624.	0.8	64
4714	Genome-Wide Copy Number Variation Detection Using NGS: Data Analysis and Interpretation. Methods in Molecular Biology, 2019, 1908, 113-124.	0.4	17
4715	Identifying loci controlling fiber composition in polyploid sugarcane ( <i>Saccharum</i> spp.) through genome-wide association study. Industrial Crops and Products, 2019, 130, 598-605.	2.5	16
4716	Phylogenetic and expression analysis of histone acetyltransferases in <i>Brachypodium distachyon</i> . Genomics, 2019, 111, 1966-1976.	1.3	5
4717	Simulation of heterogeneous tumour genomes with HeteroGenesis and in silico whole exome sequencing. Bioinformatics, 2019, 35, 2850-2852.	1.8	3
4718	Chromosome level comparative analysis of Brassica genomes. Plant Molecular Biology, 2019, 99, 237-249.	2.0	14
4719	Morphometric differentiation and gene flow in emerald shiners ( <i>Notropis atherinoides</i> ) from the lower Great Lakes and the Niagara River. Journal of Great Lakes Research, 2019, 45, 324-332.	0.8	3
4720	Convergent evolution misled taxonomy in schizothoracine fishes (Cypriniformes: Cyprinidae). Molecular Phylogenetics and Evolution, 2019, 134, 323-337.	1.2	18
4721	Identification and validation of single-nucleotide polymorphism markers linked to first flower node in kenaf by using combined specific-locus amplified fragment sequencing and bulked segregant analysis. Industrial Crops and Products, 2019, 128, 566-571.	2.5	4
4722	REDfly: the transcriptional regulatory element database for <i>Drosophila</i> . Nucleic Acids Research, 2019, 47, D828-D834.	6.5	59
4723	Targeted RNA sequencing: A routine ancillary technique in the diagnosis of bone and soft tissue neoplasms. Genes Chromosomes and Cancer, 2019, 58, 75-87.	1.5	38
4724	Resveratrol decreases the expression of genes involved in inflammation through transcriptional regulation. Free Radical Biology and Medicine, 2019, 130, 8-22.	1.3	37
4725	Characterization of the satellitome in lower vascular plants: the case of the endangered fern <i>Vandenboschia speciosa</i> . Annals of Botany, 2019, 123, 587-599.	1.4	20
4726	Whole-Genome Alignment and Comparative Annotation. Annual Review of Animal Biosciences, 2019, 7, 41-64.	3.6	62
4727	Identification of Mutated Cancer Driver Genes in Unpaired RNA-Seq Samples. Methods in Molecular Biology, 2019, 1878, 95-108.	0.4	0
4728	Transcriptomic response of the <i>Crassostrea virginica</i> gonad after exposure to a water-accommodation fraction of hydrocarbons and the potential implications in reproduction. Marine Genomics, 2019, 43, 9-18.	0.4	7
4729	Quantifying the changes in genetic diversity within sequence-discrete bacterial populations across a spatial and temporal riverine gradient. ISME Journal, 2019, 13, 767-779.	4.4	40
4730	Methylation pattern and mutational status of BRCA1 in canine mammary tumors in a Brazilian population. Comparative Clinical Pathology, 2019, 28, 63-67.	0.3	1

#	ARTICLE	IF	CITATIONS
4731	The heart of an acrobatic bird. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2019, 228, 9-17.	0.8	8
4732	Intensive allochthonous inputs along the Ganges River and their effect on microbial community composition and dynamics. <i>Environmental Microbiology</i> , 2019, 21, 182-196.	1.8	40
4733	Off- and on-target effects of genome editing in mouse embryos. <i>Journal of Reproduction and Development</i> , 2019, 65, 1-5.	0.5	24
4734	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	3.3	108
4735	Proteomics and Protein Interaction in Molecular Cell Signaling Pathways. , 2019, , 17-34.		0
4736	Genome-scale fitness profile of <i>Caulobacter crescentus</i> grown in natural freshwater. <i>ISME Journal</i> , 2019, 13, 523-536.	4.4	35
4737	<i>De novo</i> clustering of long reads by gene from transcriptomics data. <i>Nucleic Acids Research</i> , 2019, 47, e2-e2.	6.5	29
4738	Structure and evolution of double minutes in diagnosis and relapse brain tumors. <i>Acta Neuropathologica</i> , 2019, 137, 123-137.	3.9	63
4739	A Nanopore Sequencing-Based Assay for Rapid Detection of Gene Fusions. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 58-69.	1.2	34
4740	CRISPRInc: a manually curated database of validated sgRNAs for lncRNAs. <i>Nucleic Acids Research</i> , 2019, 47, D63-D68.	6.5	37
4741	MG-RAST version 4 lessons learned from a decade of low-budget ultra-high-throughput metagenome analysis. <i>Briefings in Bioinformatics</i> , 2019, 20, 1151-1159.	3.2	98
4742	Kmerind: A Flexible Parallel Library for K-mer Indexing of Biological Sequences on Distributed Memory Systems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1117-1131.	1.9	10
4743	Federation in genomics pipelines: techniques and challenges. <i>Briefings in Bioinformatics</i> , 2019, 20, 235-244.	3.2	18
4744	Chromosomal inversions promote genomic islands of concerted evolution of <i>Hsp70</i> genes in the <i>Drosophila subobscura</i> species subgroup. <i>Molecular Ecology</i> , 2019, 28, 1316-1332.	2.0	16
4745	The complete chloroplast genome sequence annotation for <i>Malania oleifera</i> , a critically endangered and important bioresource tree. <i>Conservation Genetics Resources</i> , 2019, 11, 271-274.	0.4	10
4746	VA-Store: A Virtual Approximate Store Approach to Supporting Repetitive Big Data in Genome Sequence Analyses. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020, 32, 602-616.	4.0	4
4747	OBSOLETE: Bioinformatic Platforms for Metagenomics. , 2020, , .		0
4748	Comparative assessment of long-read error correction software applied to Nanopore RNA-sequencing data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1164-1181.	3.2	33

#	ARTICLE	IF	CITATIONS
4749	Validation of a Next-Generation Sequencing Assay Targeting RNA for the Multiplexed Detection of Fusion Transcripts and Oncogenic Isoforms. <i>Archives of Pathology and Laboratory Medicine</i> , 2020, 144, 90-98.	1.2	18
4750	Insight into the epigenetic landscape of a currently endogenizing gammaretrovirus in mule deer ( <i>Odocoileus hemionus</i> ). <i>Genomics</i> , 2020, 112, 886-896.	1.3	2
4751	Satellite DNA content of B chromosomes in the characid fish <i>Characidium gomesi</i> supports their origin from sex chromosomes. <i>Molecular Genetics and Genomics</i> , 2020, 295, 195-207.	1.0	22
4752	A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 268-282.	2.2	51
4753	A chromosome-level genome assembly of <i>Pyropia haitanensis</i> (Bangiales, Rhodophyta). <i>Molecular Ecology Resources</i> , 2020, 20, 216-227.	2.2	37
4754	RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. <i>Bioinformatics</i> , 2020, 36, 1382-1390.	1.8	12
4755	Building a sequence map of the pig pan-genome from multiple de novo assemblies and Hi-C data. <i>Science China Life Sciences</i> , 2020, 63, 750-763.	2.3	47
4756	Large miRNA survival analysis reveals a prognostic four-biomarker signature for triple negative breast cancer. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180269.	0.6	16
4757	Metataxonomics of Tunisian phosphogypsum based on five bioinformatics pipelines: Insights for bioremediation. <i>Genomics</i> , 2020, 112, 981-989.	1.3	18
4758	Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 1189-1198.	3.6	3
4759	A pseudomolecule-scale genome assembly of the liverwort <i>Marchantia polymorpha</i> . <i>Plant Journal</i> , 2020, 101, 1378-1396.	2.8	35
4760	Preventive antibiotic treatment of calves: emergence of dysbiosis causing propagation of obese state-associated and mobile multidrug resistance-carrying bacteria. <i>Microbial Biotechnology</i> , 2020, 13, 669-682.	2.0	18
4761	The improved assembly of 7DL chromosome provides insight into the structure and evolution of bread wheat. <i>Plant Biotechnology Journal</i> , 2020, 18, 732-742.	4.1	6
4762	An extraordinarily stable karyotype of the woody <i>Populus</i> species revealed by chromosome painting. <i>Plant Journal</i> , 2020, 101, 253-264.	2.8	46
4763	Bioinformatics prediction and experimental validation of a novel microRNA: hsa-miR-43 within human <i>CDH4</i> gene with a potential metastasis-related function in breast cancer. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 1307-1316.	1.2	7
4764	Detection of <i>CSF1</i> rearrangements deleting the 3' UTR in tenosynovial giant cell tumors. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 96-105.	1.5	33
4765	Concordance of copy number abnormality detection using SNP arrays and Multiplex Ligation-dependent Probe Amplification (MLPA) in acute lymphoblastic leukaemia. <i>Scientific Reports</i> , 2020, 10, 45.	1.6	7
4766	Comparative genomics reveal shared genomic changes in syngnathid fishes and signatures of genetic convergence with placental mammals. <i>National Science Review</i> , 2020, 7, 964-977.	4.6	32

#	ARTICLE	IF	CITATIONS
4767	A novel F-box domain containing cyclin F like gene is required for maintaining the genome stability and survival of chicken primordial germ cells. <i>FASEB Journal</i> , 2020, 34, 1001-1017.	0.2	6
4768	SWAV: a web-based visualization browser for sliding window analysis. <i>Scientific Reports</i> , 2020, 10, 149.	1.6	10
4769	Unveiling Plant-Beneficial Function as Seen in Bacteria Genes from Termite Mound Soil. <i>Journal of Soil Science and Plant Nutrition</i> , 2020, 20, 421-430.	1.7	18
4770	A shared genetic basis of mimicry across swallowtail butterflies points to ancestral co-option of doublesex. <i>Nature Communications</i> , 2020, 11, 6.	5.8	55
4771	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab ( <i>Portunus trituberculatus</i> ). <i>GigaScience</i> , 2020, 9, .	3.3	44
4772	ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. <i>Nature Genetics</i> , 2020, 52, 187-197.	9.4	108
4773	Genome size variation in butterflies (Insecta, Lepidoptera, Papilionoidea): a thorough phylogenetic comparison. <i>Systematic Entomology</i> , 2020, 45, 571-582.	1.7	22
4774	Clonal kinetics and single-cell transcriptional profiling of CAR-T cells in patients undergoing CD19 CAR-T immunotherapy. <i>Nature Communications</i> , 2020, 11, 219.	5.8	167
4775	Contaminations in (meta)genome data: An open issue for the scientific community. <i>IUBMB Life</i> , 2020, 72, 698-705.	1.5	13
4776	Targeted viral vector transduction of relaxin-3 neurons in the rat nucleus incertus using a novel cell-type specific promoter. <i>IBRO Reports</i> , 2020, 8, 1-10.	0.3	2
4777	Identification and characterization of occult human-specific LINE-1 insertions using long-read sequencing technology. <i>Nucleic Acids Research</i> , 2020, 48, 1146-1163.	6.5	68
4778	Deciphering the microbiota data from termite mound soil in South Africa using shotgun metagenomics. <i>Data in Brief</i> , 2020, 28, 104802.	0.5	5
4779	Counting Kmers for Biological Sequences at Large Scale. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 99-108.	2.2	5
4780	The fire ant social supergene is characterized by extensive gene and transposable element copy number variation. <i>Molecular Ecology</i> , 2020, 29, 105-120.	2.0	12
4781	A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. <i>Molecular Cell</i> , 2020, 77, 352-367.e8.	4.5	48
4782	Parachute geckos free fall into synonymy: Gekko phylogeny, and a new subgeneric classification, inferred from thousands of ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106731.	1.2	31
4783	Conflicting phylogenetic signals in genomic data of the coffee family (Rubiaceae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 440-460.	1.6	36
4784	Carbon starvation reduces carbohydrate and anthocyanin accumulation in red-fleshed fruit via trehalose 6-phosphate and MYB27. <i>Plant, Cell and Environment</i> , 2020, 43, 819-835.	2.8	33

#	ARTICLE	IF	CITATIONS
4785	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020, 6, 95-106.	4.7	146
4786	A novel long noncoding RNA Linc-ASEN represses cellular senescence through multileveled reduction of p21 expression. <i>Cell Death and Differentiation</i> , 2020, 27, 1844-1861.	5.0	23
4787	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. <i>Molecular Plant</i> , 2020, 13, 336-350.	3.9	73
4788	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1444-1456.	4.1	56
4789	Sympatric lineages in the <i>Mantidactylus ambreensis</i> complex of Malagasy frogs originated allopatrically rather than by in-situ speciation. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106700.	1.2	12
4790	Long walk to genomics: History and current approaches to genome sequencing and assembly. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 9-19.	1.9	171
4791	Sensitivity of the polyDetect computational pipeline for phylogenetic analyses. <i>Analytical Biochemistry</i> , 2020, 593, 113516.	1.1	4
4792	Comparison of <i>Arachis monticola</i> with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. <i>Advanced Science</i> , 2020, 7, 1901672.	5.6	43
4793	Chromosome Translocation t(14;21)(q11;q22) Activates Both <i>OLIG1</i> and <i>OLIG2</i> in Pediatric T-cell Lymphoblastic Malignancies and May Signify Adverse Prognosis. <i>Cancer Genomics and Proteomics</i> , 2020, 17, 41-48.	1.0	3
4794	Draft Genomes of Two <i>Artocarpus</i> Plants, Jackfruit ( <i>A. heterophyllus</i> ) and Breadfruit ( <i>A. altilis</i> ). <i>Genes</i> , 2020, 11, 27.	1.0	30
4795	Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus <i>Penicillium variabile</i> HXQ-H-1. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 7.	1.5	6
4796	Benchmark study comparing liftover tools for genome conversion of epigenome sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa054.	1.5	19
4797	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
4798	An All-In-One Transcriptome-Based Assay to Identify Therapy-Guiding Genomic Aberrations in Nonsmall Cell Lung Cancer Patients. <i>Cancers</i> , 2020, 12, 2843.	1.7	6
4799	Control of Transcription Initiation by Biased Thermal Fluctuations on Repetitive Genomic Sequences. <i>Biomolecules</i> , 2020, 10, 1299.	1.8	6
4800	DeepAdd: Protein function prediction from k-mer embedding and additional features. <i>Computational Biology and Chemistry</i> , 2020, 89, 107379.	1.1	17
4801	Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. <i>Mitochondrion</i> , 2020, 55, 122-133.	1.6	24
4802	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	5.8	90

#	ARTICLE	IF	CITATIONS
4803	Identification of fruit size associated quantitative trait loci featuring SLAF based high-density linkage map of goji berry ( <i>Lycium spp.</i> ). <i>BMC Plant Biology</i> , 2020, 20, 474.	1.6	18
4804	Haplotype-resolved genome analyses of a heterozygous diploid potato. <i>Nature Genetics</i> , 2020, 52, 1018-1023.	9.4	134
4805	Functional description and development of polymorphic EST-SSR markers in bread wheat and their gene interactions network. <i>Gene Reports</i> , 2020, 21, 100902.	0.4	2
4806	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	1.3	25
4807	Metagenomes of Maize Rhizosphere Samples after Different Fertilization Treatments at Molelwane Farm, Located in North-West Province, South Africa. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
4808	Origin and adaptation to high altitude of Tibetan semi-wild wheat. <i>Nature Communications</i> , 2020, 11, 5085.	5.8	104
4809	Genomic diversity generated by a transposable element burst in a rice recombinant inbred population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26288-26297.	3.3	24
4810	Comparative genomic analyses illuminate the distinct evolution of megabats within Chiroptera. <i>DNA Research</i> , 2020, 27, .	1.5	10
4811	Catabolic Machinery of the Human Gut Microbes Bestow Resilience Against Vanillin Antimicrobial Nature. <i>Frontiers in Microbiology</i> , 2020, 11, 588545.	1.5	40
4812	The molecular structure of long non-coding RNAs: emerging patterns and functional implications. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2020, 55, 662-690.	2.3	51
4813	Metagenomic characterization of microbial communities on plasticized fabric materials exposed to harsh tropical environments. <i>International Biodeterioration and Biodegradation</i> , 2020, 154, 105061.	1.9	17
4814	A database resource and online analysis tools for coronaviruses on a historical and global scale. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2020, .	1.4	15
4815	Genome Sequence of the Euryhaline Javafish Medaka, <i>Oryzias javanicus</i> : A Small Aquarium Fish Model for Studies on Adaptation to Salinity. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 907-915.	0.8	22
4816	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	13.7	210
4817	DropSynth 2.0: high-fidelity multiplexed gene synthesis in emulsions. <i>Nucleic Acids Research</i> , 2020, 48, e95-e95.	6.5	25
4818	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , 2020, 3, 371.	2.0	34
4819	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 161-172.	3.0	18
4820	HIV-1 replication complexes accumulate in nuclear speckles and integrate into speckle-associated genomic domains. <i>Nature Communications</i> , 2020, 11, 3505.	5.8	93

#	ARTICLE	IF	CITATIONS
4821	Integrated analysis of sialotranscriptome and sialoproteome of the brown dog tick <i>Rhipicephalus sanguineus</i> (s.l.): Insights into gene expression during blood feeding. <i>Journal of Proteomics</i> , 2020, 229, 103899.	1.2	25
4822	DNA Barcoding in Nonhuman Primates Reveals Important Limitations in Retrovirus Integration Site Analysis. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 17, 796-809.	1.8	15
4823	XPA deficiency affects the ubiquitin-proteasome system function. <i>DNA Repair</i> , 2020, 94, 102937.	1.3	6
4824	Accurate Detection of HPV Integration Sites in Cervical Cancer Samples Using the Nanopore MinION Sequencer Without Error Correction. <i>Frontiers in Genetics</i> , 2020, 11, 660.	1.1	23
4825	Sequence Compression Benchmark (SCB) database—A comprehensive evaluation of reference-free compressors for FASTA-formatted sequences. <i>GigaScience</i> , 2020, 9, .	3.3	23
4826	Genomic databases. , 2020, , 47-62.		2
4827	Genome-enabled discovery of anthraquinone biosynthesis in <i>Senna tora</i> . <i>Nature Communications</i> , 2020, 11, 5875.	5.8	57
4828	Towards a better understanding of the low recall of insertion variants with short-read based variant callers. <i>BMC Genomics</i> , 2020, 21, 762.	1.2	12
4829	Molecular basis of resistance to organophosphate insecticides in the New World screw-worm fly. <i>Parasites and Vectors</i> , 2020, 13, 562.	1.0	6
4830	Genomic and Transcriptomic Analysis for Identification of Genes and Interlinked Pathways Mediating Artemisinin Resistance in <i>Leishmania donovani</i> . <i>Genes</i> , 2020, 11, 1362.	1.0	6
4831	A High Quality Asian Genome Assembly Identifies Features of Common Missing Regions. <i>Genes</i> , 2020, 11, 1350.	1.0	0
4832	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
4833	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
4834	Contributions of Adaptive Plant Architecture to Transgressive Salinity Tolerance in Recombinant Inbred Lines of Rice: Molecular Mechanisms Based on Transcriptional Networks. <i>Frontiers in Genetics</i> , 2020, 11, 594569.	1.1	7
4835	Development and validation of a 4-color multiplexing spinal muscular atrophy (SMA) genotyping assay on a novel integrated digital PCR instrument. <i>Scientific Reports</i> , 2020, 10, 19892.	1.6	17
4836	Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. <i>Genes</i> , 2020, 11, 1345.	1.0	30
4837	Optimizing performance of GATK workflows using Apache Arrow In-Memory data framework. <i>BMC Genomics</i> , 2020, 21, 683.	1.2	4
4838	Intrinsic laws of k-mer spectra of genome sequences and evolution mechanism of genomes. <i>BMC Evolutionary Biology</i> , 2020, 20, 157.	3.2	8

#	ARTICLE	IF	CITATIONS
4839	Hybrid capture of 964 nuclear genes resolves evolutionary relationships in the mimosoid legumes and reveals the polytomous origins of a large pantropical radiation. <i>American Journal of Botany</i> , 2020, 107, 1710-1735.	0.8	51
4840	The human <i>chd8</i> gene is transcribed from two distant upstream promoters. <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 190-194.	1.0	3
4841	The genome and transcriptome analysis of snake gourd provide insights into its evolution and fruit development and ripening. <i>Horticulture Research</i> , 2020, 7, 199.	2.9	22
4842	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
4843	KRAB zinc finger protein diversification drives mammalian interindividual methylation variability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31290-31300.	3.3	25
4844	The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. <i>Genome Biology</i> , 2020, 21, 291.	3.8	23
4845	Insertion variants missing in the human reference genome are widespread among human populations. <i>BMC Biology</i> , 2020, 18, 167.	1.7	7
4846	Major SCP/TAPS protein expansion in <i>Lucilia cuprina</i> is associated with novel tandem array organisation and domain architecture. <i>Parasites and Vectors</i> , 2020, 13, 598.	1.0	1
4847	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	13.7	256
4848	Comprehensive profiling of extracellular RNA in HPV-induced cancers using an improved pipeline for small RNA-seq analysis. <i>Scientific Reports</i> , 2020, 10, 19450.	1.6	18
4849	A Persisting Nontropical Focus of <i>Burkholderia pseudomallei</i> with Limited Genome Evolution over Five Decades. <i>MSystems</i> , 2020, 5, .	1.7	9
4850	An Automated Method To Predict Mouse Gene and Protein Sequences Using Variant Data. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 925-932.	0.8	1
4851	Metagenomic profiling of bacterial diversity and community structure in termite mounds and surrounding soils. <i>Archives of Microbiology</i> , 2020, 202, 2697-2709.	1.0	23
4852	The roles of climate, geography and natural selection as drivers of genetic and phenotypic differentiation in a widespread amphibian <i>Hyla annectans</i> (Anura: Hylidae). <i>Molecular Ecology</i> , 2020, 29, 3667-3683.	2.0	20
4853	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. <i>Plant Journal</i> , 2020, 104, 662-678.	2.8	52
4854	Effects of inorganic and organic treatments on the microbial community of maize rhizosphere by a shotgun metagenomics approach. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	50
4855	An evolutionary driver of interspersed segmental duplications in primates. <i>Genome Biology</i> , 2020, 21, 202.	3.8	19
4856	Multiple Anchor Staged Alignment Algorithm "Sensitive (MASAA S)"., 2020, , .		3

#	ARTICLE	IF	CITATIONS
4857	Construction of a high-density genetic linkage map and identification of gene controlling resistance to cucumber mosaic virus in <i>Luffa cylindrica</i> (L.) Roem. based on specific length amplified fragment sequencing. <i>Molecular Biology Reports</i> , 2020, 47, 5831-5841.	1.0	3
4858	SARS-CoV-2 genomic variations associated with mortality rate of COVID-19. <i>Journal of Human Genetics</i> , 2020, 65, 1075-1082.	1.1	316
4859	Privately computing set-maximal matches in genomic data. <i>BMC Medical Genomics</i> , 2020, 13, 72.	0.7	5
4860	Ultraconserved Non-coding DNA Within Diptera and Hymenoptera. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3015-3024.	0.8	3
4861	Development of a Genome-Wide Oligonucleotide Microarray Platform for Detection of DNA Copy Number Aberrations in Feline Cancers. <i>Veterinary Sciences</i> , 2020, 7, 88.	0.6	4
4862	Multi-Omics Characterization of the 4T1 Murine Mammary Gland Tumor Model. <i>Frontiers in Oncology</i> , 2020, 10, 1195.	1.3	94
4863	Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. <i>BMC Biology</i> , 2020, 18, 89.	1.7	24
4864	Chromosome-level genome assembly of the coastal horseshoe crab ( <i>Tachypleus gigas</i> ). <i>Molecular Ecology Resources</i> , 2020, 20, 1748-1760.	2.2	20
4865	Genome-wide identification and expression profile of the sox gene family in different tissues and during embryogenesis in the Pacific white shrimp ( <i>Litopenaeus vannamei</i> ). <i>Gene</i> , 2020, 763, 144956.	1.0	4
4866	Ancestral regulatory mechanisms specify conserved midbrain circuitry in arthropods and vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19544-19555.	3.3	21
4867	Morphological divergence and the Quaternary speciation of <i>Actaea purpurea</i> (Ranunculaceae) and its relatives. <i>Journal of Systematics and Evolution</i> , 2022, 60, 43-54.	1.6	2
4868	Whole-genome <i>de novo</i> assemblies reveal extensive structural variations and dynamic organelle-to-nucleus DNA transfers in African and Asian rice. <i>Plant Journal</i> , 2020, 104, 596-612.	2.8	19
4869	Construction of a High-Density Genetic Map Based on SLAF Markers and QTL Analysis of Leaf Size in Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 1143.	1.7	16
4870	smsMap: mapping single molecule sequencing reads by locating the alignment starting positions. <i>BMC Bioinformatics</i> , 2020, 21, 341.	1.2	7
4871	Fusion transcript detection using spatial transcriptomics. <i>BMC Medical Genomics</i> , 2020, 13, 110.	0.7	17
4872	Methods for the identification of mitochondrial DNA variants. , 2020, , 243-275.		0
4873	A Chromosome-Level Genome Assembly of Garlic ( <i>Allium sativum</i> ) Provides Insights into Genome Evolution and Allicin Biosynthesis. <i>Molecular Plant</i> , 2020, 13, 1328-1339.	3.9	89
4874	Metagenomic profiling of the community structure, diversity, and nutrient pathways of bacterial endophytes in maize plant. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1559-1571.	0.7	34

#	ARTICLE	IF	CITATIONS
4875	Mapping and Quantification of Non-Coding RNA Originating from the rDNA in Human Glioma Cells. <i>Cancers</i> , 2020, 12, 2090.	1.7	7
4876	MDACP: A Pathogen Genome and Metagenome Analysis Cloud Platform. <i>Frontiers in Genetics</i> , 2020, 11, 1007.	1.1	1
4877	Phased diploid genome assemblies and pan-genomes provide insights into the genetic history of apple domestication. <i>Nature Genetics</i> , 2020, 52, 1423-1432.	9.4	168
4878	The mechanism of potato resistance to <i>Globodera rostochiensis</i> : comparison of root transcriptomes of resistant and susceptible <i>Solanum phureja</i> genotypes. <i>BMC Plant Biology</i> , 2020, 20, 350.	1.6	5
4879	Progress in quickly finding orthologs as reciprocal best hits: comparing blast, last, diamond and MMseqs2. <i>BMC Genomics</i> , 2020, 21, 741.	1.2	43
4880	Temperate Bacteriophages (Prophages) in <i>Pseudomonas aeruginosa</i> Isolates Belonging to the International Cystic Fibrosis Clone (CC274). <i>Frontiers in Microbiology</i> , 2020, 11, 556706.	1.5	18
4881	pH-dependent transcriptional profile changes in iron-deficient <i>Arabidopsis</i> roots. <i>BMC Genomics</i> , 2020, 21, 694.	1.2	24
4882	LncRBase V.2: an updated resource for multispecies lncRNAs and ClinicLSNP hosting genetic variants in lncRNAs for cancer patients. <i>RNA Biology</i> , 2021, 18, 1136-1151.	1.5	14
4883	Extracellular microRNA 3' end modification across diverse body fluids. <i>Epigenetics</i> , 2021, 16, 1000-1015.	1.3	7
4884	Draft Genome Sequences of Two Virulent <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> Swine Isolates from Pennsylvania. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
4885	The <i>Eruca sativa</i> Genome and Transcriptome: A Targeted Analysis of Sulfur Metabolism and Glucosinolate Biosynthesis Pre and Postharvest. <i>Frontiers in Plant Science</i> , 2020, 11, 525102.	1.7	12
4886	Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. <i>Scientific Data</i> , 2020, 7, 324.	2.4	33
4887	Dietary Phytase- and Lactic Acid-Treated Cereals Caused Greater Taxonomic Adaptations than Functional Adaptations in the Cecal Metagenome of Growing Pigs. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	7
4888	Genome/transcriptome analysis of the chigger mite <i>Leptotrombidium pallidum</i> , a major vector for scrub typhus, with a special focus on genes more abundantly expressed in larval stage. <i>Journal of Asia-Pacific Entomology</i> , 2020, 23, 816-824.	0.4	4
4889	The <i>Phoebe</i> genome sheds light on the evolution of magnoliids. <i>Horticulture Research</i> , 2020, 7, 146.	2.9	41
4890	An integrative proteogenomics approach reveals peptides encoded by annotated lincRNA in the mouse kidney inner medulla. <i>Physiological Genomics</i> , 2020, 52, 485-491.	1.0	6
4891	Background-suppressed live visualization of genomic loci with an improved CRISPR system based on a split fluorophore. <i>Genome Research</i> , 2020, 30, 1306-1316.	2.4	12
4892	PacBio genome sequencing reveals new insights into the genomic organisation of the multi-copy <i>ToxB</i> gene of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> . <i>BMC Genomics</i> , 2020, 21, 645.	1.2	15

#	ARTICLE	IF	CITATIONS
4893	A Novel Microduplication Spanning Exons 8–16 of ATP2C1 That Was Undetectable by Standard Sanger Sequencing in a Japanese Patient With Hailey–Hailey Disease. <i>Frontiers in Medicine</i> , 2020, 7, 492.	1.2	3
4894	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295.	1.3	45
4895	Shotgun Metagenomic Survey of Maize Soil Rhizobiome. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
4896	A Novel Recurrent COL5A1 Genetic Variant Is Associated With a Dysplasia-Associated Arterial Disease Exhibiting Dissections and Fibromuscular Dysplasia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 2686-2699.	1.1	30
4897	Long-read sequencing and de novo genome assembly of marine medaka ( <i>Oryzias melastigma</i> ). <i>BMC Genomics</i> , 2020, 21, 640.	1.2	7
4898	Cytogenetically visible inversions are formed by multiple molecular mechanisms. <i>Human Mutation</i> , 2020, 41, 1979-1998.	1.1	12
4899	Ultrasensitive deletion detection links mitochondrial DNA replication, disease, and aging. <i>Genome Biology</i> , 2020, 21, 248.	3.8	48
4900	Bacterial Genome Wide Association Studies (bGWAS) and Transcriptomics Identifies Cryptic Antimicrobial Resistance Mechanisms in <i>Acinetobacter baumannii</i> . <i>Frontiers in Public Health</i> , 2020, 8, 451.	1.3	9
4901	The complete chloroplast genome sequence of Red Asparagus Lettuce ( <i>Lactuca sativa</i> var. <i>asparagine</i> L.) Tj ETQq0 0.0 rgBT /Qverlock 10	0.2	9
4902	Positive autoregulation of lag-1 in response to LIN-12 activation in cell fate decisions during <i>C. elegans</i> reproductive system development. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	8
4903	Genomic content of chemosensory receptors in two sister blister beetles facilitates characterization of chemosensory evolution. <i>BMC Genomics</i> , 2020, 21, 589.	1.2	6
4904	Comparative genomics of muskmelon reveals a potential role for retrotransposons in the modification of gene expression. <i>Communications Biology</i> , 2020, 3, 432.	2.0	29
4905	Sequencing and assembly of the Egyptian buffalo genome. <i>PLoS ONE</i> , 2020, 15, e0237087.	1.1	11
4906	New <i>Plasmodium vivax</i> Genomes From the China-Myanmar Border. <i>Frontiers in Microbiology</i> , 2020, 11, 1930.	1.5	5
4907	Identification of the SUT Gene Family in Pomegranate ( <i>Punica granatum</i> L.) and Functional Analysis of PgL0145810.1. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6608.	1.8	9
4908	Hedgehog signaling controls segmentation dynamics and diversity via msx1 in a spider embryo. <i>Science Advances</i> , 2020, 6, .	4.7	19
4909	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	17
4910	Viral Abundance and Diversity of Production Fluids in Oil Reservoirs. <i>Microorganisms</i> , 2020, 8, 1429.	1.6	3

#	ARTICLE	IF	CITATIONS
4911	The UCSC SARS-CoV-2 Genome Browser. <i>Nature Genetics</i> , 2020, 52, 991-998.	9.4	79
4912	Genomic characterization of malignant progression in neoplastic pancreatic cysts. <i>Nature Communications</i> , 2020, 11, 4085.	5.8	77
4913	Cytogenetic and molecular study of 370 infertile men in South India highlighting the importance of copy number variations by multiplex ligationâ€dependent probe amplification. <i>Andrologia</i> , 2020, 52, e13761.	1.0	1
4914	Organic Farming Enhances the Diversity and Community Structure of Endophytic Archaea and Fungi in Maize Plant: a Shotgun Approach. <i>Journal of Soil Science and Plant Nutrition</i> , 2020, 20, 2587-2599.	1.7	26
4915	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020, 370, .	6.0	105
4916	Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. <i>Nature Communications</i> , 2020, 11, 6327.	5.8	39
4917	A Chromosome-Level Genome Assembly of the Anglerfish <i>Lophius litulon</i> . <i>Frontiers in Genetics</i> , 2020, 11, 581161.	1.1	2
4918	Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9618.	1.8	8
4919	Hormonal regulation of microRNA expression dynamics in the gut of the yellow fever mosquito <i>Aedes aegypti</i> . <i>RNA Biology</i> , 2020, 18, 1-10.	1.5	3
4920	WY195, a New Inducible Promoter From the Rubber Powdery Mildew Pathogen, Can Be Used as an Excellent Tool for Genetic Engineering. <i>Frontiers in Microbiology</i> , 2020, 11, 610252.	1.5	1
4921	Use of the Illumina EPIC methylation array for epigenomic research in the crabâ€eating macaque ( <i>Macaca fascicularis</i> ). <i>Neuropsychopharmacology Reports</i> , 2020, 40, 423-426.	1.1	8
4922	An Improved Sequencing-Based Bioinformatics Pipeline to Track the Distribution and Clonal Architecture of Proviral Integration Sites. <i>Frontiers in Microbiology</i> , 2020, 11, 587306.	1.5	5
4923	LSH mediates gene repression through macroH2A deposition. <i>Nature Communications</i> , 2020, 11, 5647.	5.8	35
4924	A novel method for using RNAâ€seq data to identify imprinted genes in social Hymenoptera with multiply mated queens. <i>Journal of Evolutionary Biology</i> , 2020, 33, 1770-1782.	0.8	3
4925	Silent Infection of B and CD8 + T Lymphocytes by Influenza A Virus in Children with Tonsillar Hypertrophy. <i>Journal of Virology</i> , 2020, 94, .	1.5	5
4926	Sequencing and Functional Annotation of the Whole Genome of <i>Shiraia bambusicola</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 23-35.	0.8	8
4927	A Fast and Memoryâ€Efficient Spectral Library Search Algorithm Using Localityâ€Sensitive Hashing. <i>Proteomics</i> , 2020, 20, e2000002.	1.3	10
4928	Unique properties of a subset of human pluripotent stem cells with high capacity for self-renewal. <i>Nature Communications</i> , 2020, 11, 2420.	5.8	29

#	ARTICLE	IF	CITATIONS
4929	Allele-aware chromosome-level genome assembly and efficient transgene-free genome editing for the autotetraploid cultivated alfalfa. <i>Nature Communications</i> , 2020, 11, 2494.	5.8	224
4930	The Evolution of Human Cancer Gene Duplications across Mammals. <i>Molecular Biology and Evolution</i> , 2020, 37, 2875-2886.	3.5	31
4931	Phylogenomics unravels Quaternary vicariance and allopatric speciation patterns in temperate montane plant species: A case study on the <i>Ranunculus auricomus</i> species complex. <i>Molecular Ecology</i> , 2020, 29, 2031-2049.	2.0	41
4932	The Role of lncRNAs TAPIR-1 and -2 as Diagnostic Markers and Potential Therapeutic Targets in Prostate Cancer. <i>Cancers</i> , 2020, 12, 1122.	1.7	15
4933	Bioinformatic prediction of potential T cell epitopes for SARS-Cov-2. <i>Journal of Human Genetics</i> , 2020, 65, 569-575.	1.1	123
4934	Chromosome-level assembly of the horseshoe crab genome provides insights into its genome evolution. <i>Nature Communications</i> , 2020, 11, 2322.	5.8	57
4935	A Comparison of Two DNA Metagenomic Bioinformatic Pipelines While Evaluating the Microbial Diversity in Feces of Tanzanian Small Holder Dairy Cattle. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	16
4936	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. <i>Plant Physiology</i> , 2020, 183, 399-413.	2.3	40
4937	TGFamFinder : a novel solution for targeted gene family annotation in plants. <i>New Phytologist</i> , 2020, 227, 1568-1581.	3.5	23
4938	The third generation sequencing: the advanced approach to genetic diseases. <i>Translational Pediatrics</i> , 2020, 9, 163-173.	0.5	77
4939	Capturing Differential Allele-Level Expression and Genotypes of All Classical HLA Loci and Haplotypes by a New Capture RNA-Seq Method. <i>Frontiers in Immunology</i> , 2020, 11, 941.	2.2	45
4940	Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. <i>Cell Reports</i> , 2020, 31, 107723.	2.9	62
4941	Whole genome shotgun sequencing of POPs degrading bacterial community dwelling tannery effluents and petrol contaminated soil. <i>Microbiological Research</i> , 2020, 238, 126504.	2.5	12
4942	Differentially evolved drought stress indices determine the genetic variation of <i>Brassica napus</i> at seedling traits by genome-wide association mapping. <i>Journal of Advanced Research</i> , 2020, 24, 447-461.	4.4	29
4943	AnthOligo: automating the design of oligonucleotides for capture/enrichment technologies. <i>Bioinformatics</i> , 2020, 36, 4353-4356.	1.8	4
4944	Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 4518-4530.	0.8	34
4945	Genotyping by multiplexed sequencing (GMS): A customizable platform for genomic selection. <i>PLoS ONE</i> , 2020, 15, e0229207.	1.1	28
4946	Chromosome-scale scaffolds for the Chinese hamster reference genome assembly to facilitate the study of the CHO epigenome. <i>Biotechnology and Bioengineering</i> , 2020, 117, 2331-2339.	1.7	30

#	ARTICLE	IF	CITATIONS
4947	High-quality chromosome-scale assembly of the walnut ( <i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	3.3	83
4948	A copy number variant is associated with a spectrum of pigmentation patterns in the rock pigeon ( <i>Columba livia</i> ). <i>PLoS Genetics</i> , 2020, 16, e1008274.	1.5	34
4949	Synergistic CRISPRa-Regulated Chondrogenic Extracellular Matrix Deposition Without Exogenous Growth Factors. <i>Tissue Engineering - Part A</i> , 2020, 26, 1169-1179.	1.6	11
4950	First Genome Sequence of the Gunnisonâ€™s Prairie Dog ( <i>Cynomys gunnisoni</i> ), a Keystone Species and Player in the Transmission of Sylvatic Plague. <i>Genome Biology and Evolution</i> , 2020, 12, 618-625.	1.1	6
4951	Rapid Identification of Soybean Resistance Genes to Soybean Mosaic Virus by SLAF-seq Bulk Segregant Analysis. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 666-675.	1.0	8
4952	Whole genome sequence analysis reveals genetic structure and X-chromosome haplotype structure in indigenous Chinese pigs. <i>Scientific Reports</i> , 2020, 10, 9433.	1.6	11
4953	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. <i>Genome Biology and Evolution</i> , 2020, 12, 842-859.	1.1	13
4954	Shotgun metagenomic sequencing data of sunflower rhizosphere microbial community in South Africa. <i>Data in Brief</i> , 2020, 31, 105831.	0.5	8
4955	Dissecting the genome of star fruit ( <i>Averrhoa carambola</i> L.). <i>Horticulture Research</i> , 2020, 7, 94.	2.9	16
4956	Inducible aging in <i>Hydra oligactis</i> implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. <i>GeroScience</i> , 2020, 42, 1119-1132.	2.1	13
4957	Larger, unfiltered datasets are more effective at resolving phylogenetic conflict: Introns, exons, and UCEs resolve ambiguities in Golden-backed frogs ( <i>Anura: Ranidae</i> ; genus <i>Hylarana</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106899.	1.2	30
4958	Development and Application of a Core Genome Multilocus Sequence Typing Scheme for the Health Care-Associated Pathogen <i>Pseudomonas aeruginosa</i> . <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	20
4959	Cytogenetic Characterization of a Small Evolutionary Rearrangement Involving Chromosomes BTA21 and ÖAR18. <i>Cytogenetic and Genome Research</i> , 2020, 160, 193-198.	0.6	2
4960	Insight into the Possible Formation Mechanism of the Intersex Phenotype of Lanzhou Fat-Tailed Sheep Using Whole-Genome Resequencing. <i>Animals</i> , 2020, 10, 944.	1.0	6
4961	Genome sequence and comparative analysis of reindeer ( <i>Rangifer tarandus</i> ) in northern Eurasia. <i>Scientific Reports</i> , 2020, 10, 8980.	1.6	30
4962	The gene-rich genome of the scallop <i>Pecten maximus</i> . <i>GigaScience</i> , 2020, 9, .	3.3	53
4963	High-Quality Genome Assembly of <i>Chrysaora quinquecirrha</i> Provides Insights Into the Adaptive Evolution of Jellyfish. <i>Frontiers in Genetics</i> , 2020, 11, 535.	1.1	6
4964	Structural and Functional Annotation of Transposable Elements Revealed a Potential Regulation of Genes Involved in Rubber Biosynthesis by TE-Derived siRNA Interference in <i>Hevea brasiliensis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 4220.	1.8	6

#	ARTICLE	IF	CITATIONS
4965	The Complete Chloroplast Genome Sequencing and Comparative Analysis of Reed Canary Grass ( <i>Phalaris arundinacea</i> ) and Hardinggrass ( <i>P. aquatica</i> ). <i>Plants</i> , 2020, 9, 748.	1.6	9
4966	A chromosome-level genome assembly of the parasitoid wasp <i>Pteromalus puparum</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1384-1402.	2.2	35
4967	The genetic basis of sex determination in grapes. <i>Nature Communications</i> , 2020, 11, 2902.	5.8	118
4968	Genetic Variants of the DSF Quorum Sensing System in <i>Stenotrophomonas maltophilia</i> Influence Virulence and Resistance Phenotypes Among Genotypically Diverse Clinical Isolates. <i>Frontiers in Microbiology</i> , 2020, 11, 1160.	1.5	22
4969	Full-length transcript characterization of SF3B1 mutation in chronic lymphocytic leukemia reveals downregulation of retained introns. <i>Nature Communications</i> , 2020, 11, 1438.	5.8	273
4970	DNA markers based on retrotransposon insertion polymorphisms can detect short DNA fragments for strawberry cultivar identification. <i>Breeding Science</i> , 2020, 70, 231-240.	0.9	5
4971	AtXRN4 Affects the Turnover of Chosen miRNA*s in Arabidopsis. <i>Plants</i> , 2020, 9, 362.	1.6	7
4972	Genomic and transcriptomic analysis of <i>Candida intermedia</i> reveals the genetic determinants for its xylose-converting capacity. <i>Biotechnology for Biofuels</i> , 2020, 13, 48.	6.2	15
4973	Grape-RNA: A Database for the Collection, Evaluation, Treatment, and Data Sharing of Grape RNA-Seq Datasets. <i>Genes</i> , 2020, 11, 315.	1.0	12
4974	The bHLH transcription factor PPLS1 regulates the color of pulvinus and leaf sheath in foxtail millet ( <i>Setaria italica</i> ). <i>Theoretical and Applied Genetics</i> , 2020, 133, 1911-1926.	1.8	14
4975	Hb Rush (HBB: c.304G>C): A Rare Variant Hemoglobin Mimicking the Hb S (HBB: c.20A>T) Variant on High Performance Liquid Chromatography. <i>Hemoglobin</i> , 2020, 44, 64-66.	0.4	1
4976	Evolution and diversity of the wild rice <i>Oryza officinalis</i> complex, across continents genome types, and ploidy levels. <i>Genome Biology and Evolution</i> , 2020, 12, 413-428.	1.1	17
4977	The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , 2020, 21, 60.	3.8	104
4978	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year <i>Burkholderia pseudomallei</i> infection. <i>PLoS Pathogens</i> , 2020, 16, e1008298.	2.1	12
4979	A Partially Phase-Separated Genome Sequence Assembly of the <i>Vitis</i> Rootstock 'Traminer' ( <i>Vitis riparia</i> L.) Tj ETQq0 0 0 rgBT /Ove Science, 2020, 11, 156.	1.7	6
4980	Small circRNAs with self-cleaving ribozymes are highly expressed in diverse metazoan transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, 5054-5064.	6.5	20
4981	Cis-regulatory analysis of <i>Onecut1</i> expression in fate-restricted retinal progenitor cells. <i>Neural Development</i> , 2020, 15, 5.	1.1	13
4982	Chromosome-level analysis of the <i>Crassostrea hongkongensis</i> genome reveals extensive duplication of immune-related genes in bivalves. <i>Molecular Ecology Resources</i> , 2020, 20, 980-994.	2.2	45

#	ARTICLE	IF	CITATIONS
4983	Genomic characterization of human brain metastases identifies drivers of metastatic lung adenocarcinoma. <i>Nature Genetics</i> , 2020, 52, 371-377.	9.4	177
4984	Can we use it? On the utility of de novo and reference-based assembly of Nanopore data for plant plastome sequencing. <i>PLoS ONE</i> , 2020, 15, e0226234.	1.1	33
4985	Identification and verification of differentially expressed genes in yak mammary tissue during the lactation cycle. <i>Journal of Dairy Research</i> , 2020, 87, 158-165.	0.7	6
4986	Inferring Tunicate Relationships and the Evolution of the Tunicate Hox Cluster with the Genome of <i>Corella inflata</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 948-964.	1.1	12
4987	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. <i>Genome Research</i> , 2020, 30, 334-346.	2.4	56
4988	Evidence of constraint in the 3D genome for trans-splicing in human cells. <i>Science China Life Sciences</i> , 2020, 63, 1380-1393.	2.3	1
4989	Assembly of Mitochondrial Complex I Requires the Low-Complexity Protein AMC1 in <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2020, 214, 895-911.	1.2	5
4990	A Chromosome-Scale Assembly of the Asian Honeybee <i>Apis cerana</i> Genome. <i>Frontiers in Genetics</i> , 2020, 11, 279.	1.1	13
4991	Identification of Some Errors in the Genome Assembly of Bovidae by FISH. <i>Cytogenetic and Genome Research</i> , 2020, 160, 85-93.	0.6	5
4992	Modified nucleotides may have enhanced early RNA catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8236-8242.	3.3	17
4993	Nuclear-mitochondrial DNA segments resemble paternally inherited mitochondrial DNA in humans. <i>Nature Communications</i> , 2020, 11, 1740.	5.8	75
4994	What Is in <i>Umbilicaria pustulata</i> ? A Metagenomic Approach to Reconstruct the Holo-Genome of a Lichen. <i>Genome Biology and Evolution</i> , 2020, 12, 309-324.	1.1	37
4995	Survival in the Tropics despite isolation, inbreeding and asexual reproduction: insights from the genome of the world's southernmost poplar ( <i>Populus ilicifolia</i> ). <i>Plant Journal</i> , 2020, 103, 430-442.	2.8	23
4996	GSAAlign: an efficient sequence alignment tool for intra-species genomes. <i>BMC Genomics</i> , 2020, 21, 182.	1.2	32
4997	Expert curation of the human and mouse olfactory receptor gene repertoires identifies conserved coding regions split across two exons. <i>BMC Genomics</i> , 2020, 21, 196.	1.2	28
4998	Deep sequencing of liver explant transcriptomes reveals extensive expression from integrated hepatitis B virus DNA. <i>Journal of Viral Hepatitis</i> , 2020, 27, 1162-1170.	1.0	18
4999	Efficient Nuclease-Directed Integration of Lentivirus Vectors into the Human Ribosomal DNA Locus. <i>Molecular Therapy</i> , 2020, 28, 1858-1875.	3.7	12
5000	Chromosome-level genome assembly of the East Asian common octopus ( <i>Octopus sinensis</i> ) using PacBio sequencing and Hi-C technology. <i>Molecular Ecology Resources</i> , 2020, 20, 1572-1582.	2.2	28

#	ARTICLE	IF	CITATIONS
5001	Metagenomics: Applications of functional and structural approaches and meta-omics. , 2020, , 471-505.		4
5002	Genome assembly of the basket willow, <i>Salix viminalis</i> , reveals earliest stages of sex chromosome expansion. <i>BMC Biology</i> , 2020, 18, 78.	1.7	39
5003	Molecular dynamic simulations of full-length human purinergic receptor subtype P2X7 bonded to potent inhibitors. <i>European Journal of Pharmaceutical Sciences</i> , 2020, 152, 105454.	1.9	11
5004	A fully-automated method discovers loss of mouse-lethal and human-monogenic disease genes in 58 mammals. <i>Nucleic Acids Research</i> , 2020, 48, e91-e91.	6.5	7
5005	High-density genetic map construction and identification of loci controlling flower-type traits in <i>Chrysanthemum</i> ( <i>Chrysanthemum</i> <i>morifolium</i> Ramat.). <i>Horticulture Research</i> , 2020, 7, 108.	2.9	33
5006	Termite Societies Promote the Taxonomic and Functional Diversity of Archaeal Communities in Mound Soils. <i>Biology</i> , 2020, 9, 136.	1.3	6
5007	Stretch Profile: A pruning technique to accelerate DNA sequence search. <i>Informatics in Medicine Unlocked</i> , 2020, 19, 100323.	1.9	2
5008	Genome sequencing and transcriptome analysis of <i>Geotrichum citri-aurantii</i> on citrus reveal the potential pathogenic- and guazatine-resistance related genes. <i>Genomics</i> , 2020, 112, 4063-4071.	1.3	15
5009	CandiMeth: Powerful yet simple visualization and quantification of DNA methylation at candidate genes. <i>GigaScience</i> , 2020, 9, .	3.3	6
5010	Genome Report: Whole Genome Sequence and Annotation of the Parasitoid Jewel Wasp <i>Nasonia giraulti</i> Laboratory Strain RV2X[u]. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2565-2572.	0.8	12
5011	Suppression of adenosine-to-inosine (A-to-I) RNA editome by death associated protein 3 (DAP3) promotes cancer progression. <i>Science Advances</i> , 2020, 6, eaba5136.	4.7	29
5012	Intestinal Virome in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 72, 2182-2196.	3.6	74
5013	Comprehensive temporal reprogramming ensures dynamicity of transcriptomic profile for adaptive response in <i>Taxus contorta</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 1401-1414.	1.0	8
5014	Shotgun metagenomic data of root endophytic microbiome of maize ( <i>Zea mays</i> L.). <i>Data in Brief</i> , 2020, 31, 105893.	0.5	15
5015	Parallel and nonparallel genomic responses contribute to herbicide resistance in <i>Ipomoea purpurea</i> , a common agricultural weed. <i>PLoS Genetics</i> , 2020, 16, e1008593.	1.5	39
5016	High-Quality Genome Assembly of <i>Eriocheir japonica sinensis</i> Reveals Its Unique Genome Evolution. <i>Frontiers in Genetics</i> , 2019, 10, 1340.	1.1	32
5017	The landscape of chimeric RNAs in non-diseased tissues and cells. <i>Nucleic Acids Research</i> , 2020, 48, 1764-1778.	6.5	47
5018	The complete mitochondrial genome of <i>Talpa aquitania</i> (Talpidae; Insectivora), a mole species endemic to northern Spain and southern France. <i>Molecular Biology Reports</i> , 2020, 47, 2397-2403.	1.0	6

#	ARTICLE	IF	CITATIONS
5019	Taxonomic classification and abundance estimation using 16S and WGS—A comparison using controlled reference samples. <i>Forensic Science International: Genetics</i> , 2020, 46, 102257.	1.6	31
5020	An inferred fitness consequence map of the rice genome. <i>Nature Plants</i> , 2020, 6, 119-130.	4.7	20
5021	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <i>Current Bioinformatics</i> , 2020, 15, 2-16.	0.7	9
5022	Evolutionary Dynamics of the POTE Gene Family in Human and Nonhuman Primates. <i>Genes</i> , 2020, 11, 213.	1.0	7
5023	New genome assembly of the barn owl ( <i>Tyto alba alba</i> ). <i>Ecology and Evolution</i> , 2020, 10, 2284-2298.	0.8	11
5024	Interspecific Variation in Nematode Responses to Metals. <i>Environmental Toxicology and Chemistry</i> , 2020, 39, 1006-1016.	2.2	5
5025	Complete chloroplast genome of <i>Physalis chenopodifolia</i> Lam. (Solanaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 162-163.	0.2	5
5026	The draft genome of mandrill ( <i>Mandrillus sphinx</i> ): An Old World monkey. <i>Scientific Reports</i> , 2020, 10, 2431.	1.6	3
5027	Exploring the computational methods for protein-ligand binding site prediction. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 417-426.	1.9	112
5028	Current Trends in Diagnostics of Viral Infections of Unknown Etiology. <i>Viruses</i> , 2020, 12, 211.	1.5	49
5029	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. <i>Frontiers in Genetics</i> , 2019, 10, 1396.	1.1	10
5030	Enterovirus 71 Infection Shapes Host T Cell Receptor Repertoire and Presumably Expands VP1-Specific TCR $\beta$ CDR3 Cluster. <i>Pathogens</i> , 2020, 9, 121.	1.2	1
5031	ZEBra: Zebra finch Expression Brain Atlas—A resource for comparative molecular neuroanatomy and brain evolution studies. <i>Journal of Comparative Neurology</i> , 2020, 528, 2099-2131.	0.9	30
5032	SLAF-seq Uncovers the Genetic Diversity and Adaptation of Chinese Elm ( <i>Ulmus parvifolia</i> ) in Eastern China. <i>Forests</i> , 2020, 11, 80.	0.9	13
5033	Evolutionary dynamics of chloroplast genomes in subfamily Aroideae (Araceae). <i>Genomics</i> , 2020, 112, 2349-2360.	1.3	79
5034	Phylogenetic informativeness analyses to clarify past diversification processes in Cucurbitaceae. <i>Scientific Reports</i> , 2020, 10, 488.	1.6	17
5035	Water Deficit Transcriptomic Responses Differ in the Invasive <i>Tamarix chinensis</i> and <i>T. ramosissima</i> Established in the Southern and Northern United States. <i>Plants</i> , 2020, 9, 86.	1.6	10
5036	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020, 21, 47.	1.2	84

#	ARTICLE	IF	CITATIONS
5037	Genomic features of the fall armyworm ( <i>Spodoptera frugiperda</i> ) (J.E. Smith) yield insights into its defense system and flight capability. <i>Entomological Research</i> , 2020, 50, 100-112.	0.6	10
5038	Genome assembly and characterization of a complex zfBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. <i>PLoS Genetics</i> , 2020, 16, e1008571.	1.5	112
5039	Investigating RNA editing in deep transcriptome datasets with REDIttools and REDlportal. <i>Nature Protocols</i> , 2020, 15, 1098-1131.	5.5	94
5040	The evolutionary arms race between transposable elements and piRNAs in <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2020, 20, 14.	3.2	34
5041	Expanded complement of Niemann-Pick type C2-like protein genes in <i>Clonorchis sinensis</i> suggests functions beyond sterol binding and transport. <i>Parasites and Vectors</i> , 2020, 13, 38.	1.0	3
5042	Five mitochondrial genomes of black fungus gnats (Sciaridae) and their phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2020, 150, 200-205.	3.6	15
5043	Whole-genome and time-course dual RNA-Seq analyses reveal chronic pathogenicity-related gene dynamics in the ginseng rusty root rot pathogen <i>Ilyonectria robusta</i> . <i>Scientific Reports</i> , 2020, 10, 1586.	1.6	18
5044	O6-Methylguanine-DNA Methyltransferase (MGMT): Challenges and New Opportunities in Glioma Chemotherapy. <i>Frontiers in Oncology</i> , 2019, 9, 1547.	1.3	140
5045	Unique k-mers as Strain-Specific Barcodes for Phylogenetic Analysis and Natural Microbiome Profiling. <i>International Journal of Molecular Sciences</i> , 2020, 21, 944.	1.8	7
5046	Aging-regulated anti-apoptotic long non-coding RNA Sarrah augments recovery from acute myocardial infarction. <i>Nature Communications</i> , 2020, 11, 2039.	5.8	63
5047	Vanillin Production in <i>Pseudomonas</i> : Whole-Genome Sequencing of <i>Pseudomonas</i> sp. Strain 9.1 and Reannotation of <i>Pseudomonas putida</i> CalA as a Vanillin Reductase. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	17
5048	Genome-wide assessment of population structure and genetic diversity for <i>Anabasis aphylla</i> based on specific length amplification fragment sequencing. <i>Journal of Plant Interactions</i> , 2020, 15, 75-82.	1.0	4
5049	Tissue memory CD4+ T cells expressing IL-7 receptor-alpha (CD127) preferentially support latent HIV-1 infection. <i>PLoS Pathogens</i> , 2020, 16, e1008450.	2.1	34
5050	High-density SNP map facilitates fine mapping of QTLs and candidate genes discovery for <i>Aspergillus flavus</i> resistance in peanut ( <i>Arachis hypogaea</i> ). <i>Theoretical and Applied Genetics</i> , 2020, 133, 2239-2257.	1.8	25
5051	Development of a multiparent advanced generation intercross (MAGIC) population for genetic exploitation of complex traits in <i>Brassica juncea</i> : Glucosinolate content as an example. <i>Plant Breeding</i> , 2020, 139, 779-789.	1.0	9
5052	Horizontal gene transfer of <i>Fhb7</i> from fungus underlies <i>Fusarium</i> head blight resistance in wheat. <i>Science</i> , 2020, 368, .	6.0	398
5053	De novo Assembly of Transcriptomes From a B73 Maize Line Introgressed With a QTL for Resistance to Gray Leaf Spot Disease Reveals a Candidate Allele of a Lectin Receptor-Like Kinase. <i>Frontiers in Plant Science</i> , 2020, 11, 191.	1.7	9
5054	Expansion and Conservation of Biosynthetic Gene Clusters in Pathogenic <i>Pyrenophora</i> spp.. <i>Toxins</i> , 2020, 12, 242.	1.5	13

#	ARTICLE	IF	CITATIONS
5055	Phytochrome Coordinates with a hnRNP to Regulate Alternative Splicing via an Exonic Splicing Silencer. <i>Plant Physiology</i> , 2020, 182, 243-254.	2.3	24
5056	Comprehensive Analysis of HERV Transcriptome in HIV+ Cells: Absence of HML2 Activation and General Downregulation of Individual HERV Loci. <i>Viruses</i> , 2020, 12, 481.	1.5	9
5057	SNP discovery of <i>Camellia oleifera</i> based on RNA-seq and its application for identification of genetic relationships and locus for oil content among different cultivars. <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 687-702.	0.9	1
5058	Humans Are Selectively Exposed to <i>Pneumocystis jirovecii</i> . <i>MBio</i> , 2020, 11, .	1.8	8
5059	Exploring the success of Brazilian endemic clone <i>Pseudomonas aeruginosa</i> ST277 and its association with the CRISPR-Cas system type I-C. <i>BMC Genomics</i> , 2020, 21, 255.	1.2	15
5060	Mutational landscape and genetic signatures of cell-free DNA in tumour-induced osteomalacia. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 4931-4943.	1.6	4
5061	Draft genome and description of <i>Negativicoccus massiliensis</i> strain Marseille-P2082, a new species isolated from the gut microbiota of an obese patient. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 997-1008.	0.7	0
5062	ASFVdb: an integrative resource for genomic and proteomic analyses of African swine fever virus. Database: the <i>Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	11
5063	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	380
5064	Multifaceted Hi-C benchmarking: what makes a difference in chromosome-scale genome scaffolding?. <i>GigaScience</i> , 2020, 9, .	3.3	39
5065	Large X-Linked Palindromes Undergo Arm-to-Arm Gene Conversion across <i>Mus</i> Lineages. <i>Molecular Biology and Evolution</i> , 2020, 37, 1979-1985.	3.5	8
5066	The UCSC repeat browser allows discovery and visualization of evolutionary conflict across repeat families. <i>Mobile DNA</i> , 2020, 11, 13.	1.3	31
5067	Deficiency in the endocytic adaptor proteins PHETA1/2 impair renal and craniofacial development. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	7
5068	Evaluation of <i>Saccharomyces cerevisiae</i> Wine Yeast Competitive Fitness in Enologically Relevant Environments by Barcode Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 591-603.	0.8	10
5069	Comparison of SNP Calling Pipelines and NGS Platforms to Predict the Genomic Regions Harboring Candidate Genes for Nodulation in Cultivated Peanut. <i>Frontiers in Genetics</i> , 2020, 11, 222.	1.1	7
5070	Error, noise and bias in de novo transcriptome assemblies. <i>Molecular Ecology Resources</i> , 2021, 21, 18-29.	2.2	40
5071	Levenshtein Distance, Sequence Comparison and Biological Database Search. <i>IEEE Transactions on Information Theory</i> , 2021, 67, 3287-3294.	1.5	51
5072	FED: a web tool for foreign element detection of genome-edited organism. <i>Science China Life Sciences</i> , 2021, 64, 167-170.	2.3	8

#	ARTICLE	IF	CITATIONS
5073	Population history and genomic admixture of sea snakes of the genus <i>Laticauda</i> in the West Pacific. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 107005.	1.2	7
5074	<i>In Vivo</i> Gene Therapy for Canine SCID-X1 Using Cocal-Pseudotyped Lentiviral Vector. <i>Human Gene Therapy</i> , 2021, 32, 113-127.	1.4	8
5075	An Unbiased Molecular Approach Using 3' UTRs Resolves the Avian Family-Level Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 108-127.	3.5	99
5076	Contributions of de novo variants to systemic lupus erythematosus. <i>European Journal of Human Genetics</i> , 2021, 29, 184-193.	1.4	6
5077	High-Throughput Sequencing to Detect DNA-RNA Changes. <i>Methods in Molecular Biology</i> , 2021, 2181, 193-212.	0.4	10
5078	Congruence and Conflict in the Higher-Level Phylogenetics of Squamate Reptiles: An Expanded Phylogenomic Perspective. <i>Systematic Biology</i> , 2021, 70, 542-557.	2.7	35
5079	Allopatric sibling species pair <i>Drosophila nasuta nasuta</i> and <i>Drosophila nasuta albomicans</i> exhibit expression divergence in ovarian transcriptomes. <i>Gene</i> , 2021, 777, 145189.	1.0	2
5080	Assessing the utility of long-read nanopore sequencing for rapid and efficient characterization of mobile element insertions. <i>Laboratory Investigation</i> , 2021, 101, 442-449.	1.7	9
5081	Translation of noncoding RNAs and cancer. <i>Cancer Letters</i> , 2021, 497, 89-99.	3.2	87
5082	Interrogating Genomic-Scale Data to Resolve Recalcitrant Nodes in the Spider Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 891-903.	3.5	46
5083	Gene-Level, but Not Chromosome-Wide, Divergence between a Very Young House Fly Proto-Y Chromosome and Its Homologous Proto-X Chromosome. <i>Molecular Biology and Evolution</i> , 2021, 38, 606-618.	3.5	10
5084	Functional Genomics Platform, A Cloud-Based Platform for Studying Microbial Life at Scale. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 940-952.	1.9	18
5085	Comparative analysis of gene expression between <i>Babesia bovis</i> blood stages and kinetes allowed by improved genome annotation. <i>International Journal for Parasitology</i> , 2021, 51, 123-136.	1.3	23
5086	Genome sequencing increases diagnostic yield in clinically diagnosed Alagille syndrome patients with previously negative test results. <i>Genetics in Medicine</i> , 2021, 23, 323-330.	1.1	17
5087	dbGuide: a database of functionally validated guide RNAs for genome editing in human and mouse cells. <i>Nucleic Acids Research</i> , 2021, 49, D871-D876.	6.5	20
5088	The celery genome sequence reveals sequential paleopolyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744.	4.1	62
5089	A MicroRNA Expression Signature as Prognostic Marker for Oropharyngeal Squamous Cell Carcinoma. <i>Journal of the National Cancer Institute</i> , 2021, 113, 752-759.	3.0	10
5090	Chromosome-level genome assembly of <i>Lethenteron reissneri</i> provides insights into lamprey evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 448-463.	2.2	25

#	ARTICLE	IF	CITATIONS
5091	Comparative analysis reveals the expansion of mitochondrial DNA control region containing unusually high G-C tandem repeat arrays in <i>Nasonia vitripennis</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 166, 1246-1257.	3.6	9
5092	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
5093	Comparative Genomic Analyses Reveal Functional Insights Into Key Determinants of the Pathogenesis of <i>Pectobacterium actinidiae</i> in Kiwifruit. <i>Phytopathology</i> , 2021, 111, PHYTO-07-20-028.	1.1	3
5094	Vertebrate Chromosome Evolution. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 1-27.	3.6	34
5095	Whole Genome Sequence Resource for <i>Fusarium oxysporum</i> f. sp. <i>capsici</i> 14003, the Causative Agent of Pepper Wilt. <i>Plant Disease</i> , 2021, 105, 1183-1186.	0.7	4
5096	Whole-genome assembly and resequencing reveal genomic imprint and key genes of rapid domestication in narrow-leaved lupin. <i>Plant Journal</i> , 2021, 105, 1192-1210.	2.8	12
5097	Transcriptome assisted label free proteomics of hepatic tissue in response to both dietary restriction and compensatory growth in cattle. <i>Journal of Proteomics</i> , 2021, 232, 104048.	1.2	10
5098	Neoantigen prediction in human breast cancer using RNA sequencing data. <i>Cancer Science</i> , 2021, 112, 465-475.	1.7	13
5099	Functional diversity of microbial communities in two contrasting maize rhizosphere soils. <i>Rhizosphere</i> , 2021, 17, 100282.	1.4	16
5100	Comprehensive insights into arsenic- and iron-redox genes, their taxonomy and associated environmental drivers deciphered by a meta-analysis. <i>Environment International</i> , 2021, 146, 106234.	4.8	10
5101	Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology</i> 2000, 2021, 85, 12-27.	6.3	16
5102	Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021, 5, 231-242.	3.4	51
5103	Life-stage-dependent supergene haplotype frequencies and metapopulation neutral genetic patterns of Atlantic cod, <i>Gadus morhua</i> , from Canada's Northern cod stock region and adjacent areas. <i>Journal of Fish Biology</i> , 2021, 98, 817-828.	0.7	4
5104	The comparative genomic landscape of adaptive radiation in crater lake cichlid fishes. <i>Molecular Ecology</i> , 2021, 30, 955-972.	2.0	12
5105	Ancient microRNA profiles of 14,300-yr-old canid samples confirm taxonomic origin and provide glimpses into tissue-specific gene regulation from the Pleistocene. <i>Rna</i> , 2021, 27, 324-334.	1.6	7
5106	Time series metagenomic sampling of the Thermopyles, Greece, geothermal springs reveals stable microbial communities dominated by novel sulfur-oxidizing chemoautotrophs. <i>Environmental Microbiology</i> , 2021, 23, 3710-3726.	1.8	10
5107	Whole-Genome Sequencing of Procyonids Reveals Distinct Demographic Histories in Kinkajou ( <i>Potos flavus</i> ) and Northern Raccoon ( <i>Procyon lotor</i> ). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	5
5108	A chromosome-level genome assembly provides insights into ascorbic acid accumulation and fruit softening in guava ( <i>Psidium guajava</i> ). <i>Plant Biotechnology Journal</i> , 2021, 19, 717-730.	4.1	52

#	ARTICLE	IF	CITATIONS
5109	New methodology for repetitive sequences identification in human X and Y chromosomes. <i>Biomedical Signal Processing and Control</i> , 2021, 64, 102207.	3.5	5
5110	Molecular identification and characterisation of a novel chicken leukocyte immunoglobulin-like receptor A5. <i>British Poultry Science</i> , 2021, 62, 68-80.	0.8	2
5111	In Silico Analysis of HSP70 Gene Family in Bovine Genome. <i>Biochemical Genetics</i> , 2021, 59, 134-158.	0.8	6
5112	Environmental stability impacts the differential sensitivity of marine microbiomes to increases in temperature and acidity. <i>ISME Journal</i> , 2021, 15, 19-28.	4.4	35
5113	The genome of <i>Cleistogenes songorica</i> provides a blueprint for functional dissection of dimorphic flower differentiation and drought adaptability. <i>Plant Biotechnology Journal</i> , 2021, 19, 532-547.	4.1	21
5114	Challenges in gene-oriented approaches for pangenome content discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
5115	Disparity between morphology and genetics in <i>Urtica dioica</i> (Urticaceae). <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 606-621.	0.8	4
5116	Genetic innovations: Transposable element recruitment and de novo formation lead to the birth of orphan genes in the rice genome. <i>Journal of Systematics and Evolution</i> , 2021, 59, 341-351.	1.6	14
5117	Hepatitis delta virus-like circular RNAs from diverse metazoans encode conserved hammerhead ribozymes. <i>Virus Evolution</i> , 2021, 7, veab016.	2.2	22
5119	Pleiotropy and epistasis within and between signaling pathways defines the genetic architecture of fungal virulence. <i>PLoS Genetics</i> , 2021, 17, e1009313.	1.5	14
5120	Bioinformatics in Personalized Medicine. , 2021, , 303-315.		7
5121	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. <i>Zoological Research</i> , 2021, 42, 450-460.	0.9	9
5122	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	13.7	144
5123	Unveiling the putative functional genes present in root-associated endophytic microbiome from maize plant using the shotgun approach. <i>Journal of Applied Genetics</i> , 2021, 62, 339-351.	1.0	21
5124	A novel deletion in FLOWERING LOCUS T modulates flowering time in winter oilseed rape. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1217-1231.	1.8	16
5125	Enrichment of Circular RNA Expression Dereglulation at the Transition to Recurrent Spontaneous Seizures in Experimental Temporal Lobe Epilepsy. <i>Frontiers in Genetics</i> , 2021, 12, 627907.	1.1	13
5126	The Compact Macronuclear Genome of the Ciliate <i>Halteria grandinella</i> : A Transcriptome-Like Genome with 23,000 Nanochromosomes. <i>MBio</i> , 2021, 12, .	1.8	26
5128	Improved contiguity of the threespine stickleback genome using long-read sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	34

#	ARTICLE	IF	CITATIONS
5129	The complete chloroplast genome sequence of American elm ( <i>Ulmus americana</i> ) and comparative genomics of related species. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	3
5130	Long read sequencing of <i>Toona sinensis</i> (A. Juss) Roem: A chromosome-level reference genome for the family Meliaceae. <i>Molecular Ecology Resources</i> , 2021, 21, 1243-1255.	2.2	20
5132	Therapy-induced Deletion in 11q23 Leading to Fusion of <i>KMT2A</i> With <i>ARHGGEF12</i> and Development of B Lineage Acute Lymphoblastic Leukemia in a Child Treated for Acute Myeloid Leukemia Caused by t(9;11)(p21;q23)/ <i>KMT2A-MLLT3</i> . <i>Cancer Genomics and Proteomics</i> , 2021, 18, 67-81.	1.0	7
5133	Shotgun metagenomics reveals the functional diversity of root-associated endophytic microbiomes in maize plant. <i>Current Plant Biology</i> , 2021, 25, 100195.	2.3	17
5134	Computational Genomics. , 2021, , 213-241.		0
5135	NGS Methodologies and Computational Algorithms for the Prediction and Analysis of. <i>Methods in Molecular Biology</i> , 2021, 2362, 119-145.	0.4	2
5136	Combined genomic, transcriptomic, and metabolomic analyses provide insights into chayote ( <i>Sechium</i> ) Tj ETQq0 0,0rgBT /Overlock 10	2.9	39
5137	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560.	9.4	251
5138	Dynamic evolution of transposable elements, demographic history, and gene content of paleognathous birds. <i>Zoological Research</i> , 2021, 42, 51-61.	0.9	3
5139	Omics to Understand Drought Tolerance in Plants: An Update. , 2021, , 69-93.		0
5140	Survey of Maize Rhizosphere Microbiome Using Shotgun Metagenomics. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	7
5141	Stenoparib, an Inhibitor of Cellular Poly(ADP-Ribose) Polymerase, Blocks Replication of the SARS-CoV-2 and HCoV-NL63 Human Coronaviruses In Vitro. <i>MBio</i> , 2021, 12, .	1.8	16
5142	Diversification, Introgression, and Rampant Cytonuclear Discordance in Rocky Mountains Chipmunks ( <i>Sciuridae</i> : <i>Tamias</i> ). <i>Systematic Biology</i> , 2021, 70, 908-921.	2.7	20
5144	Metagenomic insights into the bacterial community structure and functional potentials in the rhizosphere soil of maize plants. <i>Journal of Plant Interactions</i> , 2021, 16, 258-269.	1.0	12
5145	Sp1 is a substrate of Keap1 and regulates the activity of CRL4AWDR23 ubiquitin ligase toward Nrf2. <i>Journal of Biological Chemistry</i> , 2021, 296, 100704.	1.6	10
5146	A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , 2021, , 116-126.	1.0	0
5147	A long-term conserved satellite DNA that remains unexpanded in several genomes of Characiformes fish is actively transcribed. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
5148	Draft Genome Assemblies and Annotations of <i>Agrypnia vestita</i> Walker, and <i>Hesperophylax magnus</i> Banks Reveal Substantial Repetitive Element Expansion in Tube Case-Making Caddisflies (Insecta: Trichoptera). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	14

#	ARTICLE	IF	CITATIONS
5149	CRISPR-SE: a brute force search engine for CRISPR design. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab013.	1.5	10
5150	Effective Identification of Bacterial Genomes From Short and Long Read Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2806-2816.	1.9	1
5151	Metagenomics survey unravels diversity of biogas microbiomes with potential to enhance productivity in Kenya. <i>PLoS ONE</i> , 2021, 16, e0244755.	1.1	8
5152	A mosquito small RNA genomics resource reveals dynamic evolution and host responses to viruses and transposons. <i>Genome Research</i> , 2021, 31, 512-528.	2.4	29
5153	QTL identification for nine seed-related traits in <i>Brassica juncea</i> using a multiparent advanced generation intercross (MAGIC) population. <i>Czech Journal of Genetics and Plant Breeding</i> , 2021, 57, 9-18.	0.4	3
5154	Evolution of regulatory networks associated with traits under selection in cichlids. <i>Genome Biology</i> , 2021, 22, 25.	3.8	17
5155	Genome survey sequencing and genetic diversity of cultivated <i>Akebia trifoliata</i> assessed via phenotypes and SSR markers. <i>Molecular Biology Reports</i> , 2021, 48, 241-250.	1.0	15
5156	Chromosome-level genome assembly of <i>Ophiorrhiza pumila</i> reveals the evolution of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 405.	5.8	77
5157	Significantly improving the quality of genome assemblies through curation. <i>GigaScience</i> , 2021, 10, .	3.3	739
5158	EUKulele: Taxonomic annotation of the unsung eukaryotic microbes. <i>Journal of Open Source Software</i> , 2021, 6, 2817.	2.0	19
5160	Bioinformatic Platforms for Metagenomics. , 2021, , 91-112.		0
5162	Optimization of scleroglucan production by <i>Sclerotium rolfsii</i> by lowering pH during fermentation via oxalate metabolic pathway manipulation using CRISPR/Cas9. <i>Fungal Biology and Biotechnology</i> , 2021, 8, 1.	2.5	35
5164	Detecting high-scoring local alignments in pangenome graphs. <i>Bioinformatics</i> , 2021, 37, 2266-2274.	1.8	6
5166	Gene family amplification facilitates adaptation in freshwater unionid bivalve <i>Megaloniaias nervosa</i> . <i>Molecular Ecology</i> , 2021, 30, 1155-1173.	2.0	19
5167	Diploid chromosome-scale assembly of the <i>Muscadinia rotundifolia</i> genome supports chromosome fusion and disease resistance gene expansion during <i>Vitis</i> and <i>Muscadinia</i> divergence. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	35
5169	Cyanobacteria in microbialites of Alchichica Crater Lake: a polyphasic characterization. <i>European Journal of Phycology</i> , 2021, 56, 428-443.	0.9	8
5170	A novel canine reference genome resolves genomic architecture and uncovers transcript complexity. <i>Communications Biology</i> , 2021, 4, 185.	2.0	59
5171	Population genomics in the arboviral vector <i>Aedes aegypti</i> reveals the genomic architecture and evolution of endogenous viral elements. <i>Molecular Ecology</i> , 2021, 30, 1594-1611.	2.0	37

#	ARTICLE	IF	CITATIONS
5172	The Reliability of Metagenome-Assembled Genomes (MAGs) in Representing Natural Populations: Insights from Comparing MAGs against Isolate Genomes Derived from the Same Fecal Sample. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	82
5173	The genome of <i>Tripterygium wilfordii</i> and characterization of the celastrol biosynthesis pathway. <i>GigaByte</i> , 0, 2021, 1-32.	0.0	3
5174	Identification of Novel C-Terminally Truncated Estrogen Receptor $\beta^2$ Variant Transcripts and Their Distribution in Humans. <i>Journal of Nippon Medical School</i> , 2021, 88, 54-62.	0.3	3
5175	Hybrid Genome Assembly and Gene Repertoire of the Root Endophyte <i>Clitopilus hobsonii</i> QYL-10 (Entolomataceae, Agaricales, Basidiomycetes). <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 711-714.	1.4	7
5176	The complete mitochondrial genome of <i>Glycyrrhiza uralensis</i> Fisch. (Fabales, Leguminosae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 475-477.	0.2	3
5177	Genome sequences of <i>Tropheus moorii</i> and <i>Petrochromis trewavasae</i> , two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. <i>Scientific Reports</i> , 2021, 11, 4309.	1.6	4
5178	Simple sequence repeats drive genome plasticity and promote adaptive evolution in penaeid shrimp. <i>Communications Biology</i> , 2021, 4, 186.	2.0	37
5179	A complex resistance locus in <i>Solanum americanum</i> recognizes a conserved <i>Phytophthora</i> effector. <i>Nature Plants</i> , 2021, 7, 198-208.	4.7	62
5180	Revealing the active microbiome connected with the rhizosphere soil of maize plants in Ventersdorp, South Africa. <i>Biodiversity Data Journal</i> , 2021, 9, e60245.	0.4	1
5181	The Immense Functional Attributes of Maize Rhizosphere Microbiome: A Shotgun Sequencing Approach. <i>Agriculture (Switzerland)</i> , 2021, 11, 118.	1.4	7
5182	A comprehensive review of scaffolding methods in genome assembly. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	16
5183	Divergence in alternative polyadenylation contributes to gene regulatory differences between humans and chimpanzees. <i>ELife</i> , 2021, 10, .	2.8	11
5184	Rare <i>KMT2A-ELL</i> and Novel <i>ZNF56-KMT2A</i> Fusion Genes in Pediatric T-cell Acute Lymphoblastic Leukemia. <i>Cancer Genomics and Proteomics</i> , 2021, 18, 121-131.	1.0	3
5188	First finding of free-living representatives of <i>Prokinetoplastina</i> and their nuclear and mitochondrial genomes. <i>Scientific Reports</i> , 2021, 11, 2946.	1.6	13
5189	High-Resolution Typing of <i>Staphylococcus epidermidis</i> Based on Core Genome Multilocus Sequence Typing To Investigate the Hospital Spread of Multidrug-Resistant Clones. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	4
5190	Flagellar Perturbations Activate Adhesion through Two Distinct Pathways in <i>Caulobacter crescentus</i> . <i>MBio</i> , 2021, 12, .	1.8	17
5193	Carbon fixation and rhodopsin systems in microbial mats from hypersaline lakes Brava and Tebenquiche, Salar de Atacama, Chile. <i>PLoS ONE</i> , 2021, 16, e0246656.	1.1	12
5194	Soil fertilization affects the abundance and distribution of carbon and nitrogen cycling genes in the maize rhizosphere. <i>AMB Express</i> , 2021, 11, 24.	1.4	24

#	ARTICLE	IF	CITATIONS
5195	Eliminating Target Anopheles Proteins to Non-Target Organisms based on Posterior Probability Algorithm. <i>Advances in Science, Technology and Engineering Systems</i> , 2021, 6, 710-718.	0.4	0
5197	BSGatlas: a unified <i>Bacillus subtilis</i> genome and transcriptome annotation atlas with enhanced information access. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12
5198	Latent trait modeling of tau neuropathology in progressive supranuclear palsy. <i>Acta Neuropathologica</i> , 2021, 141, 667-680.	3.9	5
5199	A chromosome-level genome of the mud crab ( <i>Scylla paramamosain</i> estampador) provides insights into the evolution of chemical and light perception in this crustacean. <i>Molecular Ecology Resources</i> , 2021, 21, 1299-1317.	2.2	17
5200	Metagenomic Insight into the Community Structure and Functional Genes in the Sunflower Rhizosphere Microbiome. <i>Agriculture (Switzerland)</i> , 2021, 11, 167.	1.4	13
5201	Functional and Pathological Roles of AHCY. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 654344.	1.8	38
5202	Deciphering the transcriptomic regulation of heat stress responses in <i>Nothofagus pumilio</i> . <i>PLoS ONE</i> , 2021, 16, e0246615.	1.1	6
5204	A Spontaneous <i>rapZ</i> Mutant Impairs Infectivity of Lytic Bacteriophage vB_EcoM_JS09 against Enterotoxigenic <i>Escherichia coli</i> . <i>MSphere</i> , 2021, 6, .	1.3	7
5205	GGVD: A goat genome variation database for tracking the dynamic evolutionary process of selective signatures and ancient introgressions. <i>Journal of Genetics and Genomics</i> , 2021, 48, 248-256.	1.7	12
5206	A chromosome-level assembly of the black tiger shrimp ( <i>Penaeus monodon</i> ) genome facilitates the identification of growth-associated genes. <i>Molecular Ecology Resources</i> , 2021, 21, 1620-1640.	2.2	43
5207	Searching the Dark Genome for Alzheimer's Disease Risk Variants. <i>Brain Sciences</i> , 2021, 11, 332.	1.1	10
5209	The complete mitochondrial genome of <i>Aconitum kusnezoffii</i> Rchb. (Ranales, Ranunculaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 779-781.	0.2	6
5210	riboCIRC: a comprehensive database of translatable circRNAs. <i>Genome Biology</i> , 2021, 22, 79.	3.8	49
5212	Benchmarking the Human Leukocyte Antigen Typing Performance of Three Assays and Seven Next-Generation Sequencing-Based Algorithms. <i>Frontiers in Immunology</i> , 2021, 12, 652258.	2.2	15
5213	Complete chloroplast genome of <i>Zingiber mioga</i> by <i>de novo</i> sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1238-1240.	0.2	1
5214	Longitudinal study of the scalp microbiome suggests coconut oil to enrich healthy scalp commensals. <i>Scientific Reports</i> , 2021, 11, 7220.	1.6	13
5215	Chromosome-scale assembly of the genome of <i>Salix dunnii</i> reveals a male heterogametic sex determination system on chromosome 7. <i>Molecular Ecology Resources</i> , 2021, 21, 1966-1982.	2.2	28
5216	Long-insert clone experimental evidence for assembly improvement and chimeric chromosomes detection in an allopolyploid beer yeast. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2

#	ARTICLE	IF	CITATIONS
5217	Comprehensive identification of somatic nucleotide variants in human brain tissue. <i>Genome Biology</i> , 2021, 22, 92.	3.8	26
5218	A multi-omic characterization of temperature stress in a halotolerant <i>Scenedesmus</i> strain for algal biotechnology. <i>Communications Biology</i> , 2021, 4, 333.	2.0	22
5219	Complete chloroplast genome and phylogenetic analysis of a wild grass, <i>Hordeum roshevitzii</i> Bowden. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1219-1221.	0.2	1
5220	Long-read assembly of a Great Dane genome highlights the contribution of GC-rich sequence and mobile elements to canine genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
5221	Comparative analysis of chloroplast genomes of kenaf cytoplasmic male sterile line and its maintainer line. <i>Scientific Reports</i> , 2021, 11, 5301.	1.6	1
5222	X chromosome-dependent disruption of placental regulatory networks in hybrid dwarf hamsters. <i>Genetics</i> , 2021, 218, .	1.2	10
5223	Primate innate immune responses to bacterial and viral pathogens reveals an evolutionary trade-off between strength and specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	30
5224	Large-scale transcriptomics to dissect 2Âyears of the life of a fungal phytopathogen interacting with its host plant. <i>BMC Biology</i> , 2021, 19, 55.	1.7	21
5225	<i>Plasmodium matutinum</i> Transmitted by <i>Culex pipiens</i> as a Cause of Avian Malaria in Captive African Penguins ( <i>Spheniscus demersus</i> ) in Italy. <i>Frontiers in Veterinary Science</i> , 2021, 8, 621974.	0.9	8
5226	Metagenomic profiling of rhizosphere microbial community structure and diversity associated with maize plant as affected by cropping systems. <i>International Microbiology</i> , 2021, 24, 325-335.	1.1	22
5227	Rapid speciation via the evolution of pre-mating isolation in the IberÃ; Seedeater. <i>Science</i> , 2021, 371, .	6.0	44
5228	SLAF-Based Linkage Map Construction and QTL Mapping of Nitrogen Use Efficiency in Rice ( <i>Oryza sativa</i> ) Tj ETQq1_1_0.784314 rgBT /D	1.0	3
5229	The stacking strategy-based hybrid framework for identifying non-coding RNAs. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	28
5231	Why are rare variants hard to impute? Coalescent models reveal theoretical limits in existing algorithms. <i>Genetics</i> , 2021, 217, .	1.2	11
5232	Whole-Genome Sequencing and Characterization of Buffalo Genetic Resources: Recent Advances and Future Challenges. <i>Animals</i> , 2021, 11, 904.	1.0	20
5234	The Complete Chloroplast Genome Sequence of <i>Melilotoides ruthenica</i> : Structural Comparative and Phylogenetic Analysis in Leguminosae. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 697, 012014.	0.2	1
5235	Effect of thermospermine on expression profiling of different gene using massive analysis of cDNA ends (MACE) and vascular maintenance in <i>Arabidopsis</i> . <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 577-586.	1.4	3
5236	Alvis: a tool for contig and read ALignment VISualisation and chimera detection. <i>BMC Bioinformatics</i> , 2021, 22, 124.	1.2	14

#	ARTICLE	IF	CITATIONS
5237	The genome of <i>Magnolia biondii</i> Pamp. provides insights into the evolution of Magnoliales and biosynthesis of terpenoids. <i>Horticulture Research</i> , 2021, 8, 38.	2.9	32
5238	The complete mitochondrial and plastid genomes of <i>Rhododendron simsii</i> , an important parent of widely cultivated azaleas. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1197-1199.	0.2	6
5239	African lungfish genome sheds light on the vertebrate water-to-land transition. <i>Cell</i> , 2021, 184, 1362-1376.e18.	13.5	99
5240	The Pan social brain: An evolutionary history of neurochemical receptor genes and their potential impact on sociocognitive differences. <i>Journal of Human Evolution</i> , 2021, 152, 102949.	1.3	12
5241	Identification and Characterization of Alternatively Spliced Transcript Isoforms of IRX4 in Prostate Cancer. <i>Genes</i> , 2021, 12, 615.	1.0	4
5243	Fast lightweight accurate xenograft sorting. <i>Algorithms for Molecular Biology</i> , 2021, 16, 2.	0.3	9
5244	ACME dissociation: a versatile cell fixation-dissociation method for single-cell transcriptomics. <i>Genome Biology</i> , 2021, 22, 89.	3.8	39
5245	Parallel computing for genome sequence processing. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
5246	Increased expression of peptides from non-coding genes in cancer proteomics datasets suggests potential tumor neoantigens. <i>Communications Biology</i> , 2021, 4, 496.	2.0	20
5247	Genome-Wide Analysis of Terpene Synthase Gene Family in <i>Mentha longifolia</i> and Catalytic Activity Analysis of a Single Terpene Synthase. <i>Genes</i> , 2021, 12, 518.	1.0	22
5248	Investigation of long interspersed element-1 retrotransposons as potential risk factors for idiopathic temporal lobe epilepsy. <i>Epilepsia</i> , 2021, 62, 1329-1342.	2.6	6
5249	Targeting of the Essential <i>acpP</i> , <i>ftsZ</i> , and <i>rne</i> Genes in Carbapenem-Resistant <i>Acinetobacter baumannii</i> by Antisense PNA Precision Antibacterials. <i>Biomedicines</i> , 2021, 9, 429.	1.4	15
5251	A novel <i>KCNQ4</i> gene variant (c.857A>G; p.Tyr286Cys) in an extended family with non-syndromic deafness 2A. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	7
5252	Single-cell transcriptome sequencing on the Nanopore platform with ScNapBar. <i>Rna</i> , 2021, 27, 763-770.	1.6	12
5253	Comparison of 15 dinoflagellate genomes reveals extensive sequence and structural divergence in family Symbiodiniaceae and genus Symbiodinium. <i>BMC Biology</i> , 2021, 19, 73.	1.7	65
5254	Universal nomenclature for oxytocin-vasotocin ligand and receptor families. <i>Nature</i> , 2021, 592, 747-755.	13.7	73
5255	SNP detection and population structure evaluation of <i>Salix gordejvii</i> Y. L. Chang et Skv. in Hunshandake Sandland, Inner Mongolia, China. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 997-1005.	1.4	1
5259	An EAV-HP insertion in the promoter region of <i>SLCO1B3</i> has pleiotropic effects on chicken liver metabolism based on the transcriptome and proteome analysis. <i>Scientific Reports</i> , 2021, 11, 7571.	1.6	3

#	ARTICLE	IF	CITATIONS
5260	Sex-Biased lncRNA Signature in Fetal Growth Restriction (FGR). <i>Cells</i> , 2021, 10, 921.	1.8	5
5261	Hapo-G, haplotype-aware polishing of genome assemblies with accurate reads. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab034.	1.5	52
5262	The genome of <i>Geosiphon pyriformis</i> reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. <i>Current Biology</i> , 2021, 31, 1570-1577.e4.	1.8	30
5263	Metagenomics Assessment of Soil Fertilization on the Chemotaxis and Disease Suppressive Genes Abundance in the Maize Rhizosphere. <i>Genes</i> , 2021, 12, 535.	1.0	8
5264	Draft Genomes and Comparative Analysis of Seven Mangrove Rhizosphere-Associated Fungi Isolated From <i>Kandelia obovata</i> and <i>Acanthus ilicifolius</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	2
5266	Complete genome sequence analysis of the peanut pathogen <i>Ralstonia solanacearum</i> strain Rs-P.362200. <i>BMC Microbiology</i> , 2021, 21, 118.	1.3	5
5267	The Chinese mitten crab genome provides insights into adaptive plasticity and developmental regulation. <i>Nature Communications</i> , 2021, 12, 2395.	5.8	38
5268	Genome-wide analysis of European sea bass provides insights into the evolution and functions of single-exon genes. <i>Ecology and Evolution</i> , 2021, 11, 6546-6557.	0.8	0
5269	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	1.6	36
5270	Ï”Np63 is a pioneer factor that binds inaccessible chromatin and elicits chromatin remodeling. <i>Epigenetics and Chromatin</i> , 2021, 14, 20.	1.8	17
5272	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021, 372, .	6.0	85
5273	Impact of different numbers of microsatellite markers on population genetic results using SLAF-seq data for <i>Rhododendron</i> species. <i>Scientific Reports</i> , 2021, 11, 8597.	1.6	12
5274	The Meishan pig genome reveals structural variation-mediated gene expression and phenotypic divergence underlying Asian pig domestication. <i>Molecular Ecology Resources</i> , 2021, 21, 2077-2092.	2.2	20
5275	Chromosomal Inversion Polymorphisms in Two Sympatric Ascidian Lineages. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
5276	The genome of a new anemone species (Actiniaria: Hormathiidae) provides insights into deep-sea adaptation. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 170, 103492.	0.6	11
5277	Whole-genome sequencing with long reads reveals complex structure and origin of structural variation in human genetic variations and somatic mutations in cancer. <i>Genome Medicine</i> , 2021, 13, 65.	3.6	43
5278	Conserved long-range base pairings are associated with pre-mRNA processing of human genes. <i>Nature Communications</i> , 2021, 12, 2300.	5.8	27
5279	High-Fiber, Whole-Food Dietary Intervention Alters the Human Gut Microbiome but Not Fecal Short-Chain Fatty Acids. <i>MSystems</i> , 2021, 6, .	1.7	69

#	ARTICLE	IF	CITATIONS
5280	Whole-genome sequencing of phenotypically distinct inflammatory breast cancers reveals similar genomic alterations to non-inflammatory breast cancers. <i>Genome Medicine</i> , 2021, 13, 70.	3.6	8
5281	Genetic Diversity and Population Structures in Chinese Miniature Pigs Revealed by SINE Retrotransposon Insertion Polymorphisms, a New Type of Genetic Markers. <i>Animals</i> , 2021, 11, 1136.	1.0	9
5282	A study of transposable element-associated structural variations (TASVs) using a de novo-assembled Korean genome. <i>Experimental and Molecular Medicine</i> , 2021, 53, 615-630.	3.2	9
5283	Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
5284	High Resolution Haplotype Analyses of Classical HLA Genes in Families With Multiple Sclerosis Highlights the Role of HLA-DP Alleles in Disease Susceptibility. <i>Frontiers in Immunology</i> , 2021, 12, 644838.	2.2	5
5285	Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. <i>Genes</i> , 2021, 12, 847.	1.0	19
5286	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. <i>Nature Communications</i> , 2021, 12, 3230.	5.8	95
5287	Designing multi-epitope vaccine against <i>Staphylococcus aureus</i> by employing subtractive proteomics, reverse vaccinology and immuno-informatics approaches. <i>Computers in Biology and Medicine</i> , 2021, 132, 104389.	3.9	73
5288	The cytochrome P450 (CYP) superfamily in cnidarians. <i>Scientific Reports</i> , 2021, 11, 9834.	1.6	7
5289	Tissue-specific activation of gene expression by the Synergistic Activation Mediator (SAM) CRISPRa system in mice. <i>Nature Communications</i> , 2021, 12, 2770.	5.8	13
5290	Comparative transcriptomic analysis highlights contrasting levels of resistance of <i>Vitis vinifera</i> and <i>Vitis amurensis</i> to <i>Botrytis cinerea</i> . <i>Horticulture Research</i> , 2021, 8, 103.	2.9	19
5291	Genome of the butterfly hillstream loach provides insights into adaptations to torrential mountain stream life. <i>Molecular Ecology Resources</i> , 2021, 21, 1922-1935.	2.2	1
5295	Introgressing the <i>Aegilops tauschii</i> genome into wheat as a basis for cereal improvement. <i>Nature Plants</i> , 2021, 7, 774-786.	4.7	65
5296	Hardware acceleration of genomics data analysis: challenges and opportunities. <i>Bioinformatics</i> , 2021, 37, 1785-1795.	1.8	8
5297	Reverse-transcribed SARS-CoV-2 RNA can integrate into the genome of cultured human cells and can be expressed in patient-derived tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	175
5299	Characterization of intermediate-sized insertions using whole-genome sequencing data and analysis of their functional impact on gene expression. <i>Human Genetics</i> , 2021, 140, 1201-1216.	1.8	3
5300	Long non-coding RNAs and their targets as potential biomarkers in breast cancer. <i>IET Systems Biology</i> , 2021, 15, 137-147.	0.8	3
5301	Taxonomic classification of metagenomic sequences from Relative Abundance Index profiles using deep learning. <i>Biomedical Signal Processing and Control</i> , 2021, 67, 102539.	3.5	12

#	ARTICLE	IF	CITATIONS
5302	Cross-Predicting Essential Genes between Two Model Eukaryotic Species Using Machine Learning. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5056.	1.8	8
5303	Long-read cDNA sequencing identifies functional pseudogenes in the human transcriptome. <i>Genome Biology</i> , 2021, 22, 146.	3.8	26
5304	Node ages, relationships, and phylogenomic incongruence in an ancient gymnosperm lineage – Phylogeny of <i>Ephedra</i> revisited. <i>Taxon</i> , 2021, 70, 701-719.	0.4	9
5305	Elephant Genomes Reveal Accelerated Evolution in Mechanisms Underlying Disease Defenses. <i>Molecular Biology and Evolution</i> , 2021, 38, 3606-3620.	3.5	33
5306	TSSFinder – fast and accurate ab initio prediction of the core promoter in eukaryotic genomes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
5308	Identification of A-to-I RNA editing profiles and their clinical relevance in lung adenocarcinoma. <i>Science China Life Sciences</i> , 2022, 65, 19-32.	2.3	6
5309	Transcriptomic Analysis of Skin Color in Anole Lizards. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
5310	Nanopore Flongle Sequencing as a Rapid, Single-Specimen Clinical Test for Fusion Detection. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 630-636.	1.2	11
5311	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	2.0	21
5312	The genome of a wild <i>Medicago</i> species provides insights into the tolerant mechanisms of legume forage to environmental stress. <i>BMC Biology</i> , 2021, 19, 96.	1.7	39
5313	Genome Sequencing and Assembly Strategies and a Comparative Analysis of the Genomic Characteristics in Penaeid Shrimp Species. <i>Frontiers in Genetics</i> , 2021, 12, 658619.	1.1	14
5314	High-Density Genetic Map Construction and Identification of QTLs Controlling Leaf Abscission Trait in <i>Poncirus trifoliata</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 5723.	1.8	7
5316	Optimising the use of gene expression data to predict plant metabolic pathway memberships. <i>New Phytologist</i> , 2021, 231, 475-489.	3.5	3
5317	Comparative Analyses of Gibbon Centromeres Reveal Dynamic Genus-Specific Shifts in Repeat Composition. <i>Molecular Biology and Evolution</i> , 2021, 38, 3972-3992.	3.5	10
5318	Optical maps refine the bread wheat <i>Triticum aestivum</i> cv. Chinese Spring genome assembly. <i>Plant Journal</i> , 2021, 107, 303-314.	2.8	237
5319	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
5320	Impact of cropping systems on the functional diversity of rhizosphere microbial communities associated with maize plant: a shotgun approach. <i>Archives of Microbiology</i> , 2021, 203, 3605-3613.	1.0	4
5322	piRNA-mediated gene regulation and adaptation to sex-specific transposon expression in <i>D. melanogaster</i> male germline. <i>Genes and Development</i> , 2021, 35, 914-935.	2.7	46

#	ARTICLE	IF	CITATIONS
5323	Sex chromosome transformation and the origin of a male-specific X chromosome in the creeping vole. <i>Science</i> , 2021, 372, 592-600.	6.0	20
5324	Defining genome architecture at base-pair resolution. <i>Nature</i> , 2021, 595, 125-129.	13.7	107
5325	SINE jumping contributes to large-scale polymorphisms in the pig genomes. <i>Mobile DNA</i> , 2021, 12, 17.	1.3	21
5327	Tracking HIV-1-Infected Cell Clones Using Integration Site-Specific qPCR. <i>Viruses</i> , 2021, 13, 1235.	1.5	10
5328	Contiguous erosion of the inactive X in human pluripotency concludes with global DNA hypomethylation. <i>Cell Reports</i> , 2021, 35, 109215.	2.9	11
5329	Candidate probiotic <i>Lactiplantibacillus plantarum</i> HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. <i>Microbiome</i> , 2021, 9, 151.	4.9	30
5330	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	4.7	53
5331	Transborder Gene Flow between Canada and the USA and Fine-scale Population Structure of Atlantic Cod in the Broader Gulf of Maine Region. <i>Transactions of the American Fisheries Society</i> , 2021, 150, 560-577.	0.6	1
5332	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. <i>Cell</i> , 2021, 184, 3542-3558.e16.	13.5	237
5334	The Influence of Soil Fertilization on the Distribution and Diversity of Phosphorus Cycling Genes and Microbes Community of Maize Rhizosphere Using Shotgun Metagenomics. <i>Genes</i> , 2021, 12, 1022.	1.0	17
5335	Cotton D genome assemblies built with long-read data unveil mechanisms of centromere evolution and stress tolerance divergence. <i>BMC Biology</i> , 2021, 19, 115.	1.7	14
5336	Wolfberry genomes and the evolution of <i>Lycium</i> (Solanaceae). <i>Communications Biology</i> , 2021, 4, 671.	2.0	40
5337	Comparative Transcriptomic Analysis Reveals the Regulatory Mechanism of Terpene Trilactones Improvement by Exogenous Methyl Jasmonate in <i>Ginkgo biloba</i> . <i>Plant Molecular Biology Reporter</i> , 0, , 1.	1.0	2
5338	A de novo transcriptional atlas in <i>Danaus plexippus</i> reveals variability in dosage compensation across tissues. <i>Communications Biology</i> , 2021, 4, 791.	2.0	9
5339	The complete mitochondrial genome of <i>Osmanthus fragrans</i> (Lamiales, Oleaceae) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2056-2057.	0.2	0
5341	Nanopore Sequencing Indicates That Tandem Amplification of Chromosome 20q11.21 in Human Pluripotent Stem Cells Is Driven by Break-Induced Replication. <i>Stem Cells and Development</i> , 2021, 30, 578-586.	1.1	4
5342	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. <i>Cancer Cell</i> , 2021, 39, 793-809.e8.	7.7	65
5343	Acute Effects on the Human Peripheral Blood Transcriptome of Decompression Sickness Secondary to Scuba Diving. <i>Frontiers in Physiology</i> , 2021, 12, 660402.	1.3	10

#	ARTICLE	IF	CITATIONS
5344	Cis-regulatory evolution spotlights species differences in the adaptive potential of gene expression plasticity. <i>Nature Communications</i> , 2021, 12, 3376.	5.8	25
5345	A porcine brain-wide RNA editing landscape. <i>Communications Biology</i> , 2021, 4, 717.	2.0	5
5346	Metagenomic Insight into the Community Structure of Maize-Rhizosphere Bacteria as Predicted by Different Environmental Factors and Their Functioning within Plant Proximity. <i>Microorganisms</i> , 2021, 9, 1419.	1.6	15
5347	Comparative transcriptome analysis of <i>Salix cupularis</i> under drought stress. <i>Global Ecology and Conservation</i> , 2021, 27, e01532.	1.0	3
5348	Variant analyses of candidate genes in orofacial clefts in multi-ethnic populations. <i>Oral Diseases</i> , 2022, 28, 1921-1935.	1.5	3
5349	SaQuant: a real-time PCR assay for quantitative assessment of <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2021, 21, 174.	1.3	5
5350	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	3.9	133
5351	Genomic insights into the fast growth of paulownias and the formation of Paulownia witches' broom. <i>Molecular Plant</i> , 2021, 14, 1668-1682.	3.9	39
5352	The nearly complete genome of <i>Ginkgo biloba</i> illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021, 7, 748-756.	4.7	98
5353	A combinatorial cis-regulatory logic restricts color-sensing Rhodopsins to specific photoreceptor subsets in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2021, 17, e1009613.	1.5	6
5354	LIQA: long-read isoform quantification and analysis. <i>Genome Biology</i> , 2021, 22, 182.	3.8	49
5355	The regulatory function of tandem repeat VNTR2 in hTERT gene involves basic Helix-loop-helix family transcription factors. <i>Environmental and Molecular Mutagenesis</i> , 2021, 62, 338-349.	0.9	0
5356	Gene Expression Modification by an Autosomal Inversion Associated With Three Male Mating Morphs. <i>Frontiers in Genetics</i> , 2021, 12, 641620.	1.1	10
5357	Complete chloroplast genome of <i>Alternanthera philoxeroides</i> by de novo sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1826-1828.	0.2	1
5358	<i>Plasmodium matutinum</i> Causing Avian Malaria in Lovebirds ( <i>Agapornis roseicollis</i> ) Hosted in an Italian Zoo. <i>Microorganisms</i> , 2021, 9, 1356.	1.6	9
5359	Schistosome W-Linked Genes Inform Temporal Dynamics of Sex Chromosome Evolution and Suggest Candidate for Sex Determination. <i>Molecular Biology and Evolution</i> , 2021, 38, 5345-5358.	3.5	12
5360	Chromosome-scale genome assembly of areca palm ( <i>Areca catechu</i> ). <i>Molecular Ecology Resources</i> , 2021, 21, 2504-2519.	2.2	20
5361	Draft de novo Genome Assembly of the Elusive Jaguarundi, <i>Puma yagouaroundi</i> . <i>Journal of Heredity</i> , 2021, 112, 540-548.	1.0	5

#	ARTICLE	IF	CITATIONS
5362	Mobile element insertions and associated structural variants in longitudinal breast cancer samples. <i>Scientific Reports</i> , 2021, 11, 13020.	1.6	3
5363	DNA-RNA Hybrid (R-Loop): From a Unified Picture of the Mammalian Telomere to the Genome-Wide Profile. <i>Cells</i> , 2021, 10, 1556.	1.8	6
5364	Computational analysis of sense-antisense chimeric transcripts reveals their potential regulatory features and the landscape of expression in human cells. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab074.	1.5	12
5365	Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2846-2867.	7.7	83
5366	Predicting future from past: The genomic basis of recurrent and rapid stickleback evolution. <i>Science Advances</i> , 2021, 7, .	4.7	62
5367	Echolocation in soft-furred tree mice. <i>Science</i> , 2021, 372, .	6.0	28
5368	A Curriculum for Genomic Education of Molecular Genetic Pathology Fellows. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 1218-1240.	1.2	4
5372	Dynamic partitioning of search patterns for approximate pattern matching using search schemes. <i>IScience</i> , 2021, 24, 102687.	1.9	3
5373	Single Copy Oligonucleotide Fluorescence In Situ Hybridization Probe Design Platforms: Development, Application and Evaluation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7124.	1.8	12
5374	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280.	5.8	9
5375	The endangered White Sands pupfish ( <i>Cyprinodon tularosa</i> ) genome reveals low diversity and heterogenous patterns of differentiation. <i>Molecular Ecology Resources</i> , 2021, 21, 2520-2532.	2.2	3
5376	Phylogeographic analysis delimits three evolutionary significant units of least chipmunks in North America and identifies unique genetic diversity within the imperiled <i>Peromyscus</i> population. <i>Ecology and Evolution</i> , 2021, 11, 12114-12128.	0.8	3
5379	Target enrichment improves phylogenetic resolution in the genus <i>Zanthoxylum</i> (Rutaceae) and indicates both incomplete lineage sorting and hybridization events. <i>Annals of Botany</i> , 2021, 128, 497-510.	1.4	12
5380	Metagenomic and viromic data mining reveals viral threats in biologically treated domestic wastewater. <i>Environmental Science and Ecotechnology</i> , 2021, 7, 100105.	6.7	23
5381	Accurate spliced alignment of long RNA sequencing reads. <i>Bioinformatics</i> , 2021, 37, 4643-4651.	1.8	28
5383	Large palindromes on the primate X Chromosome are preserved by natural selection. <i>Genome Research</i> , 2021, 31, 1337-1352.	2.4	10
5384	Taxonomic annotation of 16S rRNA sequences of pig intestinal samples using MG-RAST and QIIME2 generated different microbiota compositions. <i>Journal of Microbiological Methods</i> , 2021, 186, 106235.	0.7	8
5385	Chromosomal-scale genome assembly of <i>Eleutherococcus senticosus</i> provides insights into chromosome evolution in Araliaceae. <i>Molecular Ecology Resources</i> , 2021, 21, 2204-2220.	2.2	10

#	ARTICLE	IF	CITATIONS
5387	A chromosome-level genome assembly of the yellowfin seabream ( <i>Acanthopagrus latus</i> ; Hottuyn, 1782) provides insights into its osmoregulation and sex reversal. <i>Genomics</i> , 2021, 113, 1617-1627.	1.3	13
5389	Large parental differences in chromatin organization in pancreatic beta cell line explaining diabetes susceptibility effects. <i>Nature Communications</i> , 2021, 12, 4338.	5.8	5
5390	Distinct Retrotransposon Evolution Profile in the Genome of Rabbit ( <i>Oryctolagus cuniculus</i> ). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
5391	Genomic signatures of natural selection at phenology-related genes in a widely distributed tree species <i>Fagus sylvatica</i> L. <i>BMC Genomics</i> , 2021, 22, 583.	1.2	6
5392	Relative performance of customized and universal probe sets in target enrichment: A case study in subtribe Malinae. <i>Applications in Plant Sciences</i> , 2021, 9, e11442.	0.8	20
5393	Using Optimal Sequencing Algorithms for COVID-19 Case Study. , 2021, , .		1
5394	<i>Gossypium tomentosum</i> genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. <i>Genomics</i> , 2021, 113, 1999-2009.	1.3	8
5395	An actin-related protein that is most highly expressed in <i>Drosophila</i> testes is critical for embryonic development. <i>ELife</i> , 2021, 10, .	2.8	4
5397	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	5.8	49
5398	Landscape of tissue-specific RNA Editome provides insight into co-regulated and altered gene expression in pigs ( <i>Sus scrofa</i> ). <i>RNA Biology</i> , 2021, 18, 439-450.	1.5	5
5399	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. <i>Genome Medicine</i> , 2021, 13, 114.	3.6	5
5400	GRIDSS2: comprehensive characterisation of somatic structural variation using single breakend variants and structural variant phasing. <i>Genome Biology</i> , 2021, 22, 202.	3.8	73
5401	An epigenetic switch regulates the ontogeny of AXL-positive/EGFR-TKI-resistant cells by modulating miR-335 expression. <i>ELife</i> , 2021, 10, .	2.8	7
5405	Chromosome organization and gene expansion in the highly fragmented genome of the ciliate <i>Strombidium stylifer</i> . <i>Journal of Genetics and Genomics</i> , 2021, 48, 908-916.	1.7	13
5406	Metagenomic Study of the Community Structure and Functional Potentials in Maize Rhizosphere Microbiome: Elucidation of Mechanisms behind the Improvement in Plants under Normal and Stress Conditions. <i>Sustainability</i> , 2021, 13, 8079.	1.6	15
5407	Early-life social experience affects offspring DNA methylation and later life stress phenotype. <i>Nature Communications</i> , 2021, 12, 4398.	5.8	11
5408	Transcriptional Regulation of RUNX1: An Informatics Analysis. <i>Genes</i> , 2021, 12, 1175.	1.0	4
5409	Genome-Wide Association Study of Root and Shoot Related Traits in Spring Soybean ( <i>Glycine max</i> L.) at Seedling Stages Using SLAF-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 568995.	1.7	17

#	ARTICLE	IF	CITATIONS
5411	A consensus and saturated genetic map provides insight into genome anchoring, synteny of Solanaceae and leaf- and fruit-related QTLs in wolfberry ( <i>Lycium Linn.</i> ). <i>BMC Plant Biology</i> , 2021, 21, 350.	1.6	7
5412	Sequencing and Chromosome-Scale Assembly of Plant Genomes, <i>Brassica rapa</i> as a Use Case. <i>Biology</i> , 2021, 10, 732.	1.3	15
5413	Novel function of SART1 in HNF4 $\beta$ transcriptional regulation contributes to its antiviral role during HBV infection. <i>Journal of Hepatology</i> , 2021, 75, 1072-1082.	1.8	22
5414	Genome assembly of primitive cultivated potato <i>Solanum stenotomum</i> provides insights into potato evolution. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
5415	Prognostic Roles of BRAF, KIT, NRAS, IGF2R and SF3B1 Mutations in Mucosal Melanomas. <i>Cells</i> , 2021, 10, 2216.	1.8	8
5417	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249.	3.8	51
5418	Chromoanagenesis Event Underlies a de novo Pericentric and Multiple Paracentric Inversions in a Single Chromosome Causing Coffinâ€“Siris Syndrome. <i>Frontiers in Genetics</i> , 2021, 12, 708348.	1.1	5
5419	The first genome assembly of fungal pathogen <i>Pyrenophora tritici-repentis</i> race 1 isolate using Oxford Nanopore MinION sequencing. <i>BMC Research Notes</i> , 2021, 14, 334.	0.6	3
5420	nf-LO: A Scalable, Containerized Workflow for Genome-to-Genome Lift Over. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
5421	Exome sequencing of childâ€“parent trios with bladder exstrophy: Findings in 26 children. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 3028-3041.	0.7	4
5422	Chromosome-scale assembly of the yellow mealworm genome. <i>Open Research Europe</i> , 0, 1, 94.	2.0	1
5423	Microbial Composition and Genes for Key Metabolic Attributes in the Gut Digesta of Sea Urchins <i>Lytechinus variegatus</i> and <i>Strongylocentrotus purpuratus</i> Using Shotgun Metagenomics. <i>Current Issues in Molecular Biology</i> , 2021, 43, 978-995.	1.0	2
5424	GAMMA: a tool for the rapid identification, classification and annotation of translated gene matches from sequencing data. <i>Bioinformatics</i> , 2022, 38, 546-548.	1.8	10
5426	Evidence for and localization of proposed causative variants in cattle and pig genomes. <i>Genetics Selection Evolution</i> , 2021, 53, 67.	1.2	15
5427	Phylogenomics and evolutionary history of <i>Oreobates</i> (Anura: Craugastoridae) Neotropical frogs along elevational gradients. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107167.	1.2	1
5428	Genome, transcriptome and secretome analyses of the antagonistic, yeast-like fungus <i>Aureobasidium pullulans</i> to identify potential biocontrol genes. <i>Microbial Cell</i> , 2021, 8, 184-202.	1.4	17
5429	Identification of three novel <i>HLAâ€“DRB1</i> alleles by nextâ€“generation sequencing. <i>Hla</i> , 2021, 98, 560-562.	0.4	3
5430	Highly susceptible SARS-CoV-2 model in CAG promoterâ€“driven hACE2-transgenic mice. <i>JCI Insight</i> , 2021, 6, .	2.3	21

#	ARTICLE	IF	CITATIONS
5431	Cancer cells are highly susceptible to accumulation of templated insertions linked to MMBIR. <i>Nucleic Acids Research</i> , 2021, 49, 8714-8731.	6.5	12
5432	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	2.9	31
5434	Comparative transcriptomics provides a strategy for phylogenetic analysis and SSR marker development in <i>Chaenomeles</i> . <i>Scientific Reports</i> , 2021, 11, 16441.	1.6	2
5435	Topography drives microgeographic adaptations of closely related species in two tropical tree species complexes. <i>Molecular Ecology</i> , 2021, 30, 5080-5093.	2.0	16
5437	Evidence that toxin resistance in poison birds and frogs is not rooted in sodium channel mutations and may rely on $\alpha$ -toxin sponge proteins. <i>Journal of General Physiology</i> , 2021, 153, .	0.9	26
5438	Gender-Dependent Deregulation of Linear and Circular RNA Variants of HOMER1 in the Entorhinal Cortex of Alzheimer's Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9205.	1.8	13
5440	Genome-wide detection and classification of terpene synthase genes in <i>Aquilaria agallochum</i> . <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1711-1729.	1.4	10
5441	Molecular and functional profiling identifies therapeutically targetable vulnerabilities in plasmablastic lymphoma. <i>Nature Communications</i> , 2021, 12, 5183.	5.8	26
5442	Genome and transcriptome assemblies of the kuruma shrimp, <i>Marsupenaeus japonicus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	20
5443	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
5445	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021, 597, 119-125.	13.7	180
5446	The Easter Egg Weevil ( <i>Pachyrhynchus</i> ) genome reveals syntenic patterns in Coleoptera across 200 million years of evolution. <i>PLoS Genetics</i> , 2021, 17, e1009745.	1.5	14
5447	Planarian Anatomy Ontology: a resource to connect data within and across experimental platforms. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	11
5448	Fast and Accurate Algorithms for Mapping and Aligning Long Reads. <i>Journal of Computational Biology</i> , 2021, 28, 789-803.	0.8	2
5449	Nanopore sequencing of brain-derived full-length circRNAs reveals circRNA-specific exon usage, intron retention and microexons. <i>Nature Communications</i> , 2021, 12, 4825.	5.8	54
5450	A Genome-Wide CRISPR/Cas9 Screen Reveals the Requirement of Host Sphingomyelin Synthase 1 for Infection with Pseudorabies Virus Mutant gD <sup>Pass</sup> . <i>Viruses</i> , 2021, 13, 1574.	1.5	9
5451	Pan-genome of <i>Raphanus</i> highlights genetic variation and introgression among domesticated, wild, and weedy radishes. <i>Molecular Plant</i> , 2021, 14, 2032-2055.	3.9	56
5452	Gene trapping reveals a new transcriptionally active genome element: The chromosome-specific clustered trap region. <i>Genes To Cells</i> , 2021, 26, 874-890.	0.5	0

#	ARTICLE	IF	CITATIONS
5453	BDV Syndrome: an Emerging Syndrome With Profound Obesity and Neurodevelopmental Delay Resembling Prader-Willi Syndrome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 3413-3427.	1.8	9
5454	The relevance of chromosome fissions for major ribosomal DNA dispersion in hymenopteran insects. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1466-1476.	0.8	11
5455	Lamprey lecticans link new vertebrate genes to the origin and elaboration of vertebrate tissues. <i>Developmental Biology</i> , 2021, 476, 282-293.	0.9	5
5457	Identification and characterization of the type II toxin-antitoxin systems in the carbapenem-resistant <i>Acinetobacter baumannii</i> . <i>Microbial Pathogenesis</i> , 2021, 158, 105052.	1.3	2
5458	Afro-alpine flagships revisited II: elucidating the evolutionary relationships and species boundaries in the giant senecios ( <i>Dendrosenecio</i> , Asteraceae). <i>Alpine Botany</i> , 2022, 132, 89-105.	1.1	6
5459	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	2.9	27
5460	A near complete genome for goat genetic and genomic research. <i>Genetics Selection Evolution</i> , 2021, 53, 74.	1.2	16
5461	Transcriptomic profile of leg muscle during early growth and development in Haiyang yellow chicken. <i>Archives Animal Breeding</i> , 2021, 64, 405-416.	0.5	6
5462	A chromosome-level genome of <i>Antechinus flavipes</i> provides a reference for an Australian marsupial genus with male death after mating. <i>Molecular Ecology Resources</i> , 2022, 22, 740-754.	2.2	12
5463	Chromosome-scale assembly of the <i>Dendrobium chrysotoxum</i> genome enhances the understanding of orchid evolution. <i>Horticulture Research</i> , 2021, 8, 183.	2.9	41
5464	Genomic Epidemiology and Strain Taxonomy of <i>Corynebacterium diphtheriae</i> . <i>Journal of Clinical Microbiology</i> , 2021, 59, e0158121.	1.8	12
5465	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , 2021, 30, 6627-6641.	2.0	9
5466	High quality haplotype-resolved genome assemblies of <i>Populus tomentosa</i> Carr., a stabilized interspecific hybrid species widespread in Asia. <i>Molecular Ecology Resources</i> , 2022, 22, 786-802.	2.2	19
5467	Linkage map and QTL mapping of red flesh locus in apple using a R1R1-Å-Å-R6R6 population. <i>Horticultural Plant Journal</i> , 2021, 7, 393-400.	2.3	13
5468	Differential enrichment of yeast DNA in SARS-CoV-2 and related genomes supports synthetic origin hypothesis. <i>F1000Research</i> , 0, 10, 912.	0.8	0
5469	Chemical Inhibition of Apurinic-Apyrimidinic Endonuclease 1 Redox and DNA Repair Functions Affects the Inflammatory Response via Different but Overlapping Mechanisms. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 731588.	1.8	7
5471	Patterns of Coevolutionary Adaptations across Time and Space in Mouse Gammaretroviruses and Three Restrictive Host Factors. <i>Viruses</i> , 2021, 13, 1864.	1.5	5
5473	RetroCHMP3 blocks budding of enveloped viruses without blocking cytokinesis. <i>Cell</i> , 2021, 184, 5419-5431.e16.	13.5	8

#	ARTICLE	IF	CITATIONS
5474	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	2.8	6
5476	Genomic anatomy of male-specific microchromosomes in a gynogenetic fish. <i>PLoS Genetics</i> , 2021, 17, e1009760.	1.5	17
5477	<i>Zanthoxylum</i> -specific whole genome duplication and recent activity of transposable elements in the highly repetitive paleotetraploid <i>Z. bungeanum</i> genome. <i>Horticulture Research</i> , 2021, 8, 205.	2.9	19
5479	Protein-coding repeat polymorphisms strongly shape diverse human phenotypes. <i>Science</i> , 2021, 373, 1499-1505.	6.0	96
5480	High-Quality de novo Chromosome-Level Genome Assembly of a Single <i>Bombyx mori</i> With BmNPV Resistance by a Combination of PacBio Long-Read Sequencing, Illumina Short-Read Sequencing, and Hi-C Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 718266.	1.1	5
5481	Elucidation of the Algicidal Mechanism of the Marine Bacterium <i>Pseudoruegeria</i> sp. M32A2M Against the Harmful Alga <i>Alexandrium catenella</i> Based on Time-Course Transcriptome Analysis. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
5482	Sequence determination of phosphorothioated oligonucleotides using MALDI-TOF mass spectrometry for controlling gene doping in equestrian sports. <i>Drug Testing and Analysis</i> , 2022, 14, 175-180.	1.6	3
5483	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	66
5484	Transcriptomics analysis of the infected tissue of gibel carp ( <i>Carassius auratus gibelio</i> ) with liver myxobolosis infers the underlying defense mechanisms from the perspective of immune-metabolic interactions. <i>Aquaculture</i> , 2021, 542, 736867.	1.7	8
5485	Tiara: deep learning-based classification system for eukaryotic sequences. <i>Bioinformatics</i> , 2022, 38, 344-350.	1.8	34
5486	MINTIA: a metagenomic INserT integrated assembly and annotation tool. <i>PeerJ</i> , 2021, 9, e11885.	0.9	0
5487	A Bayesian approach for accurate de novo transcriptome assembly. <i>Scientific Reports</i> , 2021, 11, 17663.	1.6	1
5488	Chemistry and Bioinformatics Considerations in Using Next-Generation Sequencing Technologies to Inferring HIV Proviral DNA Genome-Intactness. <i>Viruses</i> , 2021, 13, 1874.	1.5	5
5489	The RNA-binding protein Musashi controls axon compartment-specific synaptic connectivity through ptp69D mRNA poly(A)-tailing. <i>Cell Reports</i> , 2021, 36, 109713.	2.9	5
5490	Transcriptional Landscapes of Long Non-coding RNAs and Alternative Splicing in <i>Pyricularia oryzae</i> Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 723636.	1.7	3
5492	Whole-Genome Sequencing and Genome-Wide Studies of Spiny Head Croaker ( <i>Collichthys lucidus</i> ) Reveals Potential Insights for Well-Developed Otoliths in the Family Sciaenidae. <i>Frontiers in Genetics</i> , 2021, 12, 730255.	1.1	0
5494	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	2.0	86
5496	Genetic and phenotypic heterogeneity in KIAA0753-related ciliopathies. <i>American Journal of Medical Genetics, Part A</i> , 2021, , .	0.7	2

#	ARTICLE	IF	CITATIONS
5497	Metagenomic Analyses of Plant Growth-Promoting and Carbon-Cycling Genes in Maize Rhizosphere Soils with Distinct Land-Use and Management Histories. <i>Genes</i> , 2021, 12, 1431.	1.0	9
5498	Transitions to asexuality and evolution of gene expression in <i>Artemia</i> brine shrimp. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211720.	1.2	6
5499	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	1.9	9
5500	Genomic analysis unveils mechanisms of northward invasion and signatures of plateau adaptation in the Asian house rat. <i>Molecular Ecology</i> , 2021, 30, 6596-6610.	2.0	10
5501	De Novo Genome Assembly of the Electric Fish <i>Brachyhypopomus occidentalis</i> (Hypopomidae). <i>Journal of Heredity</i> , 2021, 112, 1111-1121.	1.1	6
5502	FrogCap: A modular sequence capture probe set for phylogenomics and population genetics for all frogs, assessed across multiple phylogenetic scales. <i>Molecular Ecology Resources</i> , 2022, 22, 1100-1119.	2.2	17
5503	Characterization of the complete chloroplast genome of <i>Hordeum jubatum</i> (Poaceae: Pooideae). <i>Journal of Heredity</i> , 2021, 112, 1111-1121.	0.2	1
5504	Parallel subgenome structure and divergent expression evolution of allo-tetraploid common carp and goldfish. <i>Nature Genetics</i> , 2021, 53, 1493-1503.	9.4	52
5506	Inverted microbial community stratification and spatial-temporal stability in hypersaline anaerobic sediments from the Avall solar salterns. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126231.	1.2	5
5507	Protocol for HSDFinder: Identifying, annotating, categorizing, and visualizing duplicated genes in eukaryotic genomes. <i>STAR Protocols</i> , 2021, 2, 100619.	0.5	8
5508	Aptamer-mediated transcriptional gene silencing of <i>Foxp3</i> inhibits regulatory T cells and potentiates antitumor response. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 25, 143-151.	2.3	4
5509	Recombination Marks the Evolutionary Dynamics of a Recently Endogenized Retrovirus. <i>Molecular Biology and Evolution</i> , 2021, 38, 5423-5436.	3.5	2
5510	Effects of aerobic exercise on gut microbiota in adolescents with subthreshold mood syndromes and healthy adolescents: A 12-week, randomized controlled trial. <i>Journal of Affective Disorders</i> , 2021, 293, 363-372.	2.0	10
5511	A haploid diamondback moth ( <i>Plutella xylostella</i> L.) genome assembly resolves 31 chromosomes and identifies a diamide resistance mutation. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103622.	1.2	19
5512	Deciphering the animal genomics using bioinformatics approaches. , 2021, , 281-297.		1
5513	Rapid protein evolution, organellar reductions, and invasive intronic elements in the marine aerobic parasite dinoflagellate <i>Amoebophrya</i> spp. <i>BMC Biology</i> , 2021, 19, 1.	1.7	135
5514	A microbial gene catalog of anaerobic digestion from full-scale biogas plants. <i>GigaScience</i> , 2021, 10, .	3.3	23
5515	Uncovering deeply conserved motif combinations in rapidly evolving noncoding sequences. <i>Genome Biology</i> , 2021, 22, 29.	3.8	27

#	ARTICLE	IF	CITATIONS
5516	Parallel algorithm for the unsupervised binning of metagenomic sequences. , 2021, , .		0
5517	HapSolo: an optimization approach for removing secondary haplotigs during diploid genome assembly and scaffolding. BMC Bioinformatics, 2021, 22, 9.	1.2	9
5518	The<i>Physcomitrella patens</i>chromatin adaptor PpMRG1 interacts with H3K36me3 and regulates light-responsive alternative splicing. Plant Physiology, 2021, 185, 1229-1241.	2.3	3
5519	Draft genome of the herbaceous bamboo <i>Raddia distichophylla</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	6
5521	A novel terpene synthase controls differences in anti-aphrodisiac pheromone production between closely related Heliconius butterflies. PLoS Biology, 2021, 19, e3001022.	2.6	29
5522	Identification and sequencing of 59 highly polymorphic microhaplotypes for analysis of DNA mixtures. International Journal of Legal Medicine, 2021, 135, 1137-1149.	1.2	15
5523	RUNX1/RUNX1T1 mediates alternative splicing and reorganises the transcriptional landscape in leukemia. Nature Communications, 2021, 12, 520.	5.8	27
5524	InsectORâ€”Webserver for sensitive identification of insect olfactory receptor genes from non-model genomes. PLoS ONE, 2021, 16, e0245324.	1.1	14
5525	Pervasive duplication of tumor suppressors in Afrotherians during the evolution of large bodies and reduced cancer risk. ELife, 2021, 10, .	2.8	38
5526	Curation of over 10â€”000 transcriptomic studies to enable data reuse. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	21
5529	Differential Gene Expression in the Auditory System. Lecture Notes in Computer Science, 2005, , 1-8.	1.0	1
5530	A Unifying Framework for Seed Sensitivity and Its Application to Subset Seeds. Lecture Notes in Computer Science, 2005, , 251-263.	1.0	4
5531	Microarray Probe Design Using Îµ-Multi-Objective Evolutionary Algorithms with Thermodynamic Criteria. Lecture Notes in Computer Science, 2006, , 184-195.	1.0	7
5532	Using Semantic Web Tools to Integrate Experimental Measurement Data on Our Own Terms. Lecture Notes in Computer Science, 2006, , 679-688.	1.0	6
5533	Modern BLAST Programs. , 2010, , 3-19.		2
5534	Transposon Resources for Forward and Reverse Genetics in Maize. , 2009, , 561-584.		29
5535	Gene Prediction Methods. , 2009, , 99-119.		2
5536	Bioinformatics Resources for RNA Editing. Methods in Molecular Biology, 2021, 2181, 177-191.	0.4	2

#	ARTICLE	IF	CITATIONS
5537	Genome resources for the DT40 community. <i>Sub-Cellular Biochemistry</i> , 2006, 40, 25-37.	1.0	2
5538	Transcriptome Analyses to Investigate the Pathogenesis of RNA Splicing Factor Retinitis Pigmentosa. <i>Advances in Experimental Medicine and Biology</i> , 2012, 723, 519-525.	0.8	6
5539	Assessment of Mapping and SNP-Detection Algorithms for Next-Generation Sequencing Data in Cancer Genomics. , 2013, , 301-317.		1
5540	Transcriptome Sequencing (RNA-Seq). , 2015, , 31-43.		3
5541	Next-Generation Sequencing Coupled with a Cell-Free Display Technology for Reliable Interactome of Translational Factors. <i>Methods in Molecular Biology</i> , 2014, 1164, 23-32.	0.4	1
5542	GENCODE Pseudogenes. <i>Methods in Molecular Biology</i> , 2014, 1167, 129-155.	0.4	29
5543	High-Throughput Genomic Mapping of Vector Integration Sites in Gene Therapy Studies. <i>Methods in Molecular Biology</i> , 2014, 1185, 321-344.	0.4	33
5544	Case Study: Systematic Detection and Prioritization of Gene Fusions in Cancer by RNA-Seq: A DIY Toolkit. <i>Methods in Molecular Biology</i> , 2020, 2079, 69-79.	0.4	3
5545	Comparative Genomics. <i>Methods in Molecular Biology</i> , 2007, 366, 229-251.	0.4	4
5546	Identification of mRNA Polyadenylation Sites in Genomes Using cDNA Sequences, Expressed Sequence Tags, and Trace. <i>Methods in Molecular Biology</i> , 2008, 419, 23-37.	0.4	14
5547	Computational Gene Annotation in New Genome Assemblies Using GeneID. <i>Methods in Molecular Biology</i> , 2009, 537, 243-261.	0.4	28
5548	Analysis of Genomic DNA with the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2009, 537, 277-301.	0.4	8
5549	Gene Targeting in Mouse Embryonic Stem Cells. <i>Methods in Molecular Biology</i> , 2009, 530, 141-164.	0.4	14
5550	An Introduction to the Lagan Alignment Toolkit. <i>Methods in Molecular Biology</i> , 2007, 395, 205-219.	0.4	9
5551	Comparative Genomic Analysis Using the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2007, 395, 17-33.	0.4	23
5552	Visualization of Syntenic Relationships With SynBrowse. <i>Methods in Molecular Biology</i> , 2007, 396, 153-163.	0.4	9
5553	Fast Masking of Repeated Primer Binding Sites in Eukaryotic Genomes. <i>Methods in Molecular Biology</i> , 2007, 402, 201-217.	0.4	3
5554	Microarray Probe Mapping and Annotation in Cross-Species Comparative Toxicogenomics. <i>Methods in Molecular Biology</i> , 2008, 460, 159-183.	0.4	2

#	ARTICLE	IF	CITATIONS
5555	An Introduction to Mitochondrial Informatics. <i>Methods in Molecular Biology</i> , 2010, 628, 259-274.	0.4	1
5556	Gramene Database: A Hub for Comparative Plant Genomics. <i>Methods in Molecular Biology</i> , 2011, 678, 247-275.	0.4	42
5557	An Overview of the Computational Analyses and Discovery of Transcription Factor Binding Sites. <i>Methods in Molecular Biology</i> , 2010, 674, 1-22.	0.4	11
5558	Identification of Transcription Factor Binding Sites Derived from Transposable Element Sequences Using ChIP-seq. <i>Methods in Molecular Biology</i> , 2010, 674, 225-240.	0.4	5
5559	Annotating the Regulatory Genome. <i>Methods in Molecular Biology</i> , 2010, 674, 313-349.	0.4	2
5560	Computational Identification of miRNAs Involved in Cancer. <i>Methods in Molecular Biology</i> , 2011, 676, 23-41.	0.4	5
5561	Discovery of RNA Motifs Using a Computational Pipeline that Allows Insertions in Paired Regions and Filtering of Candidate Sequences. <i>Methods in Molecular Biology</i> , 2012, 848, 145-158.	0.4	4
5562	HORDE: Comprehensive Resource for Olfactory Receptor Genomics. <i>Methods in Molecular Biology</i> , 2013, 1003, 23-38.	0.4	49
5563	Heuristic Alignment Methods. <i>Methods in Molecular Biology</i> , 2014, 1079, 29-43.	0.4	4
5564	A Review of Pangenome Tools and Recent Studies. , 2020, , 89-112.		21
5565	State of the art in eukaryotic gene prediction. , 2008, , 7-39.		1
5566	Circular RNAs Are a Large Class of Animal RNAs with Regulatory Potency. <i>Springer Theses</i> , 2014, , 69-80.	0.0	7
5567	The Kiwifruit Genome. <i>Compendium of Plant Genomes</i> , 2016, , 101-114.	0.3	1
5568	Performing Local Similarity Searches with Variable Length Seeds. <i>Lecture Notes in Computer Science</i> , 2004, , 373-387.	1.0	9
5569	A Chaining Algorithm for Mapping cDNA Sequences to Multiple Genomic Sequences. , 2007, , 1-13.		4
5570	Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs. , 2008, , 372-395.		6
5571	Computing Alignment Seed Sensitivity with Probabilistic Arithmetic Automata. <i>Lecture Notes in Computer Science</i> , 2008, , 318-329.	1.0	5
5573	Using Bloom Filters for Large Scale Gene Sequence Analysis in Haskell. <i>Lecture Notes in Computer Science</i> , 2008, , 183-194.	1.0	5

#	ARTICLE	IF	CITATIONS
5574	Mining of cis-Regulatory Motifs Associated with Tissue-Specific Alternative Splicing. Lecture Notes in Computer Science, 2009, , 260-271.	1.0	3
5575	String Mining in Bioinformatics. , 2009, , 207-247.		6
5576	mpscan: Fast Localisation of Multiple Reads in Genomes. Lecture Notes in Computer Science, 2009, , 246-260.	1.0	11
5577	Designing Workflows on the Fly Using e-BioFlow. Lecture Notes in Computer Science, 2009, , 470-484.	1.0	6
5578	A Randomized Numerical Aligner (rNA). Lecture Notes in Computer Science, 2010, , 512-523.	1.0	5
5579	Statistical and Computational Studies on Alternative Splicing. , 2011, , 31-53.		4
5580	Efficient Algorithm for Microarray Probes Re-annotation. Lecture Notes in Computer Science, 2011, , 281-289.	1.0	1
5581	K-mulus: Strategies for BLAST in the Cloud. Lecture Notes in Computer Science, 2014, , 237-246.	1.0	2
5582	Efficient Indexed Alignment of Contigs to Optical Maps. Lecture Notes in Computer Science, 2014, , 68-81.	1.0	16
5583	Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96.	1.0	2
5584	Crop Genome Annotation: A Case Study for the Brassica rapa Genome. Compendium of Plant Genomes, 2015, , 53-64.	0.3	1
5585	Genomics and Transcriptomics Advance in Plant Sciences. Energy, Environment, and Sustainability, 2019, , 419-448.	0.6	5
5586	Hybrid sequencing resolves two germline ultra-complex chromosomal rearrangements consisting of 137 breakpoint junctions in a single carrier. Human Genetics, 2021, 140, 775-790.	1.8	9
5587	SoyBase and the Legume Information System: Accessing Information about the Soybean and Other Legume Genomes. , 2012, , 53-66.		3
5588	OASIS. , 2003, , 910-921.		49
5589	Tench ( <i>Tinca tinca</i> ) high-throughput transcriptomics reveal feed dependent gut profiles. Aquaculture, 2017, 479, 200-207.	1.7	1
5590	Transcriptional Signatures of Tau and Amyloid Neuropathology. Cell Reports, 2020, 30, 2040-2054.e5.	2.9	45
5591	Rapid Detection of Wheat Blast Pathogen <i>Magnaporthe oryzae</i> Triticum Pathotype Using Genome-Specific Primers and Cas12a-mediated Technology. Engineering, 2021, 7, 1326-1335.	3.2	26

#	ARTICLE	IF	CITATIONS
5592	Comparative analysis of genome sequences of the conifer tree pathogen, <i>Heterobasidion annosum</i> s.s .. Genomics Data, 2017, 14, 106-113.	1.3	10
5595	C-terminal truncated HBx initiates hepatocarcinogenesis by downregulating TXNIP and reprogramming glucose metabolism. <i>Oncogene</i> , 2021, 40, 1147-1161.	2.6	46
5596	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean ( <i>Glycine max</i> L.), 0, .		1
5597	A chromosome-level reference genome of non-heading Chinese cabbage [ <i>Brassica campestris</i> (syn.) Tj ETQq1 1 0.784314 rgBT /Overl	2.9	51
5598	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159.	9.4	123
5599	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020, 52, 342-352.	9.4	256
5600	De novo assembly and annotation of three <i>Leptosphaeria</i> genomes using Oxford Nanopore MinION sequencing. <i>Scientific Data</i> , 2018, 5, 180235.	2.4	53
5601	Draft genomic and transcriptome resources for marine chelicerate <i>Tachypleus tridentatus</i> . <i>Scientific Data</i> , 2019, 6, 190029.	2.4	15
5602	The sequence and de novo assembly of <i>Oxygymnocypris stewartii</i> genome. <i>Scientific Data</i> , 2019, 6, 190009.	2.4	29
5603	Flatworms have lost the right open reading frame kinase 3 gene during evolution. <i>Scientific Reports</i> , 2015, 5, 9417.	1.6	7
5604	Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011, 2, 118-141.	2.0	109
5605	Genome sequence of <i>Hydrangea macrophylla</i> and its application in analysis of the double flower phenotype. <i>DNA Research</i> , 2021, 28, .	1.5	13
5606	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 2020, 12, 1099-1188.	1.1	17
5607	A New Dinoflagellate Genome Illuminates a Conserved Gene Cluster Involved in Sunscreen Biosynthesis. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	31
5608	Evaluating human autosomal loci for sexually antagonistic viability selection in two large biobanks. <i>Genetics</i> , 2021, 217, 1-10.	1.2	19
5609	Long-read assembly of the <i>Brassica napus</i> reference genome Darmor-bzh. <i>GigaScience</i> , 2020, 9, .	3.3	64
5610	Genotyping of herpes simplex virus type 1 by whole-genome sequencing. <i>Journal of General Virology</i> , 2016, 97, 2732-2741.	1.3	27
5611	Detection, infection dynamics and small RNA response against <i>Culex</i> Y virus in mosquito-derived cells. <i>Journal of General Virology</i> , 2018, 99, 1739-1745.	1.3	23

#	ARTICLE	IF	CITATIONS
5612	Redefining the differences in gene content between <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> using large-scale comparative genomics. <i>Microbial Genomics</i> , 2015, 1, e000028.	1.0	9
5613	The diversity of ice algal communities on the Greenland Ice Sheet as revealed by oligotyping. <i>Microbial Genomics</i> , 2018, 4, .	1.0	39
5614	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	1.0	18
5615	A global to local genomics analysis of <i>Clostridioides difficile</i> ST1/RT027 identifies cryptic transmission events in a northern Arizona healthcare network. <i>Microbial Genomics</i> , 2019, 5, .	1.0	7
5616	Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. <i>Microbial Genomics</i> , 2020, 6, .	1.0	69
5617	Genome-wide mapping of foamy virus vector integrations into a human cell line. <i>Journal of General Virology</i> , 2006, 87, 1339-1347.	1.3	87
5787	GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis. , 2020, , .		37
5788	Persistent histone modifications at the BDNF and Cdk5 promoters following extinction of nicotine-seeking in rats. <i>Genes, Brain and Behavior</i> , 2018, 17, 98-106.	1.1	12
5789	The pseudogenes of barley. <i>Plant Journal</i> , 2018, 93, 502-514.	2.8	14
5790	Phylogeny and Comparative Genomics: the Shifting Landscape in the Genomics Era. , 0, , 84-141.		23
5791	GENRATE: A GENERATIVE MODEL THAT FINDS AND SCORES NEW GENES AND EXONS IN GENOMIC MICROARRAY DATA. , 2004, , .		3
5792	THE EFFECTS OF ALTERNATIVE SPLICING ON TRANSMEMBRANE PROTEINS IN THE MOUSE GENOME. , 2003, , 17-28.		18
5793	Large scale genomic sequence SVM classifiers. , 2005, , .		27
5794	Darwin. <i>ACM SIGPLAN Notices</i> , 2018, 53, 199-213.	0.2	41
5795	ELITE. , 2019, , .		1
5796	Designing seeds for similarity search in genomic DNA. , 2003, , .		36
5797	Transforming men into mice. , 2003, , .		21
5798	Genome-Wide Characterization of RNA Editing Sites in Primary Gastric Adenocarcinoma through RNA-seq Data Analysis. <i>International Journal of Genomics</i> , 2020, 2020, 1-16.	0.8	4

#	ARTICLE	IF	CITATIONS
5799	Intact HIV-1 proviruses accumulate at distinct chromosomal positions during prolonged antiretroviral therapy. <i>Journal of Clinical Investigation</i> , 2019, 129, 988-998.	3.9	209
5800	HIV-1 viremia not suppressible by antiretroviral therapy can originate from large T cell clones producing infectious virus. <i>Journal of Clinical Investigation</i> , 2020, 130, 5847-5857.	3.9	85
5801	Comparative genomic tools and databases: providing insights into the human genome. <i>Journal of Clinical Investigation</i> , 2003, 111, 1099-1106.	3.9	60
5802	In vivo selection of hematopoietic progenitor cells and temozolomide dose intensification in rhesus macaques through lentiviral transduction with a drug resistance gene. <i>Journal of Clinical Investigation</i> , 2009, 119, 1952-63.	3.9	53
5803	Vector design influences hepatic genotoxicity after adeno-associated virus gene therapy. <i>Journal of Clinical Investigation</i> , 2015, 125, 870-880.	3.9	287
5804	Gapless assembly of maize chromosomes using long-read technologies. <i>Genome Biology</i> , 2020, 21, 121.	3.8	101
5805	Personalized and graph genomes reveal missing signal in epigenomic data. <i>Genome Biology</i> , 2020, 21, 124.	3.8	29
5806	Identification and characterization of ERV-W-like sequences in Platyrrhini species provides new insights into the evolutionary history of ERV-W in primates. <i>Mobile DNA</i> , 2020, 11, 6.	1.3	12
5808	From zebrafish heart jogging genes to mouse and human orthologs: using Gene Ontology to investigate mammalian heart development.. <i>F1000Research</i> , 2013, 2, 242.	0.8	7
5809	From zebrafish heart jogging genes to mouse and human orthologs: using Gene Ontology to investigate mammalian heart development.. <i>F1000Research</i> , 2013, 2, 242.	0.8	6
5810	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013, 2, 244.	0.8	13
5811	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013, 2, 244.	0.8	9
5812	G-Links: a gene-centric link acquisition service. <i>F1000Research</i> , 2014, 3, 285.	0.8	3
5813	A reanalysis of mouse ENCODE comparative gene expression data. <i>F1000Research</i> , 2015, 4, 121.	0.8	91
5814	Characterization of an APC Promoter 1B deletion in a Patient Diagnosed with Familial Adenomatous Polyposis via Whole Genome Shotgun Sequencing. <i>F1000Research</i> , 2015, 4, 170.	0.8	5
5815	Accelerated Evolution of the ASPM Gene Controlling Brain Size Begins Prior to Human Brain Expansion. <i>PLoS Biology</i> , 2004, 2, e126.	2.6	176
5816	Epigenomic Consequences of Immortalized Plant Cell Suspension Culture. <i>PLoS Biology</i> , 2008, 6, e302.	2.6	179
5817	Most "Dark Matter" Transcripts Are Associated With Known Genes. <i>PLoS Biology</i> , 2010, 8, e1000371.	2.6	377

#	ARTICLE	IF	CITATIONS
5818	Evolutionary Conservation and Diversification of Puf RNA Binding Proteins and Their mRNA Targets. <i>PLoS Biology</i> , 2015, 13, e1002307.	2.6	54
5819	Comparative Developmental Transcriptomics Reveals Rewiring of a Highly Conserved Gene Regulatory Network during a Major Life History Switch in the Sea Urchin Genus <i>Heliocidaris</i> . <i>PLoS Biology</i> , 2016, 14, e1002391.	2.6	78
5820	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016, 14, e1002394.	2.6	127
5821	Spliced integrated retrotransposed element (SpIRE) formation in the human genome. <i>PLoS Biology</i> , 2018, 16, e2003067.	2.6	11
5822	Integration and Fixation Preferences of Human and Mouse Endogenous Retroviruses Uncovered with Functional Data Analysis. <i>PLoS Computational Biology</i> , 2016, 12, e1004956.	1.5	41
5823	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , 2018, 14, e1005944.	1.5	1,412
5824	Long- and Short-Term Selective Forces on Malaria Parasite Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001099.	1.5	30
5825	Analysis of 62 hybrid assembled human Y chromosomes exposes rapid structural changes and high rates of gene conversion. <i>PLoS Genetics</i> , 2017, 13, e1006834.	1.5	42
5826	A new domestic cat genome assembly based on long sequence reads empowers feline genomic medicine and identifies a novel gene for dwarfism. <i>PLoS Genetics</i> , 2020, 16, e1008926.	1.5	79
5827	Tentative Mapping of Transcription-Induced Interchromosomal Interaction using Chimeric EST and mRNA Data. <i>PLoS ONE</i> , 2007, 2, e254.	1.1	20
5828	Demographic Histories of ERV-K in Humans, Chimpanzees and Rhesus Monkeys. <i>PLoS ONE</i> , 2007, 2, e1026.	1.1	15
5829	Canine Population Structure: Assessment and Impact of Intra-Breed Stratification on SNP-Based Association Studies. <i>PLoS ONE</i> , 2007, 2, e1324.	1.1	66
5830	Genome-Wide Analysis of Abnormal H3K9 Acetylation in Cloned Mice. <i>PLoS ONE</i> , 2008, 3, e1905.	1.1	22
5831	Horizontal Gene Transfers Link a Human MRSA Pathogen to Contagious Bovine Mastitis Bacteria. <i>PLoS ONE</i> , 2008, 3, e3074.	1.1	36
5832	Identification of Nuclear and Cytoplasmic mRNA Targets for the Shuttling Protein SF2/ASF. <i>PLoS ONE</i> , 2008, 3, e3369.	1.1	98
5833	Complete Genome Sequence of the Aerobic CO-Oxidizing Thermophile <i>Thermomicrobium roseum</i> . <i>PLoS ONE</i> , 2009, 4, e4207.	1.1	113
5834	Transcription Factor Binding Sites Are Genetic Determinants of Retroviral Integration in the Human Genome. <i>PLoS ONE</i> , 2009, 4, e4571.	1.1	87
5835	A Novel Endo-Hydrogenase Activity Recycles Hydrogen Produced by Nitrogen Fixation. <i>PLoS ONE</i> , 2009, 4, e4695.	1.1	7

#	ARTICLE	IF	CITATIONS
5836	Molecular Identification and Expression Analysis of Filaggrin-2, a Member of the S100 Fused-Type Protein Family. PLoS ONE, 2009, 4, e5227.	1.1	103
5837	Genetic Structures of Copy Number Variants Revealed by Genotyping Single Sperm. PLoS ONE, 2009, 4, e5236.	1.1	3
5838	Mapping Accuracy of Short Reads from Massively Parallel Sequencing and the Implications for Quantitative Expression Profiling. PLoS ONE, 2009, 4, e6323.	1.1	19
5839	Repertoire of Bovine miRNA and miRNA-Like Small Regulatory RNAs Expressed upon Viral Infection. PLoS ONE, 2009, 4, e6349.	1.1	91
5840	Comparative Analysis of Pyrosequencing and a Phylogenetic Microarray for Exploring Microbial Community Structures in the Human Distal Intestine. PLoS ONE, 2009, 4, e6669.	1.1	719
5841	Polyploidy Did Not Predate the Evolution of Nodulation in All Legumes. PLoS ONE, 2010, 5, e11630.	1.1	88
5842	Exon-Level Transcriptome Profiling in Murine Breast Cancer Reveals Splicing Changes Specific to Tumors with Different Metastatic Abilities. PLoS ONE, 2010, 5, e11981.	1.1	23
5843	SAW: A Method to Identify Splicing Events from RNA-Seq Data Based on Splicing Fingerprints. PLoS ONE, 2010, 5, e12047.	1.1	7
5844	Genome Rearrangements Detected by SNP Microarrays in Individuals with Intellectual Disability Referred with Possible Williams Syndrome. PLoS ONE, 2010, 5, e12349.	1.1	13
5845	Aromatase Is a Direct Target of FOXL2: C134W in Granulosa Cell Tumors via a Single Highly Conserved Binding Site in the Ovarian Specific Promoter. PLoS ONE, 2010, 5, e14389.	1.1	118
5846	Neuronal Genes for Subcutaneous Fat Thickness in Human and Pig Are Identified by Local Genomic Sequencing and Combined SNP Association Study. PLoS ONE, 2011, 6, e16356.	1.1	45
5847	Abundant Human DNA Contamination Identified in Non-Primate Genome Databases. PLoS ONE, 2011, 6, e16410.	1.1	100
5848	Metatranscriptomic Approach to Analyze the Functional Human Gut Microbiota. PLoS ONE, 2011, 6, e17447.	1.1	302
5849	Chromosome Conformation Capture Uncovers Potential Genome-Wide Interactions between Human Conserved Non-Coding Sequences. PLoS ONE, 2011, 6, e17634.	1.1	19
5850	Evaluating the Fidelity of De Novo Short Read Metagenomic Assembly Using Simulated Data. PLoS ONE, 2011, 6, e19984.	1.1	65
5851	The Genome Sequence of the North-European Cucumber ( <i>Cucumis sativus</i> L.) Unravels Evolutionary Adaptation Mechanisms in Plants. PLoS ONE, 2011, 6, e22728.	1.1	112
5852	Transcriptional Profiling of Human Liver Identifies Sex-Biased Genes Associated with Polygenic Dyslipidemia and Coronary Artery Disease. PLoS ONE, 2011, 6, e23506.	1.1	143
5853	Molecular Genetic Analyses of Polytene Chromosome Region 72A-D in <i>Drosophila melanogaster</i> Reveal a Gene Desert in 72D. PLoS ONE, 2011, 6, e23509.	1.1	7

#	ARTICLE	IF	CITATIONS
5854	Common Promoter Elements in Odorant and Vomeronasal Receptor Genes. PLoS ONE, 2011, 6, e29065.	1.1	32
5855	Whole Genome Resequencing Reveals Natural Target Site Preferences of Transposable Elements in <i>Drosophila melanogaster</i> . PLoS ONE, 2012, 7, e30008.	1.1	114
5856	Exploring the Switchgrass Transcriptome Using Second-Generation Sequencing Technology. PLoS ONE, 2012, 7, e34225.	1.1	60
5857	Digital Gene Expression Analysis Based on Integrated De Novo Transcriptome Assembly of Sweet Potato [ <i>Ipomoea batatas</i> (L.) Lam.]. PLoS ONE, 2012, 7, e36234.	1.1	156
5858	Rapid Transcriptional Pulsing Dynamics of High Expressing Retroviral Transgenes in Embryonic Stem Cells. PLoS ONE, 2012, 7, e37130.	1.1	5
5859	High Accuracy Mutation Detection in Leukemia on a Selected Panel of Cancer Genes. PLoS ONE, 2012, 7, e38463.	1.1	58
5860	Skipping of Exons by Premature Termination of Transcription and Alternative Splicing within Intron-5 of the Sheep SCF Gene: A Novel Splice Variant. PLoS ONE, 2012, 7, e38657.	1.1	5
5861	Bovine Polledness â€“ An Autosomal Dominant Trait with Allelic Heterogeneity. PLoS ONE, 2012, 7, e39477.	1.1	109
5862	Novel RNAi-Mediated Approach to G Protein-Coupled Receptor Deorphanization: Proof of Principle and Characterization of a Planarian 5-HT Receptor. PLoS ONE, 2012, 7, e40787.	1.1	16
5863	FAST-SeqS: A Simple and Efficient Method for the Detection of Aneuploidy by Massively Parallel Sequencing. PLoS ONE, 2012, 7, e41162.	1.1	65
5864	Eco-Geographical Diversification of Bitter Taste Receptor Genes (TAS2Rs) among Subspecies of Chimpanzees ( <i>Pan troglodytes</i> ). PLoS ONE, 2012, 7, e43277.	1.1	24
5865	Mechanisms of Dietary Response in Mice and Primates: A Role for EGR1 in Regulating the Reaction to Human-Specific Nutritional Content. PLoS ONE, 2012, 7, e43915.	1.1	3
5866	An Alu-Based Phylogeny of Lemurs (Infraorder: Lemuriformes). PLoS ONE, 2012, 7, e44035.	1.1	21
5867	Discovery and Characterization of Human Exonic Transcriptional Regulatory Elements. PLoS ONE, 2012, 7, e46098.	1.1	14
5868	A Statistical Framework for Accurate Taxonomic Assignment of Metagenomic Sequencing Reads. PLoS ONE, 2012, 7, e46450.	1.1	23
5869	Selective Constraint on Copy Number Variation in Human Piwi-Interacting RNA Loci. PLoS ONE, 2012, 7, e46611.	1.1	5
5870	Comparative Genomics of Neuroglobin Reveals Its Early Origins. PLoS ONE, 2012, 7, e47972.	1.1	27
5871	Reanalysis of RNA-Sequencing Data Reveals Several Additional Fusion Genes with Multiple Isoforms. PLoS ONE, 2012, 7, e48745.	1.1	72

#	ARTICLE	IF	CITATIONS
5872	Deep Sequencing Reveals Differences in the Transcriptional Landscapes of Fibers from Two Cultivated Species of Cotton. PLoS ONE, 2012, 7, e48855.	1.1	37
5873	A Structural-Based Strategy for Recognition of Transcription Factor Binding Sites. PLoS ONE, 2013, 8, e52460.	1.1	13
5874	The First Symbiont-Free Genome Sequence of Marine Red Alga, <i>Susabi-nori</i> ( <i>Pyropia yezoensis</i> ). PLoS ONE, 2013, 8, e57122.	1.1	150
5875	Genome-Wide Characterization and Linkage Mapping of Simple Sequence Repeats in Mei ( <i>Prunus mume</i> ) Tj ETQq1_1_0.784314 rgBT (DOI: 10.1371/journal.pone.0078431)	1.1	41
5876	Widespread Divergence of the CEACAM/PSG Genes in Vertebrates and Humans Suggests Sensitivity to Selection. PLoS ONE, 2013, 8, e61701.	1.1	25
5877	The Development of 7E Chromosome-Specific Molecular Markers for <i>Thinopyrum elongatum</i> Based on SLAF-seq Technology. PLoS ONE, 2013, 8, e65122.	1.1	117
5878	Optimizing Information in Next-Generation-Sequencing (NGS) Reads for Improving De Novo Genome Assembly. PLoS ONE, 2013, 8, e69503.	1.1	8
5879	Genome Survey Sequencing and Genetic Background Characterization of <i>Gracilariopsis lemaneiformis</i> (Rhodophyta) Based on Next-Generation Sequencing. PLoS ONE, 2013, 8, e69909.	1.1	52
5880	Genome Sequencing and Analysis of BCG Vaccine Strains. PLoS ONE, 2013, 8, e71243.	1.1	84
5881	Breakpoint Features of Genomic Rearrangements in Neuroblastoma with Unbalanced Translocations and Chromothripsis. PLoS ONE, 2013, 8, e72182.	1.1	42
5882	Divergent Evolutionary and Expression Patterns between Lineage Specific New Duplicate Genes and Their Parental Paralogs in <i>Arabidopsis thaliana</i> . PLoS ONE, 2013, 8, e72362.	1.1	19
5883	Transcript Assembly and Quantification by RNA-Seq Reveals Differentially Expressed Genes between Soft-Endocarp and Hard-Endocarp Hawthorns. PLoS ONE, 2013, 8, e72910.	1.1	30
5884	Revealing of <i>Mycobacterium marinum</i> Transcriptome by RNA-seq. PLoS ONE, 2013, 8, e75828.	1.1	21
5885	Global Transcriptome Analysis of <i>Lactococcus garvieae</i> Strains in Response to Temperature. PLoS ONE, 2013, 8, e79692.	1.1	30
5886	A New Family of Predicted KrÄppel-Like Factor Genes and Pseudogenes in Placental Mammals. PLoS ONE, 2013, 8, e81109.	1.1	42
5887	Evaluation of Assembly Strategies Using RNA-Seq Data Associated with Grain Development of Wheat ( <i>Triticum aestivum</i> L.). PLoS ONE, 2013, 8, e83530.	1.1	33
5888	Rapid Diversification of FoxP2 in Teleosts through Gene Duplication in the Teleost-Specific Whole Genome Duplication Event. PLoS ONE, 2013, 8, e83858.	1.1	5
5889	A Penile Spine/Vibrissa Enhancer Sequence Is Missing in Modern and Extinct Humans but Is Retained in Multiple Primates with Penile Spines and Sensory Vibrissae. PLoS ONE, 2013, 8, e84258.	1.1	16

#	ARTICLE	IF	CITATIONS
5890	Detection of Chromosomal Breakpoints in Patients with Developmental Delay and Speech Disorders. PLoS ONE, 2014, 9, e90852.	1.1	41
5891	Deep RNA Sequencing Reveals Hidden Features and Dynamics of Early Gene Transcription in Paramecium bursaria Chlorella Virus 1. PLoS ONE, 2014, 9, e90989.	1.1	65
5892	The Draft Genome Sequence of European Pear ( <i>Pyrus communis</i> L. "Bartlett"). PLoS ONE, 2014, 9, e92644.	1.1	241
5893	Measuring Turnover of SIV DNA in Resting CD4+ T Cells Using Pyrosequencing: Implications for the Timing of HIV Eradication Therapies. PLoS ONE, 2014, 9, e93330.	1.1	10
5894	Characterization of Natural Antisense Transcript, Sclerotia Development and Secondary Metabolism by Strand-Specific RNA Sequencing of <i>Aspergillus flavus</i> . PLoS ONE, 2014, 9, e97814.	1.1	13
5895	Genotyping Cancer-Associated Genes in Chordoma Identifies Mutations in Oncogenes and Areas of Chromosomal Loss Involving CDKN2A, PTEN, and SMARCB1. PLoS ONE, 2014, 9, e101283.	1.1	72
5896	Systematic Identification and Characterization of RNA Editing in Prostate Tumors. PLoS ONE, 2014, 9, e101431.	1.1	15
5897	NCI-60 Whole Exome Sequencing and Pharmacological CellMiner Analyses. PLoS ONE, 2014, 9, e101670.	1.1	38
5898	Quickly Finding Orthologs as Reciprocal Best Hits with BLAT, LAST, and UBLAST: How Much Do We Miss?. PLoS ONE, 2014, 9, e101850.	1.1	133
5899	GHOSTX: An Improved Sequence Homology Search Algorithm Using a Query Suffix Array and a Database Suffix Array. PLoS ONE, 2014, 9, e103833.	1.1	76
5900	Long Non-Coding RNAs Differentially Expressed between Normal versus Primary Breast Tumor Tissues Disclose Converse Changes to Breast Cancer-Related Protein-Coding Genes. PLoS ONE, 2014, 9, e106076.	1.1	35
5901	Long Distance Linkage Disequilibrium and Limited Hybridization Suggest Cryptic Speciation in Atlantic Cod. PLoS ONE, 2014, 9, e106380.	1.1	37
5902	Evolution of an Expanded Mannose Receptor Gene Family. PLoS ONE, 2014, 9, e110330.	1.1	48
5903	Divergence of Gene Body DNA Methylation and Evolution of Plant Duplicate Genes. PLoS ONE, 2014, 9, e110357.	1.1	48
5904	Transcriptome of the Invasive Brown Marmorated Stink Bug, <i>Halyomorpha halys</i> (Stål) (Heteroptera: Pentatomidae). PLoS ONE, 2014, 9, e110367.	1.1	67
5905	Molecular Description of Eye Defects in the Zebrafish Pax6b Mutant, sunrise, Reveals a Pax6b-Dependent Genetic Network in the Developing Anterior Chamber. PLoS ONE, 2015, 10, e0117645.	1.1	32
5906	A Transcriptome Derived Female-Specific Marker from the Invasive Western Mosquitofish ( <i>Gambusia holbrooki</i> ). PLoS ONE, 2015, 10, e0122524.	1.1	26
5907	Flexible, Fast and Accurate Sequence Alignment Profiling on GPGPU with PaSWAS. PLoS ONE, 2015, 10, e0122524.	1.1	13

#	ARTICLE	IF	CITATIONS
5908	Comparative Whole-Genome Analysis of Clinical Isolates Reveals Characteristic Architecture of <i>Mycobacterium tuberculosis</i> Pangenome. PLoS ONE, 2015, 10, e0122979.	1.1	49
5909	Differential Gene Expression Profiling of Dystrophic Dog Muscle after MuStem Cell Transplantation. PLoS ONE, 2015, 10, e0123336.	1.1	17
5910	Combining Next Generation Sequencing with Bulk Segregant Analysis to Fine Map a Stem Moisture Locus in Sorghum ( <i>Sorghum bicolor</i> L. Moench). PLoS ONE, 2015, 10, e0127065.	1.1	48
5911	Identification of Pathogen Signatures in Prostate Cancer Using RNA-seq. PLoS ONE, 2015, 10, e0128955.	1.1	34
5912	Comprehensive Analysis of Disease-Related Genes in Chronic Lymphocytic Leukemia by Multiplex PCR-Based Next Generation Sequencing. PLoS ONE, 2015, 10, e0129544.	1.1	23
5913	Quantitative Trait Loci Associated with the Tocochromanol (Vitamin E) Pathway in Barley. PLoS ONE, 2015, 10, e0133767.	1.1	14
5914	Draft De Novo Transcriptome of the Rat Kangaroo Potorous <i>tridactylus</i> as a Tool for Cell Biology. PLoS ONE, 2015, 10, e0134738.	1.1	18
5915	High Resolution Consensus Mapping of Quantitative Trait Loci for Fiber Strength, Length and Micronaire on Chromosome 25 of the Upland Cotton ( <i>Gossypium hirsutum</i> L.). PLoS ONE, 2015, 10, e0135430.	1.1	51
5916	Complex Population Structure and Virulence Differences among Serotype 2 <i>Streptococcus suis</i> Strains Belonging to Sequence Type 28. PLoS ONE, 2015, 10, e0137760.	1.1	42
5917	Ovarian Transcriptome Analysis of <i>Portunus trituberculatus</i> Provides Insights into Genes Expressed during Phase III and IV Development. PLoS ONE, 2015, 10, e0138862.	1.1	20
5918	Fixing Formalin: A Method to Recover Genomic-Scale DNA Sequence Data from Formalin-Fixed Museum Specimens Using High-Throughput Sequencing. PLoS ONE, 2015, 10, e0141579.	1.1	112
5919	Exocarp Properties and Transcriptomic Analysis of Cucumber ( <i>Cucumis sativus</i> ) Fruit Expressing Age-Related Resistance to <i>Phytophthora capsici</i> . PLoS ONE, 2015, 10, e0142133.	1.1	32
5920	Mapping the Flavor Contributing Traits on "Fengwei Melon" ( <i>Cucumis melo</i> L.) Chromosomes Using Parent Resequencing and Super Bulk Segregant Analysis. PLoS ONE, 2016, 11, e0148150.	1.1	26
5921	Placenta-Enriched lincRNAs MIR503HG and LINC00629 Decrease Migration and Invasion Potential of JEG-3 Cell Line. PLoS ONE, 2016, 11, e0151560.	1.1	36
5922	Using a Candidate Gene-Based Genetic Linkage Map to Identify QTL for Winter Survival in Perennial Ryegrass. PLoS ONE, 2016, 11, e0152004.	1.1	10
5923	Reactive Oxygen Species Play a Role in the Infection of the Necrotrophic Fungi, <i>Rhizoctonia solani</i> in Wheat. PLoS ONE, 2016, 11, e0152548.	1.1	77
5924	Toward Understanding the Genetic Basis of Yak Ovary Reproduction: A Characterization and Comparative Analyses of Estrus Ovary Transcriptome in Yak and Cattle. PLoS ONE, 2016, 11, e0152675.	1.1	33
5925	Genomic Aberrations in Crizotinib Resistant Lung Adenocarcinoma Samples Identified by Transcriptome Sequencing. PLoS ONE, 2016, 11, e0153065.	1.1	18

#	ARTICLE	IF	CITATIONS
5926	Zinc Finger Domain of the PRDM9 Gene on Chromosome 1 Exhibits High Diversity in Ruminants but Its Paralog PRDM7 Contains Multiple Disruptive Mutations. PLoS ONE, 2016, 11, e0156159.	1.1	12
5927	A Chromosome 7 Pericentric Inversion Defined at Single-Nucleotide Resolution Using Diagnostic Whole Genome Sequencing in a Patient with Hand-Foot-Genital Syndrome. PLoS ONE, 2016, 11, e0157075.	1.1	5
5928	Comorbid Analysis of Genes Associated with Autism Spectrum Disorders Reveals Differential Evolutionary Constraints. PLoS ONE, 2016, 11, e0157937.	1.1	24
5929	Identification and Validation of SNP Markers Linked to Dwarf Traits Using SLAF-Seq Technology in Lagerstroemia. PLoS ONE, 2016, 11, e0158970.	1.1	23
5930	A De Novo Genome Sequence Assembly of the Arabidopsis thaliana Accession Niederzenz-1 Displays Presence/Absence Variation and Strong Synteny. PLoS ONE, 2016, 11, e0164321.	1.1	63
5931	Comparative Analysis of Vertebrate Diurnal/Circadian Transcriptomes. PLoS ONE, 2017, 12, e0169923.	1.1	29
5932	Accurate Breakpoint Mapping in Apparently Balanced Translocation Families with Discordant Phenotypes Using Whole Genome Mate-Pair Sequencing. PLoS ONE, 2017, 12, e0169935.	1.1	31
5933	The first complete chloroplast genome sequences of Ulmus species by de novo sequencing: Genome comparative and taxonomic position analysis. PLoS ONE, 2017, 12, e0171264.	1.1	80
5934	A new GTF2I-BRAF fusion mediating MAPK pathway activation in pilocytic astrocytoma. PLoS ONE, 2017, 12, e0175638.	1.1	27
5935	TRE5-A retrotransposition profiling reveals putative RNA polymerase III transcription complex binding sites on the Dictyostelium extrachromosomal rDNA element. PLoS ONE, 2017, 12, e0175729.	1.1	2
5936	Population genetic structure of Guiana dolphin ( <i>Sotalia guianensis</i> ) from the southwestern Atlantic coast of Brazil. PLoS ONE, 2017, 12, e0183645.	1.1	9
5937	Candidate genes for first flower node identified in pepper using combined SLAF-seq and BSA. PLoS ONE, 2018, 13, e0194071.	1.1	23
5938	Mitochondrial D-loop sequence variation and maternal lineage in the endangered Cleveland Bay horse. PLoS ONE, 2020, 15, e0243247.	1.1	4
5939	The full transcription map of mouse papillomavirus type 1 (MmuPV1) in mouse wart tissues. PLoS Pathogens, 2017, 13, e1006715.	2.1	47
5940	Mutations altering acetylated residues in the CTD of HIV-1 integrase cause defects in proviral transcription at early times after integration of viral DNA. PLoS Pathogens, 2020, 16, e1009147.	2.1	22
5942	Concentration-Dependent Recruitment of Mammalian Odorant Receptors. ENeuro, 2020, 7, ENEURO.0103-19.2019.	0.9	12
5943	Screening for mutations in selected miRNA genes in hypogonadotropic hypogonadism patients. Endocrine Connections, 2019, 8, 506-509.	0.8	3
5944	Independent Whole-Genome Duplications Define the Architecture of the Genomes of the Devastating West African Cacao Black Pod Pathogen <i>Phytophthora megakarya</i> and Its Close Relative <i>Phytophthora palmivora</i> . G3: Genes, Genomes, Genetics, 2020, 10, 2241-2255.	0.8	18

#	ARTICLE	IF	CITATIONS
5945	Metatranscriptomic Study of Microbes in Environment: A Community Function Based Approach. Journal of Bacteriology & Mycology Open Access, 2017, 4, .	0.2	1
5946	Genomes of <i>Strongylocentrotus franciscanus</i> and <i>Lytechinus variegatus</i> : are there any genomic explanations for the two order of magnitude difference in the lifespan of sea urchins?. <i>Aging</i> , 2016, 8, 260-271.	1.4	16
5947	The evolution of CpG density and lifespan in conserved primate and mammalian promoters. <i>Aging</i> , 2018, 10, 561-572.	1.4	23
5948	Next generation mapping reveals novel large genomic rearrangements in prostate cancer. <i>Oncotarget</i> , 2017, 8, 23588-23602.	0.8	43
5949	Deep sequencing of a recurrent oligodendroglioma and the derived xenografts reveals new insights into the evolution of human oligodendroglioma and candidate driver genes. <i>Oncotarget</i> , 2019, 10, 3641-3653.	0.8	1
5950	A novel retroviral mutagenesis screen identifies prognostic genes in RUNX1 mediated myeloid leukemogenesis. <i>Oncotarget</i> , 2015, 6, 30664-30674.	0.8	5
5951	Genome and transcriptome delineation of two major oncogenic pathways governing invasive ductal breast cancer development. <i>Oncotarget</i> , 2015, 6, 36652-36674.	0.8	24
5952	A novel gammaretroviral shuttle vector insertional mutagenesis screen identifies <i>SHARPIN</i> as a breast cancer metastasis gene and prognostic biomarker. <i>Oncotarget</i> , 2015, 6, 39507-39520.	0.8	25
5953	Bioinformatics tools for analysing viral genomic data. <i>OIE Revue Scientifique Et Technique</i> , 2016, 35, 271-285.	0.5	16
5954	Computational Approaches in Detecting Non- Coding RNA. <i>Current Genomics</i> , 2013, 14, 371-377.	0.7	41
5955	Defind: Detecting Genomic Deletions by Integrating Read Depth, GC Content, Mapping Quality and Paired-end Mapping Signatures of Next Generation Sequencing Data. <i>Current Bioinformatics</i> , 2019, 14, 130-138.	0.7	3
5956	Single-molecule Real-time (SMRT) Isoform Sequencing (Iso-Seq) in Plants: The Status of the Bioinformatics Tools to Unravel the Transcriptome Complexity. <i>Current Bioinformatics</i> , 2019, 14, 566-573.	0.7	13
5957	Target Site Preferences of Subgroup C Rous Sarcoma Virus Integration into the Chicken DNA. <i>The Open Genomics Journal</i> , 2008, 1, 6-12.	0.5	2
5958	Using Metagenomics to Connect Microbial Community Biodiversity and Functions. <i>Current Issues in Molecular Biology</i> , 2017, 24, 103-118.	1.0	47
5959	Analysis of MBOAT family reveals the diversity of MBOAT1 amplification in Solanaceae. <i>Archives of Biological Sciences</i> , 2015, 67, 1349-1356.	0.2	1
5960	Identification of common carp innate immune genes with whole-genome sequencing and RNA-Seq data. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 169.	1.0	12
5961	Improving the performance of Transposable Elements detection tools. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 231.	1.0	10
5962	COMPARATIVE METAGENOMICS ANALYSIS OF PALM OIL MILL EFFLUENT (POME) USING THREE DIFFERENT BIOINFORMATICS PIPELINES. <i>IJUM Engineering Journal</i> , 2019, 20, 1-11.	0.5	3

#	ARTICLE	IF	CITATIONS
5963	Population Structure and Antimicrobial Resistance of Invasive Serotype IV Group <i>Bacteriophage Streptococcus</i> , Toronto, Ontario, Canada. <i>Emerging Infectious Diseases</i> , 2015, 21, 585-591.	2.0	39
5964	Metagenomic Analysis of the Dynamic Changes in the Gut Microbiome of the Participants of the MARS-500 Experiment, Simulating Long Term Space Flight. <i>Acta Naturae</i> , 2013, 5, 116-125.	1.7	38
5965	An SNP-Based High-Density Genetic Linkage Map for Tetraploid Potato Using Specific Length Amplified Fragment Sequencing (SLAF-Seq) Technology. <i>Agronomy</i> , 2020, 10, 114.	1.3	11
5966	Characterization of EST-SSR markers in bread wheat EST related to drought tolerance and functional analysis of SSR-containing unigenes. , 0, , 1-12.		3
5968	LINE-1 family member GCRG123 gene is up-regulated in human gastric signet-ring cell carcinoma. <i>World Journal of Gastroenterology</i> , 2008, 14, 758.	1.4	2
5969	Microarray evaluation of bovine hepatic gene response to fescue toxicosis. <i>World Mycotoxin Journal</i> , 2013, 6, 419-426.	0.8	2
5970	An improved understanding of cancer genomics through massively parallel sequencing. <i>Translational Cancer Research</i> , 2014, 3, 243-259.	0.4	10
5971	LAS. <i>Advances in Medical Diagnosis, Treatment, and Care</i> , 2018, , 56-93.	0.1	1
5972	A Case Study of a Laboratory Information System Developed at the Institute for Cancer Research at Candiolo. , 2018, , 505-531.		1
5973	<i>Handbook of Research on Systems Biology Applications in Medicine.</i> , 2009, , .		8
5974	Computational Sequence Design Techniques for DNA Microarray Technologies. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 0, , 57-91.	0.2	1
5975	mBLAST: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. <i>Journal of Data Mining in Genomics &amp; Proteomics</i> , 2013, 04, .	0.5	16
5976	Towards a Comprehensive Search of Putative Chitinases Sequences in Environmental Metagenomic Databases. <i>Natural Science</i> , 2014, 06, 323-337.	0.2	3
5977	Bio301: A Web-Based EST Annotation Pipeline That Facilitates Functional Comparison Studies. , 2012, 2012, 1-5.		4
5978	Evaluating amplicon high-throughput sequencing data of microalgae living in melting snow: improvements and limitations. <i>Fottea</i> , 2019, 19, 115-131.	0.4	19
5979	<i>Deep Sequencing Data Analysis: Challenges and Solutions.</i> , 0, , .		4
5980	<i>Bioinformatics as a Tool for the Structural and Evolutionary Analysis of Proteins.</i> , 0, , .		7
5981	FusionScan: accurate prediction of fusion genes from RNA-Seq data. <i>Genomics and Informatics</i> , 2019, 17, e26.	0.4	10

#	ARTICLE	IF	CITATIONS
5982	Accelerating next generation sequencing data analysis: an evaluation of optimized best practices for Genome Analysis Toolkit algorithms. <i>Genomics and Informatics</i> , 2020, 18, e10.	0.4	39
5983	SNPinProbe_1.0: A database for filtering out probes in the Affymetrix GeneChip® Human Exon 1.0 ST array potentially affected by SNPs. <i>Bioinformatics</i> , 2008, 2, 469-470.	0.2	33
5984	Computational Epigenetics: the new scientific paradigm. <i>Bioinformatics</i> , 2010, 4, 331-337.	0.2	36
5985	Integrative genomic analysis of the human immune response to influenza vaccination. <i>ELife</i> , 2013, 2, e00299.	2.8	126
5986	APOBEC3A deaminates transiently exposed single-strand DNA during LINE-1 retrotransposition. <i>ELife</i> , 2014, 3, e02008.	2.8	113
5987	Metagenomic chromosome conformation capture (meta3C) unveils the diversity of chromosome organization in microorganisms. <i>ELife</i> , 2014, 3, e03318.	2.8	154
5988	Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of <i>Albugo candida</i> , a generalist parasite. <i>ELife</i> , 2015, 4, .	2.8	71
5989	Genomic variations of the mevalonate pathway in porokeratosis. <i>ELife</i> , 2015, 4, e06322.	2.8	71
5990	Viruses are a dominant driver of protein adaptation in mammals. <i>ELife</i> , 2016, 5, .	2.8	267
5991	Resolving rates of mutation in the brain using single-neuron genomics. <i>ELife</i> , 2016, 5, .	2.8	139
5992	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , 2016, 5, .	2.8	48
5993	Evolution of gene dosage on the Z-chromosome of schistosome parasites. <i>ELife</i> , 2018, 7, .	2.8	31
5994	The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , 2018, 7, .	2.8	120
5995	Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, .	2.8	26
5996	The genetic factors of bilaterian evolution. <i>ELife</i> , 2020, 9, .	2.8	44
5997	A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. <i>ELife</i> , 2019, 8, .	2.8	41
5998	Cardiac mitochondrial function depends on BUD23 mediated ribosome programming. <i>ELife</i> , 2020, 9, .	2.8	10
5999	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	2.8	33

#	ARTICLE	IF	CITATIONS
6000	Clusters of polymorphic transmembrane genes control resistance to schistosomes in snail vectors. <i>ELife</i> , 2020, 9, .	2.8	18
6001	Multiple comparative metagenomics using multiset <i>k</i> -mer counting. <i>PeerJ Computer Science</i> , 0, 2, e94.	2.7	88
6002	BiSCoT: improving large eukaryotic genome assemblies with optical maps. <i>PeerJ</i> , 2020, 8, e10150.	0.9	13
6003	GenomePeek—an online tool for prokaryotic genome and metagenome analysis. <i>PeerJ</i> , 2015, 3, e1025.	0.9	12
6004	Improving transcriptome assembly through error correction of high-throughput sequence reads. <i>PeerJ</i> , 2013, 1, e113.	0.9	38
6005	Intron gain by tandem genomic duplication: a novel case in a potato gene encoding RNA-dependent RNA polymerase. <i>PeerJ</i> , 2016, 4, e2272.	0.9	9
6006	Transcriptomic analysis of diplomonad parasites reveals a trans-spliced intron in a helicase gene in <i>Giardia</i> . <i>PeerJ</i> , 2017, 5, e2861.	0.9	7
6007	RelocaTE2: a high resolution transposable element insertion site mapping tool for population resequencing. <i>PeerJ</i> , 2017, 5, e2942.	0.9	31
6008	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. <i>PeerJ</i> , 2014, 2, e332.	0.9	265
6009	Divide and Conquer (DC) BLAST: fast and easy BLAST execution within HPC environments. <i>PeerJ</i> , 2017, 5, e3486.	0.9	10
6010	Comparative analysis of whole flower transcriptomes in the Zingiberales. <i>PeerJ</i> , 2018, 6, e5490.	0.9	5
6011	Phylogenetic analysis of the cytochrome P450 (CYP450) nucleotide sequences of the horse and predicted CYP450s of the white rhinoceros ( <i>Ceratotherium simum</i> ) and other mammalian species. <i>PeerJ</i> , 2018, 6, e5718.	0.9	2
6012	imGLAD: accurate detection and quantification of target organisms in metagenomes. <i>PeerJ</i> , 2018, 6, e5882.	0.9	24
6013	A draft genome and transcriptome of common milkweed ( <i>Asclepias syriaca</i> ) as resources for evolutionary, ecological, and molecular studies in milkweeds and Apocynaceae. <i>PeerJ</i> , 2019, 7, e7649.	0.9	19
6014	Comparative genomics and phylogenetic discordance of cultivated tomato and close wild relatives. <i>PeerJ</i> , 2015, 3, e793.	0.9	23
6015	Plastid genomics of <i>Nicotiana</i> (Solanaceae): insights into molecular evolution, positive selection and the origin of the maternal genome of Aztec tobacco ( <i>Nicotiana rustica</i> ). <i>PeerJ</i> , 2020, 8, e9552.	0.9	43
6016	Global RNA editome landscape discovers reduced RNA editing in glioma: loss of editing of gamma-amino butyric acid receptor alpha subunit 3 (GABRA3) favors glioma migration and invasion. <i>PeerJ</i> , 2020, 8, e9755.	0.9	13
6017	Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10

#	ARTICLE	IF	CITATIONS
6018	AnnoLnc: A One-Stop Portal to Systematically Annotate Novel Human Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2021, 2254, 111-131.	0.4	1
6020	High-quality genome assembly of an important biodiesel plant, <i>Euphorbia lathyris</i> L. <i>DNA Research</i> , 2021, 28, .	1.5	11
6022	RGD v2.0: a major update of the ruminant functional and evolutionary genomics database. <i>Nucleic Acids Research</i> , 2022, 50, D1091-D1099.	6.5	24
6023	Phylogenomics of <i>Salvia</i> L. subgenus <i>Calospatha</i> (Lamiaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 725900.	1.7	7
6025	Deep RNA Sequencing Revealed Fusion Junctional Heterogeneity May Predict Crizotinib Treatment Efficacy in ALK-Rearranged NSCLC. <i>Journal of Thoracic Oncology</i> , 2022, 17, 264-276.	0.5	15
6026	Chromosomal-Level Genome Assembly of a True Bug, <i>Aspongopus chinensis</i> Dallas, 1851 (Hemiptera: Dinidoridae). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
6027	Differential enrichment of yeast DNA in SARS-CoV-2 and related genomes supports synthetic origin hypothesis. <i>F1000Research</i> , 0, 10, 912.	0.8	0
6029	Phylogeny of <i>Crataegus</i> (Rosaceae) based on 257 nuclear loci and chloroplast genomes: evaluating the impact of hybridization. <i>PeerJ</i> , 2021, 9, e12418.	0.9	6
6030	MINTIE: identifying novel structural and splice variants in transcriptomes using RNA-seq data. <i>Genome Biology</i> , 2021, 22, 296.	3.8	16
6031	SeekFusion - A Clinically Validated Fusion Transcript Detection Pipeline for PCR-Based Next-Generation Sequencing of RNA. <i>Frontiers in Genetics</i> , 2021, 12, 739054.	1.1	9
6032	An <i>Emiliania huxleyi</i> pan-transcriptome reveals basal strain specificity in gene expression patterns. <i>Scientific Reports</i> , 2021, 11, 20795.	1.6	7
6036	MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. <i>Journal of Computational Biology</i> , 2021, 28, 1063-1074.	0.8	2
6037	The long non-coding RNA ET-20 mediates EMT by impairing desmosomes in breast cancer cells. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	9
6038	RBPmap: A Tool for Mapping and Predicting the Binding Sites of RNA-Binding Proteins Considering the Motif Environment. <i>Methods in Molecular Biology</i> , 2022, 2404, 53-65.	0.4	11
6039	A novel exome probe set captures phototransduction genes across birds (Aves) enabling efficient analysis of vision evolution. <i>Molecular Ecology Resources</i> , 2022, 22, 587-601.	2.2	3
6040	Evaluation of accessible regions of <i>Escherichia coli</i> fimH mRNA through computational prediction and experimental investigation. <i>Iranian Journal of Microbiology</i> , 2021, 13, 653-663.	0.8	0
6042	A DATABASE DESIGNED TO COMPUTATIONALLY AID AN EXPERIMENTAL APPROACH TO ALTERNATIVE SPLICING. , 2003, , 78-88.		10
6043	Comparative Bioinformatics for Mouse and Human Genes: Getting Started. <i>Current Protocols in Human Genetics</i> , 2004, 41, Unit 1.10.	3.5	0

#	ARTICLE	IF	CITATIONS
6047	Gene predictions and annotations.. , 2005, , 429-448.		0
6049	The GATO gene annotation tool for research laboratories. Brazilian Journal of Medical and Biological Research, 2005, 38, 1571-1574.	0.7	2
6050	Data Structures for Genome Annotation, Alternative Splicing, and Validation. Lecture Notes in Computer Science, 2006, , 114-123.	1.0	0
6051	Genome Resources and Comparative Analysis Tools for Cardiovascular Research. Methods in Molecular Medicine, 2006, 128, 101-123.	0.8	0
6053	[Special Issue: Fact Databases and Freewares] A Useful Bioinformatics Suite for Retrieving and Analyzing Microbial Genome Data (G-InforBIO). Journal of Computer Aided Chemistry, 2006, 7, 87-93.	0.3	0
6054	GENE EXPRESSION PROFILING OF BOVINE OVARIAN FOLLICULAR SELECTION. Biology of Reproduction, 2007, 77, 98-98.	1.2	0
6055	RUN PROBABILITY OF HIGH-ORDER SEED PATTERNS AND ITS APPLICATIONS TO FINDING GOOD TRANSITION SEEDS. , 2007, , .		0
6056	Web-Based Resources for Clinical Bioinformatics. Methods in Molecular Medicine, 2008, 141, 309-329.	0.8	0
6058	Mapping Techniques. Springer Protocols, 2008, , 291-310.	0.1	0
6059	Methods and application of genomic sequence alignment and alignment between genomic sequence and transcripts. Journal of Animal Genetics, 2008, 36, 177-183.	0.1	0
6060	An Integrated Approach Providing Exact SNP IDs from Sequences. Lecture Notes in Electrical Engineering, 2008, , 221-231.	0.3	0
6061	A Dynamic Neighboring Extension Search Algorithm&nbsp;for Genome Coordinate Conversion in the Presence&nbsp;of Short Sequence Duplications. Gene Expression To Genetical Genomics, 0, 2, 29-36.	1.0	0
6062	Analysis of Cis-Regulatory Motifs in Cassette Exons by Incorporating Exon Skipping Rates. Lecture Notes in Computer Science, 2009, , 272-283.	1.0	1
6063	A Reconfigurable Bloom Filter Architecture for BLASTN. Lecture Notes in Computer Science, 2009, , 40-49.	1.0	5
6064	Sequence Based Gene Expression Analysis. , 2009, , 191-207.		2
6065	Inter-Species Comparative Sequence Analysis: A Tool for Genomic Medicine. , 2009, , 120-130.		0
6066	Systems Biology and Infectious Diseases. , 2009, , 377-402.		1
6067	Animal microRNA Gene Prediction. , 2009, , 21-43.		0

#	ARTICLE	IF	CITATIONS
6068	BatchGenAna: a batch platform for large-scale genomic analysis of mammalian small RNAs. <i>Bioinformatics</i> , 2009, 3, 336-348.	0.2	0
6069	COCAW: A Genome-wide Pattern Search System for Designing Microbial Probes. <i>Genomics and Informatics</i> , 2009, 7, 178-180.	0.4	0
6070	A CNV detection algorithm based on statistical analysis of the aligned reads. <i>The KIPS Transactions PartD</i> , 2009, 16D, 661-672.	0.2	0
6071	<i>Bioinformatics Tools for Crop Research and Breeding.</i> , 2010, , 97-116.		0
6072	<i>Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions.</i> , 2010, , 315-378.		0
6073	Mapping Affymetrix Microarray Probes to the Rat Genome via a Persistent Index. <i>International Journal of Knowledge Discovery in Bioinformatics</i> , 2010, 1, 48-65.	0.8	0
6074	Comparative Gene Finding. <i>Computational Biology</i> , 2010, , 157-180.	0.1	3
6075	Spaced Seeds for Cross-species CDNA-to-genome Sequence Alignment. <i>Communications in Information and Systems</i> , 2010, 10, 115-136.	0.3	1
6076	e-BioFlow: Improving Practical Use of Workflow Systems in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2010, , 1-15.	1.0	1
6077	<i>The Draft Soybean Genome Sequence.</i> , 2010, , 223-244.		0
6078	An Integrated Genomic Resource Based on Korean Cattle (Hanwoo) Transcripts. <i>Asian-Australasian Journal of Animal Sciences</i> , 2010, 23, 1399-1404.	2.4	1
6079	<i>Bioinformatics of High-Throughput Insertional Mutagenesis.</i> , 2011, , 167-188.		0
6080	Analysis of Mutations that Influence Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2011, 703, 137-160.	0.4	0
6081	<i>Bioinformatics Resources for the Brassica Species.</i> , 2011, , 597-615.		0
6082	Mutational Data Loading Routines for Human Genome Databases: the BRCA1 Case. <i>Journal of Computing Science and Engineering</i> , 2010, 4, 291-312.	0.3	2
6083	UNION: An Efficient Mapping Tool Using UniMark with Non-overlapping Interval Indexing Strategy. <i>Communications in Computer and Information Science</i> , 2011, , 187-196.	0.4	0
6084	Identification of Hematopoietic Stem Cell Engraftment Genes in Gene Therapy Studies. <i>Journal of Stem Cell Research &amp; Therapy</i> , 2013, 2013, .	0.3	7
6085	Facing the Challenges of Genome Information Systems: A Variation Analysis Prototype. <i>Lecture Notes in Computer Science</i> , 2011, , 222-237.	1.0	3

#	ARTICLE	IF	CITATIONS
6087	Taxonomic Assignment in Metagenomics with TANGO. <i>EMBnet Journal</i> , 2011, 17, 16.	0.2	1
6088	Genome-Wide Association Studies in Disease Risk Calculation: The Role of Bioinformatics in Patient Care. , 2012, , 103-129.		0
6089	SAMasGC: Sequencing Analysis with a Multiagent System and Grid Computing. <i>Advances in Intelligent and Soft Computing</i> , 2012, , 209-216.	0.2	0
6090	How to Build a DNA Search Engine like Google?. <i>Journal of Computer Science and Systems Biology</i> , 2012, 04, .	0.0	0
6091	Comparative Evaluation of Intron Prediction Methods and Detection of Plant Genome Annotation Using Intron Length Distributions. <i>Genomics and Informatics</i> , 2012, 10, 58.	0.4	0
6092	Mapping Short Reads to a Genomic Sequence with Circular Structure. <i>International Journal of Systems Biology and Biomedical Technologies</i> , 2012, 1, 26-34.	0.2	0
6094	Functional Annotation. <i>Chapman &amp; Hall/CRC Mathematical and Computational Biology Series</i> , 2012, , .	0.1	0
6095	Dynamic Annotation Systems. <i>Chapman &amp; Hall/CRC Mathematical and Computational Biology Series</i> , 2012, , .	0.1	0
6096	Sequence Homology Handling. <i>Computational Biology</i> , 2013, , 301-334.	0.1	1
6097	An Automated Approach of Designing Multiplex PCR Primers for the Amplification of Exons. <i>Advances in Intelligent Systems and Computing</i> , 2013, , 241-252.	0.5	0
6098	MetaBin. , 2013, , 1-7.		0
6099	Absence of Genomic <i>IKZF1</i> Deletions in Pediatric B-Precursor Acute Lymphoblastic Leukemia. <i>International Journal of Molecular Medical Science</i> , 2013, 3, 72-82.	0.0	6
6100	GHOSTM. , 2013, , 1-4.		0
6102	MetaBioME. , 2013, , 1-12.		0
6103	Identification of segmental duplications in the human genome. <i>Sri Lanka Journal of Biomedical Information</i> , 2013, 3, 12.	0.1	1
6104	Parallel Two Master Method to Improve BLAST Algorithm's Performance. <i>International Journal of Computer Applications</i> , 2013, 63, 8-14.	0.2	14
6105	Staircase Method: A Novel Method for Parallelizing S-W Algorithm. <i>International Journal of Computer Applications</i> , 2013, 63, 1-7.	0.2	0
6106	Primer Design for Large-Scale Multiplex PCR and Arrayed Primer Extension. , 2013, , 199-208.		0

#	ARTICLE	IF	CITATIONS
6110	An Efficient Algorithm for Microarray Probes Re-annotation. Lecture Notes in Computer Science, 2014, , 201-218.	1.0	0
6112	High Performance Genomic Sequencing: A Filtered Approach. Advances in Intelligent Systems and Computing, 2014, , 129-136.	0.5	0
6114	Identification and Analysis of Genomic Homing Endonuclease Target Sites. Methods in Molecular Biology, 2014, 1123, 245-264.	0.4	2
6115	Implementation and Evaluation of mpiBLAST-PIO on HPC Cluster. International Journal of Computer Applications, 2014, 97, 18-23.	0.2	2
6117	Fast Model-based Protein Homology Discovery without Alignment. Asia Pacific Journal of Energy and Environment, 2014, 1, 169-184.	0.3	5
6118	A SURVEY ON NGS - SHORT READ ALIGNMENT IN HIGH PERFORMANCE COMPUTING. International Journal of Research in Engineering and Technology, 2014, 03, 84-88.	0.1	0
6119	Genome-Wide Association Study Identifies QTLs for EBV of Backfat Thickness and Average Daily Gain in Duroc Pigs. Russian Journal of Genetics, 2015, 51, 371-378.	0.4	6
6120	Annotation Pipelines for Next-Generation Sequencing Projects. Computational Biology, 2015, , 325-367.	0.1	0
6121	Fast Masking of Repeated Primer Binding Sites in Eukaryotic Genomes. Methods in Molecular Biology, 2015, 1275, 1-16.	0.4	0
6122	A Case Study of a Laboratory Information System Developed at the Institute for Cancer Research at Candiolo. Advances in Healthcare Information Systems and Administration Book Series, 2015, , 252-279.	0.2	0
6123	De Novo Genome Assembly of Next-Generation Sequencing Data. Compendium of Plant Genomes, 2015, , 41-51.	0.3	0
6124	Large-scale detection and application of expressed sequence tag single nucleotide polymorphisms in Nicotiana. Genetics and Molecular Research, 2015, 14, 7793-7800.	0.3	1
6131	BlastXtract2: Improving early exploration of (meta) genomes. Bioinformatics, 2015, 11, 173-175.	0.2	0
6138	Case Study of Genome Sequencing on an FPGA: Survey and a New Perspective. , 2015, , 73-94.		0
6139	G-Links: a gene-centric link acquisition service. F1000Research, 2014, 3, 285.	0.8	2
6140	Decrypting the Treasures of Regulatory Non-coding RNAs in Highthroughput Era. Journal of Data Mining in Genomics & Proteomics, 2016, 07, .	0.5	0
6142	Genetic Technologies and Causal Variant Discovery. Translational Bioinformatics, 2016, , 277-293.	0.0	0
6149	An Efficient Bulk Synchronous Parallelized Scheduler for Bioinformatics Application on Public Cloud. International Journal of Computer Applications, 2016, 145, 22-30.	0.2	0

#	ARTICLE	IF	CITATIONS
6151	Puffer Genome for Tracking Human Genes. , 2016, , 109-131.		1
6155	Bioinformatics for Studying Environmental Microorganisms. , 2016, , 263-282.		0
6166	Alignment and Mapping. , 2017, , 105-125.		0
6169	gb4gv: a genome browser for<i>geminivirus</i>. PeerJ, 2017, 5, e3165.	0.9	1
6179	AP4 Transcription Factor Binding Site is a Repressor Element in ek2 Promoter of Human Liver Carcinoma Cell Line, HepG2. Sains Malaysiana, 2017, 46, 1887-1893.	0.3	0
6193	Prospects for the use of third generation sequencers for quantitative profiling of transcriptome. Biomedical Chemistry Research and Methods, 2018, 1, e00086.	0.1	2
6194	Nup153 Unlocks the Nuclear Pore Complex for HIV-1 Nuclear Import in Non-Dividing Cells. SSRN Electronic Journal, 0, , .	0.4	0
6197	A BLAST-Based Algorithm to Find Evenly Distributed Unique Subsequences. Lecture Notes in Computer Science, 2018, , 265-269.	1.0	0
6241	Neem Genome Annotation. Compendium of Plant Genomes, 2019, , 73-92.	0.3	0
6242	The Genome of Prunus mume. Compendium of Plant Genomes, 2019, , 31-52.	0.3	0
6244	GMeta: A Novel Algorithm to Utilize Highly Connected Components for Metagenomic Binning. Lecture Notes in Computer Science, 2019, , 545-559.	1.0	0
6246	Transcriptional Signatures of Progressive Neuropathology in Transgenic Models of Tau and Amyloid Pathology. SSRN Electronic Journal, 0, , .	0.4	0
6247	Comparative Analyses of 35 Marine Mammal Genomes Provide Insights into the Evolution of Aquatic Life. SSRN Electronic Journal, 0, , .	0.4	0
6250	Development and Genome Sequence of a Laboratory-Inbred Miniature Pig Facilitate Study of Human Diabetic Disease. SSRN Electronic Journal, 0, , .	0.4	0
6264	The BINDS-Tree: A Space-Partitioning Based Indexing Scheme for Box Queries in Non-Ordered Discrete Data Spaces. IEICE Transactions on Information and Systems, 2019, E102.D, 745-758.	0.4	1
6272	Bioinformatic pipelines for whole transcriptome sequencing data exploitation in leukemia patients with complex structural variants. PeerJ, 2019, 7, e7071.	0.9	1
6295	From EST to structure models for functional inference of APP, BACE1, PSEN1, PSEN2 genes. Bioinformation, 2019, 15, 760-771.	0.2	0
6299	Biological Sequence Analysis. , 0, , 55-69.		2

#	ARTICLE	IF	CITATIONS
6308	Identification and Characterization of Cis-Regulatory Elements for Photoreceptor-Type-Specific Transcription in ZebraFish. <i>Methods in Molecular Biology</i> , 2020, 2092, 123-145.	0.4	2
6336	A Rapid Evolving microRNA Cluster Rewires Its Target Regulatory Networks in <i>Drosophila</i> . <i>Frontiers in Genetics</i> , 2021, 12, 760530.	1.1	1
6337	Nanopore sequencing of SARS-CoV-2: Comparison of short and long PCR-tiling amplicon protocols. <i>PLoS ONE</i> , 2021, 16, e0259277.	1.1	16
6338	Plastome sequencing reveals phylogenetic relationships among <i>Comastoma</i> and related taxa (Gentianaceae) from the Qinghai-Tibetan Plateau. <i>Ecology and Evolution</i> , 2021, 11, 16034-16046.	0.8	6
6339	Unique <i>k</i> -mer sequences for validating cancer-related substitution, insertion and deletion mutations. <i>NAR Cancer</i> , 2020, 2, zcaa034.	1.6	5
6340	Phylogenetic Manifold Regularization: A semi-supervised approach to predict transcription factor binding sites. , 2020, , .		0
6342	Shotgun Sequencing Revealed the Microbiota of Zea mays Rhizosphere of a Former Grassland and an Intensively Cultivated Agricultural Land. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
6346	Whole genome sequencing of an edible and medicinal mushroom, <i>Russula griseocarnosa</i> , and its association with mycorrhizal characteristics. <i>Gene</i> , 2022, 808, 145996.	1.0	4
6348	Updates on Legume Genome Sequencing. <i>Methods in Molecular Biology</i> , 2020, 2107, 1-18.	0.4	6
6349	Computational prediction and characterisation of miRNAs and their pathway genes in human schistosomiasis caused by <i>Schistosoma haematobium</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e190378.	0.8	4
6350	Methods for Target Enrichment Sequencing via Probe Capture in Legumes. <i>Methods in Molecular Biology</i> , 2020, 2107, 199-231.	0.4	2
6357	InsectBase 2.0: a comprehensive gene resource for insects. <i>Nucleic Acids Research</i> , 2022, 50, D1040-D1045.	6.5	74
6363	Genome-Wide Identification of Tomato Xylem Sap Fitness Factors for Three Plant-Pathogenic <i>Ralstonia</i> Species. <i>MSystems</i> , 2021, 6, e0122921.	1.7	7
6364	CSC software corrects off-target mediated gRNA depletion in CRISPR-Cas9 essentiality screens. <i>Nature Communications</i> , 2021, 12, 6461.	5.8	4
6365	Uncovering Bleomycin-Induced Genomic Alterations and Underlying Mechanisms in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0170321.	1.4	4
6366	Benchmarking pipelines for subclonal deconvolution of bulk tumour sequencing data. <i>Nature Communications</i> , 2021, 12, 6396.	5.8	10
6368	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. <i>Nature Genetics</i> , 2021, 53, 1606-1615.	9.4	93
6369	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.	4.4	20

#	ARTICLE	IF	CITATIONS
6370	Transposable elements that have recently been mobile in the human genome. BMC Genomics, 2021, 22, 789.	1.2	12
6371	Comprehensive analysis of complete mitochondrial genome of <i>Sapindus mukorossi</i> Gaertn.: an important industrial oil tree species in China. Industrial Crops and Products, 2021, 174, 114210.	2.5	16
6375	First Report of Citrus Viroid V and Citrus Viroid VI in Australia Infecting Citrus. Plant Disease, 2020, 104, 2037.	0.7	5
6377	Mapping Affymetrix Microarray Probes to the Rat Genome via a Persistent Index. , 0, , 15-32.		0
6378	Computational Sequence Design Techniques for DNA Microarray Technologies. , 0, , 884-918.		0
6379	Magnaporthe grisea Oryza sativa (MGOS) Interaction Database: Community Annotation. , 2009, , 405-415.		0
6380	Comparative genomic tools and databases: providing insights into the human genome. Journal of Clinical Investigation, 2003, 111, 1099-1106.	3.9	20
6381	Genomic Data Visualization: The Bluejay System. , 2009, , 395-409.		0
6382	Exhaustive Peptide Searching Using Relations. Lecture Notes in Computer Science, 2007, , 13-24.	1.0	2
6389	Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena ( <i>Hyaena</i> ) Tj ETQq1 1.0,784314 <sub>3</sub> rgBT /Ove 0.9		
6390	The complete mitochondrial genome of an endangered tree: <i>Malaria oleifera</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 3829-3830.	0.2	2
6394	Fusion Transcript Detection from RNA-Seq using Jaccard Distance. , 2020, , .		3
6395	Dedicated transcriptomics combined with power analysis lead to functional understanding of genes with weak phenotypic changes in knockout lines. PLoS Computational Biology, 2020, 16, e1008354.	1.5	6
6396	NEIBank: genomics and bioinformatics resources for vision research. Molecular Vision, 2008, 14, 1327-37.	1.1	30
6398	Expressed sequence tag analysis of guinea pig ( <i>Cavia porcellus</i> ) eye tissues for NEIBank. Molecular Vision, 2008, 14, 2413-27.	1.1	17
6399	MapToGenome: a comparative genomic tool that aligns transcript maps to sequenced genomes. Evolutionary Bioinformatics, 2007, 3, 15-25.	0.6	3
6400	MLGA: a cost-effective approach to the diagnosis of gene deletions in eye development anomalies. Molecular Vision, 2009, 15, 1445-8.	1.1	3
6401	PositionMatcher: A Fast Custom-Annotation Tool for Short DNA Sequences. Summit on Translational Bioinformatics, 2010, 2010, 25-9.	0.7	1

#	ARTICLE	IF	CITATIONS
6402	Metagenomic Analysis of the Dynamic Changes in the Gut Microbiome of the Participants of the MARS-500 Experiment, Simulating Long Term Space Flight. <i>Acta Naturae</i> , 2013, 5, 116-25.	1.7	22
6403	Genetic screen of African Americans with Fuchs endothelial corneal dystrophy. <i>Molecular Vision</i> , 2013, 19, 2508-16.	1.1	13
6407	Genetic variation affecting exon skipping contributes to brain structural atrophy in Alzheimer's disease. <i>AMIA Summits on Translational Science Proceedings</i> , 2018, 2017, 124-131.	0.4	6
6408	Identification of transgene flanking sequences in a pre-market safety assessed sugarcane in Argentina. <i>Crop Breeding and Applied Biotechnology</i> , 2021, 21, .	0.1	1
6409	Biological sequence analysis. , 2022, , 33-47.		0
6410	ChiTaH: a fast and accurate tool for identifying known human chimeric sequences from high-throughput sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab112.	1.5	4
6412	Shotgun metagenomics evaluation of soil fertilization effect on the rhizosphere viral community of maize plants. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 69-78.	0.7	2
6414	Transcriptome Analysis Reveals Higher Levels of Mobile Element-Associated Abnormal Gene Transcripts in Temporal Lobe Epilepsy Patients. <i>Frontiers in Genetics</i> , 2021, 12, 767341.	1.1	0
6415	Chromosome-level genome and population genomic analysis provide insights into the evolution and environmental adaptation of Jinjiang oyster <i>Crassostrea ariakensis</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 1529-1544.	2.2	16
6416	A chromosomal level genome sequence for <i>Quasipaa spinosa</i> (Dicroglossidae) reveals chromosomal evolution and population diversity. <i>Molecular Ecology Resources</i> , 2022, 22, 1545-1558.	2.2	3
6417	Massively parallel DNA target capture using long adapter single stranded oligonucleotide (LASSO) probes assembled through a novel DNA recombinase mediated methodology. <i>Biotechnology Journal</i> , 2021, , 2100240.	1.8	2
6419	The U1 snRNP component RBP45d regulates temperature-responsive flowering in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2022, 34, 834-851.	3.1	18
6420	<i>Chloranthus</i> genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, 6930.	5.8	44
6421	PCR Primer Design for the Rapidly Evolving SARS-CoV-2 Genome. <i>Methods in Molecular Biology</i> , 2022, 2392, 185-197.	0.4	2
6422	Epigenetic Dysregulation of KCNK9 Imprinting and Triple-Negative Breast Cancer. <i>Cancers</i> , 2021, 13, 6031.	1.7	1
6423	Resolving the Microalgal Gene Landscape at the Strain Level: a Novel Hybrid Transcriptome of <i>Emiliana huxleyi</i> CCMP3266. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0141821.	1.4	6
6425	Genome-wide survey and characterization of transcription factors in the silk gland of the silkworm, <i>Bombyx mori</i> . <i>PLoS ONE</i> , 2021, 16, e0259870.	1.1	3
6427	Molecular evolution of chloroplast genomes in subfamily Zingiberoideae (Zingiberaceae). <i>BMC Plant Biology</i> , 2021, 21, 558.	1.6	26

#	ARTICLE	IF	CITATIONS
6428	ASER: Animal Sex Reversal Database. Genomics, Proteomics and Bioinformatics, 2021, 19, 873-881.	3.0	5
6429	Origins and Function of VL30 lncRNA Packaging in Small Extracellular Vesicles: Implications for Cellular Physiology and Pathology. Biomedicines, 2021, 9, 1742.	1.4	3
6430	Uncovering the Role of Gut Microbiota in Amino Acid Metabolic Disturbances in Heart Failure Through Metagenomic Analysis. Frontiers in Cardiovascular Medicine, 2021, 8, 789325.	1.1	17
6431	Baiting out a full length sequence from unmapped RNA-seq data. BMC Genomics, 2021, 22, 857.	1.2	3
6432	Vertical Inheritance Facilitates Interspecies Diversification in Biosynthetic Gene Clusters and Specialized Metabolites. MBio, 2021, 12, e0270021.	1.8	23
6433	<scp>MammaPrint</scp> and <scp>BluePrint</scp> comprehensively capture the cancer hallmarks in early-stage breast cancer patients. Genes Chromosomes and Cancer, 2022, 61, 148-160.	1.5	11
6434	Systematic Identification of Endogenous Retroviral Protein-Coding Genes Expressed in Canine Oral Malignant Melanoma. Frontiers in Virology, 2021, 1, .	0.7	0
6435	Genetic and functional evidence links a missense variant in <i>B4GALT1</i> to lower LDL and fibrinogen. Science, 2021, 374, 1221-1227.	6.0	14
6436	Error-prone, stress-induced 3' flap-based Okazaki fragment maturation supports cell survival. Science, 2021, 374, 1252-1258.	6.0	9
6437	Rare and potentially pathogenic variants in hydroxycarboxylic acid receptor genes identified in breast cancer cases. BMC Medical Genomics, 2021, 14, 284.	0.7	2
6438	Hooroo mates! Phylogenomic data suggest that the closest relatives of the iconic Tasmanian cave spider Hickmania troglodytes are in Australia and New Zealand, not in South America. Invertebrate Systematics, 2021, , .	0.5	4
6439	Quantitative Trait Loci Mapping and Development of KASP Marker Smut Screening Assay Using High-Density Genetic Map and Bulk Segregant RNA Sequencing in Sugarcane (Saccharum spp.). Frontiers in Plant Science, 2021, 12, 796189.	1.7	8
6440	Whence Came These Plants Most Foul? Phylogenomics and Biogeography of Lowiaceae (Zingiberales). Frontiers in Ecology and Evolution, 2022, 9, .	1.1	1
6441	Chromosome-Level Genome Assembly of a Human Fungal Pathogen Reveals Synteny among Geographically Distinct Species. MBio, 2022, 13, e0257421.	1.8	7
6442	CLUSTER guide RNAs enable precise and efficient RNA editing with endogenous ADAR enzymes in vivo. Nature Biotechnology, 2022, 40, 759-768.	9.4	49
6443	Whole Genome Assembly of Human Papillomavirus by Nanopore Long-Read Sequencing. Frontiers in Genetics, 2021, 12, 798608.	1.1	5
6444	The genome of low-chill Chinese plum 'Sanyueli' (<i>Prunus salicina</i> Lindl.) provides insights into the regulation of the chilling requirement of flower buds. Molecular Ecology Resources, 2022, 22, 1919-1938.	2.2	11
6445	Next-generation sequencing markup language (NGSML): a medium for the representation and exchange of NGS data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	1.9	2

#	ARTICLE	IF	CITATIONS
6446	A comparative analysis of complete chloroplast genomes of seven <i>Ocotea</i> species (Lauraceae) confirms low sequence divergence within the <i>Ocotea</i> complex. <i>Scientific Reports</i> , 2022, 12, 1120.	1.6	18
6447	Comparative assessment of genes driving cancer and somatic evolution in non-cancer tissues: an update of the Network of Cancer Genes (NCC) resource. <i>Genome Biology</i> , 2022, 23, 35.	3.8	38
6448	Partitioning RNAs by length improves transcriptome reconstruction from short-read RNA-seq data. <i>Nature Biotechnology</i> , 2022, 40, 741-750.	9.4	7
6449	Genomically Hardwired Regulation of Gene Activity Orchestrates Cellular Iron Homeostasis in <i>Arabidopsis</i> . <i>RNA Biology</i> , 2022, 19, 143-161.	1.5	9
6450	A High-Density Genetic Map Enables Genome Synteny and QTL Mapping of Vegetative Growth and Leaf Traits in <i>Gardenia</i> . <i>Frontiers in Genetics</i> , 2021, 12, 802738.	1.1	2
6451	De novo mutations identified by whole-genome sequencing implicate chromatin modifications in obsessive-compulsive disorder. <i>Science Advances</i> , 2022, 8, eabi6180.	4.7	5
6452	Genome-wide assessment of genetic diversity and population structure of <i>Platostoma palustre</i> in southern China and implications for conservation and breeding strategies. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1349-1364.	0.8	0
6453	A Chromosome-Level Genome Assembly of Yellowtail Kingfish ( <i>Seriola lalandi</i> ). <i>Frontiers in Genetics</i> , 2021, 12, 825742.	1.1	1
6454	Dysgu: efficient structural variant calling using short or long reads. <i>Nucleic Acids Research</i> , 2022, 50, e53-e53.	6.5	13
6455	Somatic and Germline Genomic Alterations in Very Young Women with Breast Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2339-2348.	3.2	20
6456	A Superior Contiguous Whole Genome Assembly for Shrimp ( <i>Penaeus indicus</i> ). <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	6
6457	Genomic insight into the scale specialization of the biological control agent <i>Novius pumilus</i> (Weise.) Tj ETQq1 1 0.784314 rgBT / Over	1.2	6
6458	Mitochondrial DNA variation across 56,434 individuals in gnomAD. <i>Genome Research</i> , 2022, 32, 569-582.	2.4	59
6459	The Dark Side of Microbial Processes: Accumulation of Nitrate During Storage of Surface Water in the Dark and the Underlying Mechanism. <i>Microbiology Spectrum</i> , 2022, 10, e0223221.	1.2	0
6460	Metatranscriptome Profiling of a Specialized Microbial Consortium during the Degradation of Nixtamalized Maize Pericarp. <i>Microbiology Spectrum</i> , 2022, 10, e0231821.	1.2	4
6461	Characterisation of the Complete Mitochondrial Genome of Critically Endangered <i>Mustela lutreola</i> (Carnivora: Mustelidae) and Its Phylogenetic and Conservation Implications. <i>Genes</i> , 2022, 13, 125.	1.0	7
6462	Long-read nanopore DNA sequencing can resolve complex intragenic duplication/deletion variants, providing information to enable preimplantation genetic diagnosis. <i>Prenatal Diagnosis</i> , 2022, 42, 226-232.	1.1	6
6463	No link between population isolation and speciation rate in squamate reptiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13

#	ARTICLE	IF	CITATIONS
6464	Differential enrichment of yeast DNA in SARS-CoV-2 and related genomes supports synthetic origin hypothesis. <i>F1000Research</i> , 0, 10, 912.	0.8	0
6465	Association of Tandem Repeat Number Variabilities in Subunit S of the Type I Restriction-Modification System with Macrolide Resistance in <i>Mycoplasma pneumoniae</i> . <i>Journal of Clinical Medicine</i> , 2022, 11, 715.	1.0	2
6466	Evolution of DNA Methylation Across Ecdysozoa. <i>Journal of Molecular Evolution</i> , 2022, 90, 56-72.	0.8	12
6467	Circulating T-Cell Repertoires Correlate With the Tumor Response in Patients With Breast Cancer Receiving Neoadjuvant Chemotherapy. <i>JCO Precision Oncology</i> , 2022, 6, e2100120.	1.5	5
6468	Trade-off between sex and growth in diatoms: Molecular mechanisms and demographic implications. <i>Science Advances</i> , 2022, 8, eabj9466.	4.7	10
6470	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.4	2
6471	Genome sequence data of the antagonistic soil-borne yeast <i>Cyberlindnera sargentensis</i> (SHA 17.2). <i>Data in Brief</i> , 2022, 40, 107799.	0.5	2
6472	Genome Sequences of Two Strains of <i>Prototheca wickerhamii</i> Provide Insight Into the Protothecosis Evolution. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 797017.	1.8	2
6473	Characterizing mobile element insertions in 5675 genomes. <i>Nucleic Acids Research</i> , 2022, 50, 2493-2508.	6.5	16
6474	High Stability of the Epigenome in <i>Drosophila</i> Interspecific Hybrids. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	2
6475	Complete pan-plastome sequences enable high resolution phylogenetic classification of sugar beet and closely related crop wild relatives. <i>BMC Genomics</i> , 2022, 23, 113.	1.2	10
6476	Heterochiasmy and the establishment of <i>gsdf</i> as a novel sex determining gene in Atlantic halibut. <i>PLoS Genetics</i> , 2022, 18, e1010011.	1.5	18
6477	Capture-C: a modular and flexible approach for high-resolution chromosome conformation capture. <i>Nature Protocols</i> , 2022, 17, 445-475.	5.5	24
6478	WormBase in 2022—data, processes, and tools for analyzing <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2022, 220, .	1.2	128
6479	Novel patterns of expression and recruitment of new genes on the <i>t</i> -haplotype, a mouse selfish chromosome. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20211985.	1.2	3
6480	A Chromosome-Level Genome Assembly of the European Beech ( <i>Fagus sylvatica</i> ) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. <i>Frontiers in Genetics</i> , 2021, 12, 691058.	1.1	17
6481	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. <i>Nature Communications</i> , 2022, 13, 682.	5.8	59
6482	Multiple phylogenetically-diverse, differentially-virulent <i>Burkholderia pseudomallei</i> isolated from a single soil sample collected in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010172.	1.3	3

#	ARTICLE	IF	CITATIONS
6483	Genomic insights into the evolution of the critically endangered soft-shelled turtle <i>Rafetus swinhoei</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 1972-1985.	2.2	9
6484	HSDFinder: A BLAST-Based Strategy for Identifying Highly Similar Duplicated Genes in Eukaryotic Genomes. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	5
6485	The evolution study on by whole-genome sequencing. <i>Journal of Genetics</i> , 2019, 98, .	0.4	0
6486	A high-quality assembly reveals genomic characteristics, phylogenetic status, and causal genes for leucism plumage of Indian peafowl. <i>GigaScience</i> , 2022, 11, .	3.3	10
6487	Amplicon-based and metagenomic approaches provide insights into toxigenic potential in understudied Atlantic Canadian lakes. <i>Facets</i> , 2022, 7, 194-214.	1.1	3
6488	The haplotype-resolved chromosome pairs of a heterozygous diploid African cassava cultivar reveal novel pan-genome and allele-specific transcriptome features. <i>GigaScience</i> , 2022, 11, .	3.3	29
6490	Chromosome-scale assembly of the yellow mealworm genome. <i>Open Research Europe</i> , 0, 1, 94.	2.0	2
6491	Combined tumor and immune signals from genomes or transcriptomes predict outcomes of checkpoint inhibition in melanoma. <i>Cell Reports Medicine</i> , 2022, 3, 100500.	3.3	13
6492	Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. <i>Genome Biology</i> , 2022, 23, 46.	3.8	22
6493	Host-Species Variation and Environment Influence Endophyte Symbiosis and Mycotoxin Levels in Chinese <i>Oxytropis</i> Species. <i>Toxins</i> , 2022, 14, 181.	1.5	5
6494	Background splicing as a predictor of aberrant splicing in genetic disease. <i>RNA Biology</i> , 2022, 19, 256-265.	1.5	1
6495	Comparative genomics analysis of <i>bHLH</i> genes in cucurbits identifies a novel gene regulating cucurbitacin biosynthesis. <i>Horticulture Research</i> , 2022, 9, .	2.9	16
6497	Chromosome-level genome assembly of a xerophytic plant, <i>Haloxylon ammodendron</i> . <i>DNA Research</i> , 2022, 29, .	1.5	15
6498	Conservation of chromatin conformation in carnivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
6499	Genome-Wide Methylation Profiling in the Thalamus of Scrapie Sheep. <i>Frontiers in Veterinary Science</i> , 2022, 9, 824677.	0.9	2
6500	Comparative Genome Analysis Reveals Cis-Regulatory Elements on Gene-Sized Chromosomes of Ciliated Protists. <i>Frontiers in Microbiology</i> , 2022, 13, 775646.	1.5	5
6501	Microbial Community Structure and Functional Potential of Deep-Sea Sediments on Low Activity Hydrothermal Area in the Central Indian Ridge. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	6
6503	Gene losses may contribute to subterranean adaptations in naked mole-rat and blind mole-rat. <i>BMC Biology</i> , 2022, 20, 44.	1.7	10

#	ARTICLE	IF	CITATIONS
6504	Chromosome-level genome assembly of the diploid blueberry <i>Vaccinium darrowii</i> provides insights into its subtropical adaptation and cuticle synthesis. <i>Plant Communications</i> , 2022, 3, 100307.	3.6	10
6505	NRD: Nicotiana Resistance Database, a Comprehensive Platform of Stress Tolerance in Nicotiana. <i>Agronomy</i> , 2022, 12, 508.	1.3	0
6506	Reference genome of lumpfish <i>Cyclopterus lumpus</i> Linnaeus provides evidence of male heterogametic sex determination through the AMH pathway. <i>Molecular Ecology Resources</i> , 2022, 22, 1427-1439.	2.2	16
6507	Comparison of Immune Checkpoint Molecules PD-1 and PD-L1 in Paired Primary and Recurrent Glioma: Increasing Trend When Recurrence. <i>Brain Sciences</i> , 2022, 12, 266.	1.1	0
6508	Transcriptomic Analysis Suggests Auxin Regulation in Dorsal-Ventral Petal Asymmetry of Wild Progenitor <i>Sinningia speciosa</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 2073.	1.8	2
6509	Beyond Genes: Inclusion of Alternative Splicing and Alternative Polyadenylation to Assess the Genetic Architecture of Predisposition to Voluntary Alcohol Consumption in Brain of the HXB/BXH Recombinant Inbred Rat Panel. <i>Frontiers in Genetics</i> , 2022, 13, 821026.	1.1	2
6510	Comprehensive RNA dataset of tissue and plasma from patients with esophageal cancer or precursor lesions. <i>Scientific Data</i> , 2022, 9, 86.	2.4	1
6511	Recently Integrated Alu Elements in Capuchin Monkeys: A Resource for <i>Cebus/Sapajus</i> Genomics. <i>Genes</i> , 2022, 13, 572.	1.0	4
6512	Targeted Sanger sequencing to recover key mutations in SARS-CoV-2 variant genome assemblies produced by next-generation sequencing. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
6513	Linking genomic and epidemiologic information to advance the study of COVID-19. <i>Scientific Data</i> , 2022, 9, 121.	2.4	3
6514	Landscape of adenosine-to-inosine RNA recoding across human tissues. <i>Nature Communications</i> , 2022, 13, 1184.	5.8	46
6515	Original Leaf Colonisers Shape Fungal Decomposer Communities of <i>Phragmites australis</i> in Intermittent Habitats. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 284.	1.5	6
6516	Ethylene Response Factor109 Attunes Immunity, Photosynthesis, and Iron Homeostasis in Arabidopsis Leaves. <i>Frontiers in Plant Science</i> , 2022, 13, 841366.	1.7	7
6517	ADARs act as potent regulators of circular transcriptome in cancer. <i>Nature Communications</i> , 2022, 13, 1508.	5.8	29
6518	Integrated metagenomics identifies a crucial role for trimethylamine-producing <i>Lachnoclostridium</i> in promoting atherosclerosis. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 11.	2.9	41
6519	Transcriptome and proteome profiling reveals complex adaptations of <i>Candida parapsilosis</i> cells assimilating hydroxyaromatic carbon sources. <i>PLoS Genetics</i> , 2022, 18, e1009815.	1.5	1
6520	A point mutation in HIV-1 integrase redirects proviral integration into centromeric repeats. <i>Nature Communications</i> , 2022, 13, 1474.	5.8	6
6521	Comparative analysis of the <i>Mercenaria mercenaria</i> genome provides insights into the diversity of transposable elements and immune molecules in bivalve mollusks. <i>BMC Genomics</i> , 2022, 23, 192.	1.2	18

#	ARTICLE	IF	CITATIONS
6522	Exome sequencing identifies variants in infants with sacral agenesis. <i>Birth Defects Research</i> , 2022, 114, 215-227.	0.8	2
6523	Cupuassu ( <i>Theobroma grandiflorum</i> [Willd. ex Sprengel] Schumann) Fruit Development: Key Genes Involved in Primary Metabolism and Stress Response. <i>Agronomy</i> , 2022, 12, 763.	1.3	1
6524	PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2. <i>Npj Genomic Medicine</i> , 2022, 7, 19.	1.7	2
6525	The evolution, evolvability and engineering of gene regulatory DNA. <i>Nature</i> , 2022, 603, 455-463.	13.7	126
6526	Nanopore ReCappable sequencing maps SARS-CoV-2 5' capping sites and provides new insights into the structure of sgRNAs. <i>Nucleic Acids Research</i> , 2022, 50, 3475-3489.	6.5	12
6527	Clonal lineage tracing reveals shared origin of conventional and plasmacytoid dendritic cells. <i>Immunity</i> , 2022, 55, 405-422.e11.	6.6	37
6528	ExceS-A: an exon-centric split aligner. <i>Journal of Integrative Bioinformatics</i> , 2022, 19, .	1.0	0
6529	Dissection of molecular and histological subtypes of papillary thyroid cancer using alternative splicing profiles. <i>Experimental and Molecular Medicine</i> , 2022, 54, 263-272.	3.2	3
6530	Extensive sequence divergence between the reference genomes of two zebrafish strains, Tuebingen and AB. <i>Molecular Ecology Resources</i> , 2022, , .	2.2	1
6531	Metagenomic clustering reveals microbial contamination as an essential consideration in ultraconserved element design for phylogenomics with insect museum specimens. <i>Ecology and Evolution</i> , 2022, 12, e8625.	0.8	6
6532	Assessing the Effect of Smokeless Tobacco Consumption on Oral Microbiome in Healthy and Oral Cancer Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841465.	1.8	13
6533	Evidence for yeast artificial synthesis in SARS-CoV-2 and SARS-CoV-1 genomic sequences. <i>F1000Research</i> , 0, 10, 912.	0.8	1
6534	Transposon insertions regulate genome-wide allele-specific expression and underpin flower colour variations in apple ( <i>Malus</i> spp.). <i>Plant Biotechnology Journal</i> , 2022, 20, 1285-1297.	4.1	21
6535	The <i>Gastrodia menghaiensis</i> (Orchidaceae) genome provides new insights of orchid mycorrhizal interactions. <i>BMC Plant Biology</i> , 2022, 22, 179.	1.6	13
6536	A generalist–specialist trade-off between switchgrass cytotypes impacts climate adaptation and geographic range. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118879119.	3.3	5
6537	A Chromosome-Level Reference Genome of Chinese Balloon Flower ( <i>Platycodon grandiflorus</i> ). <i>Frontiers in Genetics</i> , 2022, 13, 869784.	1.1	7
6538	Accurate detection of tumor-specific gene fusions reveals strongly immunogenic personal neo-antigens. <i>Nature Biotechnology</i> , 2022, 40, 1276-1284.	9.4	25
6539	Precise in vivo functional analysis of DNA variants with base editing using ACEofBASEs target prediction. <i>ELife</i> , 2022, 11, .	2.8	12

#	ARTICLE	IF	CITATIONS
6540	Putting small and big pieces together: a genome assembly approach reveals the largest Lamiid plastome in a woody vine. PeerJ, 2022, 10, e13207.	0.9	3
6541	Relationship between nitrifying microorganisms and other microorganisms residing in the maize rhizosphere. Archives of Microbiology, 2022, 204, 246.	1.0	3
6542	De novo genome assembly of <i>Bradysia cellarum</i> (Diptera: Sciaridae), a notorious pest in traditional special vegetables in China. Insect Molecular Biology, 2022, 31, 508-518.	1.0	3
6543	RNA aptamers specific for transmembrane p24 trafficking protein 6 and Clusterin for the targeted delivery of imaging reagents and RNA therapeutics to human $\hat{1}^2$ cells. Nature Communications, 2022, 13, 1815.	5.8	6
6544	Dosage sensitivity and exon shuffling shape the landscape of polymorphic duplicates in <i>Drosophila</i> and humans. Nature Ecology and Evolution, 2022, 6, 273-287.	3.4	12
6545	Identification of Novel Regulatory Regions Induced by Intrauterine Growth Restriction in Rat Islets. Endocrinology, 2022, 163, .	1.4	3
6547	Medium levels of transcription and replication related chromosomal instability are associated with poor clinical outcome. Scientific Reports, 2021, 11, 23429.	1.6	1
6548	Long-read assemblies reveal structural diversity in genomes of organelles – an example with <i>Acacia pycnantha</i> . GigaByte, 0, 2021, 1-23.	0.0	6
6549	The metabolic core of the prokaryotic community from deep-sea sediments of the southern Gulf of Mexico shows different functional signatures between the continental slope and abyssal plain. PeerJ, 2021, 9, e12474.	0.9	3
6550	Genomic analysis of <i>Elsinoë arachidis</i> reveals its potential pathogenic mechanism and the biosynthesis pathway of elsinochrome toxin. PLoS ONE, 2021, 16, e0261487.	1.1	3
6551	Generation and mutational analysis of a transgenic mouse model of human <i>SRY</i> . Human Mutation, 2022, 43, 362-379.	1.1	3
6552	Identification of starch candidate genes using SLAF-seq and BSA strategies and development of related SNP-CAPS markers in tetraploid potato. PLoS ONE, 2021, 16, e0261403.	1.1	2
6553	Species-specific partial gene duplication in <i>Arabidopsis thaliana</i> evolved novel phenotypic effects on morphological traits under strong positive selection. Plant Cell, 2022, 34, 802-817.	3.1	15
6554	Genetic and Molecular Characterization of a Self-Compatible <i>Brassica rapa</i> Line Possessing a New Class II S Haplotype. Plants, 2021, 10, 2815.	1.6	5
6555	Scan of the endogenous retrovirus sequences across the swine genome and survey of their copy number variation and sequence diversity among various Chinese and Western pig breeds. Zoological Research, 2022, 43, 423-441.	0.9	5
6556	OUP accepted manuscript. Nucleic Acids Research, 2022, , .	6.5	3
6557	Intraspecific <i>de novo</i> gene birth revealed by presence-absence variant genes in <i>Caenorhabditis elegans</i> . NAR Genomics and Bioinformatics, 2022, 4, lqac031.	1.5	7
6558	Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in <i>Drosophila</i> . Nature Communications, 2022, 13, 1948.	5.8	53

#	ARTICLE	IF	CITATIONS
6559	Using iRNA-seq analysis to predict gene expression regulatory level and activity in <i>Zea mays</i> tissues. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	0
6560	Open reading frame dominance indicates protein-coding potential of RNAs. <i>EMBO Reports</i> , 2022, 23, e54321.	2.0	7
6561	A draft genome of Drung cattle reveals clues to its chromosomal fusion and environmental adaptation. <i>Communications Biology</i> , 2022, 5, 353.	2.0	1
6562	Analysis of sub-kilobase chromatin topology reveals nano-scale regulatory interactions with variable dependence on cohesin and CTCF. <i>Nature Communications</i> , 2022, 13, 2139.	5.8	48
6826	Global mapping of RNA homodimers in living cells. <i>Genome Research</i> , 2022, , .	2.4	3
6827	Using surveys of Affymetrix GeneChips to study antisense expression. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	1
6828	Automatic knowledge extraction in sequencing analysis with multiagent system and grid computing. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 206.	1.0	2
6829	ANI analysis of poxvirus genomes reveals its potential application to viral species rank demarcation. <i>Virus Evolution</i> , 2022, 8, .	2.2	7
6830	Long-read and chromosome-scale assembly of the hexaploid wheat genome achieves high resolution for research and breeding. <i>GigaScience</i> , 2022, 11, .	3.3	26
6831	Alignment-Free Analysis of Whole-Genome Sequences From Symbiodiniaceae Reveals Different Phylogenetic Signals in Distinct Regions. <i>Frontiers in Plant Science</i> , 2022, 13, 815714.	1.7	13
6833	EBV genome variations enhance clinicopathological features of nasopharyngeal carcinoma in a non-endemic region. <i>Cancer Science</i> , 2022, , .	1.7	7
6834	Evolution of coastal forests based on a full set of mangrove genomes. <i>Nature Ecology and Evolution</i> , 2022, 6, 738-749.	3.4	41
6835	Comprehensive 16S rRNA and metagenomic data from the gut microbiome of aging and rejuvenation mouse models. <i>Scientific Data</i> , 2022, 9, 197.	2.4	1
6837	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
6838	Rampant nuclear-mitochondrial-plastid phylogenomic discordance in globally distributed calcifying microalgae. <i>New Phytologist</i> , 2022, 235, 1394-1408.	3.5	11
6839	Genes and evolutionary fates of the amanitin biosynthesis pathway in poisonous mushrooms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2201113119.	3.3	10
6840	Plant Health Status Affects the Functional Diversity of the Rhizosphere Microbiome Associated With <i>Solanum lycopersicum</i> . <i>Frontiers in Sustainable Food Systems</i> , 2022, 6, .	1.8	7
6841	CircMiMi: a stand-alone software for constructing circular RNA-microRNA-mRNA interactions across species. <i>BMC Bioinformatics</i> , 2022, 23, 164.	1.2	8

#	ARTICLE	IF	CITATIONS
6842	Rare case of leptomenigeal small lymphocytic lymphoma with <i>TP53</i> mutation detected by deep next-generation sequencing. <i>Leukemia and Lymphoma</i> , 2022, , 1-5.	0.6	1
6843	The Effects of Plant Health Status on the Community Structure and Metabolic Pathways of Rhizosphere Microbial Communities Associated with <i>Solanum lycopersicum</i> . <i>Horticulturae</i> , 2022, 8, 404.	1.2	10
6844	Nitrogen fixation and other biogeochemically important features of Atacama Desert giant horsetail plant microbiomes inferred from metagenomic contig analysis. <i>Annals of Botany</i> , 2022, , .	1.4	2
6845	A Draft Reference Genome Assembly of the Critically Endangered Black Abalone, <i>Haliotis cracherodii</i> . <i>Journal of Heredity</i> , 2022, 113, 665-672.	1.0	4
6846	Phyloepigenetics. <i>Biology</i> , 2022, 11, 754.	1.3	1
6848	Genome-Based Analysis of <i>Aspergillus niger</i> Aggregate Species from China and Their Potential for Fumonisin B2 and Ochratoxin A Production. <i>Current Microbiology</i> , 2022, 79, 193.	1.0	0
6849	First Chromosome-Scale Assembly and Deep Floral-Bud Transcriptome of a Male Kiwifruit. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	9
6850	The assembled and annotated genome of the masked palm civet ( <i>Paguma larvata</i> ). <i>GigaScience</i> , 2022, 11, .	3.3	2
6857	Revealing diverse alternative splicing variants of the highly homologous SMN1 and SMN2 genes by targeted long-read sequencing. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1039-1048.	1.0	3
6858	Tri-binned genomes of the woodrats <i>Neotoma bryanti</i> and <i>Neotoma lepida</i> reveal novel gene islands and rapid copy number evolution of xenobiotic metabolizing genes. <i>Molecular Ecology Resources</i> , 2022, 22, 2713-2731.	2.2	13
6860	Semi-subterranean environment and soil metagenomic datasets of the Gyeongju Seokbinggo (stone ice) Tj ETQq0 0,0 rgBT /Qverlock 10	0.5	0
6861	<i>mebipred</i> : identifying metal-binding potential in protein sequence. <i>Bioinformatics</i> , 2022, 38, 3532-3540.	1.8	15
6862	Repetitive Elements, Sequence Turnover and Cyto-Nuclear Gene Transfer in Gymnosperm Mitogenomes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
6864	Chromosome-scale genome assembly of an important medicinal plant honeysuckle. <i>Scientific Data</i> , 2022, 9, .	2.4	7
6866	Intron losses and gains in the nematodes. <i>Biology Direct</i> , 2022, 17, .	1.9	4
6867	The chromosome-level genome for <i>Toxicodendron vernicifluum</i> provides crucial insights into Anacardiaceae evolution and urushiol biosynthesis. <i>iScience</i> , 2022, 25, 104512.	1.9	6
6868	Genome-wide specificity of plant genome editing by both CRISPR-Cas9 and TALEN. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
6869	Genetic Diversity and Population Differentiation of Chinese Lizard Gudgeon ( <i>Saurogobio dabryi</i> ) in the Upper Yangtze River. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1

#	ARTICLE	IF	CITATIONS
6871	Full-length transcripts facilitates <i>Portunus trituberculatus</i> genome structure annotation. <i>Journal of Oceanology and Limnology</i> , 2022, 40, 2042-2051.	0.6	3
6872	Chromosomal Translocation t(5;12)(p13;q14) Leading to Fusion of High-mobility Group AT-hook 2 Gene With Intergenic Sequences From Chromosome Sub-Band 5p13.2 in Benign Myoid Neoplasms of the Breast: A Second Case. <i>Cancer Genomics and Proteomics</i> , 2022, 19, 445-455.	1.0	6
6873	Chromosome-level genome assembly of the black widow spider <i>Latrodectus elegans</i> illuminates composition and evolution of venom and silk proteins. <i>GigaScience</i> , 2022, 11, .	3.3	9
6874	Computationally designed hyperactive Cas9 enzymes. <i>Nature Communications</i> , 2022, 13, .	5.8	8
6875	Expansion of a retrovirus lineage in the koala genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	3
6876	Taxonomy, comparative genomics and evolutionary insights of <i>Penicillium ucsense</i> : a novel species in series <i>Oxalica</i> . <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1009-1029.	0.7	5
6877	Blood-derived lncRNAs as biomarkers for cancer diagnosis: the Good, the Bad and the Beauty. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	50
6878	Cytogenetic Characterization and Molecular Marker Development for a <i>Triticum aestivum</i> (4A <sup>b</sup> (4B) Disomic Substitution Line with Stripe Rust Resistance. <i>Plant Disease</i> , 2023, 107, 125-130.	0.7	1
6879	Genetic and genomic architecture of species-specific cuticular hydrocarbon variation in parasitoid wasps. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	3
6880	Human Follicular Mites: Ectoparasites Becoming Symbionts. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	6
6881	Genome sequence of <i>Gossypium anomalum</i> facilitates interspecific introgression breeding. <i>Plant Communications</i> , 2022, 3, 100350.	3.6	14
6882	In Silico Models on Algal Cultivation and Processing. Impact of Meat Consumption on Health and Environmental Sustainability, 2022, , 228-255.	0.4	0
6883	Complex Feline Disease Mapping Using a Dense Genotyping Array. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
6884	Population Scale Analysis of Centromeric Satellite DNA Reveals Highly Dynamic Evolutionary Patterns and Genomic Organization in Long-Tailed and Rhesus Macaques. <i>Cells</i> , 2022, 11, 1953.	1.8	2
6885	A Novel miRNA Located in the HER2 Gene Shows an Inhibitory Effect on Wnt Signaling and Cell Cycle Progression. <i>BioMed Research International</i> , 2022, 2022, 1-9.	0.9	1
6886	Introduction to the principles and methods underlying the recovery of metagenome-assembled genomes from metagenomic data. <i>MicrobiologyOpen</i> , 2022, 11, .	1.2	8
6887	Chromosome-scale genomes reveal genomic consequences of inbreeding in the South China tiger: A comparative study with the Amur tiger. <i>Molecular Ecology Resources</i> , 2023, 23, 330-347.	2.2	11
6888	A chromosome-level genome assembly and annotation of the maize elite breeding line Dan340. <i>GigaByte</i> , 0, 2022, 1-8.	0.0	2

#	ARTICLE	IF	CITATIONS
6889	Characterization of Glutenin Genes in Bread Wheat by Third-Generation RNA Sequencing and the Development of a <i>Glu-1Dx5</i> Marker Specific for the Extra Cysteine Residue. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 7211-7219.	2.4	2
6890	Chromosome-scale assembly with a phased sex-determining region resolves features of early Z and W chromosome differentiation in a wild octoploid strawberry. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	11
6891	HISTONE DEACETYLASE 15 and MOS4-associated complex subunits 3A/3B coregulate intron retention of ABA-responsive genes. <i>Plant Physiology</i> , 2022, 190, 882-897.	2.3	10
6892	Turnover in Life-Strategies Recapitulates Marine Microbial Succession Colonizing Model Particles. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
6893	<i>De novo</i> genes in <i>Arachis hypogaea</i> cv. Tifrunner: systematic identification, molecular evolution, and potential contributions to cultivated peanut. <i>Plant Journal</i> , 0, , .	2.8	0
6895	Chromosome-level genome assembly and annotation of the native Chinese wild blueberry & <i>Vaccinium bracteatum</i> . <i>Fruit Research</i> , 2022, 2, 1-14.	0.9	5
6896	Bioinformatics Approaches for Determining the Functional Impact of Repetitive Elements on Non-coding RNAs. <i>Methods in Molecular Biology</i> , 2022, , 315-340.	0.4	2
6897	Chromosome-level assembly and annotation of the blue catfish <i>Ictalurus furcatus</i> , an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. <i>GigaScience</i> , 2022, 11, .	3.3	8
6898	Phylogeographical Pattern and Population Evolution History of Indigenous <i>Elymus sibiricus</i> L. on Qinghai-Tibetan Plateau. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
6899	Retrospective Natural History Study of RPGR-Related Cone- and Cone-Rod Dystrophies While Expanding the Mutation Spectrum of the Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7189.	1.8	7
6900	Differential Transcriptional Responses in Two Old World <i>Bemisia tabaci</i> Cryptic Species Post Acquisition of Old and New World Begomoviruses. <i>Cells</i> , 2022, 11, 2060.	1.8	11
6901	A chromosome-level genome of <i>Brachymystax tsinlingensis</i> provides resources and insights into salmonids evolution. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	0
6902	Along the <i>Bos taurus</i> genome, uncover candidate imprinting control regions. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
6903	An allozyme polymorphism is associated with a large chromosomal inversion in the marine snail <i>Littorina fabalis</i> . <i>Evolutionary Applications</i> , 2023, 16, 279-292.	1.5	7
6904	Comprehensive identification and characterization of the HML-9 (HML-9) group in the human genome. <i>Retrovirology</i> , 2022, 19, .	0.9	8
6906	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	9.4	26
6907	p53 Binding Sites in Long Terminal Repeat 5Hs (LTR5Hs) of Human Endogenous Retrovirus K Family (HML-2 Subgroup) Play Important Roles in the Regulation of LTR5Hs Transcriptional Activity. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11
6908	Efficient compression of SARS-CoV-2 genome data using Nucleotide Archival Format (NAF). <i>Patterns</i> , 2022, , 100562.	3.1	1

#	ARTICLE	IF	CITATIONS
6909	Evidence for yeast artificial synthesis in SARS-CoV-2 and SARS-CoV-1 genomic sequences. <i>F1000Research</i> , 0, 10, 912.	0.8	1
6910	Deep Sequencing Analysis of Individual HIV-1 Proviruses Reveals Frequent Asymmetric Long Terminal Repeats. <i>Journal of Virology</i> , 2022, 96, .	1.5	8
6911	Screening of Genes Related to Sex Determination and Differentiation in Mandarin Fish ( <i>Siniperca</i> ) Tj ETQq0 0 0 rgBTJ /Overlock 10 Tf 50	1.8	1
6913	Patient-Specific Assays Based on Whole-Genome Sequencing Data to Measure Residual Disease in Children With Acute Lymphoblastic Leukemia: A Proof of Concept Study. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	9
6914	REDfly: An Integrated Knowledgebase for Insect Regulatory Genomics. <i>Insects</i> , 2022, 13, 618.	1.0	9
6915	Targeted Long-Read Sequencing Identifies a Retrotransposon Insertion as a Cause of Altered GNAS Exon A/B Methylation in a Family With Autosomal Dominant Pseudohypoparathyroidism Type 1b (PHP1B). <i>Journal of Bone and Mineral Research</i> , 2020, 37, 1711-1719.	3.1	9
6916	Utilizing paralogues for phylogenetic reconstruction has the potential to increase species tree support and reduce gene tree discordance in target enrichment data. <i>Molecular Ecology Resources</i> , 2022, 22, 3018-3034.	2.2	8
6917	Robertsonian Fusion and Centromere Repositioning Contributed to the Formation of Satellite-free Centromeres During the Evolution of Zebras. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
6918	Identification of a Two-lncRNA Signature with Prognostic and Diagnostic Value for Hepatocellular Carcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-19.	0.6	0
6922	An Updated Genome Assembly Improves Understanding of the Transcriptional Regulation of Coloration in Midas Cichlid. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
6923	Exceptional diversity and selection pressure on coronavirus host receptors in bats compared to other mammals. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	13
6924	Identification of fusions with potential clinical significance in melanoma. <i>Modern Pathology</i> , 2022, 35, 1837-1847.	2.9	8
6925	Comparative repeatome analysis reveals new evidence on genome evolution in wild diploid <i>Arachis</i> (Fabaceae) species. <i>Planta</i> , 2022, 256, .	1.6	4
6927	Addressing nontarget amplification in DNA metabarcoding studies of arthropod-feeding rodents. <i>Mammal Research</i> , 0, , .	0.6	2
6928	Complete genome sequencing and investigation on the fiber-degrading potential of <i>Bacillus amyloliquefaciens</i> strain TL106 from the tibetan pig. <i>BMC Microbiology</i> , 2022, 22, .	1.3	5
6929	Chromosome-level genome assembly of largemouth bass ( <i>Micropterus salmoides</i> ) using PacBio and Hi-C technologies. <i>Scientific Data</i> , 2022, 9, .	2.4	4
6932	Chromosomal-level genome of velvet bean ( <i>Mucuna pruriens</i> ) provides resources for L-DOPA synthetic research and development. <i>DNA Research</i> , 2022, 29, .	1.5	3
6933	ZW sex-chromosome evolution and contagious parthenogenesis in <i>Artemia</i> brine shrimp. <i>Genetics</i> , 2022, 222, .	1.2	5

#	ARTICLE	IF	CITATIONS
6935	Functional Diversity of Microbial Communities in the Soybean ( <i>Glycine max</i> L.) Rhizosphere from Free State, South Africa. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9422.	1.8	5
6936	A diversified and segregated mRNA spliced-leader system in the parasitic Perkinsozoa. <i>Open Biology</i> , 2022, 12, .	1.5	3
6938	Genomic signatures and evolutionary history of the endangered blue-crowned laughingthrush and other <i>Garrulax</i> species. <i>BMC Biology</i> , 2022, 20, .	1.7	1
6939	The landscape of <i>Chlamydomonas</i> histone H3 lysine 4 methylation reveals both constant features and dynamic changes during the diurnal cycle. <i>Plant Journal</i> , 2022, 112, 352-368.	2.8	3
6940	Microbiota of the Pregnant Mouse: Characterization of the Bacterial Communities in the Oral Cavity, Lung, Intestine, and Vagina through Culture and DNA Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
6941	Multi-Omic Investigations of a 17q11.23 Translocation Links MINK1 Disruption to Autism, Epilepsy and Osteoporosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9392.	1.8	2
6942	Systematic profiling of the chicken gut microbiome reveals dietary supplementation with antibiotics alters expression of multiple microbial pathways with minimal impact on community structure. <i>Microbiome</i> , 2022, 10, .	4.9	12
6944	De Novo Long-Read Whole-Genome Assemblies and the Comparative Pan-Genome Analysis of Ascochyta Blight Pathogens Affecting Field Pea. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 884.	1.5	0
6945	A regulatory network of Sox and Six transcription factors initiate a cell fate transformation during hearing regeneration in adult zebrafish. <i>Cell Genomics</i> , 2022, 2, 100170.	3.0	13
6946	Improved genome assembly provides new insights into the environmental adaptation of the American cockroach, <i>Periplaneta americana</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 111, .	0.6	3
6947	Twinkle twinkle brittle star: the draft genome of <i>Ophioderma brevispinum</i> (Echinodermata). <i>Genome Biology and Evolution</i> , 2022, 14, 1-15.	1.2	5
6949	Cold Resistance of <i>Euonymus japonicus</i> Beihaidao Leaves and Its Chloroplast Genome Structure and Comparison with Celastraceae Species. <i>Plants</i> , 2022, 11, 2449.	1.6	1
6951	A Novel Cryptic t(2;3)(p21;q25) Translocation Fuses the <i>WWTR1</i> and <i>PRKCE</i> Genes in Uterine Leiomyoma With 3q- as the Sole Visible Chromosome Abnormality. <i>Cancer Genomics and Proteomics</i> , 2022, 19, 636-646.	1.0	3
6952	Fusion of High Mobility Group AT-hook 2 Gene ( <i>HMGAT2</i> ) With the Chromosome 12 Open Reading Frame 42 Gene ( <i>C12orf42</i> ) in an Aggressive Angiomyxoma With del(12)(q14q23) as the Sole Cytogenetic Anomaly. <i>Cancer Genomics and Proteomics</i> , 2022, 19, 576-583.	1.0	5
6953	Interpreting alignment-free sequence comparison: what makes a score a good score?. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	2
6954	Monotreme-specific conserved putative proteins derived from retroviral reverse transcriptase. <i>Virus Evolution</i> , 2022, 8, .	2.2	3
6955	16S Amplicon Sequencing of Nitrifying Bacteria and Archaea Inhabiting Maize Rhizosphere and the Influencing Environmental Factors. <i>Agriculture (Switzerland)</i> , 2022, 12, 1328.	1.4	6
6957	Multiple genome alignment in the telomere-to-telomere assembly era. <i>Genome Biology</i> , 2022, 23, .	3.8	17

#	ARTICLE	IF	CITATIONS
6959	HPV genotyping by L1 amplicon sequencing of archived invasive cervical cancer samples: a pilot study. <i>Infectious Agents and Cancer</i> , 2022, 17, .	1.2	2
6960	Chromosome-scale genome assembly of <i>Camellia sinensis</i> combined with multi-omics provides insights into its responses to infestation with green leafhoppers. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
6961	Chromosome-scale assembly of the yellow mealworm genome. <i>Open Research Europe</i> , 0, 1, 94.	2.0	7
6962	Genomic adaptation of the picoeukaryote <i>Pelagomonas calceolata</i> to iron-poor oceans revealed by a chromosome-scale genome sequence. <i>Communications Biology</i> , 2022, 5, .	2.0	6
6963	A survey of current methods to detect and genotype inversions. <i>Human Mutation</i> , 2022, 43, 1576-1589.	1.1	11
6964	Comparative genome analysis unravels pathogenicity of <i>Xanthomonas albilineans</i> causing sugarcane leaf scald disease. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
6965	Multi-omics provides new insights into the domestication and improvement of dark jute ( <i>C. tiliaceum</i> ). <i>Frontiers in Plant Science</i> , 2022, 13, 1052-1062.	2.8	1
6966	Genome-wide analysis reveals allelic variation and chromosome copy number variation in paromomycin-resistant <i>Leishmania donovani</i> . <i>Parasitology Research</i> , 2022, 121, 3121-3132.	0.6	1
6967	Evaluation and characterization of expression quantitative trait analysis methods in the Hybrid Rat Diversity Panel. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
6968	Regulation of Nodal signaling propagation by receptor interactions and positive feedback. <i>ELife</i> , 0, 11, .	2.8	5
6969	False gene and chromosome losses in genome assemblies caused by GC content variation and repeats. <i>Genome Biology</i> , 2022, 23, .	3.8	21
6970	Characterization of the Urinary Metagenome and Virome in Healthy Children. <i>Biomedicines</i> , 2022, 10, 2412.	1.4	2
6971	Unique Evolution of Antiviral Tetherin in Bats. <i>Journal of Virology</i> , 2022, 96, .	1.5	14
6972	Dynamic genome evolution in a model fern. <i>Nature Plants</i> , 2022, 8, 1038-1051.	4.7	56
6974	Comprehensive survey of transposon insertion sites and transcriptome analysis for identifying candidate genes controlling high protein content of rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
6975	Evolutionary divergence of duplicated genomes in newly described allotetraploid cottons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	19
6976	Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics. <i>Nature Genetics</i> , 2022, 54, 1553-1563.	9.4	46
6977	Tail Wags Dog's SINE: Retropositional Mechanisms of Can SINE Depend on Its A-Tail Structure. <i>Biology</i> , 2022, 11, 1403.	1.3	3

#	ARTICLE	IF	CITATIONS
6978	Comparative mitogenome analysis reveals mitochondrial genome characteristics in eight strains of <i>Beauveria</i> . PeerJ, 0, 10, e14067.	0.9	2
6980	Broad genomic workup including optical genome mapping uncovers a DDX3X: MLLT10 gene fusion in acute myeloid leukemia. Frontiers in Oncology, 0, 12, .	1.3	4
6981	Nuclear-embedded mitochondrial DNA sequences in 66,083 human genomes. Nature, 2022, 611, 105-114.	13.7	69
6982	Lineage-specific, fast-evolving GATA-like gene regulates zygotic gene activation to promote endoderm specification and pattern formation in the Theridiidae spider. BMC Biology, 2022, 20, .	1.7	5
6983	Efficacy and safety of universal (TCRKO) ARI-0001 CAR-T cells for the treatment of B-cell lymphoma. Frontiers in Immunology, 0, 13, .	2.2	4
6984	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and within-host species divergence. Transboundary and Emerging Diseases, 2022, 69, 3468-3484.	1.3	4
6986	A highly contiguous, scaffold-level nuclear genome assembly for the fever tree ( <i>Cinchona pubescens</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 0,0	0.0	1
6987	Genomic characterization of <i>Francisella tularensis</i> and other diverse <i>Francisella</i> species from complex samples. PLoS ONE, 2022, 17, e0273273.	1.1	4
6989	Mitochondrial Control Region Variants Related to Breast Cancer. Genes, 2022, 13, 1962.	1.0	0
6990	Miniature Inverted-repeat Transposable Elements Drive Rapid MicroRNA Diversification in Angiosperms. Molecular Biology and Evolution, 2022, 39, .	3.5	10
6991	Stable Transgenic Mouse Strain with Enhanced Photoactivatable Cre Recombinase for Spatiotemporal Genome Manipulation. Advanced Science, 2022, 9, .	5.6	5
6992	Spatiotemporal variations in retrovirus-host interactions among Darwin's finches. Nature Communications, 2022, 13, .	5.8	4
6993	A cryptic transcription factor regulates <i>Caulobacter</i> adhesin development. PLoS Genetics, 2022, 18, e1010481.	1.5	6
6994	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. Nature Ecology and Evolution, 2022, 6, 1891-1906.	3.4	23
6997	COX7A2L genetic variants determine cardiorespiratory fitness in mice and human. Nature Metabolism, 2022, 4, 1336-1351.	5.1	10
6998	Cebidae Alu Element Alignments and a Complex Non-Human Primate Radiation. Life, 2022, 12, 1655.	1.1	0
6999	Caecal microbial communities, functional diversity, and metabolic pathways in Ross 308 broiler chickens fed with diets containing different levels of Marama ( <i>Tylosema esculentum</i> ) bean meal. Frontiers in Microbiology, 0, 13, .	1.5	1
7000	Gapless genome assembly of azalea and multi-omics investigation into divergence between two species with distinct flower color. Horticulture Research, 2023, 10, .	2.9	11

#	ARTICLE	IF	CITATIONS
7002	An overview of online resources for intra-species detection of gene duplications. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
7003	The mitochondrial genome of the red icefish ( <i>Channichthys rugosus</i> ) casts doubt on its species status. <i>Polar Biology</i> , 2022, 45, 1541-1552.	0.5	0
7005	Thirteen Dipteroocarpoideae genomes provide insights into their evolution and borneol biosynthesis. <i>Plant Communications</i> , 2022, 3, 100464.	3.6	6
7006	A chromosome-level genome of <i>Semiothisa cinerearia</i> provides insights into its genome evolution and control. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
7007	The complete chloroplast genome sequences of three <i>Broussonetia</i> species and comparative analysis within the Moraceae. <i>PeerJ</i> , 0, 10, e14293.	0.9	5
7008	A method of large DNA fragment enrichment for nanopore sequencing in region 22q11.2. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
7009	De novo assembly and characterization of the draft genome of the cashew ( <i>Anacardium occidentale</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	4
7010	Light-Seq: light-directed in situ barcoding of biomolecules in fixed cells and tissues for spatially indexed sequencing. <i>Nature Methods</i> , 2022, 19, 1393-1402.	9.0	27
7011	Emergence of Novel RNA-Editing Sites by Changes in the Binding Affinity of a Conserved PPR Protein. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
7012	Comparative Genomic Analysis of 31 <i>Phytophthora</i> Genomes Reveals Genome Plasticity and Horizontal Gene Transfer. <i>Molecular Plant-Microbe Interactions</i> , 2023, 36, 26-46.	1.4	6
7013	Comprehensive analysis and accurate quantification of unintended large gene modifications induced by CRISPR-Cas9 gene editing. <i>Science Advances</i> , 2022, 8, .	4.7	25
7014	Target-enriched long-read sequencing (TELSeq) contextualizes antimicrobial resistance genes in metagenomes. <i>Microbiome</i> , 2022, 10, .	4.9	8
7016	Computational Genomic Signatures. <i>Synthesis Lectures on Biomedical Engineering</i> , 2011, , .	0.1	0
7017	Multigenic regulation in the ethylene biosynthesis pathway during coffee flowering. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 1657-1669.	1.4	1
7018	Somatic mutation detection: a critical evaluation through simulations and reanalyses in oaks. , 0, 2, .		5
7019	Inverted genomic regions between reference genome builds in humans impact imputation accuracy and decrease the power of association testing. <i>Human Genetics and Genomics Advances</i> , 2023, 4, 100159.	1.0	2
7020	Deeper genomic insights into tomato CLE genes repertoire identify new active peptides. <i>BMC Genomics</i> , 2022, 23, .	1.2	10
7021	Maize rhizosphere modulates the microbiome diversity and community structure to enhance plant health. <i>Saudi Journal of Biological Sciences</i> , 2023, 30, 103499.	1.8	7

#	ARTICLE	IF	CITATIONS
7022	Identification of the Telomere elongation Mutation in Drosophila. <i>Cells</i> , 2022, 11, 3484.	1.8	0
7023	Genome-wide identification, organization, and expression profiles of the chicken fibroblast growth factor genes in public databases and Vietnamese indigenous Ri chickens against highly pathogenic avian influenza H5N1 virus infection. <i>Animal Bioscience</i> , 0, , .	0.8	0
7025	Owl Monkey Alu Insertion Polymorphisms and Aotus Phylogenetics. <i>Genes</i> , 2022, 13, 2069.	1.0	2
7026	Complete mitochondrial genome of <i>Pseudoechthistatus hei</i> (Coleoptera: Cerambycidae): Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	1
7027	Structure and evolution of the squamate major histocompatibility complex as revealed by two Anolis lizard genomes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
7030	Identification of iron and zinc responsive genes in pearl millet using genome-wide RNA-sequencing approach. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	0
7032	No phylogenomic support for a Cenozoic origin of the "living fossil" <i>Isoetes</i> . <i>American Journal of Botany</i> , 2023, 110, .	0.8	2
7033	Temporal progress of gene expression analysis with RNA-Seq data: A review on the relationship between computational methods. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 86-98.	1.9	8
7034	Neoplasia-associated Chromosome Translocations Resulting in Gene Truncation. <i>Cancer Genomics and Proteomics</i> , 2022, 19, 647-672.	1.0	3
7035	Improved microbial genomes and gene catalog of the chicken gut from metagenomic sequencing of high-fidelity long reads. <i>GigaScience</i> , 2022, 11, .	3.3	12
7036	Effect of an anti-methanogenic supplement on enteric methane emission, fermentation, and whole rumen metagenome in sheep. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
7037	The UCSC Genome Browser database: 2023 update. <i>Nucleic Acids Research</i> , 2023, 51, D1188-D1195.	6.5	144
7038	Complete Mitogenome and Phylogenetic Analyses of <i>Galerita orientalis</i> Schmidt-Goebel, 1846 (Insecta): Tj ETQq0 0 0 rgBT /Overlock 10	1.0	1
7040	<i>Pseudomonas</i> cultivated from <i>Andropogon gerardii</i> rhizosphere show functional potential for promoting plant host growth and drought resilience. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
7042	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. <i>Cell</i> , 2022, 185, 4587-4603.e23.	13.5	29
7043	Comparative genomics reveals insight into the evolutionary origin of massively scrambled genomes. <i>ELife</i> , 0, 11, .	2.8	5
7044	Enhancing diagnosis of T-cell lymphoma using non-recombined T-cell receptor sequences. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
7045	The Chromatin Structure at the MECP2 Gene and In Silico Prediction of Potential Coding and Non-Coding MECP2 Splice Variants. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15643.	1.8	5

#	ARTICLE	IF	CITATIONS
7049	Complete mitochondrial genome and phylogenetic analysis of <i>Mastax latefasciata</i> (Insecta: Coleoptera: Carabidae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 2040-2043.	0.2	0
7050	Characterization of the Illumina EPIC array for optimal applications in epigenetic research targeting diverse human populations. , 2022, 2, .		0
7051	Navigating bottlenecks and trade-offs in genomic data analysis. <i>Nature Reviews Genetics</i> , 2023, 24, 235-250.	7.7	6
7052	Whole-Exome Sequencing Among Chinese Patients With Hereditary Diffuse Gastric Cancer. <i>JAMA Network Open</i> , 2022, 5, e2245836.	2.8	3
7053	Genetics of tibia bone properties of crossbred commercial laying hens in different housing systems. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	1
7058	How to survive in the world's third poplar: Insights from the genome of the highest altitude woody plant, <i>Hippophae tibetana</i> (Elaeagnaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
7059	Parallel evolution of reduced cancer risk and tumor suppressor duplications in <i>Xenarthra</i> . <i>ELife</i> , 0, 11, .	2.8	2
7060	Chromosome-scale genome assembly of <i>Glycyrrhiza uralensis</i> revealed metabolic gene cluster centred specialized metabolites biosynthesis. <i>DNA Research</i> , 2022, 29, .	1.5	3
7062	What has single-cell transcriptomics taught us about long non-coding RNAs in the ventricular-subventricular zone?. <i>Stem Cell Reports</i> , 2022, , .	2.3	1
7063	Chromosome Translocation t(10;19)(q26;q13) in a CIC-sarcoma. <i>In Vivo</i> , 2023, 37, 57-69.	0.6	1
7064	Efficient querying of genomic reference databases with <i>gget</i> . <i>Bioinformatics</i> , 2023, 39, .	1.8	11
7065	The hitchhikers' guide to RNA sequencing and functional analysis. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	8
7066	Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	39
7067	Identification of extremely GC-rich micro RNAs for RT-qPCR data normalization in human plasma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
7068	Pulmonary artery embolism: comprehensive transcriptomic analysis in understanding the pathogenic mechanisms of the disease. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
7069	A chromosome-level genome assembly of the <i>Henosepilachna vigintioctomaculata</i> provides insights into the evolution of ladybird beetles. <i>DNA Research</i> , 2023, 30, .	1.5	2
7070	Complete chloroplast genomes and comparative analysis of <i>Ligustrum</i> species. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
7071	A nuclear target sequence capture probe set for phylogeny reconstruction of the charismatic plant family Bignoniaceae. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5

#	ARTICLE	IF	CITATIONS
7072	A draft <i>Diabrotica virgifera virgifera</i> genome: insights into control and host plant adaptation by a major maize pest insect. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
7073	Anti- <i>Trypanosoma cruzi</i> antibody profiling in patients with Chagas disease treated with benznidazole assessed by genome phage display. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011019.	1.3	2
7075	Genome-wide assessment of population genetic and demographic history in <i>Magnolia odoratissima</i> based on SLAF-seq. <i>Conservation Genetics</i> , 0, , .	0.8	1
7076	Anomalies in dye-terminator DNA sequencing caused by a natural G-quadruplex. <i>PLoS ONE</i> , 2022, 17, e0279423.	1.1	0
7077	Novel <i>MYCBP::EHD2</i> and <i>RUNX1::ZNF780A</i> Fusion Genes in T-cell Acute Lymphoblastic Leukemia. <i>Cancer Genomics and Proteomics</i> , 2023, 20, 51-63.	1.0	1
7078	BLEND: a fast, memory-efficient and accurate mechanism to find fuzzy seed matches in genome analysis. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	12
7079	Analysis of IGH allele content in a sample group of rheumatoid arthritis patients demonstrates unrevealed population heterogeneity. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
7080	Variations in the Functional Diversity of Rhizosphere Microbiome of Healthy and Northern Corn Leaf Blight Infected Maize ( <i>Zea mays</i> L.). <i>Spanish Journal of Soil Science</i> , 0, 13, .	0.0	0
7081	Framework of the Alu Subfamily Evolution in the Platyrrhine Three-Family Clade of Cebidae, Callitrichidae, and Aotidae. <i>Genes</i> , 2023, 14, 249.	1.0	1
7082	Crystal lattice defects in nanocrystalline metacinnabar in contaminated streambank soils suggest a role for biogenic sulfides in the formation of mercury sulfide phases. <i>Environmental Sciences: Processes and Impacts</i> , 2023, 25, 445-460.	1.7	1
7083	Comparative Analyses Reveal the Genetic Mechanism of Ambergris Production in the Sperm Whale Based on the Chromosome-Level Genome. <i>Animals</i> , 2023, 13, 361.	1.0	1
7084	Persistent mutation burden drives sustained anti-tumor immune responses. <i>Nature Medicine</i> , 2023, 29, 440-449.	15.2	35
7085	Molecular classification and therapeutics in diffuse large B-cell lymphoma. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	0
7086	Chronic haloperidol administration downregulates select BDNF transcript and protein levels in the dorsolateral prefrontal cortex of rhesus monkeys. <i>Frontiers in Psychiatry</i> , 0, 14, .	1.3	0
7087	Comparison of Southern-by-Sequencing (SbSTM) technology and Southern Blot Analysis for Molecular Characterization of Genetically Modified Crops. , 0, , 1-14.		2
7089	An ASO therapy for Angelman syndrome that targets an evolutionarily conserved region at the start of the <i>UBE3A-AS</i> transcript. <i>Science Translational Medicine</i> , 2023, 15, .	5.8	10
7090	Recurrent 8q11-13 Aberrations Leading to <i>PLAG1</i> Rearrangements, Including Novel Chimeras <i>HNRNPA2B1::PLAG1</i> and <i>SDCBP::PLAG1</i> , in Lipomatous Tumors. <i>Cancer Genomics and Proteomics</i> , 2023, 20, 171-181.	1.0	0
7093	Complete chloroplast genome data for <i>Mimosa diplotricha</i> and <i>Mimosa diplotricha</i> var. <i>inermis</i> from China. <i>Data in Brief</i> , 2023, 48, 109045.	0.5	0

#	ARTICLE	IF	CITATIONS
7094	The Michigan Genomics Initiative: A biobank linking genotypes and electronic clinical records in Michigan Medicine patients. <i>Cell Genomics</i> , 2023, 3, 100257.	3.0	27
7095	The complete chloroplast genome of <i>Hibiscus syriacus</i> using long-read sequencing: Comparative analysis to examine the evolution of the tribe Hibisceae. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
7097	Newly identified sex chromosomes in the <i>Sphagnum</i> (peat moss) genome alter carbon sequestration and ecosystem dynamics. <i>Nature Plants</i> , 2023, 9, 238-254.	4.7	18
7098	<scp>Renalâ€hepaticâ€pancreatic</scp> dysplasia type 2: Perinatal lethal condition or a multisystemic disorder with variable expressivity. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2023, 11, .	0.6	1
7099	Genome Sequence and Analysis of <i>Nicotiana benthamiana</i> , the Model Plant for Interactions between Organisms. <i>Plant and Cell Physiology</i> , 2023, 64, 248-257.	1.5	14
7100	Dissecting the genetic basis of heterosis in elite super-hybrid rice. <i>Plant Physiology</i> , 2023, 192, 307-325.	2.3	4
7101	The genome of a vestimentiferan tubeworm ( <i>Ridgeia piscesae</i> ) provides insights into its adaptation to a deep-sea environment. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
7103	Specific-Locus Amplified Fragment Sequencing (SLAF-Seq). <i>Methods in Molecular Biology</i> , 2023, , 165-171.	0.4	1
7104	Analysis of Fowl Adenovirus 4 Transcriptome by De Novo ORF Prediction Based on Corrected Nanopore Full-Length cDNA Sequencing Data. <i>Viruses</i> , 2023, 15, 529.	1.5	1
7105	The complete plastome of <i>Glandora prostrata</i> subsp. <i>lusitanica</i> (Samp.) D.C.Thomas (Boraginaceae), the first chloroplast genome belonging to the <i>Glandora</i> genus. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 270-273.	0.2	1
7106	Precipitation is the main axis of tropical plant phylogenetic turnover across space and time. <i>Science Advances</i> , 2023, 9, .	4.7	12
7107	Metabolic Background, Not Photosynthetic Physiology, Determines Drought and Drought Recovery Responses in C3 and C2 Mricandias. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4094.	1.8	1
7108	FixItFelix: improving genomic analysis by fixing reference errors. <i>Genome Biology</i> , 2023, 24, .	3.8	7
7109	Roadmap to the study of gene and protein phylogeny and evolutionâ€”A practical guide. <i>PLoS ONE</i> , 2023, 18, e0279597.	1.1	4
7111	The diatom <i>Fragilariopsis cylindrus</i> : A model alga to understand coldâ€adapted life. <i>Journal of Phycology</i> , 2023, 59, 301-306.	1.0	4
7112	A cytosine-patch sequence motif identified in the conserved region of lincRNA-p21 interacts with the KH3 domain of hnRNPK. <i>Current Research in Structural Biology</i> , 2023, 5, 100099.	1.1	0
7113	Investigation of mutation load and rate in androgenic mutant lines of rapeseed in early generations evaluated by high-density SNP genotyping. <i>Heliyon</i> , 2023, 9, e14065.	1.4	0
7114	Exploring microbial functional biodiversity at the protein family levelâ€”From metagenomic sequence reads to annotated protein clusters. <i>Frontiers in Bioinformatics</i> , 0, 3, .	1.0	2

#	ARTICLE	IF	CITATIONS
7115	Unique gene duplications and conserved microsynteny potentially associated with resistance to wood decay in the Lauraceae. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
7116	Distinctive origin and evolution of endemic thistle of Korean volcanic island: Structural organization and phylogenetic relationships with complete chloroplast genome. <i>PLoS ONE</i> , 2023, 18, e0277471.	1.1	1
7117	Insights into the genomic evolution and the alkali tolerance mechanisms of <i>Agaricus sinodeliciosus</i> by comparative genomic and transcriptomic analyses. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
7118	Plastid Genome Assembly Using Long-read data. <i>Molecular Ecology Resources</i> , 2023, 23, 1442-1457.	2.2	4
7119	Regulatory and coding sequences of TRNP1 co-evolve with brain size and cortical folding in mammals. <i>ELife</i> , 0, 12, .	2.8	5
7121	An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	13
7122	Localized assembly for long reads enables genome-wide analysis of repetitive regions at single-base resolution in human genomes. <i>Human Genomics</i> , 2023, 17, .	1.4	2
7123	Improved chromosomal-level genome assembly and re-annotation of leopard coral grouper. <i>Scientific Data</i> , 2023, 10, .	2.4	2
7125	New proposal of viral genome representation applied in the classification of SARS-CoV-2 with deep learning. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	1
7126	Pan-cancer analysis identifies tumor-specific antigens derived from transposable elements. <i>Nature Genetics</i> , 2023, 55, 631-639.	9.4	32
7127	Simultaneous Ultra-Sensitive Detection of Structural and Single Nucleotide Variants Using Multiplex Droplet Digital PCR in Liquid Biopsies from Children with Medulloblastoma. <i>Cancers</i> , 2023, 15, 1972.	1.7	5
7128	Determining chromatin architecture with Micro Capture-C. <i>Nature Protocols</i> , 2023, 18, 1687-1711.	5.5	7
7129	Crystal Structure of an iâ€Motif from the <i>HRAS</i> Oncogene Promoter. <i>Angewandte Chemie - International Edition</i> , 2023, 62, .	7.2	5
7130	Crystal Structure of an iâ€Motif from the <i>HRAS</i> Oncogene Promoter. <i>Angewandte Chemie</i> , 2023, 135, .	1.6	0
7131	CRISPR/Cas9-Mediated Genome Editing in Zebrafish. <i>Methods in Molecular Biology</i> , 2023, , 371-380.	0.4	0
7132	Target-capture probes for phylogenomics of the Caenogastropoda. <i>Molecular Ecology Resources</i> , 0, , .	2.2	1
7134	Shine: A novel strategy to extract specific, sensitive and well-conserved biomarkers from massive microbial genomic datasets. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	0
7135	Identification and validation of new MADS-box homologous genes in 3010 rice pan-genome. <i>Plant Cell Reports</i> , 0, , .	2.8	1

#	ARTICLE	IF	CITATIONS
7137	Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species. <i>Nature Genetics</i> , 2023, 55, 852-860.	9.4	43
7138	Genomic and transcriptomic analysis of checkpoint blockade response in advanced non-small cell lung cancer. <i>Nature Genetics</i> , 2023, 55, 807-819.	9.4	18
7139	Expanding known viral diversity in the healthy infant gut. <i>Nature Microbiology</i> , 2023, 8, 986-998.	5.9	31
7141	Definition of the transcriptional units of inherited retinal disease genes by meta-analysis of human retinal transcriptome data. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
7142	The Complete Chloroplast Genomes of <i>Gynostemma</i> Reveal the Phylogenetic Relationships of Species within the Genus. <i>Genes</i> , 2023, 14, 929.	1.0	2
7188	Tackling Tissue Macrophage Heterogeneity by SplitCre Transgenesis. <i>Methods in Molecular Biology</i> , 2024, , 481-503.	0.4	0
7223	Accurate Detection of Fusion Genes in Long-Read Transcriptome Datasets from Multiple Cancer Cell Lines. , 2024, , .		0
7227	In Silico Models on Algal Cultivation and Processing. , 2023, , 989-1016.		0