

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

Genome Research

12, 656-664

DOI: 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. | 7.1 | 31 |
| 4 | Identification of Candidate Genes Regulating HDL Cholesterol Using a Chromosomal Region Expression Array. Genome Research, 2002, 12, 1693-1702. | 5.5 | 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. | 7.1 | 75 |
| 6 | Comparison of whole genome assemblies of the human genome. Nucleic Acids Research, 2002, 30, 5004-5014. | 14.5 | 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. | 5.5 | 8,776 |
| 10 | The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. Science, 2002, 298, 2157-2167. | 12.6 | 1,539 |
| 11 | Computational comparison of two mouse draft genomes and the human golden path. Genome Biology, 2002, 4, R1. | 9.6 | 34 |
| 12 | Apollo: a sequence annotation editor. Genome Biology, 2002, 3, research0082.1. | 9.6 | 369 |
| 13 | Assessing the impact of comparative genomic sequence data on the functional annotation of the Drosophila genome. Genome Biology, 2002, 3, research0086.1. | 9.6 | 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. | 6.2 | 144 |
| 17 | Visualizing the genome: techniques for presenting human genome data and annotations. BMC Bioinformatics, 2002, 3, 19. | 2.6 | 30 |
| 18 | Development and production of an oligonucleotide MuscleChip: use for validation of ambiguous ESTs. BMC Bioinformatics, 2002, 3, 33. | 2.6 | 8 |
| 19 | Genetics of the immune response: identifying immune variation within the MHC and throughout the genome. Immunological Reviews, 2002, 190, 69-85. | 6.0 | 49 |
| 20 | A physical map of the mouse genome. Nature, 2002, 418, 743-750. | 27.8 | 316 |
| 21 | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573. | 27.8 | 1,548 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 35 | Commentary: keeping biology in mind. <i>Nature Genetics</i> , 2002, 32, 74-75. | 21.4 | 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. | 21.4 | 255 |
| 37 | The UCSC Genome Browser Database. <i>Nucleic Acids Research</i> , 2003, 31, 51-54. | 14.5 | 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. | 2.2 | 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. | 2.2 | 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. | 2.3 | 5 |
| 41 | Binformatics: 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. | 2.6 | 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. | 2.8 | 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. | 27.8 | 108 |
| 48 | Introduction: putting it together. <i>Nature Genetics</i> , 2003, 35, 5-8. | 21.4 | 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. | 21.4 | 32 |
| 50 | Question 2—How can sequence-tagged sites within a DNA sequence be identified?. <i>Nature Genetics</i> , 2003, 35, 18-20. | 21.4 | 0 |
| 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. | 21.4 | 2 |
| 52 | Question 4—A user wishes to find all the single nucleotide polymorphisms that lie between two sequence-tagged sites. Do any of these single nucleotide polymorphisms fall within the coding region of a gene? Where can any additional information about the function of these genes be found?. <i>Nature Genetics</i> , 2003, 35, 29-32. | 21.4 | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 53 | Question 5ÂGiven a fragment of mRNA sequence, how would one find where that piece of DNA mapped in the human genome? Once its position has been determined, how would one find alternatively-spliced transcripts?. Nature Genetics, 2003, 35, 33-39. | 21.4 | 0 |
| 54 | Question 7ÂHow would an investigator easily find compiled information describing the structure of a gene of interest? Is it possible to obtain the sequence of any putative promoter regions?. Nature Genetics, 2003, 35, 44-48. | 21.4 | 0 |
| 55 | Question 10ÂFor 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?. Nature Genetics, 2003, 35, 57-62. | 21.4 | 2 |
| 56 | Question 11ÂAn investigator has identified and cloned a human gene, but no corresponding mouse ortholog has yet been identified. How can a mouse genomic sequence with similarity to the human gene sequence be retrieved?. Nature Genetics, 2003, 35, 63-65. | 21.4 | 0 |
| 57 | Question 12ÂHow does a user find characterized mouse mutants corresponding to human genes?. Nature Genetics, 2003, 35, 66-69. | 21.4 | 0 |
| 58 | Commentary: keeping biology in mind. Nature Genetics, 2003, 35, 74-74. | 21.4 | 1 |
| 59 | Clonality analysis after retroviral-mediated gene transfer to CD34+ cells from the cord blood of ADA-deficient SCID neonates. Nature Medicine, 2003, 9, 463-468. | 30.7 | 134 |
| 60 | Comparative genomics: genome-wide analysis in metazoan eukaryotes. Nature Reviews Genetics, 2003, 4, 251-262. | 16.3 | 203 |
| 61 | The UCSC Genome Browser. Current Protocols in Bioinformatics, 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. Reproductive Biology and Endocrinology, 2003, 1, 54. | 3.3 | 33 |
| 63 | Structural Context of Exons in Protein Domains: Implications for Protein Modelling and Design. Journal of Molecular Biology, 2003, 333, 1045-1059. | 4.2 | 9 |
| 64 | Genome Rearrangements in Mammalian Evolution: Lessons From Human and Mouse Genomes. Genome Research, 2003, 13, 37-45. | 5.5 | 302 |
| 65 | Dissecting the transcription networks of a cell using computational genomics. Current Opinion in Genetics and Development, 2003, 13, 611-616. | 3.3 | 27 |
| 66 | Vertebrate gene predictions and the problem of large genes. Nature Reviews Genetics, 2003, 4, 741-749. | 16.3 | 56 |
| 67 | Is there an evolutionary relationship between WARP (von Willebrand factor A-domain-related protein) and the FACIT and FACIT-like collagens?. FEBS Letters, 2003, 552, 91-94. | 2.8 | 6 |
| 68 | Identification of a Novel Bardet-Biedl Syndrome Protein, BBS7, That Shares Structural Features with BBS1 and BBS2. American Journal of Human Genetics, 2003, 72, 650-658. | 6.2 | 207 |
| 69 | Large Differences between LINE-1 Amplification Rates in the Human and Chimpanzee Lineages. American Journal of Human Genetics, 2003, 72, 739-748. | 6.2 | 30 |
| 70 | ATLAS: A System to Selectively Identify Human-Specific L1 Insertions. American Journal of Human Genetics, 2003, 72, 823-838. | 6.2 | 105 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 71 | Mutations in the Fumarate Hydratase Gene Cause Hereditary Leiomyomatosis and Renal Cell Cancer in Families in North America. American Journal of Human Genetics, 2003, 73, 95-106. | 6.2 | 563 |
| 72 | Identification, characterization and expression analysis of a new fibrillar collagen gene, COL27A1. Matrix Biology, 2003, 22, 3-14. | 3.6 | 112 |
| 73 | In silico searching of human and mouse genome data identifies known and unknown HNF1 binding sites upstream of β -cell genes. Molecular Genetics and Metabolism, 2003, 78, 145-151. | 1.1 | 15 |
| 74 | Two promoters within the human LMO4 gene contribute to its overexpression in breast cancer cells. Genomics, 2003, 82, 280-287. | 2.9 | 13 |
| 75 | Farnesoid X Receptor Activates Transcription of the Phospholipid Pump MDR3. Journal of Biological Chemistry, 2003, 278, 51085-51090. | 3.4 | 195 |
| 76 | Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26. | 5.5 | 263 |
| 77 | Enrichment of Gene-Coding Sequences in Maize by Genome Filtration. Science, 2003, 302, 2118-2120. | 12.6 | 207 |
| 78 | Expressed sequence tag profiling identifies developmental and anatomic partitioning of gene expression in the mouse prostate. Genome Biology, 2003, 4, R79. | 9.6 | 21 |
| 79 | Whole-genome screening indicates a possible burst of formation of processed pseudogenes and Alu repeats by particular L1 subfamilies in ancestral primates. Genome Biology, 2003, 4, R74. | 9.6 | 172 |
| 80 | ProSplicer: a database of putative alternative splicing information derived from protein, mRNA and expressed sequence tag sequence data. Genome Biology, 2003, 4, R29. | 9.6 | 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. Genome Research, 2003, 13, 1290-1300. | 5.5 | 168 |
| 85 | Aligning ESTs to genome using multilayer unique makers. , 0, , . | | 1 |
| 86 | A coming of age for bioinformatics. Journal of Cell Science, 2003, 116, 6-7. | 2.0 | 1 |
| 87 | Mastering seeds for genomic size nucleotide BLAST searches. Nucleic Acids Research, 2003, 31, 6935-6941. | 14.5 | 25 |
| 88 | Strategies and Tools for Whole-Genome Alignments. Genome Research, 2003, 13, 73-80. | 5.5 | 190 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 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. | 5.5 | 7 |
| 90 | A Complexity Reduction Algorithm for Analysis and Annotation of Large Genomic Sequences. <i>Genome Research</i> , 2003, 13, 313-322. | 5.5 | 15 |
| 91 | Glocal alignment: finding rearrangements during alignment. <i>Bioinformatics</i> , 2003, 19, i54-i62. | 4.1 | 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. | 14.5 | 15 |
| 93 | Locating Sequence on FPC Maps and Selecting a Minimal Tiling Path. <i>Genome Research</i> , 2003, 13, 2152-2163. | 5.5 | 37 |
| 94 | GeneLynx Mouse: Integrated Portal to the Mouse Genome. <i>Genome Research</i> , 2003, 13, 1501-1504. | 5.5 | 13 |
| 95 | A comparative analysis of HGSC and Celera human genome assemblies and gene sets. <i>Bioinformatics</i> , 2003, 19, 1597-1605. | 4.1 | 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. | 7.1 | 222 |
| 97 | Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. <i>Genome Research</i> , 2003, 13, 1-12. | 5.5 | 210 |
| 98 | GeneAnnot: Interfacing GeneCards with high-throughput gene expression compendia. <i>Briefings in Bioinformatics</i> , 2003, 4, 349-360. | 6.5 | 17 |
| 99 | Computational Discovery of Internal Micro-Exons. <i>Genome Research</i> , 2003, 13, 1216-1221. | 5.5 | 62 |
| 100 | PromoSer: a large-scale mammalian promoter and transcription start site identification service. <i>Nucleic Acids Research</i> , 2003, 31, 3554-3559. | 14.5 | 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. | 5.5 | 0 |
| 102 | Elevated Rates of Protein Secretion, Evolution, and Disease Among Tissue-Specific Genes. <i>Genome Research</i> , 2003, 14, 54-61. | 5.5 | 160 |
| 103 | Global disruption of the cerebellar transcriptome in a Down syndrome mouse model. <i>Human Molecular Genetics</i> , 2003, 12, 2013-2019. | 2.9 | 143 |
| 104 | Multiple, dispersed human U6 small nuclear RNA genes with varied transcriptional efficiencies. <i>Nucleic Acids Research</i> , 2003, 31, 2344-2352. | 14.5 | 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. | 14.5 | 199 |
| 106 | Annotating Large Genomes With Exact Word Matches. <i>Genome Research</i> , 2003, 13, 2306-2315. | 5.5 | 62 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 107 | Multiple Variable First Exons: A Mechanism for Cell- and Tissue-Specific Gene Regulation. <i>Genome Research</i> , 2003, 14, 79-89. | 5.5 | 123 |
| 108 | A General Approach for Identifying Distant Regulatory Elements Applied to the Gdf6 Gene. <i>Genome Research</i> , 2003, 13, 2069-2081. | 5.5 | 85 |
| 109 | 1-Mb Resolution Array-Based Comparative Genomic Hybridization Using a BAC Clone Set Optimized for Cancer Gene Analysis. <i>Genome Research</i> , 2004, 14, 179-187. | 5.5 | 100 |
| 110 | Physical evidence of Mcs5, a QTL controlling mammary carcinoma susceptibility, in congenic rats. <i>Carcinogenesis</i> , 2003, 24, 1455-1460. | 2.8 | 21 |
| 111 | gff2aplot: Plotting sequence comparisons. <i>Bioinformatics</i> , 2003, 19, 2477-2479. | 4.1 | 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. | 5.5 | 21 |
| 113 | G Protein-Coupled Receptor Genes in the FANTOM2 Database. <i>Genome Research</i> , 2003, 13, 1466-1477. | 5.5 | 32 |
| 114 | Continued Discovery of Transcriptional Units Expressed in Cells of the Mouse Mononuclear Phagocyte Lineage. <i>Genome Research</i> , 2003, 13, 1360-1365. | 5.5 | 41 |
| 115 | Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , 2003, 31, 5654-5666. | 14.5 | 1,597 |
| 116 | Molecular classification of familial non- <i>BRCA1/BRCA2</i> breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2532-2537. | 7.1 | 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. | 0.8 | 7 |
| 118 | Reevaluating Human Gene Annotation: A Second-Generation Analysis of Chromosome 22. <i>Genome Research</i> , 2003, 13, 27-36. | 5.5 | 73 |
| 119 | WormBase: a cross-species database for comparative genomics. <i>Nucleic Acids Research</i> , 2003, 31, 133-137. | 14.5 | 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. | 5.5 | 115 |
| 121 | DNannotator: annotation software tool kit for regional genomic sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3729-3735. | 14.5 | 4 |
| 122 | Assessment of SAGE in Transcript Identification. <i>Genome Research</i> , 2003, 13, 1203-1215. | 5.5 | 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. | 0.8 | 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. | 6.2 | 1 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 125 | Identification of a gene causing human cytochrome <i>c</i> oxidase deficiency by integrative genomics. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 605-610. | 7.1 | 526 |
| 126 | The Role of Declarative Querying in Bioinformatics. OMICS A Journal of Integrative Biology, 2003, 7, 89-91. | 2.0 | 12 |
| 127 | The Histone Deacetylase 9 Gene Encodes Multiple Protein Isoforms. Journal of Biological Chemistry, 2003, 278, 16059-16072. | 3.4 | 128 |
| 128 | LAGAN and Multi-LAGAN: Efficient Tools for Large-Scale Multiple Alignment of Genomic DNA. Genome Research, 2003, 13, 721-731. | 5.5 | 960 |
| 129 | A 1-Mb resolution radiation hybrid map of the canine genome. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5296-5301. | 7.1 | 219 |
| 130 | Discovery of the breast cancer gene <i>BASE</i> using a molecular approach to enrich for genes encoding membrane and secreted proteins. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1099-1104. | 7.1 | 55 |
| 131 | Human-Mouse Alignments with BLASTZ. Genome Research, 2003, 13, 103-107. | 5.5 | 1,071 |
| 132 | PRIMEX: rapid identification of oligonucleotide matches in whole genomes. Bioinformatics, 2003, 19, 2486-2488. | 4.1 | 31 |
| 133 | Alignment of BLAST high-scoring segment pairs based on the longest increasing subsequence algorithm. Bioinformatics, 2003, 19, 1391-1396. | 4.1 | 31 |
| 134 | Genome Sequencing, Assembly and Gene Prediction in Fungi. Applied Mycology and Biotechnology, 2003, 3, 65-81. | 0.3 | 1 |
| 135 | Detecting protein sequence conservation via metric embeddings. Bioinformatics, 2003, 19, i122-i129. | 4.1 | 25 |
| 136 | GS-Aligner: A Novel Tool for Aligning Genomic Sequences Using Bit-Level Operations. Molecular Biology and Evolution, 2003, 20, 1299-1309. | 8.9 | 9 |
| 137 | Match Chaining Algorithms for cDNA Mapping. Lecture Notes in Computer Science, 2003, , 462-475. | 1.3 | 23 |
| 138 | Vector Seeds: An Extension to Spaced Seeds Allows Substantial Improvements in Sensitivity and Specificity. Lecture Notes in Computer Science, 2003, , 39-54. | 1.3 | 22 |
| 139 | Transcriptome Analysis of Mouse Stem Cells and Early Embryos. PLoS Biology, 2003, 1, e74. | 5.6 | 156 |
| 140 | The ND-Tree. , 2003, , 620-631. | | 14 |
| 141 | Large-scale RT-PCR recovery of full-length cDNA clones. BioTechniques, 2004, 36, 690-700. | 1.8 | 11 |
| 142 | Bioinformatic Approaches to Assigning Protein Function From Novel Sequence Data. , 2005, 104, 313-332. | | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 143 | A Neutral Model of Transcriptome Evolution. PLoS Biology, 2004, 2, e132. | 5.6 | 294 |
| 144 | DoOP: Databases of Orthologous Promoters, collections of clusters of orthologous upstream sequences from chordates and plants. Nucleic Acids Research, 2004, 33, D86-D90. | 14.5 | 26 |
| 145 | Efficient combination of multiple word models for improved sequence comparison. Bioinformatics, 2004, 20, 2529-2533. | 4.1 | 12 |
| 146 | SPD--a web-based secreted protein database. Nucleic Acids Research, 2004, 33, D169-D173. | 14.5 | 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. Human Molecular Genetics, 2004, 13, 1479-1485. | 2.9 | 56 |
| 148 | Designing multiple simultaneous seeds for DNA similarity search. , 2004, , . | | 26 |
| 149 | The UniMarker (UM) method for synteny mapping of large genomes. Bioinformatics, 2004, 20, 3156-3165. | 4.1 | 9 |
| 150 | Multiple organism gene finding by collapsed gibbs sampling. , 2004, , . | | 4 |
| 151 | T1DBase, a community web-based resource for type 1 diabetes research. Nucleic Acids Research, 2004, 33, D544-D549. | 14.5 | 44 |
| 152 | Pooled Genomic Indexing (PGI): Analysis and Design of Experiments. Journal of Computational Biology, 2004, 11, 1001-1021. | 1.6 | 8 |
| 153 | Computational Searches for Missing Orthologs: The Case of S100A12 in Mice. OMICS A Journal of Integrative Biology, 2004, 8, 334-340. | 2.0 | 22 |
| 154 | Inferred Functions of "Novel" Genes Identified in Fibroblasts Chondroinduced by Demineralized Bone. DNA and Cell Biology, 2004, 23, 15-24. | 1.9 | 1 |
| 155 | HGVbase: a curated resource describing human DNA variation and phenotype relationships. Nucleic Acids Research, 2004, 32, 516D-519. | 14.5 | 60 |
| 156 | Natural Genetic Variation Caused by Transposable Elements in Humans. Genetics, 2004, 168, 933-951. | 2.9 | 138 |
| 157 | HemoPDB: Hematopoiesis Promoter Database, an information resource of transcriptional regulation in blood cell development. Nucleic Acids Research, 2004, 32, 86D-90. | 14.5 | 14 |
| 158 | Identifying gene regulatory elements by genome-wide recovery of DNase hypersensitive sites. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 992-997. | 7.1 | 166 |
| 159 | A novel TEAD1 mutation is the causative allele in Sveinsson's chorioretinal atrophy (helicoid) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 T | 2.9 | 118 |
| 160 | Comparative Recombination Rates in the Rat, Mouse, and Human Genomes. Genome Research, 2004, 14, 528-538. | 5.5 | 452 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 161 | Using MoBloS' scalable genome join to find conserved primer pair candidates between two genomes. Bioinformatics, 2004, 20, i355-i362. | 4.1 | 15 |
| 162 | 1274 Full-Open Reading Frames of Transcripts Expressed in the Developing Mouse Nervous System. Genome Research, 2004, 14, 2053-2063. | 5.5 | 17 |
| 163 | The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. Nucleic Acids Research, 2004, 32, 3977-3983. | 14.5 | 77 |
| 164 | Building Genomic Profiles for Uncovering Segmental Homology in the Twilight Zone. Genome Research, 2004, 14, 1095-1106. | 5.5 | 62 |
| 165 | Full-malaria 2004: an enlarged database for comparative studies of full-length cDNAs of malaria parasites, Plasmodium species. Nucleic Acids Research, 2004, 32, 334D-338. | 14.5 | 26 |
| 166 | ORFcurator: molecular curation of genes and gene clusters in prokaryotic organisms. Bioinformatics, 2004, 20, 3462-3465. | 4.1 | 12 |
| 167 | Comparative Evolutionary Genomics of Androgen-Binding Protein Genes. Genome Research, 2004, 14, 1516-1529. | 5.5 | 79 |
| 168 | A comparative method for identification of gene structures and alternatively spliced variants. Bioinformatics, 2004, 20, 3064-3079. | 4.1 | 14 |
| 169 | The Ensembl Automatic Gene Annotation System. Genome Research, 2004, 14, 942-950. | 5.5 | 352 |
| 170 | Parallel Genotyping of Over 10,000 SNPs Using a One-Primer Assay on a High-Density Oligonucleotide Array. Genome Research, 2004, 14, 414-425. | 5.5 | 281 |
| 171 | Noncoding Sequences Conserved in a Limited Number of Mammals in the SIM2 Interval are Frequently Functional. Genome Research, 2004, 14, 367-372. | 5.5 | 73 |
| 172 | Genomic Analysis of the Nuclear Receptor Family: New Insights Into Structure, Regulation, and Evolution From the Rat Genome. Genome Research, 2004, 14, 580-590. | 5.5 | 187 |
| 173 | RTCGD: retroviral tagged cancer gene database. Nucleic Acids Research, 2004, 32, 523D-527. | 14.5 | 289 |
| 174 | Automated Whole-Genome Multiple Alignment of Rat, Mouse, and Human. Genome Research, 2004, 14, 685-692. | 5.5 | 79 |
| 175 | Gene trap as a tool for genome annotation and analysis of X chromosome inactivation in human embryonic stem cells. Nucleic Acids Research, 2004, 32, 3995-4002. | 14.5 | 69 |
| 176 | Molecular structure of double-minute chromosomes bearing amplified copies of the epidermal growth factor receptor gene in gliomas. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11368-11373. | 7.1 | 145 |
| 177 | Discovery of functional noncoding elements by digital analysis of chromatin structure. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16837-16842. | 7.1 | 135 |
| 178 | Novel Antigen Identification Method for Discovery of Protective Malaria Antigens by Rapid Testing of DNA Vaccines Encoding Exons from the Parasite Genome. Infection and Immunity, 2004, 72, 1594-1602. | 2.2 | 28 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 179 | Evolution and Comparative Genomics of Odorant- and Pheromone-Associated Genes in Rodents. <i>Genome Research</i> , 2004, 14, 591-602. | 5.5 | 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. | 5.5 | 36 |
| 181 | WormBase: a comprehensive data resource for <i>Caenorhabditis</i> biology and genomics. <i>Nucleic Acids Research</i> , 2004, 33, D383-D389. | 14.5 | 155 |
| 182 | WormBase as an Integrated Platform for the <i>C. elegans</i> ORFeome. <i>Genome Research</i> , 2004, 14, 2155-2161. | 5.5 | 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. | 1.6 | 45 |
| 184 | Identification of MEF2-regulated genes during muscle differentiation. <i>Physiological Genomics</i> , 2004, 20, 143-151. | 2.3 | 22 |
| 185 | OPTIMAL SPACED SEEDS FOR HOMOLOGOUS CODING REGIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 01, 595-610. | 0.8 | 48 |
| 186 | From masking repeats to identifying functional repeats in the mouse transcriptome. <i>Briefings in Bioinformatics</i> , 2004, 5, 107-117. | 6.5 | 5 |
| 187 | Integrated analysis of the genome and the transcriptome by FANTOM. <i>Briefings in Bioinformatics</i> , 2004, 5, 249-258. | 6.5 | 12 |
| 188 | Gene structure prediction from consensus spliced alignment of multiple ESTs matching the same genomic locus. <i>Bioinformatics</i> , 2004, 20, 1157-1169. | 4.1 | 97 |
| 189 | GeneAnnot: comprehensive two-way linking between oligonucleotide array probesets and GeneCards genes. <i>Bioinformatics</i> , 2004, 20, 1457-1458. | 4.1 | 53 |
| 190 | Eukaryotic Regulatory Element Conservation Analysis and Identification Using Comparative Genomics. <i>Genome Research</i> , 2004, 14, 451-458. | 5.5 | 130 |
| 191 | Differential <i>Alu</i> Mobilization and Polymorphism Among the Human and Chimpanzee Lineages. <i>Genome Research</i> , 2004, 14, 1068-1075. | 5.5 | 108 |
| 192 | HERVd: the Human Endogenous RetroViruses Database: update. <i>Nucleic Acids Research</i> , 2004, 32, 50D-50. | 14.5 | 63 |
| 193 | Hembase: browser and genome portal for hematology and erythroid biology. <i>Nucleic Acids Research</i> , 2004, 32, 572D-574. | 14.5 | 21 |
| 194 | The mouse genome: Experimental examination of gene predictions and transcriptional start sites. <i>Genome Research</i> , 2004, 14, 2424-2429. | 5.5 | 11 |
| 195 | Good spaced seeds for homology search. <i>Bioinformatics</i> , 2004, 20, 1053-1059. | 4.1 | 69 |
| 196 | Identifying estrogen receptor α target genes using integrated computational genomics and chromatin immunoprecipitation microarray. <i>Nucleic Acids Research</i> , 2004, 32, 6627-6635. | 14.5 | 79 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 197 | MAVID: Constrained Ancestral Alignment of Multiple Sequences. <i>Genome Research</i> , 2004, 14, 693-699. | 5.5 | 232 |
| 198 | me-PCR: a refined ultrafast algorithm for identifying sequence-defined genomic elements. <i>Bioinformatics</i> , 2004, 20, 588-590. | 4.1 | 12 |
| 199 | Gene expression changes associated with fibronectin-induced cardiac myocyte hypertrophy. <i>Physiological Genomics</i> , 2004, 18, 273-283. | 2.3 | 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. | 14.5 | 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. | 14.5 | 462 |
| 203 | siRNA Selection Server: an automated siRNA oligonucleotide prediction server. <i>Nucleic Acids Research</i> , 2004, 32, W130-W134. | 14.5 | 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. | 14.5 | 17 |
| 205 | PromoSer: improvements to the algorithm, visualization and accessibility. <i>Nucleic Acids Research</i> , 2004, 32, W191-W194. | 14.5 | 22 |
| 206 | ProbeLynx: a tool for updating the association of microarray probes to genes. <i>Nucleic Acids Research</i> , 2004, 32, W471-W474. | 14.5 | 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. | 14.5 | 10 |
| 208 | ChickVD: a sequence variation database for the chicken genome. <i>Nucleic Acids Research</i> , 2004, 33, D438-D441. | 14.5 | 33 |
| 209 | The UCSC Proteome Browser. <i>Nucleic Acids Research</i> , 2004, 33, D454-D458. | 14.5 | 43 |
| 210 | Systematic Recovery and Analysis of Full-ORF Human cDNA Clones. <i>Genome Research</i> , 2004, 14, 2083-2092. | 5.5 | 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. | 7.1 | 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. | 3.4 | 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. | 7.1 | 26 |
| 214 | Pash: Efficient Genome-Scale Sequence Anchoring by Positional Hashing. <i>Genome Research</i> , 2004, 14, 672-678. | 5.5 | 33 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 215 | Genetic Divergence of the Rhesus Macaque Major Histocompatibility Complex. <i>Genome Research</i> , 2004, 14, 1501-1515. | 5.5 | 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. | 5.5 | 26 |
| 217 | Packaging and reverse transcription of snRNAs by retroviruses may generate pseudogenes. <i>Rna</i> , 2004, 10, 299-307. | 3.5 | 33 |
| 218 | CHARACTERIZATION OF THE SPLICE SITES IN GTâ€‘AG AND GCâ€‘AG INTRONS IN HIGHER EUKARYOTES USING FULL-LENGTH cDNAs. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 309-331. | 0.8 | 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. | 0.8 | 22 |
| 220 | FREP: a database of functional repeats in mouse cDNAs. <i>Nucleic Acids Research</i> , 2004, 32, 471D-475. | 14.5 | 6 |
| 221 | EXPRESSION OF TESTIS SPECIFIC ANKYRIN REPEAT AND SOCS BOX-CONTAINING 17 GENE. <i>Archives of Andrology</i> , 2004, 50, 155-161. | 1.0 | 10 |
| 222 | Predicting rules on organization of cis-regulatory elements, taking the order of elements into account. <i>Bioinformatics</i> , 2004, 20, 1119-1128. | 4.1 | 17 |
| 223 | Speeding up whole-genome alignment by indexing frequency vectors. <i>Bioinformatics</i> , 2004, 20, 2122-2134. | 4.1 | 15 |
| 224 | Distinct Genomic Integration of MLV and SIV Vectors in Primate Hematopoietic Stem and Progenitor Cells. <i>PLoS Biology</i> , 2004, 2, e423. | 5.6 | 243 |
| 225 | Site2genome: locating short DNA sequences in whole genomes. <i>Bioinformatics</i> , 2004, 20, 1468-1469. | 4.1 | 3 |
| 226 | Over 20% of human transcripts might form sense-antisense pairs. <i>Nucleic Acids Research</i> , 2004, 32, 4812-4820. | 14.5 | 287 |
| 227 | Integration of the Rat Recombination and EST Maps in the Rat Genomic Sequence and Comparative Mapping Analysis With the Mouse Genome. <i>Genome Research</i> , 2004, 14, 758-765. | 5.5 | 22 |
| 228 | Characterization of a human colonic cDNA encoding a structurally novel urea transporter, hUT-A6. <i>American Journal of Physiology - Cell Physiology</i> , 2004, 287, C1087-C1093. | 4.6 | 60 |
| 229 | An online database for the detection of novel archaeal sequences in human ESTs. <i>Bioinformatics</i> , 2004, 20, 2361-2362. | 4.1 | 1 |
| 230 | New human and mouse microRNA genes found by homology search. <i>FEBS Journal</i> , 2005, 272, 59-73. | 4.7 | 268 |
| 231 | Identification of putative homology between horse microsatellite flanking sequences and crossâ€‘species ESTs, mRNAs and genomic sequences. <i>Animal Genetics</i> , 2004, 35, 28-33. | 1.7 | 17 |
| 232 | High-throughput screening of genome fragments bound to differentially acetylated histones. <i>Genes To Cells</i> , 2004, 9, 1167-1174. | 1.2 | 10 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 233 | The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535. | 27.8 | 298 |
| 234 | Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521. | 27.8 | 1,943 |
| 235 | A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722. | 27.8 | 391 |
| 236 | The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994. | 27.8 | 156 |
| 237 | Retrotransposition of Alu elements: how many sources?. <i>Trends in Genetics</i> , 2004, 20, 464-467. | 6.7 | 103 |
| 238 | Mammalian phylogenomics comes of age. <i>Trends in Genetics</i> , 2004, 20, 631-639. | 6.7 | 327 |
| 239 | Comprehensive analysis of keratin gene clusters in humans and rodents. <i>European Journal of Cell Biology</i> , 2004, 83, 19-26. | 3.6 | 176 |
| 240 | Improved hit criteria for DNA local alignment. <i>BMC Bioinformatics</i> , 2004, 5, 149. | 2.6 | 49 |
| 241 | Combining gene expression data from different generations of oligonucleotide arrays. <i>BMC Bioinformatics</i> , 2004, 5, 159. | 2.6 | 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. | 2.8 | 25 |
| 243 | A genome-wide screen identifies a single β -defensin gene cluster in the chicken: implications for the origin and evolution of mammalian defensins. <i>BMC Genomics</i> , 2004, 5, 56. | 2.8 | 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. | 2.8 | 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. | 2.8 | 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. | 3.8 | 19 |
| 248 | Evolutionary implication of human endogenous retrovirus HERV-H family. <i>Journal of Human Genetics</i> , 2004, 49, 215-219. | 2.3 | 8 |
| 249 | Comprehensive association analysis of APOE regulatory region polymorphisms in Alzheimer disease. <i>Neurogenetics</i> , 2004, 5, 201-208. | 1.4 | 22 |
| 250 | An interactive bovine in silico SNP database (IBISS). <i>Mammalian Genome</i> , 2004, 15, 819-827. | 2.2 | 60 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 251 | Comparative genomics: methods and applications. Die Naturwissenschaften, 2004, 91, 405-21. | 1.6 | 20 |
| 252 | Open reading frame sequencing and structure-based alignment of polypeptides encoded by RT1-Bb, RT1-Ba, RT1-Db, and RT1-Da alleles. Immunogenetics, 2004, 56, 585-596. | 2.4 | 15 |
| 253 | A digenic cause of cleft lip in A-strain mice and definition of candidate genes for the two loci. Birth Defects Research Part A: Clinical and Molecular Teratology, 2004, 70, 509-518. | 1.6 | 35 |
| 254 | Recent developments in computational approaches for uncovering genomic homology. BioEssays, 2004, 26, 1225-1235. | 2.5 | 22 |
| 255 | Prognostic classification of relapsing favorable histology Wilms tumor using cDNA microarray expression profiling and support vector machines. Genes Chromosomes and Cancer, 2004, 41, 65-79. | 2.8 | 48 |
| 256 | PromoLign: A database for upstream region analysis and SNPs. Human Mutation, 2004, 23, 534-539. | 2.5 | 33 |
| 257 | Two-color multiplex ligation-dependent probe amplification: Detecting genomic rearrangements in hereditary multiple exostoses. Human Mutation, 2004, 24, 86-92. | 2.5 | 142 |
| 258 | Characterization of a mutagenic B1 retrotransposon insertion in the jittery mouse. Human Mutation, 2004, 24, 9-13. | 2.5 | 21 |
| 259 | Gene expression analysis in the hippocampal formation of tree shrews chronically treated with cortisol. Journal of Neuroscience Research, 2004, 78, 702-710. | 2.9 | 33 |
| 260 | MAGIC Database and Interfaces: An Integrated Package for Gene Discovery and Expression. Comparative and Functional Genomics, 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. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 116-129. | 3.0 | 88 |
| 263 | Xpro: database of eukaryotic protein-encoding genes. Nucleic Acids Research, 2004, 32, 59D-63. | 14.5 | 21 |
| 264 | A metric model of amino acid substitution. Bioinformatics, 2004, 20, 1214-1221. | 4.1 | 35 |
| 265 | Evolution of the tumor suppressor BRCA1 locus in primates: implications for cancer predisposition. Human Molecular Genetics, 2004, 13, 2737-2751. | 2.9 | 88 |
| 266 | Creation of the whole human genome microarray. Expert Review of Proteomics, 2004, 1, 19-28. | 3.0 | 33 |
| 267 | Genome-wide mutagenesis of Zea mays L. using RescueMu transposons. Genome Biology, 2004, 5, R82. | 9.6 | 66 |
| 268 | Alternative splicing of mouse transcription factors affects their DNA-binding domain architecture and is tissue specific. Genome Biology, 2004, 5, R75. | 9.6 | 67 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 269 | Evolutionary conservation and selection of human disease gene orthologs in the rat and mouse genomes. <i>Genome Biology</i> , 2004, 5, R47. | 9.6 | 116 |
| 270 | ELXR: a resource for rapid exon-directed sequence analysis. <i>Genome Biology</i> , 2004, 5, R36. | 9.6 | 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. | 2.2 | 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. | 2.1 | 33 |
| 273 | Odorant and vomeronasal receptor genes in two mouse genome assemblies. <i>Genomics</i> , 2004, 83, 802-811. | 2.9 | 149 |
| 274 | Comparative sequence analysis of the Gdf6 locus reveals a duplicon-mediated chromosomal rearrangement in rodents and rapidly diverging coding and regulatory sequences. <i>Genomics</i> , 2004, 84, 814-823. | 2.9 | 8 |
| 275 | Interpreting mammalian evolution using Fugu genome comparisons. <i>Genomics</i> , 2004, 84, 890-895. | 2.9 | 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. | 2.9 | 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. | 2.3 | 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. | 2.7 | 98 |
| 279 | A transcriptional profile of human fetal cartilage. <i>Matrix Biology</i> , 2004, 23, 299-307. | 3.6 | 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. | 4.2 | 36 |
| 281 | Analysis of the Human Alu Ya-lineage. <i>Journal of Molecular Biology</i> , 2004, 342, 109-118. | 4.2 | 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. | 7.1 | 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. | 5.5 | 210 |
| 284 | VISTA: computational tools for comparative genomics. <i>Nucleic Acids Research</i> , 2004, 32, W273-W279. | 14.5 | 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. | 5.5 | 311 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 287 | Bioinformatics and Management Science: Some Common Tools and Techniques. Operations Research, 2004, 52, 165-190. | 1.9 | 15 |
| 288 | Identification of the major promoter and non-coding exons of the human arylamine N-acetyltransferase 1 gene (NAT1). Pharmacogenetics and Genomics, 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. Nucleic Acids Research, 2004, 33, D141-D146. | 14.5 | 140 |
| 290 | Detecting Copy Number Changes in Genomic DNA: MAPH and MLPA. Methods in Cell Biology, 2004, 75, 751-768. | 1.1 | 25 |
| 291 | Good spaced seeds for homology search. , 0, , . | | 0 |
| 292 | Parkin and relatives: the RBR family of ubiquitin ligases. Physiological Genomics, 2004, 17, 253-263. | 2.3 | 103 |
| 293 | Searching WormBase for Information AboutCaenorhabditis elegans. Current Protocols in Bioinformatics, 2004, 6, 1.8.1. | 25.8 | 1 |
| 294 | Rapid evolution and diversification of mammalian β -defensins as revealed by comparative analysis of rodent and primate genes. Physiological Genomics, 2004, 20, 1-11. | 2.3 | 145 |
| 295 | Large-scale gene discovery in human airway epithelia reveals novel transcripts. Physiological Genomics, 2004, 17, 69-77. | 2.3 | 23 |
| 296 | Gene structure prediction in plant genomes. , 2005, , . | | 1 |
| 297 | Databases for Comparative Analysis of Human-Mouse Orthologous Alternative Splicing. Lecture Notes in Computer Science, 2005, , 123-131. | 1.3 | 3 |
| 298 | AN ASSESSMENT OF A METRIC SPACE DATABASE INDEX TO SUPPORT SEQUENCE HOMOLOGY. International Journal on Artificial Intelligence Tools, 2005, 14, 867-885. | 1.0 | 12 |
| 299 | Neighboring-Nucleotide Effects on the Mutation Patterns of the Rice Genome. Genomics, Proteomics and Bioinformatics, 2005, 3, 158-168. | 6.9 | 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. Nucleic Acids Research, 2005, 33, W56-W64. | 14.5 | 32 |
| 303 | Efficient q-Gram Filters for Finding All $\hat{\mu}$ -Matches over a Given Length. Lecture Notes in Computer Science, 2005, , 189-203. | 1.3 | 21 |
| 304 | Genomic rearrangements by LINE-1 insertion-mediated deletion in the human and chimpanzee lineages. Nucleic Acids Research, 2005, 33, 4040-4052. | 14.5 | 127 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 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. | 1.4 | 64 |
| 306 | A newly discovered human $\hat{\pm}$ -globin gene. <i>Blood</i> , 2005, 106, 1466-1472. | 1.4 | 59 |
| 307 | Characterization of CA XV, a new GPI-anchored form of carbonic anhydrase. <i>Biochemical Journal</i> , 2005, 392, 83-92. | 3.7 | 152 |
| 308 | Comparisons of Long Genomic Sequences. <i>Chapman & 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. | 0.8 | 13 |
| 311 | Designing seeds for similarity search in genomic DNA. <i>Journal of Computer and System Sciences</i> , 2005, 70, 342-363. | 1.2 | 64 |
| 312 | Vector seeds: An extension to spaced seeds. <i>Journal of Computer and System Sciences</i> , 2005, 70, 364-380. | 1.2 | 42 |
| 313 | A mobile element based phylogeny of Old World monkeys. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 872-880. | 2.7 | 90 |
| 314 | Tri-nucleotide repeats and their association with genes in rice genome. <i>BioSystems</i> , 2005, 82, 248-256. | 2.0 | 5 |
| 315 | Engineering a software tool for gene structure prediction in higher organisms. <i>Information and Software Technology</i> , 2005, 47, 965-978. | 4.4 | 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. | 2.3 | 14 |
| 317 | Complete reannotation of the Arabidopsis genome: methods, tools, protocols and the final release. <i>BMC Biology</i> , 2005, 3, 7. | 3.8 | 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. | 21.4 | 38 |
| 320 | Computational screening of conserved genomic DNA in search of functional noncoding elements. <i>Nature Methods</i> , 2005, 2, 535-545. | 19.0 | 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. | 2.8 | 75 |
| 322 | Retroviral insertional mutagenesis: past, present and future. <i>Oncogene</i> , 2005, 24, 7656-7672. | 5.9 | 250 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 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. | 2.4 | 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. | 3.7 | 149 |
| 325 | Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731. | 27.8 | 85 |
| 326 | Transcription of mammalian messenger RNAs by a nuclear RNA polymerase of mitochondrial origin. <i>Nature</i> , 2005, 436, 735-739. | 27.8 | 61 |
| 327 | DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555. | 27.8 | 53 |
| 328 | Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87. | 27.8 | 2,222 |
| 329 | Natural selection on protein-coding genes in the human genome. <i>Nature</i> , 2005, 437, 1153-1157. | 27.8 | 718 |
| 330 | $\hat{\text{I}}^3\text{N}$ -crystallin and the evolution of the $\hat{\text{I}}^2\hat{\text{I}}^3$ -crystallin superfamily in vertebrates. <i>FEBS Journal</i> , 2005, 272, 2276-2291. | 4.7 | 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. | 2.0 | 0 |
| 332 | Tissue distribution of a human Cav1.2 $\hat{\text{I}}_{\pm 1}$ subunit splice variant with a 75bp insertion $\hat{\text{I}}^{\dagger}$. <i>Cell Calcium</i> , 2005, 38, 11-21. | 2.4 | 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. | 6.4 | 101 |
| 335 | A limited role for balancing selection. <i>Trends in Genetics</i> , 2005, 21, 30-32. | 6.7 | 103 |
| 336 | Refined repetitive sequence searches utilizing a fast hash function and cross species information retrievals. <i>BMC Bioinformatics</i> , 2005, 6, 111. | 2.6 | 10 |
| 337 | A multistep bioinformatic approach detects putative regulatory elements in gene promoters. <i>BMC Bioinformatics</i> , 2005, 6, 121. | 2.6 | 18 |
| 338 | Satellog: a database for the identification and prioritization of satellite repeats in disease association studies. <i>BMC Bioinformatics</i> , 2005, 6, 145. | 2.6 | 16 |
| 339 | A computational approach for identifying pathogenicity islands in prokaryotic genomes. <i>BMC Bioinformatics</i> , 2005, 6, 184. | 2.6 | 55 |
| 340 | A method for finding single-nucleotide polymorphisms with allele frequencies in sequences of deep coverage. <i>BMC Bioinformatics</i> , 2005, 6, 220. | 2.6 | 10 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 341 | ASPIC: a novel method to predict the exon-intron structure of a gene that is optimally compatible to a set of transcript sequences. BMC Bioinformatics, 2005, 6, 244. | 2.6 | 32 |
| 342 | A method of precise mRNA/DNA homology-based gene structure prediction. BMC Bioinformatics, 2005, 6, 261. | 2.6 | 6 |
| 343 | Statistical Viewer: a tool to upload and integrate linkage and association data as plots displayed within the Ensembl genome browser. BMC Bioinformatics, 2005, 6, 95. | 2.6 | 11 |
| 344 | Phylogenomic approaches to common problems encountered in the analysis of low copy repeats: the sulfotransferase 1A gene family example. BMC Evolutionary Biology, 2005, 5, 22. | 3.2 | 21 |
| 345 | A systematic search for new mammalian noncoding RNAs indicates little conserved intergenic transcription. BMC Genomics, 2005, 6, 104. | 2.8 | 72 |
| 346 | Construction and characterization of a genomic BAC library for the Mus m. musculus mouse subspecies (PWD/Ph inbred strain). BMC Genomics, 2005, 6, 161. | 2.8 | 12 |
| 347 | Characterization of 954 bovine full-CDS cDNA sequences. BMC Genomics, 2005, 6, 166. | 2.8 | 26 |
| 348 | Efficient single nucleotide polymorphism discovery in laboratory rat strains using wild rat-derived SNP candidates. BMC Genomics, 2005, 6, 170. | 2.8 | 17 |
| 349 | Identification of functional SNPs in the 5-prime flanking sequences of human genes. BMC Genomics, 2005, 6, 18. | 2.8 | 44 |
| 350 | A method for accurate detection of genomic microdeletions using real-time quantitative PCR. BMC Genomics, 2005, 6, 180. | 2.8 | 89 |
| 351 | Genome-scale analysis of positional clustering of mouse testis-specific genes. BMC Genomics, 2005, 6, 7. | 2.8 | 47 |
| 352 | Linkage mapping bovine EST-based SNP. BMC Genomics, 2005, 6, 74. | 2.8 | 58 |
| 353 | Molecular profile of catabolic versus anabolic treatment regimens of parathyroid hormone (PTH) in rat bone: An analysis by DNA microarray. Journal of Cellular Biochemistry, 2005, 95, 403-418. | 2.6 | 92 |
| 354 | Identification and validation of novelERBB2(HER2,NEU) targets including genes involved in angiogenesis. International Journal of Cancer, 2005, 114, 590-597. | 5.1 | 53 |
| 355 | Investigations of the genomic region that contains theclf1 mutation, a causal gene in multifactorial cleft lip and palate in mice. Birth Defects Research Part A: Clinical and Molecular Teratology, 2005, 73, 103-113. | 1.6 | 54 |
| 356 | Analysis ofNF1 transcriptional regulatory elements. American Journal of Medical Genetics, Part A, 2005, 137A, 130-135. | 1.2 | 10 |
| 357 | The synthetic form of a novel chicken γ -defensin identified in silico is predominantly active against intestinal pathogens. Immunogenetics, 2005, 57, 90-98. | 2.4 | 74 |
| 358 | Validation of mRNA/EST-based gene predictions in human Xp11.4 revealed differences to the organization of the orthologous mouse locus. Mammalian Genome, 2005, 16, 934-941. | 2.2 | 1 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 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. Theoretical and Applied Genetics, 2005, 111, 1596-1607. | 3.6 | 36 |
| 360 | DING proteins are from <i>Pseudomonas</i> . FEMS Microbiology Letters, 2005, 252, 215-222. | 1.8 | 20 |
| 361 | Cataloging transcription factor and major signaling molecule genes for functional genomic studies in <i>Ciona intestinalis</i> . Development Genes and Evolution, 2005, 215, 580-596. | 0.9 | 22 |
| 362 | Analysis of porcine MHC expression profile. Science Bulletin, 2005, 50, 880-890. | 1.7 | 2 |
| 363 | Test Data Sets and Evaluation of Gene Prediction Programs on the Rice Genome. Journal of Computer Science and Technology, 2005, 20, 446-453. | 1.5 | 14 |
| 364 | Analysis of 70,000 EST sequences to study divergence between two closely related <i>Populus</i> species. Tree Genetics and Genomes, 2005, 1, 109-115. | 1.6 | 11 |
| 365 | Characterisation and application of a bovine U6 promoter for expression of short hairpin RNAs. BMC Biotechnology, 2005, 5, 13. | 3.3 | 26 |
| 366 | Exploring hepatic hormone actions using a compilation of gene expression profiles. BMC Physiology, 2005, 5, 8. | 3.6 | 39 |
| 367 | The Genomes of <i>Oryza sativa</i> : A History of Duplications. PLoS Biology, 2005, 3, e38. | 5.6 | 808 |
| 369 | Restriction fragment fingerprinting software. , 2005, , . | | 0 |
| 370 | Tools and strategies for physiological genomics: the Rat Genome Database. Physiological Genomics, 2005, 23, 246-256. | 2.3 | 25 |
| 371 | Learning Interpretable SVMs for Biological Sequence Classification. Lecture Notes in Computer Science, 2005, , 389-407. | 1.3 | 24 |
| 372 | Mapping of genetic determinants of the sympathoneural response to stress. Physiological Genomics, 2005, 20, 183-187. | 2.3 | 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. Bioinformatics, 2005, 21, 2867-2874. | 4.1 | 29 |
| 375 | LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. Bioinformatics, 2005, 21, 2814-2820. | 4.1 | 202 |
| 376 | The Evolution of Transcription-Initiation Sites. Molecular Biology and Evolution, 2005, 22, 1137-1146. | 8.9 | 60 |
| 377 | Differential Effects of Estrogen and Raloxifene on Messenger RNA and Matrix Metalloproteinase 2 Activity in the Rat Uterus. Biology of Reproduction, 2005, 72, 830-841. | 2.7 | 37 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 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. | 3.2 | 114 |
| 379 | Global analysis of IL-2 target genes: identification of chromosomal clusters of expressed genes. <i>International Immunology</i> , 2005, 17, 1009-1021. | 4.0 | 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. | 3.4 | 80 |
| 381 | A retrocopy of a gene can functionally displace the source gene in evolution. <i>Nucleic Acids Research</i> , 2005, 33, 6654-6661. | 14.5 | 41 |
| 382 | Comparative EST Analyses in Plant Systems. <i>Methods in Enzymology</i> , 2005, 395, 400-418. | 1.0 | 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. | 6.6 | 56 |
| 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. | 5.5 | 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. | 5.5 | 38 |
| 386 | ItC31 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. | 5.5 | 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. | 5.5 | 30 |
| 389 | A Genetic Linkage Map for the Tiger Pufferfish, <i>Takifugu rubripes</i> . <i>Genetics</i> , 2005, 171, 227-238. | 2.9 | 93 |
| 390 | Assembly of polymorphic genomes: Algorithms and application to <i>Ciona savignyi</i> . <i>Genome Research</i> , 2005, 15, 1127-1135. | 5.5 | 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. | 3.2 | 85 |
| 392 | The evolutionary fate of MULE-mediated duplications of host gene fragments in rice. <i>Genome Research</i> , 2005, 15, 1292-1297. | 5.5 | 210 |
| 393 | Multiple Fates of L1 Retrotransposition Intermediates in Cultured Human Cells. <i>Molecular and Cellular Biology</i> , 2005, 25, 7780-7795. | 2.3 | 255 |
| 394 | Identification and characterization of the peroxiredoxin gene family in chickens. <i>Poultry Science</i> , 2005, 84, 1432-1438. | 3.4 | 19 |
| 395 | Inferring gene transcriptional modulatory relations: a genetical genomics approach. <i>Human Molecular Genetics</i> , 2005, 14, 1119-1125. | 2.9 | 76 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 396 | Large-scale structure of genomic methylation patterns. <i>Genome Research</i> , 2005, 16, 157-163. | 5.5 | 325 |
| 397 | ECgene: Genome-based EST clustering and gene modeling for alternative splicing. <i>Genome Research</i> , 2005, 15, 566-576. | 5.5 | 86 |
| 398 | Direct crossregulation between retinoic acid receptor $\hat{1}^2$ and Hox genes during hindbrain segmentation. <i>Development (Cambridge)</i> , 2005, 132, 503-513. | 2.5 | 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. | 8.9 | 31 |
| 400 | RASE: recognition of alternatively spliced exons in <i>C.elegans</i> . <i>Bioinformatics</i> , 2005, 21, i369-i377. | 4.1 | 109 |
| 401 | Pooled genomic indexing of rhesus macaque. <i>Genome Research</i> , 2005, 15, 292-301. | 5.5 | 14 |
| 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. | 7.1 | 203 |
| 403 | A large-scale analysis of mRNA polyadenylation of human and mouse genes. <i>Nucleic Acids Research</i> , 2005, 33, 201-212. | 14.5 | 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. | 7.1 | 75 |
| 405 | AnoEST: Toward <i>A. gambiae</i> functional genomics. <i>Genome Research</i> , 2005, 15, 893-899. | 5.5 | 19 |
| 406 | Genome-wide assembly and analysis of alternative transcripts in mouse. <i>Genome Research</i> , 2005, 15, 748-754. | 5.5 | 49 |
| 407 | Using multiple alignments to improve seeded local alignment algorithms. <i>Nucleic Acids Research</i> , 2005, 33, 4563-4577. | 14.5 | 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. | 14.5 | 222 |
| 409 | Quick, Practical Selection of Effective Seeds for Homology Search. <i>Journal of Computational Biology</i> , 2005, 12, 1137-1152. | 1.6 | 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. | 2.0 | 6 |
| 412 | ESTmapper: Efficiently Aligning DNA Sequences to Genomes. , 0, , . | | 4 |
| 413 | Cross-species analysis of the mammalian $\hat{1}^2$ -defensin gene family: presence of syntenic gene clusters and preferential expression in the male reproductive tract. <i>Physiological Genomics</i> , 2005, 23, 5-17. | 2.3 | 191 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 414 | Symmetrical base preferences surrounding HIV-1, avian sarcoma/leukosis virus, and murine leukemia virus integration sites. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6103-6107. | 7.1 | 158 |
| 415 | Complex genomic rearrangements lead to novel primate gene function. Genome Research, 2005, 15, 343-351. | 5.5 | 104 |
| 416 | EVOPRINTER, a multigenomic comparative tool for rapid identification of functionally important DNA. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14700-14705. | 7.1 | 62 |
| 417 | MAASE: An alternative splicing database designed for supporting splicing microarray applications. Rna, 2005, 11, 1767-1776. | 3.5 | 23 |
| 418 | Using shared genomic synteny and shared protein functions to enhance the identification of orthologous gene pairs. Bioinformatics, 2005, 21, 703-710. | 4.1 | 85 |
| 419 | Designing Multiple Simultaneous Seeds for DNA Similarity Search. Journal of Computational Biology, 2005, 12, 847-861. | 1.6 | 46 |
| 420 | High-Performance Direct Pairwise Comparison of Large Genomic Sequences. , 0, , . | | 1 |
| 421 | Genome-Wide Screening for Target Regions of Histone Deacetylases in Cardiomyocytes. Circulation Research, 2005, 97, 210-218. | 4.5 | 26 |
| 423 | Large-Scale Analysis of Adeno-Associated Virus Vector Integration Sites in Normal Human Cells. Journal of Virology, 2005, 79, 11434-11442. | 3.4 | 148 |
| 424 | Substitution Rate and Structural Divergence of 5'UTR Evolution: Comparative Analysis Between Human and Cynomolgus Monkey cDNAs. Molecular Biology and Evolution, 2005, 22, 1976-1982. | 8.9 | 21 |
| 425 | MuPlex: multi-objective multiplex PCR assay design. Nucleic Acids Research, 2005, 33, W544-W547. | 14.5 | 76 |
| 426 | Gene identification in novel eukaryotic genomes by self-training algorithm. Nucleic Acids Research, 2005, 33, 6494-6506. | 14.5 | 746 |
| 427 | Identification of transposable elements using multiple alignments of related genomes. Genome Research, 2005, 16, 260-270. | 5.5 | 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. Bioinformatics, 2005, 21, 1859-1875. | 4.1 | 2,121 |
| 430 | JIGSAW: integration of multiple sources of evidence for gene prediction. Bioinformatics, 2005, 21, 3596-3603. | 4.1 | 147 |
| 431 | Coupling of Metabotropic Glutamate Receptor 8 to N-Type Ca ²⁺ Channels in Rat Sympathetic Neurons. Molecular Pharmacology, 2005, 67, 1840-1851. | 2.3 | 22 |
| 432 | Comparing low coverage random shotgun sequence data from Brassica oleracea and Oryza sativa genome sequence for their ability to add to the annotation of Arabidopsis thaliana. Genome Research, 2005, 15, 496-504. | 5.5 | 27 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 433 | Under the genomic radar: The Stealth model of Alu amplification. <i>Genome Research</i> , 2005, 15, 655-664. | 5.5 | 65 |
| 434 | Survey of allelic expression using EST mining. <i>Genome Research</i> , 2005, 15, 1584-1591. | 5.5 | 115 |
| 435 | The Institute for Genomic Research Osa1 Rice Genome Annotation Database. <i>Plant Physiology</i> , 2005, 138, 18-26. | 4.8 | 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. | 8.9 | 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. | 4.1 | 31 |
| 439 | Multiple mechanisms are implicated in the generation of 5q35 microdeletions in Sotos syndrome. <i>Journal of Medical Genetics</i> , 2005, 42, 307-313. | 3.2 | 60 |
| 440 | ASePCR: alternative splicing electronic RT-PCR in multiple tissues and organs. <i>Nucleic Acids Research</i> , 2005, 33, W681-W685. | 14.5 | 9 |
| 441 | Retropseudogenes derived from the human Ro/SS-A autoantigen-associated hY RNAs. <i>Nucleic Acids Research</i> , 2005, 33, 2032-2041. | 14.5 | 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. | 14.5 | 89 |
| 443 | miBLAST: scalable evaluation of a batch of nucleotide sequence queries with BLAST. <i>Nucleic Acids Research</i> , 2005, 33, 4335-4344. | 14.5 | 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. | 14.5 | 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. | 14.5 | 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. | 3.4 | 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. | 5.5 | 3,517 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 451 | Evolution of the secretoglobins: a genomic and proteomic view. Biological Journal of the Linnean Society, 2005, 84, 493-501. | 1.6 | 18 |
| 452 | An Integrated Database of the Ascidian, <i>Ciona intestinalis</i> : Towards Functional Genomics. Zoological Science, 2005, 22, 837-843. | 0.7 | 173 |
| 453 | Nine unknown rearrangements in 16p13.3 and 11p15.4 causing α - and β -thalassaemia characterised by high resolution multiplex ligation-dependent probe amplification. Journal of Medical Genetics, 2005, 42, 922-931. | 3.2 | 213 |
| 454 | Composite genome map and recombination parameters derived from three archetypal lineages of <i>Toxoplasma gondii</i> . Nucleic Acids Research, 2005, 33, 2980-2992. | 14.5 | 147 |
| 455 | Computational prediction of miRNAs in <i>Arabidopsis thaliana</i> . Genome Research, 2005, 15, 78-91. | 5.5 | 324 |
| 456 | Finding Keywords for Intergenic and Gene Regions for Human Genome. Nucleosides, Nucleotides and Nucleic Acids, 2005, 24, 191-198. | 1.1 | 0 |
| 457 | Cloning and characterization a novel human 1-acyl-sn-glycerol-3-phosphate acyltransferase gene AGPAT7. DNA Sequence, 2005, 16, 386-390. | 0.7 | 35 |
| 458 | EST-Based Analysis of Gene Expression in the Human Cochlea. , 2005, 2005, . | | 0 |
| 459 | Alu Retrotransposition-mediated Deletion. Journal of Molecular Biology, 2005, 348, 791-800. | 4.2 | 114 |
| 460 | SVA Elements: A Hominid-specific Retroposon Family. Journal of Molecular Biology, 2005, 354, 994-1007. | 4.2 | 319 |
| 461 | Genome-wide localization of histone 4 arginine 3 methylation in a differentiation primed myeloid leukemia cell line. Immunobiology, 2005, 210, 141-152. | 1.9 | 11 |
| 462 | SVM classification of human intergenic and gene sequences. Mathematical Biosciences, 2005, 195, 168-178. | 1.9 | 5 |
| 463 | Optimised real-time quantitative PCR assays for RANKL regulated genes. Molecular and Cellular Probes, 2005, 19, 119-126. | 2.1 | 22 |
| 464 | Evaluation of EST-data using the genome assembly. Biochemical and Biophysical Research Communications, 2005, 331, 1566-1576. | 2.1 | 14 |
| 465 | Identification and analysis of the human neural polypyrimidine tract binding protein (nPTB) gene promoter region. Gene, 2005, 356, 11-18. | 2.2 | 9 |
| 466 | Endogenous retrovirus long terminal repeats as ready-to-use mobile promoters: The case of primate β 2GAL-T5. Gene, 2005, 364, 2-12. | 2.2 | 50 |
| 467 | Chromosomal aberrations induced by double strand DNA breaks. DNA Repair, 2005, 4, 1038-1046. | 2.8 | 69 |
| 468 | Comparison of the current RefSeq, Ensembl and EST databases for counting genes and gene discovery. FEBS Letters, 2005, 579, 690-698. | 2.8 | 31 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 469 | Genome-wide prediction of human VNTRs. <i>Genomics</i> , 2005, 85, 24-35. | 2.9 | 47 |
| 470 | Application of functional genomic technologies in a mouse model of retinal degeneration. <i>Genomics</i> , 2005, 85, 309-321. | 2.9 | 9 |
| 471 | Detecting false expression signals in high-density oligonucleotide arrays by an in silico approach. <i>Genomics</i> , 2005, 85, 297-308. | 2.9 | 50 |
| 472 | Discovery of 342 putative new genes from the analysis of 5' end-sequenced full-length-enriched cDNA human transcripts. <i>Genomics</i> , 2005, 85, 739-751. | 2.9 | 5 |
| 473 | Nested genes in the human genome. <i>Genomics</i> , 2005, 86, 414-422. | 2.9 | 71 |
| 474 | Comparative genomic analysis of human and chimpanzee proteases. <i>Genomics</i> , 2005, 86, 638-647. | 2.9 | 78 |
| 475 | The HSP90 family of genes in the human genome: Insights into their divergence and evolution. <i>Genomics</i> , 2005, 86, 627-637. | 2.9 | 317 |
| 476 | Computational analysis of protein tyrosine phosphatases: practical guide to bioinformatics and data resources. <i>Methods</i> , 2005, 35, 90-114. | 3.8 | 40 |
| 477 | Computational searches for splicing signals. <i>Methods</i> , 2005, 37, 292-305. | 3.8 | 50 |
| 478 | Identification of Chicken Transmembrane Channel-like (TMC) genes: Expression analysis in the cochlea. <i>Neuroscience</i> , 2005, 132, 1115-1122. | 2.3 | 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. | 3.0 | 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. | 14.5 | 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. | 12.6 | 221 |
| 485 | Genetic Analysis and Attribution of Microbial Forensics Evidence. <i>Critical Reviews in Microbiology</i> , 2005, 31, 233-254. | 6.1 | 66 |
| 486 | A novel approach to identifying regulatory motifs in distantly related genomes. <i>Genome Biology</i> , 2005, 6, R113. | 9.6 | 12 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 487 | Genome-wide promoter extraction and analysis in human, mouse, and rat. <i>Genome Biology</i> , 2005, 6, R72. | 9.6 | 60 |
| 488 | Transcript copy number estimation using a mouse whole-genome oligonucleotide microarray. <i>Genome Biology</i> , 2005, 6, R61. | 9.6 | 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. | 9.6 | 41 |
| 490 | Genome-wide prediction and identification of cis-natural antisense transcripts in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2005, 6, R30. | 9.6 | 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. | 9.6 | 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. | 9.6 | 188 |
| 493 | Ancient genomic architecture for mammalian olfactory receptor clusters. <i>Genome Biology</i> , 2006, 7, R88. | 9.6 | 47 |
| 494 | Prediction of trans-antisense transcripts in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2006, 7, R92. | 9.6 | 72 |
| 495 | Sex-specific expression of alternative transcripts in <i>Drosophila</i> . <i>Genome Biology</i> , 2006, 7, R79. | 9.6 | 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. | 9.6 | 162 |
| 497 | Reference based annotation with GeneMapper. <i>Genome Biology</i> , 2006, 7, R29. | 9.6 | 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. | 9.6 | 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. | 8.8 | 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. | 9.6 | 263 |
| 501 | Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. <i>Genome Biology</i> , 2006, 7, S5. | 9.6 | 15 |
| 502 | Exogean: a framework for annotating protein-coding genes in eukaryotic genomic DNA. <i>Genome Biology</i> , 2006, 7, S7. | 9.6 | 14 |
| 503 | JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. <i>Genome Biology</i> , 2006, 7, S9. | 9.6 | 61 |
| 504 | Identifying repeat domains in large genomes. <i>Genome Biology</i> , 2006, 7, R7. | 9.6 | 31 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 505 | Comparisons of Annotation Predictions for Affymetrix GeneChips??. Applied Bioinformatics, 2006, 5, 237-248. | 1.6 | 4 |
| 506 | Alternative mRNA Polyadenylation Can Potentially Affect Detection of Gene Expression by Affymetrix GeneChip?? Arrays. Applied Bioinformatics, 2006, 5, 249-253. | 1.6 | 15 |
| 508 | Exploring I/O Strategies for Parallel Sequence-Search Tools with S3aSim. , 0, , . | | 9 |
| 509 | fjoin: Simple and Efficient Computation of Feature Overlaps. Journal of Computational Biology, 2006, 13, 1457-1464. | 1.6 | 34 |
| 510 | Efficient q-Gram Filters for Finding All $\hat{\mu}$ -Matches over a Given Length. Journal of Computational Biology, 2006, 13, 296-308. | 1.6 | 90 |
| 511 | Parallel Genomic Sequence-Searching on an Ad-Hoc Grid: Experiences, Lessons Learned, and Implications. , 2006, , . | | 7 |
| 512 | Ultra-high resolution array painting facilitates breakpoint sequencing. Journal of Medical Genetics, 2006, 44, 51-58. | 3.2 | 26 |
| 513 | A hitchhiker's guide to expressed sequence tag (EST) analysis. Briefings in Bioinformatics, 2006, 8, 6-21. | 6.5 | 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. Plant Cell, 2006, 18, 1791-1802. | 6.6 | 207 |
| 516 | Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. American Journal of Human Genetics, 2006, 79, 500-513. | 6.2 | 261 |
| 517 | Comparative Analysis of Eubacterial DNA Polymerase III Alpha Subunits. Genomics, Proteomics and Bioinformatics, 2006, 4, 203-211. | 6.9 | 28 |
| 518 | Characterization of Phagosome Trafficking and Identification of PhoP-Regulated Genes Important for Survival of Yersinia pestis in Macrophages. Infection and Immunity, 2006, 74, 3727-3741. | 2.2 | 131 |
| 519 | Whole Genome Alignment with BLAST on Grid Environment. , 2006, , . | | 1 |
| 520 | C. elegans: an invaluable model organism for the proteomics studies of the cholesterol-mediated signalling pathway. Expert Review of Proteomics, 2006, 3, 439-453. | 3.0 | 15 |
| 521 | Asymptotic behaviour and optimal word size for exact and approximate word matches between random sequences. BMC Bioinformatics, 2006, 7, S21. | 2.6 | 22 |
| 522 | Positive selection on the nonhomologous end-joining factor Cernunnos-XLF in the human lineage. Biology Direct, 2006, 1, 15. | 4.6 | 12 |
| 523 | Bioinformatics Packages for Sequence Analysis. Applied Mycology and Biotechnology, 2006, 6, 143-160. | 0.3 | 8 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 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. International Journal of Antimicrobial Agents, 2006, 27, 138-151. | 2.5 | 94 |
| 526 | A Deterministic Finite Automaton for Faster Protein Hit Detection in BLAST. Journal of Computational Biology, 2006, 13, 965-978. | 1.6 | 31 |
| 527 | High-Performance Direct Pairwise Comparison of Large Genomic Sequences. IEEE Transactions on Parallel and Distributed Systems, 2006, 17, 764-772. | 5.6 | 6 |
| 528 | Identification and characterization of an interleukin-15 homologue from <i>Tetraodon nigroviridis</i> . Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2006, 143, 335-343. | 1.6 | 36 |
| 529 | Origin and diversification of minisatellites derived from human Alu sequences. Gene, 2006, 365, 21-26. | 2.2 | 18 |
| 530 | Identification of highly specific localized sequence motifs in human ribosomal protein gene promoters. Gene, 2006, 365, 48-56. | 2.2 | 20 |
| 531 | mNSC1 shows no evidence of protein-coding capacity. Gene, 2006, 370, 83-85. | 2.2 | 2 |
| 532 | A novel primate specific gene, CEI, is located in the homeobox gene IRXA2 promoter in <i>Homo sapiens</i> . Gene, 2006, 371, 167-173. | 2.2 | 8 |
| 533 | Identification and analysis of putative regulatory sequences for the MYF5/MYF6 locus in different vertebrate species. Gene, 2006, 379, 141-147. | 2.2 | 33 |
| 534 | Integration Specificity of Phage ϕ C31 Integrase in the Human Genome. Journal of Molecular Biology, 2006, 357, 28-48. | 4.2 | 228 |
| 535 | Use of competitive DNA hybridization to identify differences in the genomes of bacteria. Journal of Microbiological Methods, 2006, 66, 321-330. | 1.6 | 19 |
| 536 | Characterization and expression sites of newly identified chicken collectins. Molecular Immunology, 2006, 43, 1604-1616. | 2.2 | 49 |
| 537 | Mutation analyses of genes on 6p12-p11 in patients with juvenile myoclonic epilepsy. Neuroscience Letters, 2006, 405, 126-131. | 2.1 | 12 |
| 538 | Thioredoxin1 Upregulates Mitochondrial Proteins Related to Oxidative Phosphorylation and TCA Cycle in the Heart. Antioxidants and Redox Signaling, 2006, 8, 1635-1650. | 5.4 | 47 |
| 539 | Genome conservation between the bovine and human interleukin-8 receptor complex: Improper annotation of bovine interleukin-8 receptor b identified. Veterinary Immunology and Immunopathology, 2006, 114, 335-340. | 1.2 | 18 |
| 540 | The echinoderm adhesome. Developmental Biology, 2006, 300, 252-266. | 2.0 | 158 |
| 541 | Analysis of cytoskeletal and motility proteins in the sea urchin genome assembly. Developmental Biology, 2006, 300, 219-237. | 2.0 | 53 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 542 | The presence of GC-AG introns in <i>Neurospora crassa</i> and other euascomycetes determined from analyses of complete genomes: implications for automated gene prediction. <i>Genomics</i> , 2006, 87, 338-347. | 2.9 | 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. | 2.9 | 19 |
| 544 | Conservation patterns in different functional sequence categories of divergent <i>Drosophila</i> species. <i>Genomics</i> , 2006, 88, 431-442. | 2.9 | 18 |
| 545 | ChickGCE: A novel germ cell EST database for studying the early developmental stage in chickens. <i>Genomics</i> , 2006, 88, 252-257. | 2.9 | 10 |
| 546 | Novel genes identified by manual annotation and microarray expression analysis in the pancreas. <i>Genomics</i> , 2006, 88, 752-761. | 2.9 | 6 |
| 547 | In silico identification and Bayesian phylogenetic analysis of multiple new mammalian kallikrein gene families. <i>Genomics</i> , 2006, 88, 591-599. | 2.9 | 31 |
| 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. | 2.9 | 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. | 2.3 | 27 |
| 553 | MGOS: A Resource for Studying <i>Magnaporthe grisea</i> and <i>Oryza sativa</i> Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1055-1061. | 2.6 | 24 |
| 554 | A Homeodomain-Zinc Finger Protein, ZFX4, Is Expressed in Neuronal Differentiation Manner and Suppressed in Muscle Differentiation Manner. <i>Biological and Pharmaceutical Bulletin</i> , 2006, 29, 1830-1835. | 1.4 | 35 |
| 555 | NF-Y, AP2, Nrf1 and Sp1 regulate the fragile X-related gene 2 (FXR2). <i>Biochemical Journal</i> , 2006, 400, 327-335. | 3.7 | 9 |
| 557 | Comparison of human (and other) genome browsers. <i>Human Genomics</i> , 2006, 2, 266. | 2.9 | 18 |
| 558 | A Hybrid, Recursive Algorithm for Clustering Expressed Sequence Tags in <i>Chlamydomonas reinhardtii</i> . , 2006, , . | | 0 |
| 559 | LINE-1 RNA splicing and influences on mammalian gene expression. <i>Nucleic Acids Research</i> , 2006, 34, 1512-1521. | 14.5 | 180 |
| 560 | ChimerDB--a knowledgebase for fusion sequences. <i>Nucleic Acids Research</i> , 2006, 34, D21-D24. | 14.5 | 34 |
| 561 | Novel Tools for Plant Genome Annotation and Applications to <i>Arabidopsis</i> and <i>Rice</i> . , 2005, , 63-76. | | 2 |
| 562 | Genomic overview of mRNA 5'-leader trans-splicing in the ascidian <i>Ciona intestinalis</i> . <i>Nucleic Acids Research</i> , 2006, 34, 3378-3388. | 14.5 | 62 |
| 563 | ARTS: accurate recognition of transcription starts in human. <i>Bioinformatics</i> , 2006, 22, e472-e480. | 4.1 | 101 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 564 | The PLAC1-homology region of the ZP domain is sufficient for protein polymerisation. BMC Biochemistry, 2006, 7, 11. | 4.4 | 71 |
| 565 | Genomic characterization of five deletions in the LDL receptor gene in Danish Familial Hypercholesterolemic subjects. BMC Medical Genetics, 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). BMC Medical Genetics, 2006, 7, 69. | 2.1 | 9 |
| 567 | Composition-based statistics and translated nucleotide searches: Improving the TBLASTN module of BLAST. BMC Biology, 2006, 4, 41. | 3.8 | 420 |
| 568 | EMMA: An Efficient Massive Mapping Algorithm Using Improved Approximate Mapping Filtering. Acta Biochimica Et Biophysica Sinica, 2006, 38, 857-864. | 2.0 | 0 |
| 569 | Bioinformatic analysis of expressed sequence tags derived from a compatible Alternaria brassicicola-Brassica oleracea interaction. Molecular Plant Pathology, 2006, 7, 113-124. | 4.2 | 30 |
| 570 | A sequence-oriented comparison of gene expression measurements across different hybridization-based technologies. Nature Biotechnology, 2006, 24, 832-840. | 17.5 | 144 |
| 571 | Genome-wide transcription analyses in rice using tiling microarrays. Nature Genetics, 2006, 38, 124-129. | 21.4 | 154 |
| 572 | Mutations in the gene encoding pejvakin, a newly identified protein of the afferent auditory pathway, cause DFNB59 auditory neuropathy. Nature Genetics, 2006, 38, 770-778. | 21.4 | 262 |
| 573 | Genome-wide analysis of estrogen receptor binding sites. Nature Genetics, 2006, 38, 1289-1297. | 21.4 | 1,227 |
| 574 | Genome assembly comparison identifies structural variants in the human genome. Nature Genetics, 2006, 38, 1413-1418. | 21.4 | 150 |
| 575 | Regional copy number-independent deregulation of transcription in cancer. Nature Genetics, 2006, 38, 1386-1396. | 21.4 | 198 |
| 576 | Segmental duplication density decrease with distance to human-mouse breaks of synteny. European Journal of Human Genetics, 2006, 14, 216-221. | 2.8 | 4 |
| 577 | Identification of cryptic imbalance in phenotypically normal and abnormal translocation carriers. European Journal of Human Genetics, 2006, 14, 1255-1262. | 2.8 | 25 |
| 578 | Two-dimensional electrophoretic mobility shift assay: Identification and mapping of transcription factor CTCF target sequences within an FXVD5â€‘COX7A1 region of human chromosome 19. Analytical Biochemistry, 2006, 354, 85-93. | 2.4 | 16 |
| 579 | Comparative genomics as a tool for gene discovery. Current Opinion in Biotechnology, 2006, 17, 161-167. | 6.6 | 40 |
| 580 | Evolution of glyoxylate cycle enzymes in Metazoa: evidence of multiple horizontal transfer events and pseudogene formation. Biology Direct, 2006, 1, 31. | 4.6 | 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. Chromosome Research, 2006, 14, 203-211. | 2.2 | 84 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 582 | Characterization of a complex rearrangement with interstitial deletions and inversion on human chromosome 1. <i>Chromosome Research</i> , 2006, 14, 277-282. | 2.2 | 19 |
| 583 | Tempo and mode of ERV-K evolution in human and chimpanzee genomes. <i>Archives of Virology</i> , 2006, 151, 2215-2228. | 2.1 | 24 |
| 584 | A founder mutation for ichthyosis prematurity syndrome restricted to 76Åkb by haplotype association. <i>Journal of Human Genetics</i> , 2006, 51, 864-871. | 2.3 | 18 |
| 585 | Identification of alternatively spliced dab1 isoforms in zebrafish. <i>Development Genes and Evolution</i> , 2006, 216, 291-299. | 0.9 | 14 |
| 586 | Grey, a novel mutation in the murine Lyst gene, causes the beige phenotype by skipping of exon 25. <i>Mammalian Genome</i> , 2006, 17, 203-210. | 2.2 | 26 |
| 587 | Expression profiling identifies novel candidate genes for ethanol sensitivity QTLs. <i>Mammalian Genome</i> , 2006, 17, 147-156. | 2.2 | 21 |
| 588 | Identification, genome mapping, and CTCF binding of potential insulators within the FXD5-COX7A1 locus of human Chromosome 19q13.12. <i>Mammalian Genome</i> , 2006, 17, 1042-1049. | 2.2 | 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. | 1.8 | 16 |
| 590 | Nonrandom Representation of Sex-Biased Genes on Chicken Z Chromosome. <i>Journal of Molecular Evolution</i> , 2006, 63, 676-681. | 1.8 | 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. | 2.6 | 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. | 2.6 | 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. | 3.3 | 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. | 0.8 | 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. | 15.5 | 32 |
| 598 | Differential expression of a new isoform of DLG2 in renal oncocytoma. <i>BMC Cancer</i> , 2006, 6, 106. | 2.6 | 14 |
| 599 | Fast-Find: a novel computational approach to analyzing combinatorial motifs. <i>BMC Bioinformatics</i> , 2006, 7, 1. | 2.6 | 467 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 600 | Choosing the best heuristic for seeded alignment of DNA sequences. BMC Bioinformatics, 2006, 7, 133. | 2.6 | 21 |
| 601 | GENOMEMASKER package for designing unique genomic PCR primers. BMC Bioinformatics, 2006, 7, 172. | 2.6 | 37 |
| 602 | Ebbie: automated analysis and storage of small RNA cloning data using a dynamic web server. BMC Bioinformatics, 2006, 7, 185. | 2.6 | 3 |
| 603 | Automatic generation of gene finders for eukaryotic species. BMC Bioinformatics, 2006, 7, 263. | 2.6 | 25 |
| 604 | Using ESTs to improve the accuracy of de novo gene prediction. BMC Bioinformatics, 2006, 7, 327. | 2.6 | 47 |
| 605 | G-InforBIO: integrated system for microbial genomics. BMC Bioinformatics, 2006, 7, 368. | 2.6 | 11 |
| 606 | Detecting the limits of regulatory element conservation and divergence estimation using pairwise and multiple alignments. BMC Bioinformatics, 2006, 7, 376. | 2.6 | 46 |
| 607 | MICA: desktop software for comprehensive searching of DNA databases. BMC Bioinformatics, 2006, 7, 427. | 2.6 | 4 |
| 608 | CGAT: a comparative genome analysis tool for visualizing alignments in the analysis of complex evolutionary changes between closely related genomes. BMC Bioinformatics, 2006, 7, 472. | 2.6 | 22 |
| 609 | CAFTAN: a tool for fast mapping, and quality assessment of cDNAs. BMC Bioinformatics, 2006, 7, 473. | 2.6 | 0 |
| 610 | Quantitative comparison of EST libraries requires compensation for systematic biases in cDNA generation. BMC Bioinformatics, 2006, 7, 77. | 2.6 | 31 |
| 611 | Learning Interpretable SVMs for Biological Sequence Classification. BMC Bioinformatics, 2006, 7, S9. | 2.6 | 58 |
| 612 | Phylogenetic analysis of the tenascin gene family: evidence of origin early in the chordate lineage. BMC Evolutionary Biology, 2006, 6, 60. | 3.2 | 92 |
| 613 | Widespread ectopic expression of olfactory receptor genes. BMC Genomics, 2006, 7, 121. | 2.8 | 216 |
| 614 | Gene expression profiling in the striatum of inbred mouse strains with distinct opioid-related phenotypes. BMC Genomics, 2006, 7, 146. | 2.8 | 48 |
| 615 | Comparative analysis of cancer genes in the human and chimpanzee genomes. BMC Genomics, 2006, 7, 15. | 2.8 | 94 |
| 616 | Gene order data from a model amphibian (Ambystoma): new perspectives on vertebrate genome structure and evolution. BMC Genomics, 2006, 7, 219. | 2.8 | 30 |
| 617 | Gene expression profiling of chicken primordial germ cell ESTs. BMC Genomics, 2006, 7, 220. | 2.8 | 26 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 618 | Comparison of methods for genomic localization of gene trap sequences. BMC Genomics, 2006, 7, 236. | 2.8 | 1 |
| 619 | Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. BMC Genomics, 2006, 7, 246. | 2.8 | 173 |
| 620 | Design factors that influence PCR amplification success of cross-species primers among 1147 mammalian primer pairs. BMC Genomics, 2006, 7, 253. | 2.8 | 35 |
| 621 | Evolution and comparative analysis of the MHC Class III inflammatory region. BMC Genomics, 2006, 7, 281. | 2.8 | 54 |
| 622 | SAGE detects microRNA precursors. BMC Genomics, 2006, 7, 285. | 2.8 | 12 |
| 623 | Simultaneous host and parasite expression profiling identifies tissue-specific transcriptional programs associated with susceptibility or resistance to experimental cerebral malaria. BMC Genomics, 2006, 7, 295. | 2.8 | 62 |
| 624 | Comprehensive analysis of alternative splicing in rice and comparative analyses with Arabidopsis. BMC Genomics, 2006, 7, 327. | 2.8 | 375 |
| 625 | Duplication and relocation of the functional DPY19L2 gene within low copy repeats. BMC Genomics, 2006, 7, 45. | 2.8 | 28 |
| 626 | Periodicity of SNP distribution around transcription start sites. BMC Genomics, 2006, 7, 66. | 2.8 | 19 |
| 627 | Analysis of 10,000 ESTs from lymphocytes of the cynomolgus monkey to improve our understanding of its immune system. BMC Genomics, 2006, 7, 82. | 2.8 | 13 |
| 628 | Sex-dependent gene expression in early brain development of chicken embryos. BMC Neuroscience, 2006, 7, 12. | 1.9 | 59 |
| 629 | Piloting the zebrafish genome browser. Developmental Dynamics, 2006, 235, 747-753. | 1.8 | 5 |
| 630 | Identification of candidates for tumor-specific alternative splicing in the thyroid. Genes Chromosomes and Cancer, 2006, 45, 540-553. | 2.8 | 15 |
| 631 | Nonsynonymous SNPs: validation characteristics, derived allele frequency patterns, and suggestive evidence for natural selection. Human Mutation, 2006, 27, 173-186. | 2.5 | 9 |
| 632 | dbRIP: A highly integrated database of retrotransposon insertion polymorphisms in humans. Human Mutation, 2006, 27, 323-329. | 2.5 | 177 |
| 633 | Frequency of genomic rearrangements involving the SHFM3 locus at chromosome 10q24 in syndromic and non-syndromic split-hand/foot malformation. American Journal of Medical Genetics, Part A, 2006, 140A, 1375-1383. | 1.2 | 22 |
| 634 | Split-hand/split-foot malformation 3 (SHFM3) at 10q24, development of rapid diagnostic methods and gene expression from the region. American Journal of Medical Genetics, Part A, 2006, 140A, 1384-1395. | 1.2 | 33 |
| 635 | Tetrahymena Genome Database (TGD): a new genomic resource for Tetrahymena thermophila research. Nucleic Acids Research, 2006, 34, D500-D503. | 14.5 | 107 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 636 | Regions of extreme synonymous codon selection in mammalian genes. Nucleic Acids Research, 2006, 34, 1700-1710. | 14.5 | 47 |
| 637 | Indel seeds for homology search. Bioinformatics, 2006, 22, e341-e349. | 4.1 | 28 |
| 638 | Meisetz and the birth of the KRAB motif. Bioinformatics, 2006, 22, 2841-2845. | 4.1 | 90 |
| 639 | CisView: A Browser and Database of cis-regulatory Modules Predicted in the Mouse Genome. DNA Research, 2006, 13, 123-134. | 3.4 | 28 |
| 640 | TISA: Tissue-specific Alternative Splicing in Human and Mouse Genes. DNA Research, 2006, 13, 229-243. | 3.4 | 29 |
| 641 | snoRNA-LBME-db, a comprehensive database of human H/ACA and C/D box snoRNAs. Nucleic Acids Research, 2006, 34, D158-D162. | 14.5 | 463 |
| 642 | VMD: a community annotation database for oomycetes and microbial genomes. Nucleic Acids Research, 2006, 34, D379-D381. | 14.5 | 28 |
| 643 | The TIGR Maize Database. Nucleic Acids Research, 2006, 34, D771-D776. | 14.5 | 35 |
| 644 | The Mouse Functional Genome Database (MfunGD): functional annotation of proteins in the light of their cellular context. Nucleic Acids Research, 2006, 34, D568-D571. | 14.5 | 15 |
| 645 | MPromDb: an integrated resource for annotation and visualization of mammalian gene promoters and ChIP-chip experimental data. Nucleic Acids Research, 2006, 34, D98-D103. | 14.5 | 41 |
| 646 | The UCSC Archaeal Genome Browser. Nucleic Acids Research, 2006, 34, D407-D410. | 14.5 | 107 |
| 647 | The UCSC Genome Browser Database: update 2006. Nucleic Acids Research, 2006, 34, D590-D598. | 14.5 | 1,156 |
| 648 | Application of a superword array in genome assembly. Nucleic Acids Research, 2006, 34, 201-205. | 14.5 | 29 |
| 649 | Dynamic use of multiple parameter sets in sequence alignment. Nucleic Acids Research, 2006, 35, 678-686. | 14.5 | 26 |
| 650 | MutScreener: primer design tool for PCR-direct sequencing. Nucleic Acids Research, 2006, 34, W660-W664. | 14.5 | 7 |
| 651 | An open-access long oligonucleotide microarray resource for analysis of the human and mouse transcriptomes. Nucleic Acids Research, 2006, 34, e87-e87. | 14.5 | 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. Endocrinology, 2006, 147, 2357-2367. | 2.8 | 40 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 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. Molecular Biology and Evolution, 2006, 23, 2392-2404. | 8.9 | 154 |
| 657 | Chromosome-wide identification of novel imprinted genes using microarrays and uniparental disomies. Nucleic Acids Research, 2006, 34, e88-e88. | 14.5 | 61 |
| 658 | Alternative isoform discrimination by the next generation of expression profiling microarrays. Expert Opinion on Therapeutic Targets, 2006, 10, 613-625. | 3.4 | 9 |
| 659 | Accurate anchoring alignment of divergent sequences. Bioinformatics, 2006, 22, 29-34. | 4.1 | 36 |
| 660 | A space-partitioning-based indexing method for multidimensional non-ordered discrete data spaces. ACM Transactions on Information Systems, 2006, 24, 79-110. | 4.9 | 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. | 2.8 | 20 |
| 663 | Aligning DNA sequences using dynamic programming. Xrds, 2006, 13, 9-9. | 0.3 | 2 |
| 664 | A Map of Recent Positive Selection in the Human Genome. PLoS Biology, 2006, 4, e72. | 5.6 | 2,329 |
| 665 | Functionality of Intergenic Transcription: An Evolutionary Comparison. PLoS Genetics, 2006, 2, e171. | 3.5 | 73 |
| 666 | A large quantity of novel human antisense transcripts detected by LongSAGE. Bioinformatics, 2006, 22, 2475-2479. | 4.1 | 49 |
| 667 | Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. PLoS Biology, 2006, 4, e46. | 5.6 | 150 |
| 668 | Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33. | 3.2 | 439 |
| 669 | Unusual Intron Conservation near Tissue-Regulated Exons Found by Splicing Microarrays. PLoS Computational Biology, 2006, 2, e4. | 3.2 | 175 |
| 670 | Parametric Alignment of Drosophila Genomes. PLoS Computational Biology, 2006, 2, e73. | 3.2 | 38 |
| 671 | An Integrative Method for Accurate Comparative Genome Mapping. PLoS Computational Biology, 2006, 2, e75. | 3.2 | 25 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 672 | Identification and Analysis of Genes and Pseudogenes within Duplicated Regions in the Human and Mouse Genomes. PLoS Computational Biology, 2006, 2, e76. | 3.2 | 22 |
| 673 | A High-Resolution Map of Synteny Disruptions in Gibbon and Human Genomes. PLoS Genetics, 2006, 2, e223. | 3.5 | 48 |
| 674 | Gene Losses during Human Origins. PLoS Biology, 2006, 4, e52. | 5.6 | 188 |
| 675 | SPA: A Probabilistic Algorithm for Spliced Alignment. PLoS Genetics, 2006, 2, e24. | 3.5 | 21 |
| 676 | Mammalian Small Nucleolar RNAs Are Mobile Genetic Elements. PLoS Genetics, 2006, 2, e205. | 3.5 | 131 |
| 677 | Recent Assembly of an Imprinted Domain from Non-Imprinted Components. PLoS Genetics, 2006, 2, e182. | 3.5 | 84 |
| 678 | The Rice Annotation Project Database (RAP-DB): hub for Oryza sativa ssp. japonica genome information. Nucleic Acids Research, 2006, 34, D741-D744. | 14.5 | 219 |
| 679 | Heterogeneous Genomic Molecular Clocks in Primates. PLoS Genetics, 2006, 2, e163. | 3.5 | 89 |
| 680 | The G Proteinâ€“Coupled Receptor Subset of the Chicken Genome. PLoS Computational Biology, 2006, 2, e54. | 3.2 | 104 |
| 681 | Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. PLoS Genetics, 2006, 2, e62. | 3.5 | 165 |
| 682 | Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcription and organismic complexity. Genome Research, 2006, 16, 922-933. | 5.5 | 40 |
| 683 | Bioinformatics of alternative splicing and its regulation. Briefings in Bioinformatics, 2006, 7, 55-69. | 6.5 | 29 |
| 684 | In Vivo Requirement of the Small Subunit of U2AF for Recognition of a Weak 3' Splice Site. Molecular and Cellular Biology, 2006, 26, 8183-8190. | 2.3 | 56 |
| 685 | A computational screen for mammalian pseudouridylation guide H/ACA RNAs. Rna, 2006, 12, 15-25. | 3.5 | 84 |
| 686 | Conserved distances between vertebrate highly conserved elements. Human Molecular Genetics, 2006, 15, 2911-2922. | 2.9 | 28 |
| 687 | U1-like snRNAs lacking complementarity to canonical 5' splice sites. Rna, 2006, 12, 1603-1611. | 3.5 | 28 |
| 688 | Water stress-responsive genes in loblolly pine (Pinus taeda) roots identified by analyses of expressed sequence tag libraries. Tree Physiology, 2006, 26, 1-16. | 3.1 | 84 |
| 689 | MYC-containing double minutes in hematologic malignancies: evidence in favor of the episome model and exclusion of MYC as the target gene. Human Molecular Genetics, 2006, 15, 933-942. | 2.9 | 116 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 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. | 5.5 | 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. | 2.9 | 31 |
| 692 | Genome-wide analysis of mRNAs bound to the histone stem-loop binding protein. <i>Rna</i> , 2006, 12, 1853-1867. | 3.5 | 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. | 8.9 | 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. | 4.8 | 13 |
| 695 | Decoding the fine-scale structure of a breast cancer genome and transcriptome. <i>Genome Research</i> , 2006, 16, 394-404. | 5.5 | 49 |
| 696 | Foamy virus vector integration sites in normal human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1498-1503. | 7.1 | 226 |
| 697 | Common origin of the human synovial sarcoma associated <i>SS18</i> and <i>SS18L1</i> gene loci. <i>Cytogenetic and Genome Research</i> , 2006, 112, 222-226. | 1.1 | 8 |
| 698 | Isolation and functional analysis of human HMBOX1, a homeobox containing protein with transcriptional repressor activity. <i>Cytogenetic and Genome Research</i> , 2006, 114, 131-136. | 1.1 | 44 |
| 699 | Genome-wide in silico identification and analysis of cis natural antisense transcripts (cis-NATs) in ten species. <i>Nucleic Acids Research</i> , 2006, 34, 3465-3475. | 14.5 | 155 |
| 700 | Evolution of the vertebrate DNMT3 gene family: a possible link between existence of <i>DNMT3L</i> and genomic imprinting. <i>Cytogenetic and Genome Research</i> , 2006, 113, 75-80. | 1.1 | 67 |
| 701 | GenRate: A Generative Model that Reveals Novel Transcripts in Genome-Tiling Microarray Data. <i>Journal of Computational Biology</i> , 2006, 13, 200-214. | 1.6 | 1 |
| 702 | AGRIS and AtRegNet. A Platform to Link cis-Regulatory Elements and Transcription Factors into Regulatory Networks. <i>Plant Physiology</i> , 2006, 140, 818-829. | 4.8 | 249 |
| 703 | Mammalian \hat{A} -spectrin is a neofunctionalized polypeptide adapted to small highly deformable erythrocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 643-648. | 7.1 | 43 |
| 704 | SyMAP: A system for discovering and viewing syntenic regions of FPC maps. <i>Genome Research</i> , 2006, 16, 1159-1168. | 5.5 | 176 |
| 705 | Characterization of a cancer/testis (CT) antigen gene family capable of eliciting humoral response in cancer patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18066-18071. | 7.1 | 32 |
| 706 | Sequence analysis of the complete mitochondrial DNA in 10 commonly used inbred rat strains. <i>American Journal of Physiology - Cell Physiology</i> , 2006, 291, C1183-C1192. | 4.6 | 39 |
| 707 | A UNIFYING FRAMEWORK FOR SEED SENSITIVITY AND ITS APPLICATION TO SUBSET SEEDS. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 553-569. | 0.8 | 58 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 709 | A high throughput method for genome-wide analysis of retroviral integration. <i>Nucleic Acids Research</i> , 2006, 34, e134-e134. | 14.5 | 8 |
| 710 | Computational methods for alternative splicing prediction. <i>Briefings in Functional Genomics & Proteomics</i> , 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. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2006, 319, 369-375. | 2.5 | 33 |
| 712 | A First-Generation Metric Linkage Disequilibrium Map of Bovine Chromosome 6. <i>Genetics</i> , 2006, 174, 79-85. | 2.9 | 35 |
| 713 | Flexibility and constraint in the nucleosome core landscape of <i>Caenorhabditis elegans</i> chromatin. <i>Genome Research</i> , 2006, 16, 1505-1516. | 5.5 | 169 |
| 714 | Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964. | 7.1 | 286 |
| 715 | Gallus GBrowse: a unified genomic database for the chicken. <i>Nucleic Acids Research</i> , 2007, 36, D719-D723. | 14.5 | 9 |
| 716 | OVERLAPPING ALTERNATIVE DONOR SPLICE SITES IN THE HUMAN GENOME. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 991-1004. | 0.8 | 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. | 7.1 | 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. | 7.1 | 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. | 3.4 | 156 |
| 720 | Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , 2007, 17, 1763-1773. | 5.5 | 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. | 5.5 | 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. | 7.1 | 45 |
| 723 | Widely variable endogenous retroviral methylation levels in human placenta. <i>Nucleic Acids Research</i> , 2007, 35, 4743-4754. | 14.5 | 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. | 14.5 | 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. | 2.4 | 32 |
| 726 | Sampling the Arabidopsis Transcriptome with Massively Parallel Pyrosequencing. <i>Plant Physiology</i> , 2007, 144, 32-42. | 4.8 | 298 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 727 | Genetic analysis of albuminuria in a cross between C57BL/6J and DBA/2J mice. American Journal of Physiology - Renal Physiology, 2007, 293, F1649-F1656. | 2.7 | 35 |
| 728 | Alu Recombination-Mediated Structural Deletions in the Chimpanzee Genome. PLoS Genetics, 2007, 3, e184. | 3.5 | 94 |
| 729 | Evolutionary Conservation of UTR Intron Boundaries in Cryptococcus. Molecular Biology and Evolution, 2007, 24, 1140-1148. | 8.9 | 18 |
| 730 | Genome-Wide Expression Profiling of the Arabidopsis Female Gametophyte Identifies Families of Small, Secreted Proteins. PLoS Genetics, 2007, 3, e171. | 3.5 | 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. Human Molecular Genetics, 2007, 16, 1381-1390. | 2.9 | 18 |
| 733 | Genome browsing with Ensembl: a practical overview. Briefings in Functional Genomics & Proteomics, 2007, 6, 202-219. | 3.8 | 31 |
| 734 | Population Genomics: Whole-Genome Analysis of Polymorphism and Divergence in Drosophila simulans. PLoS Biology, 2007, 5, e310. | 5.6 | 583 |
| 735 | Divergent Evolution of Human p53 Binding Sites: Cell Cycle Versus Apoptosis. PLoS Genetics, 2007, 3, e127. | 3.5 | 88 |
| 736 | A Screen for Retrotransposed Imprinted Genes Reveals an Association between X Chromosome Homology and Maternal Germ-Line Methylation. PLoS Genetics, 2007, 3, e20. | 3.5 | 103 |
| 737 | GeneHub-GEPIS: digital expression profiling for normal and cancer tissues based on an integrated gene database. Nucleic Acids Research, 2007, 35, W152-W158. | 14.5 | 30 |
| 738 | FK506, a Calcineurin Inhibitor, Prevents Cadmium-Induced Testicular Toxicity in Mice. Toxicological Sciences, 2007, 100, 474-485. | 3.1 | 23 |
| 739 | cGMP-dependent protein kinase I interacts with TRIM39R, a novel Rpp21 domain-containing TRIM protein. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2007, 293, L903-L912. | 2.9 | 15 |
| 740 | Improving the Caenorhabditis elegans Genome Annotation Using Machine Learning. PLoS Computational Biology, 2007, 3, e20. | 3.2 | 57 |
| 741 | Comparative Genomics Search for Losses of Long-Established Genes on the Human Lineage. PLoS Computational Biology, 2007, 3, e247. | 3.2 | 103 |
| 742 | A High-Resolution Map of Segmental DNA Copy Number Variation in the Mouse Genome. PLoS Genetics, 2007, 3, e3. | 3.5 | 196 |
| 743 | Genome Analysis of Minibacterium massiliensis Highlights the Convergent Evolution of Water-Living Bacteria. PLoS Genetics, 2007, 3, e138. | 3.5 | 64 |
| 744 | Adaptive Evolution of Conserved Noncoding Elements in Mammals. PLoS Genetics, 2007, 3, e147. | 3.5 | 79 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 745 | Extragenic Accumulation of RNA Polymerase II Enhances Transcription by RNA Polymerase III. PLoS Genetics, 2007, 3, e212. | 3.5 | 56 |
| 746 | Transcriptional Interferences in cis Natural Antisense Transcripts of Humans and Mice. Genetics, 2007, 176, 1299-1306. | 2.9 | 124 |
| 747 | Comparative Physical Mapping Between Oryza sativa (AA Genome Type) and O. punctata (BB Genome) Tj ETQq0 0.0 rgBT /Overlock 10 | 2.9 | 49 |
| 748 | Sex-specific regulation of gene expression in the aging monkey aorta. Physiological Genomics, 2007, 29, 169-180. | 2.3 | 43 |
| 749 | Hairpin structure within the 3'UTR of DNA polymerase β mRNA acts as a post-transcriptional regulatory element and interacts with Hax-1. Nucleic Acids Research, 2007, 35, 5499-5510. | 14.5 | 43 |
| 750 | Context Dependence, Ancestral Misidentification, and Spurious Signatures of Natural Selection. Molecular Biology and Evolution, 2007, 24, 1792-1800. | 8.9 | 162 |
| 751 | Mapping Human Genetic Ancestry. Molecular Biology and Evolution, 2007, 24, 2266-2276. | 8.9 | 117 |
| 752 | The TIGR Plant Transcript Assemblies database. Nucleic Acids Research, 2007, 35, D846-D851. | 14.5 | 173 |
| 753 | The UCSC genome browser database: update 2007. Nucleic Acids Research, 2007, 35, D668-D673. | 14.5 | 260 |
| 754 | A role for microRNAs in maintenance of mouse mammary epithelial progenitor cells. Genes and Development, 2007, 21, 3238-3243. | 5.9 | 195 |
| 755 | Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). Genome Research, 2007, 17, 828-838. | 5.5 | 86 |
| 756 | Differing patterns of selection in alternative and constitutive splice sites. Genome Research, 2007, 17, 1015-1022. | 5.5 | 32 |
| 757 | VectorBase: a home for invertebrate vectors of human pathogens. Nucleic Acids Research, 2007, 35, D503-D505. | 14.5 | 107 |
| 758 | Bird and Mammal Sex-Chromosome Orthologs Map to the Same Autosomal Region in a Salamander (Ambystoma). Genetics, 2007, 177, 607-613. | 2.9 | 25 |
| 759 | Drosophila Polymorphism Database (DPDB)A Portal for Nucleotide Polymorphism in Drosophila. Fly, 2007, 1, 205-211. | 1.7 | 3 |
| 760 | Ro-Associated Y RNAs in Metazoans: Evolution and Diversification. Molecular Biology and Evolution, 2007, 24, 1678-1689. | 8.9 | 93 |
| 761 | Systematic variation in mRNA 3 β 2-processing signals during mouse spermatogenesis. Nucleic Acids Research, 2007, 35, 234-246. | 14.5 | 114 |
| 762 | PolyA_DB 2: mRNA polyadenylation sites in vertebrate genes. Nucleic Acids Research, 2007, 35, D165-D168. | 14.5 | 156 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 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. | 8.2 | 104 |
| 764 | Common Functions for Diverse Small RNAs of Land Plants. <i>Plant Cell</i> , 2007, 19, 1750-1769. | 6.6 | 387 |
| 765 | Identification of the circadian transcriptome in adult mouse skeletal muscle. <i>Physiological Genomics</i> , 2007, 31, 86-95. | 2.3 | 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. | 5.5 | 65 |
| 767 | Towards pathogenomics: a web-based resource for pathogenicity islands. <i>Nucleic Acids Research</i> , 2007, 35, D395-D400. | 14.5 | 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. | 1.6 | 48 |
| 769 | Large-scale Discovery of Regulatory Motifs Involved in Alternative Splicing. , 2007, , . | | 0 |
| 770 | Correcting Base-Assignment Errors in Repeat Regions of Shotgun Assembly. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 54-64. | 3.0 | 9 |
| 771 | Generalized Correlation Functions and Their Applications in Selection of Optimal Multiple Spaced Seeds for Homology Search. <i>Journal of Computational Biology</i> , 2007, 14, 238-254. | 1.6 | 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. <i>DNA Sequence</i> , 2007, 18, 73-79. | 0.7 | 7 |
| 773 | Bayesian Inference of MicroRNA Targets from Sequence and Expression Data. <i>Journal of Computational Biology</i> , 2007, 14, 550-563. | 1.6 | 106 |
| 774 | A complex system of small RNAs in the unicellular green alga <i>Chlamydomonas reinhardtii</i> . <i>Genes and Development</i> , 2007, 21, 1190-1203. | 5.9 | 367 |
| 775 | Widespread mRNA polyadenylation events in introns indicate dynamic interplay between polyadenylation and splicing. <i>Genome Research</i> , 2007, 17, 156-165. | 5.5 | 184 |
| 776 | Comparative Cross-Species Alternative Splicing in Plants. <i>Plant Physiology</i> , 2007, 144, 1632-1641. | 4.8 | 73 |
| 777 | Adaptive Evolution of Recently Duplicated Accessory Gland Protein Genes in Desert <i>Drosophila</i> . <i>Genetics</i> , 2007, 177, 1023-1030. | 2.9 | 45 |
| 778 | Analysis of the Unassembled Part of the Dog Genome Sequence: Chromosomal Localization of 115 Genes Inferred from Multispecies Comparative Genomics. <i>Journal of Heredity</i> , 2007, 98, 461-467. | 2.4 | 5 |
| 779 | Toward a universal microarray: prediction of gene expression through nearest-neighbor probe sequence identification. <i>Nucleic Acids Research</i> , 2007, 35, e99-e99. | 14.5 | 63 |
| 780 | Functional Analysis of the Human N-Acetyltransferase 1 Major Promoter: Quantitation of Tissue Expression and Identification of Critical Sequence Elements. <i>Drug Metabolism and Disposition</i> , 2007, 35, 1649-1656. | 3.3 | 49 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 781 | Homology search for genes. <i>Bioinformatics</i> , 2007, 23, i97-i103. | 4.1 | 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. <i>Genetics</i> , 2007, 176, 763-772. | 2.9 | 77 |
| 783 | Phylogenetic Footprinting Analysis in the Upstream Regulatory Regions of the <i>Drosophila</i> Enhancer of split Genes. <i>Genetics</i> , 2007, 177, 1377-1394. | 2.9 | 22 |
| 784 | Quantitating tissue specificity of human genes to facilitate biomarker discovery. <i>Bioinformatics</i> , 2007, 23, 1348-1355. | 4.1 | 19 |
| 785 | Dual-specificity splice sites function alternatively as 5â€² and 3â€² splice sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15028-15033. | 7.1 | 36 |
| 786 | Dual Modes of Natural Selection on Upstream Open Reading Frames. <i>Molecular Biology and Evolution</i> , 2007, 24, 1744-1751. | 8.9 | 46 |
| 787 | Assessing the need for sequence-based normalization in tiling microarray experiments. <i>Bioinformatics</i> , 2007, 23, 988-997. | 4.1 | 36 |
| 788 | The UCSC Genome Browser Database: 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D773-D779. | 14.5 | 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. | 3.3 | 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. | 8.9 | 50 |
| 791 | Discovering and detecting transposable elements in genome sequences. <i>Briefings in Bioinformatics</i> , 2007, 8, 382-392. | 6.5 | 189 |
| 792 | Multiple whole genome alignments and novel biomedical applications at the VISTA portal. <i>Nucleic Acids Research</i> , 2007, 35, W669-W674. | 14.5 | 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. | 3.1 | 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. | 3.1 | 30 |
| 795 | Optimized design and assessment of whole genome tiling arrays. <i>Bioinformatics</i> , 2007, 23, i195-i204. | 4.1 | 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. | 14.5 | 75 |
| 797 | LINE-1 retrotransposition in human embryonic stem cells. <i>Human Molecular Genetics</i> , 2007, 16, 1569-1577. | 2.9 | 204 |
| 798 | UTRome.org: a platform for 3'UTR biology in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2007, 36, D57-D62. | 14.5 | 20 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 799 | CTCFBSDB: a CTCF-binding site database for characterization of vertebrate genomic insulators. <i>Nucleic Acids Research</i> , 2007, 36, D83-D87. | 14.5 | 98 |
| 800 | <i>C. elegans</i> sequences that control trans-splicing and operon pre-mRNA processing. <i>Rna</i> , 2007, 13, 1409-1426. | 3.5 | 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. | 4.1 | 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. | 1.1 | 26 |
| 804 | Biodiversity of 20 chicken breeds assessed by SNPs located in gene regions. <i>Cytogenetic and Genome Research</i> , 2007, 117, 319-326. | 1.1 | 22 |
| 805 | Purifying Selection Maintains Highly Conserved Noncoding Sequences in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 2222-2234. | 8.9 | 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. | 14.5 | 34 |
| 807 | CG dinucleotide clustering is a species-specific property of the genome. <i>Nucleic Acids Research</i> , 2007, 35, 6798-6807. | 14.5 | 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. | 14.5 | 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. | 5.5 | 13 |
| 811 | Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. <i>Genome Research</i> , 2007, 17, 1296-1303. | 5.5 | 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, , . | 2.6 | 15 |
| 816 | MapToGenome: A Comparative Genomic Tool that Aligns Transcript Maps to Sequenced Genomes. <i>Evolutionary Bioinformatics</i> , 2007, 3, 117693430700300. | 1.2 | 2 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 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. | 1.5 | 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. | 2.9 | 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. | 2.9 | 5 |
| 821 | Patterns of gene duplication and intron loss in the ENCODE regions suggest a confounding factor. <i>Genomics</i> , 2007, 90, 44-48. | 2.9 | 5 |
| 822 | Identification of six putative human transporters with structural similarity to the drug transporter SLC22 family. <i>Genomics</i> , 2007, 90, 595-609. | 2.9 | 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. | 1.1 | 29 |
| 824 | Molecular determinants of AMPA receptor subunit assembly. <i>Trends in Neurosciences</i> , 2007, 30, 407-416. | 8.6 | 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. | 2.7 | 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. | 2.2 | 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. | 2.2 | 213 |
| 828 | Identification of three mouse μ -opioid receptor (MOR) gene (Oprm1) splice variants containing a newly identified alternatively spliced exon. <i>Gene</i> , 2007, 388, 135-147. | 2.2 | 30 |
| 829 | Comparative analysis of cis-encoded antisense RNAs in eukaryotes. <i>Gene</i> , 2007, 392, 134-141. | 2.2 | 29 |
| 830 | Identification of five mouse μ -opioid receptor (MOR) gene (Oprm1) splice variants containing a newly identified alternatively spliced exon. <i>Gene</i> , 2007, 395, 98-107. | 2.2 | 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. | 2.2 | 13 |
| 832 | Origin and evolution of vertebrate ABCA genes: A story from Amphioxus. <i>Gene</i> , 2007, 405, 88-95. | 2.2 | 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. | 4.2 | 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. | 2.1 | 8 |
| 835 | ZXDC, a novel zinc finger protein that binds CIITA and activates MHC gene transcription. <i>Molecular Immunology</i> , 2007, 44, 311-321. | 2.2 | 20 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 836 | Bioinformatic analysis of post-transcriptional regulation by uORF in human and mouse. FEBS Letters, 2007, 581, 4184-4188. | 2.8 | 64 |
| 837 | The Strength of Selection on Ultraconserved Elements in the Human Genome. American Journal of Human Genetics, 2007, 80, 692-704. | 6.2 | 62 |
| 838 | Restaura-G: A Rapid Genome Re-Annotation System for Comparative Genomics. Genomics, Proteomics and Bioinformatics, 2007, 5, 53-58. | 6.9 | 17 |
| 839 | Gene copy number variation spanning 60 million years of human and primate evolution. Genome Research, 2007, 17, 1266-1277. | 5.5 | 153 |
| 840 | A cross-species alignment tool (CAT). BMC Bioinformatics, 2007, 8, 349. | 2.6 | 4 |
| 841 | Genome-wide Detection and Analysis of Alternative Splicing for Nucleotide Binding Site-Leucine-Rich Repeats Sequences in Rice. Journal of Genetics and Genomics, 2007, 34, 247-257. | 3.9 | 17 |
| 842 | Origin and Evolution of Human microRNAs From Transposable Elements. Genetics, 2007, 176, 1323-1337. | 2.9 | 311 |
| 843 | CONTRAST: a discriminative, phylogeny-free approach to multiple informant de novo gene prediction. Genome Biology, 2007, 8, R269. | 9.6 | 79 |
| 844 | Contribution of telomerase RNA retrotranscription to DNA double-strand break repair during mammalian genome evolution. Genome Biology, 2007, 8, R260. | 9.6 | 68 |
| 845 | The ribosomal protein genes and Minute loci of Drosophila melanogaster. Genome Biology, 2007, 8, R216. | 9.6 | 330 |
| 846 | A physical map of the bovine genome. Genome Biology, 2007, 8, R165. | 9.6 | 73 |
| 847 | PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171. | 9.6 | 170 |
| 848 | Genome position and gene amplification. Genome Biology, 2007, 8, R120. | 9.6 | 24 |
| 849 | Morphine effects on striatal transcriptome in mice. Genome Biology, 2007, 8, R128. | 9.6 | 74 |
| 850 | Large-scale identification of human genes implicated in epidermal barrier function. Genome Biology, 2007, 8, R107. | 9.6 | 130 |
| 851 | LongSAGE profiling of nine human embryonic stem cell lines. Genome Biology, 2007, 8, R113. | 9.6 | 21 |
| 852 | cis-Decoder discovers constellations of conserved DNA sequences shared among tissue-specific enhancers. Genome Biology, 2007, 8, R75. | 9.6 | 24 |
| 853 | Regulatory conservation of protein coding and microRNA genes in vertebrates: lessons from the opossum genome. Genome Biology, 2007, 8, R84. | 9.6 | 26 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 854 | Discovery of tissue-specific exons using comprehensive human exon microarrays. <i>Genome Biology</i> , 2007, 8, R64. | 9.6 | 255 |
| 855 | Sense-antisense pairs in mammals: functional and evolutionary considerations. <i>Genome Biology</i> , 2007, 8, R40. | 9.6 | 55 |
| 856 | CAGE-TSSchip: promoter-based expression profiling using the 5'-leading label of capped transcripts. <i>Genome Biology</i> , 2007, 8, R42. | 9.6 | 3 |
| 857 | A haplome alignment and reference sequence of the highly polymorphic <i>Ciona savignyi</i> genome. <i>Genome Biology</i> , 2007, 8, R41. | 9.6 | 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. | 5.5 | 1,586 |
| 859 | Finding cis-regulatory modules in <i>Drosophila</i> using phylogenetic hidden Markov models. <i>Bioinformatics</i> , 2007, 23, 2031-2037. | 4.1 | 9 |
| 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. | 2.7 | 73 |
| 861 | Comparing Compressed Sequences for Faster Nucleotide BLAST Searches. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 349-364. | 3.0 | 16 |
| 862 | Superiority of Spaced Seeds for Homology Search. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 496-505. | 3.0 | 13 |
| 863 | A practical guide to the art of RNA gene prediction. <i>Briefings in Bioinformatics</i> , 2007, 8, 396-414. | 6.5 | 37 |
| 864 | Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234. | 12.6 | 1,283 |
| 865 | SmedGD: the <i>Schmidtea mediterranea</i> genome database. <i>Nucleic Acids Research</i> , 2007, 36, D599-D606. | 14.5 | 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. | 5.5 | 184 |
| 867 | Variation of CNV distribution in five different ethnic populations. <i>Cytogenetic and Genome Research</i> , 2007, 118, 19-30. | 1.1 | 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. | 1.6 | 8 |
| 869 | <i>Ellobius lutescens</i>: Sex Determination and Sex Chromosome. <i>Sexual Development</i> , 2007, 1, 211-221. | 2.0 | 46 |
| 870 | A chromosome inversion near the <i>KIT</i> gene and the Tobiano spotting pattern in horses. <i>Cytogenetic and Genome Research</i> , 2007, 119, 225-230. | 1.1 | 96 |
| 871 | Aligning Multiple Whole Genomes with Mercator and MAVID. <i>Methods in Molecular Biology</i> , 2007, 395, 221-235. | 0.9 | 83 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 872 | Automated Querying of Genome Databases. PLoS Computational Biology, 2007, 3, e1. | 3.2 | 17 |
| 873 | A Family of Human MicroRNA Genes from Miniature Inverted-Repeat Transposable Elements. PLoS ONE, 2007, 2, e203. | 2.5 | 264 |
| 874 | Extensive Polycistronism and Antisense Transcription in the Mammalian Hox Clusters. PLoS ONE, 2007, 2, e356. | 2.5 | 78 |
| 875 | Gene Organization in Rice Revealed by Full-Length cDNA Mapping and Gene Expression Analysis through Microarray. PLoS ONE, 2007, 2, e1235. | 2.5 | 51 |
| 876 | Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. Genome Research, 2007, 17, 720-731. | 5.5 | 31 |
| 877 | BLAST-off for genomes. Nature Reviews Genetics, 2007, 8, S14-S14. | 16.3 | 1 |
| 878 | In silico-initiated cloning and molecular characterization of cortxin 3, a novel human gene specifically expressed in the kidney and brain, and well conserved in vertebrates. International Journal of Molecular Medicine, 0, , . | 4.0 | 5 |
| 881 | PhenCode: connecting ENCODE data with mutations and phenotype. Human Mutation, 2007, 28, 554-562. | 2.5 | 79 |
| 882 | Complex genomic rearrangement in CCS-LacZ transgenic mice. Genesis, 2007, 45, 76-82. | 1.6 | 15 |
| 883 | FluoMEP: A new genotyping method combining the advantages of randomly amplified polymorphic DNA and amplified fragment length polymorphism. Electrophoresis, 2007, 28, 525-534. | 2.4 | 14 |
| 884 | Review of the literature examining the correlation among DNA microarray technologies. Environmental and Molecular Mutagenesis, 2007, 48, 380-394. | 2.2 | 75 |
| 885 | A high performance grid-web service framework for the identification of "conserved sequence tags"™. Future Generation Computer Systems, 2007, 23, 371-381. | 7.5 | 0 |
| 886 | Indexing schemes for similarity search in datasets of short protein fragments. Information Systems, 2007, 32, 1145-1165. | 3.6 | 16 |
| 887 | Rod-derived Cone Viability Factor-2 is a novel bifunctional-thioredoxin-like protein with therapeutic potential. BMC Molecular Biology, 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. BMC Women's Health, 2007, 7, 5. | 2.0 | 24 |
| 889 | Comparative analysis of structured RNAs in S. cerevisiae indicates a multitude of different functions. BMC Biology, 2007, 5, 25. | 3.8 | 32 |
| 890 | A mobile element-based evolutionary history of guenons (tribe Cercopithecini). BMC Biology, 2007, 5, 5. | 3.8 | 58 |
| 891 | Asymptotic behaviour and optimal word size for exact and approximate word matches between random sequences. Proceedings in Applied Mathematics and Mechanics, 2007, 7, 1121801-1121802. | 0.2 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 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. | 5.9 | 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. | 5.9 | 12 |
| 894 | Recurrent DNA copy number variation in the laboratory mouse. <i>Nature Genetics</i> , 2007, 39, 1384-1389. | 21.4 | 129 |
| 895 | A retroviral strategy that efficiently creates chromosomal deletions in mammalian cells. <i>Nature Methods</i> , 2007, 4, 263-268. | 19.0 | 14 |
| 896 | Processing of intronic microRNAs. <i>EMBO Journal</i> , 2007, 26, 775-783. | 7.8 | 714 |
| 897 | The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467. | 27.8 | 3,384 |
| 898 | Constraint and turnover in sex-biased gene expression in the genus <i>Drosophila</i> . <i>Nature</i> , 2007, 450, 233-237. | 27.8 | 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. | 2.6 | 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. | 3.6 | 41 |
| 901 | Interpretation of multiple probe sets mapping to the same gene in Affymetrix GeneChips. <i>BMC Bioinformatics</i> , 2007, 8, 13. | 2.6 | 66 |
| 902 | antiCODE: a natural sense-antisense transcripts database. <i>BMC Bioinformatics</i> , 2007, 8, 319. | 2.6 | 24 |
| 903 | Considerations in the identification of functional RNA structural elements in genomic alignments. <i>BMC Bioinformatics</i> , 2007, 8, 33. | 2.6 | 56 |
| 904 | How accurately is ncRNA aligned within whole-genome multiple alignments?. <i>BMC Bioinformatics</i> , 2007, 8, 417. | 2.6 | 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. | 2.6 | 23 |
| 906 | Gene models from ESTs (GeneModelEST): an application on the <i>Solanum lycopersicum</i> genome. <i>BMC Bioinformatics</i> , 2007, 8, S9. | 2.6 | 10 |
| 907 | Accurate splice site prediction using support vector machines. <i>BMC Bioinformatics</i> , 2007, 8, S7. | 2.6 | 135 |
| 908 | Simultaneous identification of long similar substrings in large sets of sequences. <i>BMC Bioinformatics</i> , 2007, 8, S7. | 2.6 | 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 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 910 | Conserved and species-specific alternative splicing in mammalian genomes. BMC Evolutionary Biology, 2007, 7, 249. | 3.2 | 26 |
| 911 | A cricket Gene Index: a genomic resource for studying neurobiology, speciation, and molecular evolution. BMC Genomics, 2007, 8, 109. | 2.8 | 32 |
| 912 | Gene-resolution analysis of DNA copy number variation using oligonucleotide expression microarrays. BMC Genomics, 2007, 8, 111. | 2.8 | 19 |
| 913 | Global repeat discovery and estimation of genomic copy number in a large, complex genome using a high-throughput 454 sequence survey. BMC Genomics, 2007, 8, 132. | 2.8 | 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. BMC Genomics, 2007, 8, 190. | 2.8 | 22 |
| 915 | WASP: a Web-based Allele-Specific PCR assay designing tool for detecting SNPs and mutations. BMC Genomics, 2007, 8, 275. | 2.8 | 107 |
| 916 | The G protein-coupled receptor subset of the rat genome. BMC Genomics, 2007, 8, 338. | 2.8 | 170 |
| 917 | Short sequence motifs, overrepresented in mammalian conserved non-coding sequences. BMC Genomics, 2007, 8, 378. | 2.8 | 7 |
| 918 | A screen for nuclear transcripts identifies two linked noncoding RNAs associated with SC35 splicing domains. BMC Genomics, 2007, 8, 39. | 2.8 | 836 |
| 919 | Large-scale analysis by SAGE reveals new mechanisms of v-erbA oncogene action. BMC Genomics, 2007, 8, 390. | 2.8 | 15 |
| 920 | Exonization of active mouse L1s: a driver of transcriptome evolution?. BMC Genomics, 2007, 8, 392. | 2.8 | 41 |
| 921 | Mapping of transcription start sites of human retina expressed genes. BMC Genomics, 2007, 8, 42. | 2.8 | 14 |
| 922 | A gene-based radiation hybrid map of the gilthead sea bream Sparus aurata refines and exploits conserved synteny with Tetraodon nigroviridis. BMC Genomics, 2007, 8, 44. | 2.8 | 52 |
| 923 | Ashbya Genome Database 3.0: a cross-species genome and transcriptome browser for yeast biologists. BMC Genomics, 2007, 8, 9. | 2.8 | 46 |
| 924 | Bacterial flora-typing with targeted, chip-based Pyrosequencing. BMC Microbiology, 2007, 7, 108. | 3.3 | 205 |
| 925 | Isolation, sequencing, and functional analysis of the TATA-less murine ATPase II promoter and structural analysis of the ATPase II gene. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2007, 1769, 61-75. | 2.4 | 7 |
| 926 | Translational regulation of human methionine synthase by upstream open reading frames. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 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. Cancer Genetics and Cytogenetics, 2007, 174, 116-120. | 1.0 | 19 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 928 | SGA: A grammar-based alignment algorithm. Computer Methods and Programs in Biomedicine, 2007, 86, 17-20. | 4.7 | 2 |
| 929 | GRATâ€”genome-scale rapid alignment tool. Computer Methods and Programs in Biomedicine, 2007, 86, 87-92. | 4.7 | 3 |
| 930 | Chaperonomics, a new tool to study ageing and associated diseases. Mechanisms of Ageing and Development, 2007, 128, 125-136. | 4.6 | 18 |
| 931 | Reciprocal gene loss between Tetraodon and zebrafish after whole genome duplication in their ancestor. Trends in Genetics, 2007, 23, 108-112. | 6.7 | 116 |
| 932 | Reconsidering the significance of genomic word frequencies. Trends in Genetics, 2007, 23, 543-546. | 6.7 | 31 |
| 933 | Gross Genomic Rearrangement Involving the TSC2-PKD1 Contiguous Deletion Syndrome: Characterization of the Deletion Event by Quantitative Polymerase Chain Reaction Deletion Assay. American Journal of Kidney Diseases, 2007, 49, e11-e21. | 1.9 | 17 |
| 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. | 1.8 | 38 |
| 937 | Evolutionary Pathways of the tirant LTR Retrotransposon in the Drosophila melanogaster Subgroup of Species. Journal of Molecular Evolution, 2007, 64, 438-447. | 1.8 | 9 |
| 938 | Comparative genomics reveals functional transcriptional control sequences in the Prop1 gene. Mammalian Genome, 2007, 18, 521-537. | 2.2 | 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. | 1.8 | 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. | 2.1 | 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. | 2.2 | 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. | 3.7 | 13 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 946 | Different Evolutionary Strategies for the Origin of Caspase-1 Inhibitors. <i>Journal of Molecular Evolution</i> , 2008, 66, 591-597. | 1.8 | 14 |
| 947 | Gene Duplication in Early Vertebrates Results in Tissue-Specific Subfunctionalized Adaptor Proteins: CASP and GRASP. <i>Journal of Molecular Evolution</i> , 2008, 67, 168-178. | 1.8 | 5 |
| 948 | Evolution, expression and effectiveness in a cluster of novel bovine β^2 -defensins. <i>Immunogenetics</i> , 2008, 60, 147-156. | 2.4 | 73 |
| 949 | The effect of temperature on Natural Antisense Transcript (NAT) expression in <i>Aspergillus flavus</i> . <i>Current Genetics</i> , 2008, 54, 241-269. | 1.7 | 41 |
| 950 | An imputed genotype resource for the laboratory mouse. <i>Mammalian Genome</i> , 2008, 19, 199-208. | 2.2 | 79 |
| 951 | Characterization of mouse Dactylaplasia mutations: a model for human ectrodactyly SHFM3. <i>Mammalian Genome</i> , 2008, 19, 272-278. | 2.2 | 23 |
| 952 | An epigenetic aberration increased in intergenic regions of cloned mice. <i>Mammalian Genome</i> , 2008, 19, 667-674. | 2.2 | 5 |
| 953 | The Genome Browser at UCSC for Locating Genes, and Much More!. <i>Molecular Biotechnology</i> , 2008, 38, 269-275. | 2.4 | 15 |
| 954 | Linking the Genomes of Nonmodel Teleosts Through Comparative Genomics. <i>Marine Biotechnology</i> , 2008, 10, 227-233. | 2.4 | 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. | 1.6 | 22 |
| 957 | Genotype-phenotype correlations in MYCN-related Feingold syndrome. <i>Human Mutation</i> , 2008, 29, 1125-1132. | 2.5 | 72 |
| 958 | An unusual haplotype structure on human chromosome 8p23 derived from the inversion polymorphism. <i>Human Mutation</i> , 2008, 29, 1209-1216. | 2.5 | 30 |
| 959 | Characterization of TRIM31, upregulated in gastric adenocarcinoma, as a novel RBCC protein. <i>Journal of Cellular Biochemistry</i> , 2008, 105, 1081-1091. | 2.6 | 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. | 1.7 | 8 |
| 961 | An automated, high-throughput sequence read classification pipeline for preliminary genome characterization. <i>Analytical Biochemistry</i> , 2008, 373, 78-87. | 2.4 | 5 |
| 962 | A small trip in the untranquil world of genomes. <i>Theoretical Computer Science</i> , 2008, 395, 171-192. | 0.9 | 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. | 5.9 | 739 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 964 | A novel insertion variant of the human IL-23 receptor-Î± chain transcript. <i>Genes and Immunity</i> , 2008, 9, 566-569. | 4.1 | 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. | 4.5 | 12 |
| 966 | Proportionally more deleterious genetic variation in European than in African populations. <i>Nature</i> , 2008, 451, 994-997. | 27.8 | 365 |
| 967 | A discontinuous hammerhead ribozyme embedded in a mammalian messenger RNA. <i>Nature</i> , 2008, 454, 899-902. | 27.8 | 156 |
| 968 | The impact of microRNAs on protein output. <i>Nature</i> , 2008, 455, 64-71. | 27.8 | 3,270 |
| 969 | Design and analysis of ChIP-seq experiments for DNA-binding proteins. <i>Nature Biotechnology</i> , 2008, 26, 1351-1359. | 17.5 | 825 |
| 970 | Primary microRNA transcripts are processed co-transcriptionally. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 902-909. | 8.2 | 335 |
| 971 | Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , 2008, 5, 613-619. | 19.0 | 952 |
| 972 | Steady progress and recent breakthroughs in the accuracy of automated genome annotation. <i>Nature Reviews Genetics</i> , 2008, 9, 62-73. | 16.3 | 133 |
| 973 | Towards a cyberinfrastructure for the biological sciences: progress, visions and challenges. <i>Nature Reviews Genetics</i> , 2008, 9, 678-688. | 16.3 | 145 |
| 974 | The DISC locus in psychiatric illness. <i>Molecular Psychiatry</i> , 2008, 13, 36-64. | 7.9 | 554 |
| 975 | Identification of the sensory neuron specific regulatory region for the mouse gene encoding the voltage-gated sodium channel Na _V 1.8. <i>Journal of Neurochemistry</i> , 2008, 106, 1209-1224. | 3.9 | 14 |
| 976 | Development of an <i>in silico</i> coding gene SNP map in pigs. <i>Animal Genetics</i> , 2008, 39, 446-450. | 1.7 | 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. | 1.2 | 10 |
| 978 | Multiple organism algorithm for finding ultraconserved elements. <i>BMC Bioinformatics</i> , 2008, 9, 15. | 2.6 | 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. | 2.6 | 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. | 2.6 | 137 |
| 981 | SynBlast: Assisting the analysis of conserved syntenic information. <i>BMC Bioinformatics</i> , 2008, 9, 351. | 2.6 | 12 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 982 | Identification and correction of abnormal, incomplete and mispredicted proteins in public databases. BMC Bioinformatics, 2008, 9, 353. | 2.6 | 55 |
| 983 | SQUAT: A web tool to mine human, murine and avian SAGE data. BMC Bioinformatics, 2008, 9, 378. | 2.6 | 7 |
| 984 | Optimal neighborhood indexing for protein similarity search. BMC Bioinformatics, 2008, 9, 534. | 2.6 | 3 |
| 985 | Supervised Lowess normalization of comparative genome hybridization data “ application to lactococcal strain comparisons. BMC Bioinformatics, 2008, 9, 93. | 2.6 | 20 |
| 986 | Functional analysis of novel SNPs and mutations in human and mouse genomes. BMC Bioinformatics, 2008, 9, S10. | 2.6 | 16 |
| 987 | hsp70 genes in the human genome: Conservation and differentiation patterns predict a wide array of overlapping and specialized functions. BMC Evolutionary Biology, 2008, 8, 19. | 3.2 | 224 |
| 988 | A genomic view of the NOD-like receptor family in teleost fish: identification of a novel NLR subfamily in zebrafish. BMC Evolutionary Biology, 2008, 8, 42. | 3.2 | 199 |
| 989 | Opossum carboxylesterases: sequences, phylogeny and evidence for CES gene duplication events predating the marsupial-eutherian common ancestor. BMC Evolutionary Biology, 2008, 8, 54. | 3.2 | 12 |
| 990 | The amphioxus (<i>Branchiostoma floridae</i>) genome contains a highly diversified set of G protein-coupled receptors. BMC Evolutionary Biology, 2008, 8, 9. | 3.2 | 87 |
| 991 | Rapid detection and curation of conserved DNA via enhanced-BLAT and EvoPrinterHD analysis. BMC Genomics, 2008, 9, 106. | 2.8 | 31 |
| 992 | A novel method of differential gene expression analysis using multiple cDNA libraries applied to the identification of tumour endothelial genes. BMC Genomics, 2008, 9, 153. | 2.8 | 47 |
| 993 | Detailed characterization of the mouse embryonic stem cell transcriptome reveals novel genes and intergenic splicing associated with pluripotency. BMC Genomics, 2008, 9, 155. | 2.8 | 13 |
| 994 | Hidden layers of human small RNAs. BMC Genomics, 2008, 9, 157. | 2.8 | 255 |
| 995 | How many human genes can be defined as housekeeping with current expression data?. BMC Genomics, 2008, 9, 172. | 2.8 | 125 |
| 996 | Non-random retention of protein-coding overlapping genes in Metazoa. BMC Genomics, 2008, 9, 174. | 2.8 | 26 |
| 997 | Comparative analysis of sequence features involved in the recognition of tandem splice sites. BMC Genomics, 2008, 9, 202. | 2.8 | 9 |
| 998 | Repeats and EST analysis for new organisms. BMC Genomics, 2008, 9, 23. | 2.8 | 12 |
| 999 | The RHNumtS compilation: Features and bioinformatics approaches to locate and quantify Human NumtS. BMC Genomics, 2008, 9, 267. | 2.8 | 34 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 1000 | Genome-wide identification of coding and non-coding conserved sequence tags in human and mouse genomes. BMC Genomics, 2008, 9, 277. | 2.8 | 3 |
| 1001 | Genome-wide analysis of alternative promoters of human genes using a custom promoter tiling array. BMC Genomics, 2008, 9, 349. | 2.8 | 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. BMC Genomics, 2008, 9, 354. | 2.8 | 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. BMC Genomics, 2008, 9, 407. | 2.8 | 28 |
| 1004 | WebScipio: An online tool for the determination of gene structures using protein sequences. BMC Genomics, 2008, 9, 422. | 2.8 | 30 |
| 1005 | Retrocopy contributions to the evolution of the human genome. BMC Genomics, 2008, 9, 466. | 2.8 | 93 |
| 1006 | Analysis of the <i>Pythium ultimum</i> transcriptome using Sanger and Pyrosequencing approaches. BMC Genomics, 2008, 9, 542. | 2.8 | 78 |
| 1007 | LTR retrotransposons reveal recent extensive inter-subspecies nonreciprocal recombination in Asian cultivated rice. BMC Genomics, 2008, 9, 565. | 2.8 | 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. BMC Genomics, 2008, 9, 57. | 2.8 | 68 |
| 1009 | ProSeeK: A web server for MLPA probe design. BMC Genomics, 2008, 9, 573. | 2.8 | 6 |
| 1010 | Methylation-sensitive linking libraries enhance gene-enriched sequencing of complex genomes and map DNA methylation domains. BMC Genomics, 2008, 9, 621. | 2.8 | 11 |
| 1011 | Identification of novel homologous microRNA genes in the rhesus macaque genome. BMC Genomics, 2008, 9, 8. | 2.8 | 38 |
| 1012 | Complementary RNA amplification methods enhance microarray identification of transcripts expressed in the <i>C. elegans</i> nervous system. BMC Genomics, 2008, 9, 84. | 2.8 | 34 |
| 1013 | Gene conversion in the rice genome. BMC Genomics, 2008, 9, 93. | 2.8 | 42 |
| 1014 | xMAN: extreme MApping of OligoNucleotides. BMC Genomics, 2008, 9, S20. | 2.8 | 19 |
| 1015 | Fast comparison of DNA sequences by oligonucleotide profiling. BMC Research Notes, 2008, 1, 5. | 1.4 | 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. BMC Research Notes, 2008, 1, 95. | 1.4 | 36 |
| 1017 | Patterns of Codon Usage in two Ciliates that Reassign the Genetic Code: <i>Tetrahymena thermophila</i> and <i>Paramecium tetraurelia</i> . Protist, 2008, 159, 283-298. | 1.5 | 32 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 1018 | Effect of ergot alkaloids associated with fescue toxicosis on hepatic cytochrome P450 and antioxidant proteins. Toxicology and Applied Pharmacology, 2008, 227, 347-356. | 2.8 | 25 |
| 1019 | Bioinformatics challenges of new sequencing technology. Trends in Genetics, 2008, 24, 142-149. | 6.7 | 438 |
| 1020 | The impact of next-generation sequencing technology on genetics. Trends in Genetics, 2008, 24, 133-141. | 6.7 | 1,848 |
| 1021 | <i>Cassandra</i> retrotransposons carry independently transcribed 5S RNA. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5833-5838. | 7.1 | 127 |
| 1022 | HTLV-1 Integration into Transcriptionally Active Genomic Regions Is Associated with Proviral Expression and with HAM/TSP. PLoS Pathogens, 2008, 4, e1000027. | 4.7 | 91 |
| 1024 | Clinical Uses of Microarrays in Cancer Research. Methods in Molecular Medicine, 2008, 141, 87-113. | 0.8 | 18 |
| 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. | 2.6 | 3 |
| 1027 | HIV-1 latency in actively dividing human T cell lines. Retrovirology, 2008, 5, 37. | 2.0 | 45 |
| 1028 | Splign: algorithms for computing spliced alignments with identification of paralogs. Biology Direct, 2008, 3, 20. | 4.6 | 329 |
| 1029 | Molecular Identification and Functional Characterization of the Kisspeptin/Kisspeptin Receptor System in Lower Vertebrates1. Biology of Reproduction, 2008, 79, 776-786. | 2.7 | 211 |
| 1030 | Genome-Wide Association of Histone H3 Lysine Nine Methylation with CHG DNA Methylation in Arabidopsis thaliana. PLoS ONE, 2008, 3, e3156. | 2.5 | 293 |
| 1031 | Genome Annotation. Methods in Molecular Biology, 2008, 452, 125-139. | 0.9 | 7 |
| 1032 | Essential Concepts in Toxicogenomics. Methods in Molecular Biology, 2008, , . | 0.9 | 1 |
| 1033 | CompostBin: A DNA Composition-Based Algorithm for Binning Environmental Shotgun Reads. Lecture Notes in Computer Science, 2008, , 17-28. | 1.3 | 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. | 9.6 | 192 |
| 1035 | Genomic analysis of the relationship between gene expression variation and DNA polymorphism in Drosophila simulans. Genome Biology, 2008, 9, R125. | 9.6 | 17 |
| 1036 | Cross-kingdom patterns of alternative splicing and splice recognition. Genome Biology, 2008, 9, R50. | 9.6 | 126 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1037 | Transcriptional analysis of highly syntenic regions between <i>Medicago truncatula</i> and <i>Glycine max</i> using tiling microarrays. <i>Genome Biology</i> , 2008, 9, R57. | 9.6 | 13 |
| 1038 | A sequence-based survey of the complex structural organization of tumor genomes. <i>Genome Biology</i> , 2008, 9, R59. | 9.6 | 31 |
| 1039 | Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Biology</i> , 2008, 9, R45. | 9.6 | 82 |
| 1040 | The Groucho/TLE/Grg family of transcriptional co-repressors. <i>Genome Biology</i> , 2008, 9, 205. | 9.6 | 141 |
| 1041 | Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. <i>Genome Biology</i> , 2008, 9, R3. | 9.6 | 53 |
| 1042 | Automated eukaryotic gene structure annotation using EvidenceModeler and the Program to Assemble Spliced Alignments. <i>Genome Biology</i> , 2008, 9, R7. | 9.6 | 2,484 |
| 1043 | Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008, 18, 1851-1858. | 5.5 | 2,275 |
| 1044 | Inferring Function from Homology. <i>Methods in Molecular Biology</i> , 2008, 453, 149-168. | 0.9 | 9 |
| 1045 | Bioinformatics Detection of Alternative Splicing. <i>Methods in Molecular Biology</i> , 2008, 452, 179-197. | 0.9 | 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. | 3.2 | 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. | 2.2 | 77 |
| 1048 | Combinatorial effects of four histone modifications in transcription and differentiation. <i>Genomics</i> , 2008, 91, 41-51. | 2.9 | 45 |
| 1049 | UCSC genome browser tutorial. <i>Genomics</i> , 2008, 92, 75-84. | 2.9 | 108 |
| 1050 | Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008, 9, R175. | 9.6 | 210 |
| 1051 | Retrotransposition as a Source of New Promoters. <i>Molecular Biology and Evolution</i> , 2008, 25, 1231-1238. | 8.9 | 38 |
| 1052 | Molecular cloning and analysis of breakpoints on ring chromosome 17 in a patient with autism. <i>Gene</i> , 2008, 407, 186-192. | 2.2 | 14 |
| 1053 | Bioinformatic prediction and analysis of eukaryotic protein kinases in the rat genome. <i>Gene</i> , 2008, 410, 147-153. | 2.2 | 20 |
| 1054 | Zebrafish U6 small nuclear RNA gene promoters contain a SPH element in an unusual location. <i>Gene</i> , 2008, 421, 89-94. | 2.2 | 11 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1055 | Comparative analysis of an unusual gene arrangement in the human chromosome 1. <i>Gene</i> , 2008, 423, 172-179. | 2.2 | 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. | 1.0 | 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. | 1.6 | 15 |
| 1058 | High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322. | 28.9 | 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. | 28.9 | 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. | 7.0 | 79 |
| 1061 | Translational control of intron splicing in eukaryotes. <i>Nature</i> , 2008, 451, 359-362. | 27.8 | 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. | 5.5 | 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. | 2.1 | 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. | 1.4 | 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. | 5.5 | 698 |
| 1071 | Comparative and Evolutionary Genomics of Globin Genes in Fish. <i>Methods in Enzymology</i> , 2008, 436, 511-538. | 1.0 | 6 |
| 1072 | Conserved chromosomal clustering of genes governed by chromatin regulators in <i>Drosophila</i> . <i>Genome Biology</i> , 2008, 9, R134. | 9.6 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1073 | Chromatin structure analyses identify miRNA promoters. <i>Genes and Development</i> , 2008, 22, 3172-3183. | 5.9 | 541 |
| 1074 | Designating eukaryotic orthology via processed transcription units. <i>Nucleic Acids Research</i> , 2008, 36, 3436-3442. | 14.5 | 4 |
| 1075 | Species-specific Differences among KCNMB3 BK β 3 Auxiliary Subunits: Some β 3 N-terminal Variants May Be Primate-specific Subunits. <i>Journal of General Physiology</i> , 2008, 132, 115-129. | 1.9 | 20 |
| 1076 | SeqMap: mapping massive amount of oligonucleotides to the genome. <i>Bioinformatics</i> , 2008, 24, 2395-2396. | 4.1 | 459 |
| 1077 | OREST: the online resource for EST analysis. <i>Nucleic Acids Research</i> , 2008, 36, W140-W144. | 14.5 | 6 |
| 1078 | Tissue-specific splicing factor gene expression signatures. <i>Nucleic Acids Research</i> , 2008, 36, 4823-4832. | 14.5 | 172 |
| 1079 | Gene prediction in novel fungal genomes using an ab initio algorithm with unsupervised training. <i>Genome Research</i> , 2008, 18, 1979-1990. | 5.5 | 800 |
| 1080 | Predicting functional regulatory polymorphisms. <i>Bioinformatics</i> , 2008, 24, 1787-1792. | 4.1 | 21 |
| 1081 | Database indexing for production MegaBLAST searches. <i>Bioinformatics</i> , 2008, 24, 1757-1764. | 4.1 | 993 |
| 1082 | Large-scale gene trapping in C57BL/6N mouse embryonic stem cells. <i>Genome Research</i> , 2008, 18, 1670-1679. | 5.5 | 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. | 3.5 | 9 |
| 1084 | Comparative expression analysis uncovers novel features of endogenous antisense transcription. <i>Human Molecular Genetics</i> , 2008, 17, 1631-1640. | 2.9 | 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. | 8.9 | 96 |
| 1086 | WAMIDEX: A web atlas of murine genomic imprinting and differential expression. <i>Epigenetics</i> , 2008, 3, 89-96. | 2.7 | 51 |
| 1087 | Using whole genome presence/absence data to untangle function in 12 <i>Drosophila</i> genomes. <i>Fly</i> , 2008, 2, 291-299. | 1.7 | 10 |
| 1088 | Run Probabilities of Seed-Like Patterns and Identifying Good Transition Seeds. <i>Journal of Computational Biology</i> , 2008, 15, 1295-1313. | 1.6 | 16 |
| 1089 | G9a Histone Methyltransferase Contributes to Imprinting in the Mouse Placenta. <i>Molecular and Cellular Biology</i> , 2008, 28, 1104-1113. | 2.3 | 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. | 7.1 | 70 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1091 | Transcriptional Autoregulation Controls Pancreatic <i>Ptf1a</i> Expression during Development and Adulthood. <i>Molecular and Cellular Biology</i> , 2008, 28, 5458-5468. | 2.3 | 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. | 5.5 | 261 |
| 1093 | The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111. | 5.5 | 456 |
| 1094 | Nested Patch PCR enables highly multiplexed mutation discovery in candidate genes. <i>Genome Research</i> , 2008, 18, 1844-1850. | 5.5 | 55 |
| 1095 | Molecular profiling in the age of cancer genomics. <i>Expert Review of Molecular Diagnostics</i> , 2008, 8, 263-276. | 3.1 | 8 |
| 1096 | FishMap: A Community Resource for Zebrafish Genomics. <i>Zebrafish</i> , 2008, 5, 125-130. | 1.1 | 20 |
| 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. | 0.8 | 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. | 7.1 | 247 |
| 1099 | Genome-Wide Pattern of TCF7L2/TCF4 Chromatin Occupancy in Colorectal Cancer Cells. <i>Molecular and Cellular Biology</i> , 2008, 28, 2732-2744. | 2.3 | 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. | 2.5 | 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. | 5.5 | 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. | 3.6 | 26 |
| 1103 | Characterization of genome-wide p53-binding sites upon stress response. <i>Nucleic Acids Research</i> , 2008, 36, 3639-3654. | 14.5 | 199 |
| 1104 | DNAlive: a tool for the physical analysis of DNA at the genomic scale. <i>Bioinformatics</i> , 2008, 24, 1731-1732. | 4.1 | 28 |
| 1105 | Navigating the genome. <i>Journal of Cell Science</i> , 2008, 121, 921-923. | 2.0 | 0 |
| 1106 | Using retroviruses as a mutagenesis tool to explore the zebrafish genome. <i>Briefings in Functional Genomics & 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. | 2.0 | 3 |
| 1108 | Multilocus Patterns of Nucleotide Polymorphism and the Demographic History of <i>Populus tremula</i> . <i>Genetics</i> , 2008, 180, 329-340. | 2.9 | 173 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1109 | Genotypic Features of Lentivirus Transgenic Mice. <i>Journal of Virology</i> , 2008, 82, 7111-7119. | 3.4 | 30 |
| 1110 | A microRNA catalog of the developing chicken embryo identified by a deep sequencing approach. <i>Genome Research</i> , 2008, 18, 957-964. | 5.5 | 282 |
| 1111 | ZOOM! Zillions of oligos mapped. <i>Bioinformatics</i> , 2008, 24, 2431-2437. | 4.1 | 187 |
| 1112 | Fast Evolution of Core Promoters in Primate Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1239-1244. | 8.9 | 15 |
| 1113 | Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. <i>PLoS Genetics</i> , 2008, 4, e1000271. | 3.5 | 143 |
| 1114 | Direct mapping and alignment of protein sequences onto genomic sequence. <i>Bioinformatics</i> , 2008, 24, 2438-2444. | 4.1 | 53 |
| 1115 | High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. <i>PLoS Genetics</i> , 2008, 4, e1000249. | 3.5 | 99 |
| 1116 | High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. <i>PLoS Genetics</i> , 2008, 4, e1000214. | 3.5 | 510 |
| 1117 | Near Intron Positions Are Reliable Phylogenetic Markers: An Application to Holometabolous Insects. <i>Molecular Biology and Evolution</i> , 2008, 25, 821-830. | 8.9 | 39 |
| 1118 | A robust framework for detecting structural variations in a genome. <i>Bioinformatics</i> , 2008, 24, i59-i67. | 4.1 | 49 |
| 1119 | Agglomerative Epigenetic Aberrations Are a Common Event in Human Breast Cancer. <i>Cancer Research</i> , 2008, 68, 8616-8625. | 0.9 | 146 |
| 1120 | Using native and syntenically mapped cDNA alignments to improve <i>de novo</i> gene finding. <i>Bioinformatics</i> , 2008, 24, 637-644. | 4.1 | 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. | 8.9 | 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. | 8.3 | 36 |
| 1123 | Chromosomal Gene Movements Reflect the Recent Origin and Biology of Therian Sex Chromosomes. <i>PLoS Biology</i> , 2008, 6, e80. | 5.6 | 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. | 3.5 | 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. | 3.5 | 262 |
| 1126 | The Status of Dosage Compensation in the Multiple X Chromosomes of the Platypus. <i>PLoS Genetics</i> , 2008, 4, e1000140. | 3.5 | 102 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1127 | Identification of ancient remains through genomic sequencing. <i>Genome Research</i> , 2008, 18, 1347-1353. | 5.5 | 47 |
| 1128 | genBlastA: Enabling BLAST to identify homologous gene sequences. <i>Genome Research</i> , 2009, 19, 143-149. | 5.5 | 249 |
| 1129 | Genome level analysis of rice mRNA 3' end processing signals and alternative polyadenylation. <i>Nucleic Acids Research</i> , 2008, 36, 3150-3161. | 14.5 | 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. | 3.1 | 16 |
| 1131 | Splicing factor SFRS1 recognizes a functionally diverse landscape of RNA transcripts. <i>Genome Research</i> , 2009, 19, 381-394. | 5.5 | 284 |
| 1132 | Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403. | 5.5 | 117 |
| 1133 | Analysis of Alternative Splicing in Plants with Bioinformatics Tools. <i>Current Topics in Microbiology and Immunology</i> , 2008, 326, 17-37. | 1.1 | 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. | 8.9 | 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. | 2.3 | 60 |
| 1136 | Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. <i>Rna</i> , 2008, 14, 2455-2459. | 3.5 | 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. | 14.5 | 91 |
| 1138 | On the origin of new genes in <i>Drosophila</i> . <i>Genome Research</i> , 2008, 18, 1446-1455. | 5.5 | 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. | 14.5 | 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. | 3.4 | 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. | 3.3 | 45 |
| 1142 | Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009, 15, 85-96. | 3.5 | 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. | 7.1 | 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. | 8.3 | 101 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 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. | 2.9 | 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. | 5.5 | 129 |
| 1147 | Dispensability of mammalian DNA. <i>Genome Research</i> , 2008, 18, 1743-1751. | 5.5 | 42 |
| 1148 | Properties of Wild-Type and Fluorescent Protein-Tagged Mouse Tetrodotoxin-Resistant Sodium Channel (Na _V 1.8) Heterologously Expressed in Rat Sympathetic Neurons. <i>Journal of Neurophysiology</i> , 2008, 99, 1917-1927. | 1.8 | 12 |
| 1149 | SOX17 directly activates <i>Zfp202</i> transcription during in vitro endoderm differentiation. <i>Physiological Genomics</i> , 2008, 34, 277-284. | 2.3 | 8 |
| 1150 | Haplotype sorting using human fosmid clone end-sequence pairs. <i>Genome Research</i> , 2008, 18, 2016-2023. | 5.5 | 25 |
| 1151 | Specific expression of long noncoding RNAs in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 716-721. | 7.1 | 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. <i>Genetical Research</i> , 2008, 90, 243-252. | 0.9 | 18 |
| 1154 | Mutation Detection Using Automated Fluorescence-Based Sequencing. <i>Current Protocols in Human Genetics</i> , 2008, 57, Unit7.9. | 3.5 | 5 |
| 1155 | $\frac{1}{4}$ mutation patterns suggest different progression pathways in follicular lymphoma: early direct or late from FL progenitor cells. <i>Blood</i> , 2008, 112, 1951-1959. | 1.4 | 54 |
| 1156 | Calcitonin receptor-like receptor guides arterial differentiation in zebrafish. <i>Blood</i> , 2008, 111, 4965-4972. | 1.4 | 38 |
| 1157 | Global Sequencing: A Review of Current Molecular Data and New Methods Available to Assess Microbial Diversity. <i>Microbes and Environments</i> , 2008, 23, 253-268. | 1.6 | 64 |
| 1158 | CoCoNUT: an efficient system for the comparison and analysis of genomes. <i>BMC Bioinformatics</i> , 2008, 9, 476. | 2.6 | 23 |
| 1159 | Strategies for Reliable Exploitation of Evolutionary Concepts in High Throughput Biology. <i>Evolutionary Bioinformatics</i> , 2008, 4, EBO.S597. | 1.2 | 15 |
| 1160 | On the Extent and Origins of Genic Novelty in the Phylum Nematoda. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e258. | 3.0 | 68 |
| 1161 | GPCR Genes Are Preferentially Retained after Whole Genome Duplication. <i>PLoS ONE</i> , 2008, 3, e1903. | 2.5 | 22 |
| 1162 | Width of Gene Expression Profile Drives Alternative Splicing. <i>PLoS ONE</i> , 2008, 3, e3587. | 2.5 | 13 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1163 | The Human Microbiome and Infectious Diseases: Beyond Koch. Interdisciplinary Perspectives on Infectious Diseases, 2008, 2008, 1-2. | 1.4 | 11 |
| 1164 | The Human Vaginal Bacterial Biota and Bacterial Vaginosis. Interdisciplinary Perspectives on Infectious Diseases, 2008, 2008, 1-22. | 1.4 | 185 |
| 1165 | Affymetrix Whole-Transcript Human Gene 1.0 ST array is highly concordant with standard 3â€² expression arrays. BioTechniques, 2008, 44, 759-762. | 1.8 | 31 |
| 1166 | Largeâ€”Scale Discovery of Geneâ€”Enriched SNPs. Plant Genome, 2009, 2, . | 2.8 | 55 |
| 1167 | High Performance Protein Sequence Database Scanning on the Cell Broadband Engine. Scientific Programming, 2009, 17, 97-111. | 0.7 | 5 |
| 1168 | A novel L1 retrotransposon marker for HeLa cell line identification. BioTechniques, 2009, 46, 277-284. | 1.8 | 115 |
| 1169 | High-throughput verification of transcriptional starting sites by Deep-RACE. BioTechniques, 2009, 46, 130-132. | 1.8 | 33 |
| 1170 | Structural Fingerprints of Transcription Factor Binding Site Regions. Algorithms, 2009, 2, 448-469. | 2.1 | 1 |
| 1171 | Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. PLoS ONE, 2009, 4, e6524. | 2.5 | 568 |
| 1172 | Fine-Scale Phylogenetic Discordance across the House Mouse Genome. PLoS Genetics, 2009, 5, e1000729. | 3.5 | 104 |
| 1173 | Sequencing, Mapping, and Analysis of 27,455 Maize Full-Length cDNAs. PLoS Genetics, 2009, 5, e1000740. | 3.5 | 145 |
| 1174 | Big Genomes Facilitate the Comparative Identification of Regulatory Elements. PLoS ONE, 2009, 4, e4688. | 2.5 | 41 |
| 1175 | A Scalable Method for Analysis and Display of DNA Sequences. PLoS ONE, 2009, 4, e7051. | 2.5 | 23 |
| 1176 | BFAST: An Alignment Tool for Large Scale Genome Resequencing. PLoS ONE, 2009, 4, e7767. | 2.5 | 444 |
| 1177 | A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in Arabidopsis thaliana. PLoS Genetics, 2009, 5, e1000551. | 3.5 | 554 |
| 1178 | Identification of Lympho-Epithelial Kazal-Type Inhibitor 2 in Human Skin as a Kallikrein-Related Peptidase 5-Specific Protease Inhibitor. PLoS ONE, 2009, 4, e4372. | 2.5 | 60 |
| 1179 | The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333. | 5.5 | 125 |
| 1180 | Mapping short reads to a genome without using hash look-up table algorithm and Burrows Wheeler Transformation. , 2009, , . | | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1181 | VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587. | 14.5 | 234 |
| 1182 | Recent de novo origin of human protein-coding genes. Genome Research, 2009, 19, 1752-1759. | 5.5 | 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. Nucleic Acids Research, 2009, 37, 3276-3287. | 14.5 | 60 |
| 1185 | RazerS—fast read mapping with sensitivity control. Genome Research, 2009, 19, 1646-1654. | 5.5 | 125 |
| 1186 | Cell contact-dependent acquisition of cellular and viral nonautonomously encoded small RNAs. Genes and Development, 2009, 23, 1971-1979. | 5.9 | 106 |
| 1187 | A Domestic cat X Chromosome Linkage Map and the Sex-Linked Locus: Mapping of, Multiple Origins and Epistasis Over nonagouti. Genetics, 2009, 181, 1415-1425. | 2.9 | 30 |
| 1188 | Identification and Characterization of a Novel Gene, dapr, Involved in Skeletal Muscle Differentiation and Protein Kinase B Signaling. Journal of Biological Chemistry, 2009, 284, 1636-1643. | 3.4 | 3 |
| 1189 | Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. Journal of Immunology, 2009, 182, 7738-7748. | 0.8 | 221 |
| 1190 | mGene: Accurate SVM-based gene finding with an application to nematode genomes. Genome Research, 2009, 19, 2133-2143. | 5.5 | 79 |
| 1191 | Blimp-1/Prdm1 Alternative Promoter Usage during Mouse Development and Plasma Cell Differentiation. Molecular and Cellular Biology, 2009, 29, 5813-5827. | 2.3 | 57 |
| 1192 | Response of Gastric Epithelial Progenitors to Helicobacter pylori Isolates Obtained from Swedish Patients with Chronic Atrophic Gastritis. Journal of Biological Chemistry, 2009, 284, 30383-30394. | 3.4 | 25 |
| 1193 | Genetic Regulatory Network Analysis for App-Based on Genetical Genomics Approach. Experimental Aging Research, 2009, 36, 79-93. | 1.2 | 14 |
| 1194 | Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875. | 8.9 | 50 |
| 1195 | Detection of intergenic non-coding RNAs expressed in the main developmental stages in Drosophila melanogaster. Nucleic Acids Research, 2009, 37, 4308-4314. | 14.5 | 21 |
| 1196 | Exon-trapping mediated by the human retrotransposon SVA. Genome Research, 2009, 19, 1983-1991. | 5.5 | 94 |
| 1197 | Translation of an STR-based biomarker into a clinically compatible SNP-based platform for loss of heterozygosity. Cancer Biomarkers, 2009, 5, 143-158. | 1.7 | 8 |
| 1198 | Analysis of Transcriptome Changes Induced by Ptr ToxA in Wheat Provides Insights into the Mechanisms of Plant Susceptibility. Molecular Plant, 2009, 2, 1067-1083. | 8.3 | 54 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1199 | PerM: efficient mapping of short sequencing reads with periodic full sensitive spaced seeds. <i>Bioinformatics</i> , 2009, 25, 2514-2521. | 4.1 | 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. | 7.1 | 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. | 5.9 | 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. | 8.9 | 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. | 14.5 | 33 |
| 1204 | HAPLOWSER: a whole-genome haplotype browser for personal genome and metagenome. <i>Bioinformatics</i> , 2009, 25, 2430-2431. | 4.1 | 2 |
| 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. | 14.5 | 13 |
| 1206 | The UCSC Genome Browser Database: update 2009. <i>Nucleic Acids Research</i> , 2009, 37, D755-D761. | 14.5 | 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. | 14.5 | 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. | 2.5 | 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. | 0.9 | 156 |
| 1211 | A High-Density Single Nucleotide Polymorphism Map for <i>Neurospora crassa</i> . <i>Genetics</i> , 2009, 181, 767-781. | 2.9 | 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. | 2.6 | 9 |
| 1213 | Characterizing the D2 Statistic: Word Matches in Biological Sequences. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-21. | 0.6 | 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. | 2.0 | 32 |
| 1215 | Transcriptional Enhancers Induce Insertional Gene Dereglulation Independently From the Vector Type and Design. <i>Molecular Therapy</i> , 2009, 17, 851-856. | 8.2 | 79 |
| 1216 | Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731. | 5.5 | 295 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1217 | High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. <i>Genome Research</i> , 2009, 19, 1133-1140. | 5.5 | 69 |
| 1218 | Extensive Structural Renovation of Retrogenes in the Evolution of the Populus Genome. <i>Plant Physiology</i> , 2009, 151, 1943-1951. | 4.8 | 66 |
| 1219 | SNP-o-matic. <i>Bioinformatics</i> , 2009, 25, 2434-2435. | 4.1 | 23 |
| 1220 | Evolutionary Breakpoints in the Gibbon Suggest Association between Cytosine Methylation and Karyotype Evolution. <i>PLoS Genetics</i> , 2009, 5, e1000538. | 3.5 | 81 |
| 1221 | GASZ Is Essential for Male Meiosis and Suppression of Retrotransposon Expression in the Male Germline. <i>PLoS Genetics</i> , 2009, 5, e1000635. | 3.5 | 151 |
| 1222 | WebGMAP: a web service for mapping and aligning cDNA sequences to genomes. <i>Nucleic Acids Research</i> , 2009, 37, W77-W83. | 14.5 | 5 |
| 1223 | Using microarrays to identify positional candidate genes for QTL: the case study of ACTH response in pigs. <i>BMC Proceedings</i> , 2009, 3, S14. | 1.6 | 10 |
| 1224 | A Genome-Wide Association Study of Pulmonary Function Measures in the Framingham Heart Study. <i>PLoS Genetics</i> , 2009, 5, e1000429. | 3.5 | 292 |
| 1225 | Comparison of three microarray probe annotation pipelines: differences in strategies and their effect on downstream analysis. <i>BMC Proceedings</i> , 2009, 3, S1. | 1.6 | 7 |
| 1226 | Evolutionary Processes Acting on Candidate cis-Regulatory Regions in Humans Inferred from Patterns of Polymorphism and Divergence. <i>PLoS Genetics</i> , 2009, 5, e1000592. | 3.5 | 123 |
| 1227 | MFEprimer: multiple factor evaluation of the specificity of PCR primers. <i>Bioinformatics</i> , 2009, 25, 276-278. | 4.1 | 62 |
| 1228 | Global discovery of primate-specific genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12019-12024. | 7.1 | 66 |
| 1229 | Fine-Scale Variation and Genetic Determinants of Alternative Splicing across Individuals. <i>PLoS Genetics</i> , 2009, 5, e1000766. | 3.5 | 81 |
| 1230 | Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. <i>Bioinformatics</i> , 2009, 25, 1587-1593. | 4.1 | 6 |
| 1231 | G-compass: a web-based comparative genome browser between human and other vertebrate genomes. <i>Bioinformatics</i> , 2009, 25, 3321-3322. | 4.1 | 7 |
| 1232 | A comprehensive in silico expression analysis of RNA binding proteins in normal and tumor tissue; identification of potential players in tumor formation. <i>RNA Biology</i> , 2009, 6, 426-433. | 3.1 | 51 |
| 1233 | Age-Associated Inflammation and Toll-Like Receptor Dysfunction Prime the Lungs for Pneumococcal Pneumonia. <i>Journal of Infectious Diseases</i> , 2009, 200, 546-554. | 4.0 | 131 |
| 1234 | k-link EST clustering: evaluating error introduced by chimeric sequences under different degrees of linkage. <i>Bioinformatics</i> , 2009, 25, 2302-2308. | 4.1 | 4 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1235 | Conserved introns reveal novel transcripts in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2009, 19, 1289-1300. | 5.5 | 38 |
| 1236 | Seq-SNPing: Multiple-Alignment Tool for SNP Discovery, SNP ID Identification, and RFLP Genotyping. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 253-260. | 2.0 | 13 |
| 1237 | Modulation of gene expression in U251 glioblastoma cells by binding of mutant p53 R273H to intronic and intergenic sequences. <i>Nucleic Acids Research</i> , 2009, 37, 1486-1500. | 14.5 | 56 |
| 1238 | A <i>Caenorhabditis elegans</i> RNA-Directed RNA Polymerase in Sperm Development and Endogenous RNA Interference. <i>Genetics</i> , 2009, 183, 1297-1314. | 2.9 | 80 |
| 1239 | Lowly Expressed Human MicroRNA Genes Evolve Rapidly. <i>Molecular Biology and Evolution</i> , 2009, 26, 1195-1198. | 8.9 | 86 |
| 1240 | RiceGeneThresher: a web-based application for mining genes underlying QTL in rice genome. <i>Nucleic Acids Research</i> , 2009, 37, D996-D1000. | 14.5 | 10 |
| 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. | 6.6 | 128 |
| 1242 | MachiBase: a <i>Drosophila melanogaster</i> 5'-end mRNA transcription database. <i>Nucleic Acids Research</i> , 2009, 37, D49-D53. | 14.5 | 23 |
| 1243 | Evolution of Vault RNAs. <i>Molecular Biology and Evolution</i> , 2009, 26, 1975-1991. | 8.9 | 130 |
| 1244 | Gramene QTL database: development, content and applications. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap005. | 3.0 | 95 |
| 1245 | Sim4cc: a cross-species spliced alignment program. <i>Nucleic Acids Research</i> , 2009, 37, e80-e80. | 14.5 | 16 |
| 1246 | Computational and analytical framework for small RNA profiling by high-throughput sequencing. <i>Rna</i> , 2009, 15, 992-1002. | 3.5 | 112 |
| 1247 | Orphelia: predicting genes in metagenomic sequencing reads. <i>Nucleic Acids Research</i> , 2009, 37, W101-W105. | 14.5 | 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. | 3.6 | 75 |
| 1249 | Conservation of Domain Structure in a Fast-Evolving Heterochromatic SUUR Protein in <i>Drosophilids</i> . <i>Genetics</i> , 2009, 183, 119-129. | 2.9 | 4 |
| 1250 | Multiple whole-genome alignments without a reference organism. <i>Genome Research</i> , 2009, 19, 682-689. | 5.5 | 63 |
| 1251 | Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009, 37, D136-D140. | 14.5 | 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. | 5.5 | 135 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1253 | Local alignment of two-base encoded DNA sequence. BMC Bioinformatics, 2009, 10, 175. | 2.6 | 32 |
| 1254 | miRExpress: Analyzing high-throughput sequencing data for profiling microRNA expression. BMC Bioinformatics, 2009, 10, 328. | 2.6 | 165 |
| 1255 | BLAST+: architecture and applications. BMC Bioinformatics, 2009, 10, 421. | 2.6 | 14,935 |
| 1256 | QSRA – a quality-value guided de novo short read assembler. BMC Bioinformatics, 2009, 10, 69. | 2.6 | 53 |
| 1257 | CNV-seq, a new method to detect copy number variation using high-throughput sequencing. BMC Bioinformatics, 2009, 10, 80. | 2.6 | 495 |
| 1258 | Short read DNA fragment anchoring algorithm. BMC Bioinformatics, 2009, 10, S17. | 2.6 | 12 |
| 1259 | EasyCluster: a fast and efficient gene-oriented clustering tool for large-scale transcriptome data. BMC Bioinformatics, 2009, 10, S10. | 2.6 | 15 |
| 1260 | Statistical assessment of discriminative features for protein-coding and non coding cross-species conserved sequence elements. BMC Bioinformatics, 2009, 10, S2. | 2.6 | 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. | 2.8 | 47 |
| 1270 | A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. BMC Genomics, 2009, 10, 163. | 2.8 | 205 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1271 | ESTPiper – a web-based analysis pipeline for expressed sequence tags. BMC Genomics, 2009, 10, 174. | 2.8 | 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. | 2.8 | 72 |
| 1273 | Genic regions of a large salamander genome contain long introns and novel genes. BMC Genomics, 2009, 10, 19. | 2.8 | 81 |
| 1274 | Improving Gene-finding in <i>Chlamydomonas reinhardtii</i> : GreenGenie2. BMC Genomics, 2009, 10, 210. | 2.8 | 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. | 2.8 | 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. | 2.8 | 27 |
| 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. | 2.8 | 41 |
| 1278 | Characterization of the <i>Zoarces viviparus</i> liver transcriptome using massively parallel pyrosequencing. BMC Genomics, 2009, 10, 345. | 2.8 | 65 |
| 1279 | Mining for single nucleotide polymorphisms in pig genome sequence data. BMC Genomics, 2009, 10, 4. | 2.8 | 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. | 2.8 | 42 |
| 1281 | Computational prediction of splicing regulatory elements shared by Tetrapoda organisms. BMC Genomics, 2009, 10, 508. | 2.8 | 5 |
| 1282 | Genome and gene alterations by insertions and deletions in the evolution of human and chimpanzee chromosome 22. BMC Genomics, 2009, 10, 51. | 2.8 | 17 |
| 1283 | An expression database for roots of the model legume <i>Medicago truncatula</i> under salt stress. BMC Genomics, 2009, 10, 517. | 2.8 | 65 |
| 1284 | The effect of sequencing errors on metagenomic gene prediction. BMC Genomics, 2009, 10, 520. | 2.8 | 84 |
| 1285 | Correlation of microsynteny conservation and disease gene distribution in mammalian genomes. BMC Genomics, 2009, 10, 521. | 2.8 | 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. | 2.8 | 30 |
| 1287 | Complexity of genome evolution by segmental rearrangement in <i>Brassica rapa</i> revealed by sequence-level analysis. BMC Genomics, 2009, 10, 539. | 2.8 | 33 |
| 1288 | Expression profiling of rainbow trout testis development identifies evolutionary conserved genes involved in spermatogenesis. BMC Genomics, 2009, 10, 546. | 2.8 | 76 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1289 | Combining next-generation pyrosequencing with microarray for large scale expression analysis in non-model species. BMC Genomics, 2009, 10, 555. | 2.8 | 72 |
| 1290 | FragIdent – Automatic identification and characterisation of cDNA-fragments. BMC Genomics, 2009, 10, 95. | 2.8 | 0 |
| 1291 | MapNext: a software tool for spliced and unspliced alignments and SNP detection of short sequence reads. BMC Genomics, 2009, 10, S13. | 2.8 | 14 |
| 1292 | BOAT: Basic Oligonucleotide Alignment Tool. BMC Genomics, 2009, 10, S2. | 2.8 | 7 |
| 1293 | An empirical study of choosing efficient discriminative seeds for oligonucleotide design. BMC Genomics, 2009, 10, S3. | 2.8 | 3 |
| 1294 | PDbase: a database of Parkinson's Disease-related genes and genetic variation using substantia nigra ESTs. BMC Genomics, 2009, 10, S32. | 2.8 | 20 |
| 1295 | COMUS: Clinician-Oriented locus-specific MUtation detection and deposition System. BMC Genomics, 2009, 10, S35. | 2.8 | 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. | 2.8 | 22 |
| 1297 | Genomic analysis of Campylobacter fetus subspecies: identification of candidate virulence determinants and diagnostic assay targets. BMC Microbiology, 2009, 9, 86. | 3.3 | 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. | 3.6 | 55 |
| 1299 | ECRG4 is a candidate tumor suppressor gene frequently hypermethylated in colorectal carcinoma and glioma. BMC Cancer, 2009, 9, 447. | 2.6 | 77 |
| 1300 | Collection of Macaca fascicularis cDNAs derived from bone marrow, kidney, liver, pancreas, spleen, and thymus. BMC Research Notes, 2009, 2, 199. | 1.4 | 11 |
| 1301 | MicroRNAs and Cancer – The Search Begins!. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 67-77. | 3.2 | 18 |
| 1302 | An expanded clade of rodent Trim5 genes. Virology, 2009, 385, 473-483. | 2.4 | 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. | 11.7 | 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. | 16.8 | 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. | 1.2 | 17 |
| 1306 | Distribution and neuronal expression of phosphatidylinositol phosphate kinase II β in the mouse brain. Journal of Comparative Neurology, 2009, 517, 296-312. | 1.6 | 48 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1307 | Regucalcin is underexpressed in human breast and prostate cancers: Effect of sex steroid hormones. Journal of Cellular Biochemistry, 2009, 107, 667-676. | 2.6 | 47 |
| 1308 | Zebrafish <i>intron1</i> plays a fundamental role in controlling spatiotemporal gene expression during embryonic development. Journal of Cellular Biochemistry, 2009, 108, 1364-1375. | 2.6 | 7 |
| 1309 | Methylation analysis by DNA immunoprecipitation. Journal of Cellular Physiology, 2010, 222, 522-531. | 4.1 | 23 |
| 1310 | Hematopoietic immortalizing function of the NKX2-5 subclass homeobox gene <i>TLX1</i> . Genes Chromosomes and Cancer, 2010, 49, 119-131. | 2.8 | 2 |
| 1311 | Drosophila P transposons of the urochordata Ciona intestinalis. Molecular Genetics and Genomics, 2009, 282, 165-172. | 2.1 | 8 |
| 1312 | Evolution of Tom, 297, 17.6 and rover retrotransposons in Drosophilidae species. Molecular Genetics and Genomics, 2009, 282, 351-362. | 2.1 | 15 |
| 1313 | Meiotic behavior of aneuploid chromatin in mouse models of Down syndrome. Chromosoma, 2009, 118, 723-736. | 2.2 | 20 |
| 1314 | Identification of a novel human lactate dehydrogenase gene LDHAL6A, which activates transcriptional activities of AP1(PMA). Molecular Biology Reports, 2009, 36, 669-676. | 2.3 | 4 |
| 1315 | Influence of genetic background on tumor karyotypes: Evidence for breed-associated cytogenetic aberrations in canine appendicular osteosarcoma. Chromosome Research, 2009, 17, 365-377. | 2.2 | 74 |
| 1316 | Microarray-based cytogenetic profiling reveals recurrent and subtype-associated genomic copy number aberrations in feline sarcomas. Chromosome Research, 2009, 17, 987-1000. | 2.2 | 14 |
| 1317 | Isolation of Plant Gene Space-Related Sequence Elements by High C+G Patch (HCGP) Filtration: Model Study on Rice. Plant Molecular Biology Reporter, 2009, 27, 79-85. | 1.8 | 2 |
| 1318 | Characterization of new hAT transposable elements in 12 Drosophila genomes. Genetica, 2009, 135, 67-75. | 1.1 | 22 |
| 1319 | Search for informative polymorphisms in candidate genes: clock genes and circadian behaviour in blue tits. Genetica, 2009, 136, 109-117. | 1.1 | 42 |
| 1320 | The role of gene DCDC2 in German dyslexics. Annals of Dyslexia, 2009, 59, 1-11. | 1.7 | 64 |
| 1321 | Computational evidence of A-to-I RNA editing in nucleus transcriptome of Arabidopsis thaliana. Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities, 2009, 4, 349-361. | 0.6 | 0 |
| 1322 | Gene structures, biochemical characterization and distribution of rat melatonin receptors. Journal of Physiological Sciences, 2009, 59, 37-47. | 2.1 | 56 |
| 1323 | Single feature polymorphisms between two rice cultivars detected using a median polish method. Theoretical and Applied Genetics, 2009, 119, 151-164. | 3.6 | 13 |
| 1324 | Short Homologous Sequences Are Strongly Associated with the Generation of Chimeric RNAs in Eukaryotes. Journal of Molecular Evolution, 2009, 68, 56-65. | 1.8 | 77 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1325 | Tandem Stop Codons in Ciliates That Reassign Stop Codons. <i>Journal of Molecular Evolution</i> , 2009, 68, 424-431. | 1.8 | 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. | 1.8 | 39 |
| 1327 | Non-coding RNAs revealed during identification of genes involved in chicken immune responses. <i>Immunogenetics</i> , 2009, 61, 55-70. | 2.4 | 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. | 2.7 | 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. | 3.8 | 497 |
| 1331 | Genetical genomic determinants of alcohol consumption in rats and humans. <i>BMC Biology</i> , 2009, 7, 70. | 3.8 | 148 |
| 1332 | Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. <i>BMC Biology</i> , 2009, 7, 78. | 3.8 | 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. | 5.7 | 273 |
| 1335 | The transcriptionally active regions in the genome of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2009, 73, 1043-1057. | 2.5 | 146 |
| 1336 | Whole genome scan to detect quantitative trait loci for bovine milk protein composition. <i>Animal Genetics</i> , 2009, 40, 524-537. | 1.7 | 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. | 2.8 | 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. | 2.8 | 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. | 4.5 | 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. | 4.5 | 9 |
| 1341 | Transcriptome sequencing to detect gene fusions in cancer. <i>Nature</i> , 2009, 458, 97-101. | 27.8 | 791 |
| 1342 | ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858. | 27.8 | 1,526 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1343 | Copy number variation at 1q21.1 associated with neuroblastoma. <i>Nature</i> , 2009, 459, 987-991. | 27.8 | 329 |
| 1344 | Direct RNA sequencing. <i>Nature</i> , 2009, 461, 814-818. | 27.8 | 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. | 17.5 | 69 |
| 1346 | Comprehensive genomic access to vector integration in clinical gene therapy. <i>Nature Medicine</i> , 2009, 15, 1431-1436. | 30.7 | 173 |
| 1347 | Somatic cell nuclear transfer in zebrafish. <i>Nature Methods</i> , 2009, 6, 733-735. | 19.0 | 42 |
| 1348 | Application of 'next-generation' sequencing technologies to microbial genetics. <i>Nature Reviews Microbiology</i> , 2009, 7, 96-97. | 28.6 | 269 |
| 1349 | In the News. <i>Nature Reviews Microbiology</i> , 2009, 7, 260-261. | 28.6 | 158 |
| 1350 | The evolutionary history of the SSX family of human C/T-antigens. <i>Molecular Biology</i> , 2009, 43, 954-960. | 1.3 | 2 |
| 1351 | Detecting positive selection in the budding yeast genome. <i>Journal of Evolutionary Biology</i> , 2009, 22, 2430-2437. | 1.7 | 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. | 0.8 | 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. | 7.3 | 208 |
| 1354 | Acceleration of ungapped extension in Mercury BLAST. <i>Microprocessors and Microsystems</i> , 2009, 33, 281-289. | 2.8 | 18 |
| 1355 | A fully resolved genus level phylogeny of neotropical primates (Platyrrhini). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 694-702. | 2.7 | 102 |
| 1356 | Computational identification of novel microRNA homologs in the chimpanzee genome. <i>Computational Biology and Chemistry</i> , 2009, 33, 62-70. | 2.3 | 39 |
| 1357 | Sequence assembly. <i>Computational Biology and Chemistry</i> , 2009, 33, 121-136. | 2.3 | 39 |
| 1358 | Molecular mechanisms regulating bovine ovarian follicular selection. <i>Molecular Reproduction and Development</i> , 2009, 76, 351-366. | 2.0 | 28 |
| 1359 | TopHat: discovering splice junctions with RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1105-1111. | 4.1 | 11,265 |
| 1360 | On Subset Seeds for Protein Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 483-494. | 3.0 | 20 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1361 | “Changing by doubling” the impact of Whole Genome Duplications in the evolution of eukaryotes. <i>Comptes Rendus - Biologies</i> , 2009, 332, 241-253. | 0.2 | 48 |
| 1362 | The avian Toll-Like receptor pathway”Subtle differences amidst general conformity. <i>Developmental and Comparative Immunology</i> , 2009, 33, 967-973. | 2.3 | 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. | 7.0 | 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. | 7.0 | 259 |
| 1365 | Characterisation of circulating DNA by parallel tagged sequencing on the 454 platform. <i>Clinica Chimica Acta</i> , 2009, 409, 21-27. | 1.1 | 32 |
| 1366 | Dissecting Regulatory Networks in Host-Pathogen Interaction Using ChIP-on-chip Technology. <i>Cell Host and Microbe</i> , 2009, 5, 430-437. | 11.0 | 14 |
| 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. | 3.3 | 76 |
| 1368 | UTR dinucleotide simple sequence repeat evolution exhibits recurring patterns including regulatory sequence motif replacements. <i>Gene</i> , 2009, 429, 80-86. | 2.2 | 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. | 2.2 | 4 |
| 1370 | Internal priming: An opportunistic pathway for L1 and Alu retrotransposition in hominins. <i>Gene</i> , 2009, 448, 233-241. | 2.2 | 21 |
| 1371 | Loss of epigenetic silencing in tumors preferentially affects primate-specific retroelements. <i>Gene</i> , 2009, 448, 151-167. | 2.2 | 108 |
| 1372 | Identification of an ancient Bmp4 mesoderm enhancer located 46Âkb from the promoter. <i>Developmental Biology</i> , 2009, 327, 590-602. | 2.0 | 30 |
| 1373 | Cis-regulation and chromosomal rearrangement of the fgf8 locus after the teleost/tetrapod split. <i>Developmental Biology</i> , 2009, 336, 301-312. | 2.0 | 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. | 2.9 | 44 |
| 1375 | An alternative pathway for Alu retrotransposition suggests a role in DNA double-strand break repair. <i>Genomics</i> , 2009, 93, 205-212. | 2.9 | 36 |
| 1376 | Characterization and functional analysis of cis-acting elements of the human farnesyl diphosphate synthetase (FDPS) gene 5â€² flanking region. <i>Genomics</i> , 2009, 93, 227-234. | 2.9 | 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. | 2.9 | 34 |
| 1378 | Critical evaluation of the FANTOM3 non-coding RNA transcripts. <i>Genomics</i> , 2009, 94, 169-176. | 2.9 | 15 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1379 | Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. <i>Genomics</i> , 2009, 94, 308-316. | 2.9 | 11 |
| 1380 | Genome-wide high throughput analysis of DNA methylation in eukaryotes. <i>Methods</i> , 2009, 47, 142-150. | 3.8 | 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. | 3.8 | 9 |
| 1382 | Photoperiod modifies the diurnal expression profile of VvPHYA and VvPHYB transcripts in field-grown grapevine leaves. <i>Journal of Plant Physiology</i> , 2009, 166, 1172-1180. | 3.5 | 42 |
| 1383 | Overexpression of Nrp/b (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. | 2.5 | 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. | 3.4 | 255 |
| 1385 | Mining SNPs from DNA Sequence Data; Computational Approaches to SNP Discovery and Analysis. <i>Methods in Molecular Biology</i> , 2009, 578, 73-91. | 0.9 | 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. | 5.5 | 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. | 5.5 | 141 |
| 1389 | A Parallel Pairwise Local Sequence Alignment Algorithm. <i>IEEE Transactions on Nanobioscience</i> , 2009, 8, 139-146. | 3.3 | 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. | 3.3 | 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. | 2.0 | 65 |
| 1392 | The DAWGPAWS pipeline for the annotation of genes and transposable elements in plant genomes. <i>Plant Methods</i> , 2009, 5, 8. | 4.3 | 21 |
| 1393 | The Role of CLCA Proteins in Inflammatory Airway Disease. <i>Annual Review of Physiology</i> , 2009, 71, 425-449. | 13.1 | 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. | 0.9 | 72 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 1397 | Proteolytic Systems: Constructing Degradomes. <i>Methods in Molecular Biology</i> , 2009, 539, 33-47. | 0.9 | 15 |
| 1399 | iTriplet, a rule-based nucleic acid sequence motif finder. <i>Algorithms for Molecular Biology</i> , 2009, 4, 14. | 1.2 | 25 |
| 1400 | Tandem repeats modify the structure of human genes hosted in segmental duplications. <i>Genome Biology</i> , 2009, 10, R137. | 9.6 | 32 |
| 1401 | High resolution discovery and confirmation of copy number variants in 90 Yoruba Nigerians. <i>Genome Biology</i> , 2009, 10, R125. | 9.6 | 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. | 9.6 | 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. | 9.6 | 183 |
| 1404 | Many LINE1 elements contribute to the transcriptome of human somatic cells. <i>Genome Biology</i> , 2009, 10, R100. | 8.8 | 84 |
| 1405 | The bovine lactation genome: insights into the evolution of mammalian milk. <i>Genome Biology</i> , 2009, 10, R43. | 9.6 | 164 |
| 1406 | Widespread evidence for horizontal transfer of transposable elements across <i>Drosophila</i> genomes. <i>Genome Biology</i> , 2009, 10, R22. | 9.6 | 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. | 9.6 | 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. | 0.9 | 67 |
| 1409 | Pan-vertebrate conserved non-coding sequences associated with developmental regulation. <i>Briefings in Functional Genomics & 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. | 3.4 | 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. | 2.0 | 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. | 1.6 | 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. | 3.0 | 14 |
| 1415 | Geometric Aspects of Biological Sequence Comparison. <i>Journal of Computational Biology</i> , 2009, 16, 579-610. | 1.6 | 10 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1416 | Dynamic Programming for Single Nucleotide Polymorphism ID Identification in Systematic Association Studies. Kaohsiung Journal of Medical Sciences, 2009, 25, 165-176. | 1.9 | 1 |
| 1417 | Bioinformatic analysis of microRNA biogenesis and function related proteins in eleven animal genomes. Journal of Genetics and Genomics, 2009, 36, 591-601. | 3.9 | 16 |
| 1418 | EvoOligo: Oligonucleotide Probe Design With Multiobjective Evolutionary Algorithms. IEEE Transactions on Systems, Man, and Cybernetics, 2009, 39, 1606-1616. | 5.0 | 11 |
| 1419 | Setting CAGE Tags in a Genomic Context. , 2009, , 93-100. | | 0 |
| 1420 | Orientation, distance, regulation and function of neighbouring genes. Human Genomics, 2009, 3, 143-56. | 2.9 | 22 |
| 1421 | Evolution of a Bitter Taste Receptor Gene Cluster in a New World Sparrow. Genome Biology and Evolution, 2010, 2, 358-370. | 2.5 | 38 |
| 1422 | Quantitative Gene Expression Profiles in Real Time From Expressed Sequence Tag Databases. Gene Expression, 2010, 14, 321-336. | 1.2 | 4 |
| 1423 | Validation of Rearrangement Break Points Identified by Paired-End Sequencing in Natural Populations of <i>Drosophila melanogaster</i> . Genome Biology and Evolution, 2010, 2, 83-101. | 2.5 | 46 |
| 1424 | Gene Duplication and Environmental Adaptation within Yeast Populations. Genome Biology and Evolution, 2010, 2, 591-601. | 2.5 | 44 |
| 1425 | Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. Standards in Genomic Sciences, 2010, 2, 142-148. | 1.5 | 509 |
| 1426 | Whole-Genome Positive Selection and Habitat-Driven Evolution in a Shallow and a Deep-Sea Urchin. Genome Biology and Evolution, 2010, 2, 800-814. | 2.5 | 52 |
| 1427 | Alterations in Gene Expression in MEN1-Associated Insulinoma Development. Pancreas, 2010, 39, 1140-1146. | 1.1 | 7 |
| 1428 | Heritability in the Efficiency of Nonsense-Mediated mRNA Decay in Humans. PLoS ONE, 2010, 5, e11657. | 2.5 | 17 |
| 1433 | Agrobacterium-mediated gene disruption using split-marker in <i>Grosmannia clavigera</i> , a mountain pine beetle associated pathogen. Current Genetics, 2010, 56, 297-307. | 1.7 | 39 |
| 1434 | Characterization of the zebrafish T cell receptor $\hat{1}^2$ locus. Immunogenetics, 2010, 62, 23-29. | 2.4 | 46 |
| 1435 | Organization of the variable region of the immunoglobulin heavy-chain gene locus of the rat. Immunogenetics, 2010, 62, 479-486. | 2.4 | 13 |
| 1436 | Reducing non-determinism of k-NN searching in non-ordered discrete data spaces. Information Processing Letters, 2010, 110, 420-423. | 0.6 | 0 |
| 1437 | Positional variations among heterogeneous nucleosome maps give dynamical information on chromatin. Chromosoma, 2010, 119, 391-404. | 2.2 | 8 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 1438 | Large intron 14 rearrangement in APC results in splice defect and attenuated FAP. Human Genetics, 2010, 127, 359-369. | 3.8 | 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> . Population Ecology, 2010, 52, 159-169. | 1.2 | 6 |
| 1440 | A comprehensive analysis of protein phosphatases in rice and Arabidopsis. Plant Systematics and Evolution, 2010, 289, 111-126. | 0.9 | 7 |
| 1441 | Prediction and identification of tumor-specific noncoding RNAs from human UniGene. Medical Oncology, 2010, 27, 894-898. | 2.5 | 7 |
| 1442 | An N- and C-terminal truncated isoform of zinc finger X-linked duplicated C protein represses MHC class II transcription. Molecular and Cellular Biochemistry, 2010, 337, 1-7. | 3.1 | 4 |
| 1443 | Characterization of a novel human HMBOX1 splicing variant lacking the homeodomain and with attenuated transcription repressor activity. Molecular Biology Reports, 2010, 37, 2767-2772. | 2.3 | 5 |
| 1444 | Strategies to develop polymorphic markers for <i>Coffea arabica</i> L.. Euphytica, 2010, 173, 243-253. | 1.2 | 2 |
| 1445 | hAT transposable elements and their derivatives: an analysis in the 12 <i>Drosophila</i> genomes. Genetica, 2010, 138, 649-655. | 1.1 | 13 |
| 1446 | Genome-wide SNP association-based localization of a dwarfism gene in Friesian dwarf horses. Animal Genetics, 2010, 41, 2-7. | 1.7 | 31 |
| 1447 | Transcription of LINE-derived sequences in exercise-induced stress in horses. Animal Genetics, 2010, 41, 23-27. | 1.7 | 22 |
| 1448 | Mitochondrial DNA insertions in the nuclear horse genome. Animal Genetics, 2010, 41, 176-185. | 1.7 | 35 |
| 1449 | Histone H3 trimethylated at lysine 4 is enriched at probable transcription start sites in <i>Trypanosoma brucei</i> . Molecular and Biochemical Parasitology, 2010, 172, 141-144. | 1.1 | 77 |
| 1450 | BS Seeker: precise mapping for bisulfite sequencing. BMC Bioinformatics, 2010, 11, 203. | 2.6 | 212 |
| 1451 | A method of predicting changes in human gene splicing induced by genetic variants in context of cis-acting elements. BMC Bioinformatics, 2010, 11, 22. | 2.6 | 15 |
| 1452 | Cgaln: fast and space-efficient whole-genome alignment. BMC Bioinformatics, 2010, 11, 224. | 2.6 | 14 |
| 1453 | eHive: An Artificial Intelligence workflow system for genomic analysis. BMC Bioinformatics, 2010, 11, 240. | 2.6 | 37 |
| 1454 | Analysing 454 amplicon resequencing experiments using the modular and database oriented Variant Identification Pipeline. BMC Bioinformatics, 2010, 11, 269. | 2.6 | 15 |
| 1455 | Improving de novo sequence assembly using machine learning and comparative genomics for overlap correction. BMC Bioinformatics, 2010, 11, 33. | 2.6 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1456 | Local alignment of generalized k-base encoded DNA sequence. BMC Bioinformatics, 2010, 11, 347. | 2.6 | 1 |
| 1457 | Geoseq: a tool for dissecting deep-sequencing datasets. BMC Bioinformatics, 2010, 11, 506. | 2.6 | 4 |
| 1458 | Gen Htr : a tool for comparative assessment of genetic heterogeneity in microbial genomes generated by massive short-read sequencing. BMC Bioinformatics, 2010, 11, 508. | 2.6 | 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. BMC Bioinformatics, 2010, 11, 572. | 2.6 | 48 |
| 1460 | Initial steps towards a production platform for DNA sequence analysis on the grid. BMC Bioinformatics, 2010, 11, 598. | 2.6 | 7 |
| 1461 | A computational screen for site selective A-to-I editing detects novel sites in neuron specific Hu proteins. BMC Bioinformatics, 2010, 11, 6. | 2.6 | 35 |
| 1462 | Parameters for accurate genome alignment. BMC Bioinformatics, 2010, 11, 80. | 2.6 | 180 |
| 1463 | Quail Genomics: a knowledgebase for Northern bobwhite. BMC Bioinformatics, 2010, 11, S13. | 2.6 | 14 |
| 1464 | Assessment of genetic variation for the LINE-1 retrotransposon from next generation sequence data. BMC Bioinformatics, 2010, 11, S12. | 2.6 | 7 |
| 1465 | The molecular evolution of PL10 homologs. BMC Evolutionary Biology, 2010, 10, 127. | 3.2 | 26 |
| 1466 | Some novel intron positions in conserved Drosophila genes are caused by intron sliding or tandem duplication. BMC Evolutionary Biology, 2010, 10, 156. | 3.2 | 17 |
| 1467 | Periostin shows increased evolutionary plasticity in its alternatively spliced region. BMC Evolutionary Biology, 2010, 10, 30. | 3.2 | 87 |
| 1468 | Evolution of Rhizaria: new insights from phylogenomic analysis of uncultivated protists. BMC Evolutionary Biology, 2010, 10, 377. | 3.2 | 130 |
| 1469 | Evolution of spliceosomal introns following endosymbiotic gene transfer. BMC Evolutionary Biology, 2010, 10, 57. | 3.2 | 23 |
| 1470 | Chaperonin genes on the rise: new divergent classes and intense duplication in human and other vertebrate genomes. BMC Evolutionary Biology, 2010, 10, 64. | 3.2 | 30 |
| 1471 | Genomic organization of duplicated short wave-sensitive and long wave-sensitive opsin genes in the green swordtail, Xiphophorus helleri. BMC Evolutionary Biology, 2010, 10, 87. | 3.2 | 32 |
| 1472 | Genome-wide analysis of alternative splicing in Chlamydomonas reinhardtii. BMC Genomics, 2010, 11, 114. | 2.8 | 69 |
| 1473 | An EST resource for tilapia based on 17 normalized libraries and assembly of 116,899 sequence tags. BMC Genomics, 2010, 11, 278. | 2.8 | 39 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1474 | A manual collection of Syt, Esyt, Rph3a, Rph3al, Doc2, and Dbic2 genes from 46 metazoan genomes - an open access resource for neuroscience and evolutionary biology. BMC Genomics, 2010, 11, 37. | 2.8 | 53 |
| 1475 | Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. BMC Genomics, 2010, 11, 383. | 2.8 | 97 |
| 1476 | Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. BMC Genomics, 2010, 11, 384. | 2.8 | 161 |
| 1477 | Gene discovery for the bark beetle-vectored fungal tree pathogen <i>Grosmannia clavigera</i> . BMC Genomics, 2010, 11, 536. | 2.8 | 25 |
| 1478 | Gene expression in a paleopolyploid: a transcriptome resource for the ciliate <i>Paramecium tetraurelia</i> . BMC Genomics, 2010, 11, 547. | 2.8 | 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. BMC Genomics, 2010, 11, 565. | 2.8 | 67 |
| 1480 | Comparing de novo assemblers for 454 transcriptome data. BMC Genomics, 2010, 11, 571. | 2.8 | 217 |
| 1481 | Annotation and comparative analysis of the glycoside hydrolase genes in <i>Brachypodium distachyon</i> . BMC Genomics, 2010, 11, 600. | 2.8 | 53 |
| 1482 | Genomic tools development for <i>Aquilegia</i> : construction of a BAC-based physical map. BMC Genomics, 2010, 11, 621. | 2.8 | 13 |
| 1483 | The rapid generation of chimerical genes expanding protein diversity in zebrafish. BMC Genomics, 2010, 11, 657. | 2.8 | 36 |
| 1484 | Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. BMC Genomics, 2010, 11, 663. | 2.8 | 201 |
| 1485 | Genomic and transcriptomic analysis of the AP2/ERF superfamily in <i>Vitis vinifera</i> . BMC Genomics, 2010, 11, 719. | 2.8 | 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. | 2.2 | 67 |
| 1487 | Analysis of the genome content of <i>Lactococcus garvieae</i> by genomic interspecies microarray hybridization. BMC Microbiology, 2010, 10, 79. | 3.3 | 11 |
| 1488 | Long noncoding RNAs in neuronal-glial fate specification and oligodendrocyte lineage maturation. BMC Neuroscience, 2010, 11, 14. | 1.9 | 381 |
| 1489 | Transcriptional profiles underlying parent-of-origin effects in seeds of <i>Arabidopsis thaliana</i> . BMC Plant Biology, 2010, 10, 72. | 3.6 | 71 |
| 1490 | Expression profiling in canine osteosarcoma: identification of biomarkers and pathways associated with outcome. BMC Cancer, 2010, 10, 506. | 2.6 | 47 |
| 1491 | Alterations in the steroid hormone receptor co-chaperone FKBP are associated with male infertility: a case-control study. Reproductive Biology and Endocrinology, 2010, 8, 22. | 3.3 | 31 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 1492 | Cloning and characterization of a novel alternatively spliced transcript of the human CHD7 putative helicase. BMC Research Notes, 2010, 3, 252. | 1.4 | 7 |
| 1493 | Rapid pair-wise synteny analysis of large bacterial genomes using web-based GeneOrder4.0. BMC Research Notes, 2010, 3, 41. | 1.4 | 15 |
| 1494 | Vertebrate β -thymosins: Conserved synteny reveals the relationship between those of bony fish and of land vertebrates. FEBS Letters, 2010, 584, 1047-1053. | 2.8 | 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. | 1.6 | 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. | 2.5 | 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. | 2.8 | 12 |
| 1498 | Validation and application of normalization factors for gene expression studies in rubella virus-infected cell lines with quantitative real-time PCR. Journal of Cellular Biochemistry, 2010, 110, 118-128. | 2.6 | 25 |
| 1499 | OCT3/4 regulates transcription of histone deacetylase 4 (<i>Hdac4</i>) in mouse embryonic stem cells. Journal of Cellular Biochemistry, 2010, 111, 391-401. | 2.6 | 10 |
| 1500 | Cabin1 expression suggests roles in neuronal development. Developmental Dynamics, 2010, 239, 2443-2451. | 1.8 | 19 |
| 1501 | Recurrent interstitial 1p36 deletions: Evidence for germline mosaicism and complex rearrangement breakpoints. American Journal of Medical Genetics, Part A, 2010, 152A, 3074-3083. | 1.2 | 31 |
| 1502 | Intracisternal A particle genes: Distribution in the mouse genome, active subtypes, and potential roles as species-specific mediators of susceptibility to cancer. Molecular Carcinogenesis, 2010, 49, 54-67. | 2.7 | 44 |
| 1503 | Hox expression in the American alligator and evolution of archosaurian axial patterning. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2010, 314B, 629-644. | 1.3 | 38 |
| 1504 | Quantitative erythrocyte membrane proteome analysis with Blue-Native/SDS PAGE. Journal of Proteomics, 2010, 73, 456-465. | 2.4 | 60 |
| 1505 | Computational identification and characterization of primate-specific microRNAs in human genome. Computational Biology and Chemistry, 2010, 34, 232-241. | 2.3 | 57 |
| 1506 | Human T-cell memory consists mainly of unexpanded clones. Immunology Letters, 2010, 133, 42-48. | 2.5 | 89 |
| 1507 | Characterization of the first beta-class carbonic anhydrase from an arthropod (<i>Drosophila</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf50 Biochemistry, 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. BMC Genetics, 2010, 11, 42. | 2.7 | 96 |
| 1509 | Identifying novel genes in <i>C. elegans</i> using SAGE tags. BMC Molecular Biology, 2010, 11, 96. | 3.0 | 5 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1510 | Serious limitations of the QTL/Microarray approach for QTL gene discovery. BMC Biology, 2010, 8, 96. | 3.8 | 29 |
| 1511 | Phylogenetic comparative assembly. Algorithms for Molecular Biology, 2010, 5, 3. | 1.2 | 15 |
| 1512 | Heads or tails: L1 insertion-associated 5' homopolymeric sequences. Mobile DNA, 2010, 1, 7. | 3.6 | 10 |
| 1513 | Computational analysis of unassigned high-quality MS/MS spectra in proteomic data sets. Proteomics, 2010, 10, 2712-2718. | 2.2 | 58 |
| 1514 | Detecting Gene Duplications in the Human Lineage. Annals of Human Genetics, 2010, 74, 555-565. | 0.8 | 6 |
| 1515 | Characterization of the <i>Arabidopsis thaliana</i> exocyst complex gene families by phylogenetic, expression profiling, and subcellular localization studies. New Phytologist, 2010, 185, 401-419. | 7.3 | 77 |
| 1516 | Increased vitamin D-driven signalling and expression of the vitamin D receptor, MSX2, and RANKL in tooth resorption in cats. European Journal of Oral Sciences, 2010, 118, 39-46. | 1.5 | 22 |
| 1517 | A genetic linkage map of red drum, <i>Sciaenops ocellatus</i> . Animal Genetics, 2010, 41, 630-641. | 1.7 | 12 |
| 1518 | Comparative analysis of nuclear tRNA genes of <i>Nasonia vitripennis</i> and other arthropods, and relationships to codon usage bias. Insect Molecular Biology, 2010, 19, 49-58. | 2.0 | 32 |
| 1519 | Molecular Evolution of the Thyrotrophin-Releasing Hormone Precursor in Vertebrates: Insights From Comparative Genomics. Journal of Neuroendocrinology, 2010, 22, 608-619. | 2.6 | 19 |
| 1520 | Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. Molecular Ecology, 2010, 19, 266-276. | 3.9 | 105 |
| 1521 | A syndrome of short stature, microcephaly and speech delay is associated with duplications reciprocal to the common Sotos syndrome deletion. European Journal of Human Genetics, 2010, 18, 258-261. | 2.8 | 41 |
| 1522 | A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65. | 27.8 | 9,342 |
| 1523 | Building the sequence map of the human pan-genome. Nature Biotechnology, 2010, 28, 57-63. | 17.5 | 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> . Plant Journal, 2010, 63, 990-1003. | 5.7 | 47 |
| 1525 | Mutation spectrum revealed by breakpoint sequencing of human germline CNVs. Nature Genetics, 2010, 42, 385-391. | 21.4 | 211 |
| 1526 | Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. Nature Genetics, 2010, 42, 1053-1059. | 21.4 | 987 |
| 1527 | De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912. | 19.0 | 886 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1528 | Defining transcribed regions using RNA-seq. Nature Protocols, 2010, 5, 255-266. | 12.0 | 70 |
| 1529 | Genome-wide high-throughput integrome analyses by nrLAM-PCR and next-generation sequencing. Nature Protocols, 2010, 5, 1379-1395. | 12.0 | 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. Journal of Evolutionary Biology, 2010, 23, 518-527. | 1.7 | 15 |
| 1531 | Testing the Coding Potential of Conserved Short Genomic Sequences. Advances in Bioinformatics, 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. PLoS ONE, 2010, 5, e9154. | 2.5 | 44 |
| 1533 | A Novel Role for Minimal Introns: Routing mRNAs to the Cytosol. PLoS ONE, 2010, 5, e10144. | 2.5 | 27 |
| 1534 | HMMSplicer: A Tool for Efficient and Sensitive Discovery of Known and Novel Splice Junctions in RNA-Seq Data. PLoS ONE, 2010, 5, e13875. | 2.5 | 50 |
| 1535 | Multiplexed DNA Sequence Capture of Mitochondrial Genomes Using PCR Products. PLoS ONE, 2010, 5, e14004. | 2.5 | 471 |
| 1536 | Analyses of Copy Number Variation of GK Rat Reveal New Putative Type 2 Diabetes Susceptibility Loci. PLoS ONE, 2010, 5, e14077. | 2.5 | 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. | 2.5 | 29 |
| 1538 | Microarray probes and probe sets. Frontiers in Bioscience - Elite, 2010, E2, 325-338. | 1.8 | 45 |
| 1539 | Scaffolding a <i>Caenorhabditis</i> nematode genome with RNA-seq. Genome Research, 2010, 20, 1740-1747. | 5.5 | 83 |
| 1540 | Analysis of Human Small Nucleolar RNAs (snoRNA) and the Development of snoRNA Modulator of Gene Expression Vectors. Molecular Biology of the Cell, 2010, 21, 1569-1584. | 2.1 | 40 |
| 1541 | Mutation@A Glance: An Integrative Web Application for Analysing Mutations from Human Genetic Diseases. DNA Research, 2010, 17, 197-208. | 3.4 | 26 |
| 1542 | Classification of DNA sequences using Bloom filters. Bioinformatics, 2010, 26, 1595-1600. | 4.1 | 57 |
| 1543 | BAGEL2: mining for bacteriocins in genomic data. Nucleic Acids Research, 2010, 38, W647-W651. | 14.5 | 144 |
| 1544 | ChimerDB 2.0—a knowledgebase for fusion genes updated. Nucleic Acids Research, 2010, 38, D81-D85. | 14.5 | 78 |
| 1545 | Rapid identification of heterozygous mutations in <i>Drosophila melanogaster</i> using genomic capture sequencing. Genome Research, 2010, 20, 981-988. | 5.5 | 30 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1546 | Genome-wide synteny through highly sensitive sequence alignment: <i>Satsuma</i> . <i>Bioinformatics</i> , 2010, 26, 1145-1151. | 4.1 | 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. | 14.5 | 39 |
| 1548 | Evidence for bacterial origin of heat shock RNA-1. <i>Rna</i> , 2010, 16, 274-279. | 3.5 | 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. | 2.7 | 49 |
| 1550 | Cost-Effective Sequencing of Full-Length cDNA Clones Powered by a De Novo-Reference Hybrid Assembly. <i>PLoS ONE</i> , 2010, 5, e10517. | 2.5 | 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. | 14.5 | 89 |
| 1552 | EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. <i>Bioinformatics</i> , 2010, 26, 2076-2084. | 4.1 | 7 |
| 1553 | Genome-wide mapping and assembly of structural variant breakpoints in the mouse genome. <i>Genome Research</i> , 2010, 20, 623-635. | 5.5 | 257 |
| 1554 | DARNED: a DAtabase of RNA EDiting in humans. <i>Bioinformatics</i> , 2010, 26, 1772-1776. | 4.1 | 225 |
| 1555 | PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 623-634. | 3.8 | 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. | 14.5 | 200 |
| 1557 | A network of conserved co-occurring motifs for the regulation of alternative splicing. <i>Nucleic Acids Research</i> , 2010, 38, 7916-7926. | 14.5 | 12 |
| 1558 | Characterization of C1q in Teleosts. <i>Journal of Biological Chemistry</i> , 2010, 285, 28777-28786. | 3.4 | 45 |
| 1559 | Genome of <i>Helicobacter pylori</i> Strain 908. <i>Journal of Bacteriology</i> , 2010, 192, 6488-6489. | 2.2 | 25 |
| 1560 | FragGeneScan: predicting genes in short and error-prone reads. <i>Nucleic Acids Research</i> , 2010, 38, e191-e191. | 14.5 | 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. | 14.5 | 55 |
| 1562 | Metagenomics: seeking for the human gut microbial communities. <i>Reviews in Medical Microbiology</i> , 2010, 21, 51-55. | 0.9 | 1 |
| 1563 | Challenges of sequencing human genomes. <i>Briefings in Bioinformatics</i> , 2010, 11, 484-498. | 6.5 | 134 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1564 | Detection, Validation, and Downstream Analysis of Allelic Variation in Gene Expression. <i>Genetics</i> , 2010, 184, 119-128. | 2.9 | 60 |
| 1565 | Population dynamics of PIWI-interacting RNAs (piRNAs) and their targets in <i>Drosophila</i> . <i>Genome Research</i> , 2010, 20, 212-227. | 5.5 | 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. | 5.5 | 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. | 3.4 | 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. | 8.9 | 56 |
| 1569 | The UCSC Genome Browser database: update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D613-D619. | 14.5 | 537 |
| 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. | 14.5 | 28 |
| 1571 | Chromosomal position effects on AAV-mediated gene targeting. <i>Nucleic Acids Research</i> , 2010, 38, 3582-3594. | 14.5 | 14 |
| 1572 | Efficient k-nearest neighbor searching in nonordered discrete data spaces. <i>ACM Transactions on Information Systems</i> , 2010, 28, 1-33. | 4.9 | 7 |
| 1573 | Detection of human interchromosomal trans-splicing in sequence databanks. <i>Briefings in Bioinformatics</i> , 2010, 11, 198-209. | 6.5 | 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. | 2.9 | 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. | 5.5 | 40 |
| 1576 | MicroRNA Gene Evolution in <i>Arabidopsis lyrata</i> and <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2010, 22, 1074-1089. | 6.6 | 234 |
| 1577 | Different Phylogenomic Approaches to Resolve the Evolutionary Relationships among Model Fish Species. <i>Molecular Biology and Evolution</i> , 2010, 27, 2757-2774. | 8.9 | 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. | 2.2 | 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 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1582 | BeetleBase in 2010: revisions to provide comprehensive genomic information for <i>Tribolium castaneum</i> . <i>Nucleic Acids Research</i> , 2010, 38, D437-D442. | 14.5 | 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. | 1.6 | 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. | 14.5 | 28 |
| 1587 | PanCGHweb: a web tool for genotype calling in pangenome CGH data. <i>Bioinformatics</i> , 2010, 26, 1256-1257. | 4.1 | 20 |
| 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. | 3.5 | 306 |
| 1590 | MicroRNA Regulation of IFN- γ Protein Expression: Rapid and Sensitive Modulation of the Innate Immune Response. <i>Journal of Immunology</i> , 2010, 184, 2369-2376. | 0.8 | 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. | 3.4 | 114 |
| 1592 | Isolation of SPINK6 in Human Skin. <i>Journal of Biological Chemistry</i> , 2010, 285, 32174-32181. | 3.4 | 75 |
| 1593 | Targets of the Tal1 Transcription Factor in Erythrocytes. <i>Journal of Biological Chemistry</i> , 2010, 285, 5338-5346. | 3.4 | 16 |
| 1594 | Discovery and Characterization of Mammalian Endogenous Parvoviruses. <i>Journal of Virology</i> , 2010, 84, 12628-12635. | 3.4 | 68 |
| 1595 | PLANdbAffy: probe-level annotation database for Affymetrix expression microarrays. <i>Nucleic Acids Research</i> , 2010, 38, D726-D730. | 14.5 | 25 |
| 1596 | Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189. | 5.5 | 239 |
| 1597 | MouseIndelDB: a database integrating genomic indel polymorphisms that distinguish mouse strains. <i>Nucleic Acids Research</i> , 2010, 38, D600-D606. | 14.5 | 19 |
| 1598 | The Role of Nucleosome Positioning in the Evolution of Gene Regulation. <i>PLoS Biology</i> , 2010, 8, e1000414. | 5.6 | 202 |
| 1599 | The Parental Non-Equivalence of Imprinting Control Regions during Mammalian Development and Evolution. <i>PLoS Genetics</i> , 2010, 6, e1001214. | 3.5 | 61 |
| 1600 | Human and Non-Human Primate Genomes Share Hotspots of Positive Selection. <i>PLoS Genetics</i> , 2010, 6, e1000840. | 3.5 | 58 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1601 | r2cat: syntenic plots and comparative assembly. <i>Bioinformatics</i> , 2010, 26, 570-571. | 4.1 | 134 |
| 1602 | Genome-Wide Interrogation of Mammalian Stem Cell Fate Determinants by Nested Chromosome Deletions. <i>PLoS Genetics</i> , 2010, 6, e1001241. | 3.5 | 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. | 4.7 | 234 |
| 1604 | Smed454 dataset: unravelling the transcriptome of <i>Schmidtea mediterranea</i> . <i>BMC Genomics</i> , 2010, 11, 731. | 2.8 | 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. | 14.5 | 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. | 4.7 | 72 |
| 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. | 3.2 | 72 |
| 1608 | Deletion of CREB1 from the Dorsal Telencephalon Reduces Motivational Properties of Cocaine. <i>Cerebral Cortex</i> , 2010, 20, 941-952. | 2.9 | 24 |
| 1609 | Evolution of an X-Linked Primate-Specific Micro RNA Cluster. <i>Molecular Biology and Evolution</i> , 2010, 27, 671-683. | 8.9 | 64 |
| 1610 | GenomeRNAi: a database for cell-based RNAi phenotypes. 2009 update. <i>Nucleic Acids Research</i> , 2010, 38, D448-D452. | 14.5 | 37 |
| 1611 | The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803. | 5.5 | 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. | 14.5 | 136 |
| 1613 | KRAB—Zinc Finger Proteins and KAP1 Can Mediate Long-Range Transcriptional Repression through Heterochromatin Spreading. <i>PLoS Genetics</i> , 2010, 6, e1000869. | 3.5 | 309 |
| 1614 | inGAP: an integrated next-generation genome analysis pipeline. <i>Bioinformatics</i> , 2010, 26, 127-129. | 4.1 | 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. | 6.2 | 11 |
| 1617 | FANGS. , 2010, , . | | 4 |
| 1618 | REAL. , 2010, , . | | 24 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1619 | EuGene-maize: a web site for maize gene prediction. <i>Bioinformatics</i> , 2010, 26, 1254-1255. | 4.1 | 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. | 6.6 | 253 |
| 1621 | mRNA deep sequencing reveals 75 new genes and a complex transcriptional landscape in Mimivirus. <i>Genome Research</i> , 2010, 20, 664-674. | 5.5 | 160 |
| 1622 | Gene Family Size Conservation Is a Good Indicator of Evolutionary Rates. <i>Molecular Biology and Evolution</i> , 2010, 27, 1750-1758. | 8.9 | 31 |
| 1623 | An annotated k-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. | 5.5 | 156 |
| 1625 | A SNP discovery method to assess variant allele probability from next-generation resequencing data. <i>Genome Research</i> , 2010, 20, 273-280. | 5.5 | 168 |
| 1626 | The FLIGHT <i>Drosophila</i> RNAi database. <i>Fly</i> , 2010, 4, 344-348. | 1.7 | 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. | 2.5 | 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. | 9.6 | 150 |
| 1634 | Epigenetic Databases and Computational Methodologies in the Analysis of Epigenetic Datasets. <i>Advances in Genetics</i> , 2010, 71, 259-295. | 1.8 | 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. | 1.1 | 25 |
| 1636 | FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. <i>Genome Biology</i> , 2010, 11, R104. | 8.8 | 137 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1637 | Prevalence of alternative splicing choices in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2010, 10, 102. | 3.6 | 34 |
| 1638 | Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010, 7, 111. | 2.0 | 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. | 1.3 | 85 |
| 1640 | A Restriction Enzyme-PCR-Based Technique to Determine Transgene Insertion Sites. <i>Methods in Molecular Biology</i> , 2010, 597, 287-299. | 0.9 | 12 |
| 1641 | DNA barcoding: a six-question tour to improve users' awareness about the method. <i>Briefings in Bioinformatics</i> , 2010, 11, 440-453. | 6.5 | 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. | 3.7 | 37 |
| 1643 | Insights from the Comparison of Plant Genome Sequences. <i>Annual Review of Plant Biology</i> , 2010, 61, 349-372. | 18.7 | 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. | 9.7 | 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. | 2.4 | 50 |
| 1647 | Magnesium sulfate treatment alters fetal cerebellar gene expression responses to hypoxia. <i>International Journal of Developmental Neuroscience</i> , 2010, 28, 207-216. | 1.6 | 6 |
| 1648 | Alternative promoter usage and alternative splicing of the rat estrogen receptor β gene generate numerous mRNA variants with distinct 5' ends. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2010, 118, 59-69. | 2.5 | 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. | 2.1 | 6 |
| 1650 | The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. <i>Cell</i> , 2010, 140, 631-642. | 28.9 | 399 |
| 1651 | LINE-1 Retrotransposition Activity in Human Genomes. <i>Cell</i> , 2010, 141, 1159-1170. | 28.9 | 531 |
| 1652 | Efficient discovery of ASCL1 regulatory sequences through transgene pooling. <i>Genomics</i> , 2010, 95, 363-369. | 2.9 | 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. | 2.9 | 32 |
| 1654 | Genomic SELEX: A discovery tool for genomic aptamers. <i>Methods</i> , 2010, 52, 125-132. | 3.8 | 55 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1655 | MetaBioME: a database to explore commercially useful enzymes in metagenomic datasets. <i>Nucleic Acids Research</i> , 2010, 38, D468-D472. | 14.5 | 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. | 3.8 | 140 |
| 1657 | Runx2 regulates survivin expression in prostate cancer cells. <i>Laboratory Investigation</i> , 2010, 90, 222-233. | 3.7 | 72 |
| 1658 | Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. <i>Nature</i> , 2010, 466, 612-616. | 27.8 | 210 |
| 1659 | A survey of sequence alignment algorithms for next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 473-483. | 6.5 | 765 |
| 1660 | Fast and SNP-tolerant detection of complex variants and splicing in short reads. <i>Bioinformatics</i> , 2010, 26, 873-881. | 4.1 | 1,774 |
| 1661 | Databases and Genome Browsers. , 2010, , 905-921. | | 0 |
| 1662 | Cellâ€™type specific analysis of translating RNAs in developing flowers reveals new levels of control. <i>Molecular Systems Biology</i> , 2010, 6, 419. | 7.2 | 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. | 6.5 | 141 |
| 1665 | Characterization of microRNAs encoded by the bovine herpesvirus 1 genome. <i>Journal of General Virology</i> , 2010, 91, 32-41. | 2.9 | 44 |
| 1666 | Computational Methods for Ab Initio and Comparative Gene Finding. <i>Methods in Molecular Biology</i> , 2010, 609, 269-284. | 0.9 | 45 |
| 1667 | Bioinformatics for Next Generation Sequencing Data. <i>Genes</i> , 2010, 1, 294-307. | 2.4 | 65 |
| 1668 | Sequencing and Genome Assembly Using Next-Generation Technologies. <i>Methods in Molecular Biology</i> , 2010, 673, 1-17. | 0.9 | 47 |
| 1669 | Genetic diversity in India and the inference of Eurasian population expansion. <i>Genome Biology</i> , 2010, 11, R113. | 8.8 | 60 |
| 1670 | Design and evaluation of genome-wide libraries for RNA interference screens. <i>Genome Biology</i> , 2010, 11, R61. | 9.6 | 69 |
| 1671 | Towards a comprehensive structural variation map of an individual human genome. <i>Genome Biology</i> , 2010, 11, R52. | 9.6 | 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. | 9.6 | 93 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1673 | SL RNA Genes of the Ascidian Tunicates <i>Ciona intestinalis</i> and <i>Ciona savignyi</i> . Zoological Science, 2010, 27, 171-180. | 0.7 | 7 |
| 1674 | Fast and accurate long-read alignment with Burrows-Wheeler transform. Bioinformatics, 2010, 26, 589-595. | 4.1 | 10,002 |
| 1675 | Whole-genome sequencing and intensive analysis of the undomesticated soybean (<i>Glycine soja</i>) Tj ETQq0 0 0 rgBT /Overlock 10 America, 2010, 107, 22032-22037. | 7.1 | 299 |
| 1676 | Development of a DNA Microarray to Detect Antimicrobial Resistance Genes Identified in the National Center for Biotechnology Information Database. Microbial Drug Resistance, 2010, 16, 9-19. | 2.0 | 55 |
| 1677 | The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222. | 14.5 | 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. MBio, 2011, 2, . | 4.1 | 86 |
| 1679 | Sequencing and disease variation detection tools and techniques. , 2011, , . | | 1 |
| 1680 | The human gut virome: Inter-individual variation and dynamic response to diet. Genome Research, 2011, 21, 1616-1625. | 5.5 | 825 |
| 1681 | Evolution of C4 Photosynthesis in the Genus <i>Flaveria</i> : How Many and Which Genes Does It Take to Make C4?. Plant Cell, 2011, 23, 2087-2105. | 6.6 | 185 |
| 1682 | Rigid region pairwise sequence alignment. , 2011, , . | | 2 |
| 1683 | Analysis of Transcriptome Complexity Through RNA Sequencing in Normal and Failing Murine Hearts. Circulation Research, 2011, 109, 1332-1341. | 4.5 | 194 |
| 1684 | CUDA-BLASTP: Accelerating BLASTP on CUDA-Enabled Graphics Hardware. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1678-1684. | 3.0 | 69 |
| 1685 | Comparative analysis of RNA-Seq alignment algorithms and the RNA-Seq unified mapper (RUM). Bioinformatics, 2011, 27, 2518-2528. | 4.1 | 298 |
| 1686 | GnomCmp: a quantitative approach for comparative analysis of closely related genomes of bacterial pathogens. Genome, 2011, 54, 402-418. | 2.0 | 1 |
| 1687 | DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. Genome Biology, 2011, 12, R10. | 8.8 | 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. Immunopharmacology and Immunotoxicology, 2011, 33, 754-758. | 2.4 | 9 |
| 1690 | Alternative Splicing in the Fly and the Worm: Splicing Databases for <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> . , 2011, , . | | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1691 | Sequence Analysis of the Genome of an Oil-Bearing Tree, <i>Jatropha curcas</i> L.. DNA Research, 2011, 18, 65-76. | 3.4 | 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. Genome Research, 2011, 21, 216-226. | 5.5 | 146 |
| 1694 | Three Periods of Regulatory Innovation During Vertebrate Evolution. Science, 2011, 333, 1019-1024. | 12.6 | 127 |
| 1695 | Drosophila Duplication Hotspots Are Associated with Late-Replicating Regions of the Genome. PLoS Genetics, 2011, 7, e1002340. | 3.5 | 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 Overlooked | 2.0 | 5 |
| 1697 | Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. Nature Biotechnology, 2011, 29, 723-730. | 17.5 | 113 |
| 1699 | Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. Nature Genetics, 2011, 43, 956-963. | 21.4 | 910 |
| 1700 | Discovery of lost diversity of paternal horse lineages using ancient DNA. Nature Communications, 2011, 2, 450. | 12.8 | 72 |
| 1701 | Mesozoic retroposons reveal parrots as the closest living relatives of passerine birds. Nature Communications, 2011, 2, 443. | 12.8 | 175 |
| 1702 | Genome wide SNP discovery, analysis and evaluation in mallard (<i>Anas platyrhynchos</i>). BMC Genomics, 2011, 12, 150. | 2.8 | 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. BMC Research Notes, 2011, 4, 200. | 1.4 | 6 |
| 1704 | The complexity of <i>Rhipicephalus (Boophilus) microplus</i> genome characterised through detailed analysis of two BAC clones. BMC Research Notes, 2011, 4, 254. | 1.4 | 6 |
| 1705 | Cross-species protein sequence and gene structure prediction with fine-tuned Webscipio 2.0 and Scipio. BMC Research Notes, 2011, 4, 265. | 1.4 | 38 |
| 1706 | Integrating fragmented software applications into holistic solutions: focus on drug discovery. Expert Opinion on Drug Discovery, 2011, 6, 383-392. | 5.0 | 1 |
| 1707 | Next generation sequencing has lower sequence coverage and poorer SNP-detection capability in the regulatory regions. Scientific Reports, 2011, 1, 55. | 3.3 | 67 |
| 1708 | Transcriptome Sequencing Demonstrates that Human Papillomavirus Is Not Active in Cutaneous Squamous Cell Carcinoma. Journal of Investigative Dermatology, 2011, 131, 1745-1753. | 0.7 | 127 |
| 1709 | Probabilistic Analysis of Probe Reliability in Differential Gene Expression Studies with Short Oligonucleotide Arrays. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 217-225. | 3.0 | 29 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1710 | Post-transcriptional exon shuffling events in humans can be evolutionarily conserved and abundant. <i>Genome Research</i> , 2011, 21, 1788-1799. | 5.5 | 56 |
| 1711 | Waveform Mapping and Time-Frequency Processing of DNA and Protein Sequences. <i>IEEE Transactions on Signal Processing</i> , 2011, 59, 4210-4224. | 5.3 | 7 |
| 1712 | Plant Reverse Genetics. <i>Methods in Molecular Biology</i> , 2011, , . | 0.9 | 7 |
| 1713 | CREST maps somatic structural variation in cancer genomes with base-pair resolution. <i>Nature Methods</i> , 2011, 8, 652-654. | 19.0 | 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. | 9.6 | 183 |
| 1716 | The draft genome and transcriptome of <i>Cannabis sativa</i> . <i>Genome Biology</i> , 2011, 12, R102. | 9.6 | 479 |
| 1717 | TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. <i>Genome Biology</i> , 2011, 12, R72. | 9.6 | 670 |
| 1718 | The head-regeneration transcriptome of the planarian <i>Schmidtea mediterranea</i> . <i>Genome Biology</i> , 2011, 12, R76. | 9.6 | 109 |
| 1719 | Refinement of primate copy number variation hotspots identifies candidate genomic regions evolving under positive selection. <i>Genome Biology</i> , 2011, 12, R52. | 8.8 | 58 |
| 1720 | A vertebrate case study of the quality of assemblies derived from next-generation sequences. <i>Genome Biology</i> , 2011, 12, R31. | 9.6 | 32 |
| 1721 | Genome sequence of the stramenopile <i>Blastocystis</i> , a human anaerobic parasite. <i>Genome Biology</i> , 2011, 12, R29. | 9.6 | 159 |
| 1722 | A cost-effective and universal strategy for complete prokaryotic genome sequencing proposed by computer simulation. <i>Genome Biology</i> , 2011, 12, . | 9.6 | 1 |
| 1723 | Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi. <i>Genome Biology</i> , 2011, 12, R7. | 9.6 | 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. | 2.3 | 28 |
| 1725 | Bioinformatics challenges for personalized medicine. <i>Bioinformatics</i> , 2011, 27, 1741-1748. | 4.1 | 223 |
| 1726 | Development and characterization of two mini-X chromosomal short tandem repeat multiplexes. <i>Forensic Science International: Genetics</i> , 2011, 5, 415-421. | 3.1 | 29 |
| 1727 | Dating Primate Divergences through an Integrated Analysis of Palaeontological and Molecular Data. <i>Systematic Biology</i> , 2011, 60, 16-31. | 5.6 | 195 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 9.7 | 77 |
| 1729 | Identification of novel splicing events and post-transcriptional regulation of human estrogen receptor α isoforms. <i>Molecular and Cellular Endocrinology</i> , 2011, 333, 55-61. | 3.2 | 24 |
| 1730 | Identification of C-terminally and N-terminally truncated estrogen receptor α variants in the mouse. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2011, 124, 38-46. | 2.5 | 14 |
| 1731 | Complex organization of the 5'-untranslated region of the mouse estrogen receptor α gene: Identification of numerous mRNA transcripts with distinct 5'-ends. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2011, 125, 211-218. | 2.5 | 18 |
| 1732 | Mapping in vivo protein-RNA interactions at single-nucleotide resolution from HITS-CLIP data. <i>Nature Biotechnology</i> , 2011, 29, 607-614. | 17.5 | 384 |
| 1733 | Sequence overlap between autosomal and sex-linked probes on the Illumina HumanMethylation27 microarray. <i>Genomics</i> , 2011, 97, 214-222. | 2.9 | 67 |
| 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. | 2.9 | 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. | 6.9 | 26 |
| 1736 | Identification of Alternatively Spliced Transcripts Using a Proteomic Informatics Approach. <i>Methods in Molecular Biology</i> , 2011, 696, 319-326. | 0.9 | 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. | 17.5 | 488 |
| 1739 | Weak seed-pairing stability and high target-site abundance decrease the proficiency of lsi-6 and other microRNAs. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1139-1146. | 8.2 | 803 |
| 1740 | Museum genomics: low-cost and high-accuracy genetic data from historical specimens. <i>Molecular Ecology Resources</i> , 2011, 11, 1082-1092. | 4.8 | 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. | 0.9 | 22 |
| 1743 | Deep Sequencing of the Human TCR β and TCR α Repertoires Suggests that TCR α Rearranges After β and β T Cell Commitment. <i>Science Translational Medicine</i> , 2011, 3, 90ra61. | 12.4 | 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. | 17.5 | 428 |
| 1745 | Using Bacterial Artificial Chromosomes to Refine Genome Assemblies and to Build Virtual Genomes. , 0, , . | | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 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. Molecular Systems Biology, 2011, 7, 504. | 7.2 | 32 |
| 1749 | Adaptation of the AFLP technique as a new tool to detect genetic instability and transposition in interspecific hybrids. BioTechniques, 2011, 50, 247-250. | 1.8 | 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. Frontiers in Plant Science, 2011, 2, 34. | 3.6 | 396 |
| 1752 | Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont Piriformospora indica. PLoS Pathogens, 2011, 7, e1002290. | 4.7 | 361 |
| 1753 | Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two Bos Taurus Assemblies. PLoS ONE, 2011, 6, e21400. | 2.5 | 65 |
| 1754 | Phylogenetic Comparison of F-Box (FBX) Gene Superfamily within the Plant Kingdom Reveals Divergent Evolutionary Histories Indicative of Genomic Drift. PLoS ONE, 2011, 6, e16219. | 2.5 | 116 |
| 1755 | Considering Transposable Element Diversification in De Novo Annotation Approaches. PLoS ONE, 2011, 6, e16526. | 2.5 | 477 |
| 1756 | Quantitative Trait Loci Involved in Sex Determination and Body Growth in the Gilthead Sea Bream (Sparus aurata L.) through Targeted Genome Scan. PLoS ONE, 2011, 6, e16599. | 2.5 | 70 |
| 1757 | Genome-Wide Linkage Analysis of Global Gene Expression in Loin Muscle Tissue Identifies Candidate Genes in Pigs. PLoS ONE, 2011, 6, e16766. | 2.5 | 45 |
| 1758 | Fast Identification and Removal of Sequence Contamination from Genomic and Metagenomic Datasets. PLoS ONE, 2011, 6, e17288. | 2.5 | 630 |
| 1759 | CORE: A Phylogenetically-Curated 16S rDNA Database of the Core Oral Microbiome. PLoS ONE, 2011, 6, e19051. | 2.5 | 154 |
| 1760 | The First Sequenced Carnivore Genome Shows Complex Host-Endogenous Retrovirus Relationships. PLoS ONE, 2011, 6, e19832. | 2.5 | 32 |
| 1761 | Towards the Human Colorectal Cancer Microbiome. PLoS ONE, 2011, 6, e20447. | 2.5 | 470 |
| 1762 | Nuclear Outsourcing of RNA Interference Components to Human Mitochondria. PLoS ONE, 2011, 6, e20746. | 2.5 | 249 |
| 1763 | Poly (A)+ Transcriptome Assessment of ERBB2-Induced Alterations in Breast Cell Lines. PLoS ONE, 2011, 6, e21022. | 2.5 | 17 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1764 | Microbial Diversity in the Midguts of Field and Lab-Reared Populations of the European Corn Borer <i>Ostrinia nubilalis</i> . PLoS ONE, 2011, 6, e21751. | 2.5 | 71 |
| 1765 | The Fat Body Transcriptomes of the Yellow Fever Mosquito <i>Aedes aegypti</i> , Pre- and Post- Blood Meal. PLoS ONE, 2011, 6, e22573. | 2.5 | 77 |
| 1766 | Addressing Inter-Gene Heterogeneity in Maximum Likelihood Phylogenomic Analysis: Yeasts Revisited. PLoS ONE, 2011, 6, e22783. | 2.5 | 24 |
| 1767 | Protein-Binding Microarray Analysis of Tumor Suppressor AP2 β Target Gene Specificity. PLoS ONE, 2011, 6, e22895. | 2.5 | 5 |
| 1768 | Very Few RNA and DNA Sequence Differences in the Human Transcriptome. PLoS ONE, 2011, 6, e25842. | 2.5 | 69 |
| 1769 | Regional Selection Acting on the OFD1 Gene Family. PLoS ONE, 2011, 6, e26195. | 2.5 | 9 |
| 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. | 2.5 | 45 |
| 1771 | Genome-Wide Signatures of "Rearrangement Hotspots"™ within Segmental Duplications in Humans. PLoS ONE, 2011, 6, e28853. | 2.5 | 14 |
| 1772 | A genomic approach to investigate expression profiles in Slovenian patients with gastric cancer. Oncology Letters, 2011, 2, 1003-1014. | 1.8 | 7 |
| 1773 | Evolution of Synonymous Codon Usage in <i>Neurospora tetrasperma</i> and <i>Neurospora discreta</i> . Genome Biology and Evolution, 2011, 3, 332-343. | 2.5 | 32 |
| 1774 | Familial hemophagocytic lymphohistiocytosis type 3 (FHL3) caused by deep intronic mutation and inversion in UNC13D. Blood, 2011, 118, 5783-5793. | 1.4 | 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, <i>Bombyx mori</i> . Genome Biology and Evolution, 2011, 3, 491-504. | 2.5 | 53 |
| 1780 | Characterization of a divergent chromosome region in the willow warbler <i>Phylloscopus trochilus</i> using avian genomic resources. Journal of Evolutionary Biology, 2011, 24, 1241-1253. | 1.7 | 8 |
| 1781 | Comparative deep transcriptional profiling of four developing oilseeds. Plant Journal, 2011, 68, 1014-1027. | 5.7 | 241 |
| 1782 | Characterization of a genomic divergence island between black and yellow and gopher <i>Sebastes</i> rockfishes. Molecular Ecology, 2011, 20, 2603-2618. | 3.9 | 14 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1783 | Isolation and gene flow: inferring the speciation history of European house mice. <i>Molecular Ecology</i> , 2011, 20, 5248-5264. | 3.9 | 99 |
| 1784 | Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. <i>Journal of Neurochemistry</i> , 2011, 116, 459-466. | 3.9 | 152 |
| 1785 | Understanding the pathogenesis of Alzheimer's disease: will RNA-seq realize the promise of transcriptomics?. <i>Journal of Neurochemistry</i> , 2011, 116, 937-946. | 3.9 | 65 |
| 1786 | Expression Profiling of Cassava Storage Roots Reveals an Active Process of Glycolysis/Gluconeogenesis. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 193-211. | 8.5 | 89 |
| 1787 | A CASE-BY-CASE EVOLUTIONARY ANALYSIS OF FOUR IMPRINTED RETROGENES. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 1413-1427. | 2.3 | 26 |
| 1788 | Soil-specific limitations for access and analysis of soil microbial communities by metagenomics. <i>FEMS Microbiology Ecology</i> , 2011, 78, 31-49. | 2.7 | 185 |
| 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. | 3.3 | 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. | 21.4 | 814 |
| 1791 | Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477. | 19.0 | 919 |
| 1792 | Next-generation transcriptome assembly. <i>Nature Reviews Genetics</i> , 2011, 12, 671-682. | 16.3 | 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. | 17.5 | 356 |
| 1794 | Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652. | 17.5 | 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. | 2.3 | 10 |
| 1796 | Gene expression in <i>Trypanosoma brucei</i> : lessons from high-throughput RNA sequencing. <i>Trends in Parasitology</i> , 2011, 27, 434-441. | 3.3 | 71 |
| 1797 | Effects of genome-wide copy number variation on expression in mammalian cells. <i>BMC Genomics</i> , 2011, 12, 562. | 2.8 | 19 |
| 1798 | Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. <i>BMC Genomics</i> , 2011, 12, 590. | 2.8 | 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. | 3.6 | 25 |
| 1800 | Spliceosomal intron size expansion in domesticated grapevine (<i>Vitis vinifera</i>). <i>BMC Research Notes</i> , 2011, 4, 52. | 1.4 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1801 | The physiological, transcriptional and genetic responses of an ozone- sensitive and an ozone tolerant poplar and selected extremes of their F 2 progeny. <i>Environmental Pollution</i> , 2011, 159, 45-54. | 7.5 | 32 |
| 1802 | Analysis of High-Throughput Sequencing Data. <i>Methods in Molecular Biology</i> , 2011, 678, 1-11. | 0.9 | 6 |
| 1803 | <i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533. | 27.8 | 246 |
| 1804 | Next-generation sequencing and its applications in molecular diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 333-343. | 3.1 | 146 |
| 1805 | CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638. | 21.4 | 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. | 2.9 | 41 |
| 1807 | Bioinformatic identification of novel protein phosphatases in the dog genome. <i>Molecular and Cellular Biochemistry</i> , 2011, 351, 149-156. | 3.1 | 1 |
| 1808 | Pseudogene: lessons from PCR bias, identification and resurrection. <i>Molecular Biology Reports</i> , 2011, 38, 3709-3715. | 2.3 | 10 |
| 1809 | A novel mitofusin 2 mutation causes canine fetal-onset neuroaxonal dystrophy. <i>Neurogenetics</i> , 2011, 12, 223-232. | 1.4 | 24 |
| 1810 | Functional Divergences of GAPDH Isoforms During Early Development in Two Perciform Fish Species. <i>Marine Biotechnology</i> , 2011, 13, 1115-1124. | 2.4 | 11 |
| 1811 | Ecological genetics of invasive alien species. <i>BioControl</i> , 2011, 56, 409-428. | 2.0 | 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. | 3.6 | 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. | 1.8 | 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. | 1.8 | 4 |
| 1815 | Reproductive tissue-specific expression profiling and genetic variation across a 19 gene bovine β -defensin cluster. <i>Immunogenetics</i> , 2011, 63, 641-651. | 2.4 | 33 |
| 1816 | Finding Cancer-Associated miRNAs: Methods and Tools. <i>Molecular Biotechnology</i> , 2011, 49, 97-107. | 2.4 | 7 |
| 1817 | De novo transcriptome assembly of RNA-Seq reads with different strategies. <i>Science China Life Sciences</i> , 2011, 54, 1129-1133. | 4.9 | 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 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 1819 | Identification, characterization, and comparative genomic distribution of the HERV-K (HML-2) group of human endogenous retroviruses. <i>Retrovirology</i> , 2011, 8, 90. | 2.0 | 340 |
| 1820 | Fast local fragment chaining using sum-of-pair gap costs. <i>Algorithms for Molecular Biology</i> , 2011, 6, 4. | 1.2 | 15 |
| 1821 | Enhancing genome assemblies by integrating non-sequence based data. <i>BMC Proceedings</i> , 2011, 5, S7. | 1.6 | 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. | 1.5 | 40 |
| 1823 | Distinct influences of tandem repeats and retrotransposons on CENH3 nucleosome positioning. <i>Epigenetics and Chromatin</i> , 2011, 4, 3. | 3.9 | 30 |
| 1824 | Alu pair exclusions in the human genome. <i>Mobile DNA</i> , 2011, 2, 10. | 3.6 | 15 |
| 1825 | RAPSearch: a fast protein similarity search tool for short reads. <i>BMC Bioinformatics</i> , 2011, 12, 159. | 2.6 | 128 |
| 1826 | Parallelized short read assembly of large genomes using de Bruijn graphs. <i>BMC Bioinformatics</i> , 2011, 12, 354. | 2.6 | 64 |
| 1827 | Support vector machines-based identification of alternative splicing in <i>Arabidopsis thaliana</i> from whole-genome tiling arrays. <i>BMC Bioinformatics</i> , 2011, 12, 55. | 2.6 | 21 |
| 1828 | Optimizing de novo transcriptome assembly from short-read RNA-Seq data: a comparative study. <i>BMC Bioinformatics</i> , 2011, 12, S2. | 2.6 | 462 |
| 1829 | ClipCrop: a tool for detecting structural variations with single-base resolution using soft-clipping information. <i>BMC Bioinformatics</i> , 2011, 12, S7. | 2.6 | 41 |
| 1830 | STELLAR: fast and exact local alignments. <i>BMC Bioinformatics</i> , 2011, 12, S15. | 2.6 | 28 |
| 1831 | Human teneurin-1 is a direct target of the homeobox transcription factor EMX2 at a novel alternate promoter. <i>BMC Developmental Biology</i> , 2011, 11, 35. | 2.1 | 15 |
| 1832 | The sequence, structure and evolutionary features of HOTAIR in mammals. <i>BMC Evolutionary Biology</i> , 2011, 11, 102. | 3.2 | 118 |
| 1833 | Rhythms and synchronization patterns in gene expression in the <i>Aedes aegypti</i> mosquito. <i>BMC Genomics</i> , 2011, 12, 153. | 2.8 | 47 |
| 1834 | Rice-Map: a new-generation rice genome browser. <i>BMC Genomics</i> , 2011, 12, 165. | 2.8 | 10 |
| 1835 | A high-resolution linkage map for comparative genome analysis and QTL fine mapping in Asian seabass, <i>Lates calcarifer</i> . <i>BMC Genomics</i> , 2011, 12, 174. | 2.8 | 93 |
| 1836 | Building a model: developing genomic resources for common milkweed (<i>Asclepias syriaca</i>) with low coverage genome sequencing. <i>BMC Genomics</i> , 2011, 12, 211. | 2.8 | 104 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 1837 | A systematic evaluation of expression of HERV-W elements; influence of genomic context, viral structure and orientation. BMC Genomics, 2011, 12, 22. | 2.8 | 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. | 2.8 | 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. | 2.8 | 33 |
| 1840 | Exome-wide DNA capture and next generation sequencing in domestic and wild species. BMC Genomics, 2011, 12, 347. | 2.8 | 88 |
| 1841 | Identification of genomic indels and structural variations using split reads. BMC Genomics, 2011, 12, 375. | 2.8 | 57 |
| 1842 | Deep sequencing reveals as-yet-undiscovered small RNAs in Escherichia coli. BMC Genomics, 2011, 12, 428. | 2.8 | 51 |
| 1843 | A comparative physical map reveals the pattern of chromosomal evolution between the turkey (Meleagris gallopavo) and chicken (Gallus gallus) genomes. BMC Genomics, 2011, 12, 447. | 2.8 | 24 |
| 1844 | De novo sequence assembly of Albugo candida reveals a small genome relative to other biotrophic oomycetes. BMC Genomics, 2011, 12, 503. | 2.8 | 123 |
| 1845 | RNA-Seq improves annotation of protein-coding genes in the cucumber genome. BMC Genomics, 2011, 12, 540. | 2.8 | 232 |
| 1846 | The repertoire of G protein-coupled receptors in the human parasite Schistosoma mansoni and the model organism Schmidtea mediterranea. BMC Genomics, 2011, 12, 596. | 2.8 | 72 |
| 1847 | The mosquito Aedes aegypti has a large genome size and high transposable element load but contains a low proportion of transposon-specific piRNAs. BMC Genomics, 2011, 12, 606. | 2.8 | 99 |
| 1848 | Genomic sequencing and analysis of a Chinese hamster ovary cell line using Illumina sequencing technology. BMC Genomics, 2011, 12, 67. | 2.8 | 37 |
| 1849 | Interrogation of alternative splicing events in duplicated genes during evolution. BMC Genomics, 2011, 12, S16. | 2.8 | 13 |
| 1850 | Profiling ascidian promoters as the primordial type of vertebrate promoter. BMC Genomics, 2011, 12, S7. | 2.8 | 7 |
| 1851 | Mutational analysis of 12 patients with the phenotype of Ehlersâ€“Danlos syndrome type VIB shows no linkage to the zinc transporter gene <i>SLC39A13</i>. American Journal of Medical Genetics, Part A, 2011, 155, 2011-2014. | 1.2 | 0 |
| 1852 | An experience report: porting the MG-RAST rapid metagenomics analysis pipeline to the cloud. Concurrency Computation Practice and Experience, 2011, 23, 2250-2257. | 2.2 | 13 |
| 1853 | In silico bioinformatic tools for determining core genes from sets of genomes. Drug Development Research, 2011, 72, 147-152. | 2.9 | 0 |
| 1854 | SNP uniqueness problem: a proofâ€“ofâ€“principle in HapMap SNPs. Human Mutation, 2011, 32, 355-357. | 2.5 | 7 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 1855 | Genome-wide identification of conserved regulatory function in diverged sequences. <i>Genome Research</i> , 2011, 21, 1139-1149. | 5.5 | 72 |
| 1856 | A method for visualization of genomic datasets for sphingolipid metabolism to predict potentially interesting differences. <i>Journal of Lipid Research</i> , 2011, 52, 1073-1083. | 4.2 | 24 |
| 1857 | Identifying viral integration sites using SeqMap 2.0. <i>Bioinformatics</i> , 2011, 27, 720-722. | 4.1 | 33 |
| 1858 | Adaptive seeds tame genomic sequence comparison. <i>Genome Research</i> , 2011, 21, 487-493. | 5.5 | 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. | 5.5 | 123 |
| 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. | 3.5 | 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. | 2.2 | 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. | 5.5 | 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. | 4.8 | 222 |
| 1866 | Genome of Multidrug-Resistant Uropathogenic <i>Escherichia coli</i> Strain NA114 from India. <i>Journal of Bacteriology</i> , 2011, 193, 4272-4273. | 2.2 | 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. | 14.5 | 513 |
| 1869 | Multimodal RNA-seq using single-strand, double-strand, and CircLigase-based capture yields a refined and extended description of the <i>C. elegans</i> transcriptome. <i>Genome Research</i> , 2011, 21, 265-275. | 5.5 | 38 |
| 1870 | Expression, Splicing, and Evolution of the Myosin Gene Family in Plants. <i>Plant Physiology</i> , 2011, 155, 1191-1204. | 4.8 | 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. | 2.9 | 9 |
| 1872 | Identification of piRNAs in the central nervous system. <i>Rna</i> , 2011, 17, 1090-1099. | 3.5 | 265 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 4.1 | 39 |
| 1874 | PE-Assembler: <i>de novo</i> assembler using short paired-end reads. <i>Bioinformatics</i> , 2011, 27, 167-174. | 4.1 | 98 |
| 1875 | The effects of EBV transformation on gene expression levels and methylation profiles. <i>Human Molecular Genetics</i> , 2011, 20, 1643-1652. | 2.9 | 124 |
| 1876 | Meta-IDBA: a <i>de Novo</i> assembler for metagenomic data. <i>Bioinformatics</i> , 2011, 27, i94-i101. | 4.1 | 267 |
| 1877 | Epigenetic Control of Retrotransposon Expression in Human Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2011, 31, 300-316. | 2.3 | 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. | 14.5 | 114 |
| 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. | 14.5 | 123 |
| 1880 | Zygomycetes, Microsporidia, and the Evolutionary Ancestry of Sex Determination. <i>Genome Biology and Evolution</i> , 2011, 3, 186-194. | 2.5 | 24 |
| 1881 | Genome-wide analysis of retrogene polymorphisms in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011, 21, 2087-2095. | 5.5 | 58 |
| 1882 | Anatomy of a hash-based long read sequence mapping algorithm for next generation DNA sequencing. <i>Bioinformatics</i> , 2011, 27, 189-195. | 4.1 | 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. | 2.3 | 20 |
| 1884 | Annotating genes and genomes with DNA sequences extracted from biomedical articles. <i>Bioinformatics</i> , 2011, 27, 980-986. | 4.1 | 23 |
| 1885 | <i>S</i> -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. | 2.5 | 42 |
| 1886 | Whole Genome Sequence Comparisons in Taxonomy. <i>Methods in Microbiology</i> , 2011, 38, 409-436. | 0.8 | 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. | 14.5 | 19 |
| 1888 | Cell envelope gene expression in phosphate-limited <i>Bacillus subtilis</i> cells. <i>Microbiology (United Kingdom)</i> 10.1093/mic/dkq114 | 1.8 | 35 |
| 1889 | Silencing, Positive Selection and Parallel Evolution: Busy History of Primate Cytochromes c. <i>PLoS ONE</i> , 2011, 6, e26269. | 2.5 | 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. | 3.5 | 196 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 14.5 | 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. | 2.2 | 42 |
| 1893 | dbDNV: a resource of duplicated gene nucleotide variants in human genome. <i>Nucleic Acids Research</i> , 2011, 39, D920-D925. | 14.5 | 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. | 3.4 | 67 |
| 1895 | Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. <i>Genome Research</i> , 2011, 21, 634-641. | 5.5 | 105 |
| 1896 | Molecular Description and Industrial Potential of Tn <i>6098</i> Conjugative Transfer Conferring Alpha-Galactoside Metabolism in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 555-563. | 3.1 | 30 |
| 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. | 2.3 | 12 |
| 1898 | <i>Sim4db</i> and <i>Leaff</i> : utilities for fast batch spliced alignment and sequence indexing. <i>Bioinformatics</i> , 2011, 27, 1869-1870. | 4.1 | 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. | 3.0 | 15 |
| 1900 | Transcriptome Analysis of <i>Sarracenia</i> , an Insectivorous Plant. <i>DNA Research</i> , 2011, 18, 253-261. | 3.4 | 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. | 6.6 | 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. | 8.9 | 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. | 14.5 | 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. | 3.1 | 34 |
| 1905 | Kaviar: an accessible system for testing SNV novelty. <i>Bioinformatics</i> , 2011, 27, 3216-3217. | 4.1 | 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. | 8.9 | 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. | 4.1 | 84 |
| 1908 | Computational challenges of sequence classification in microbiomic data. <i>Briefings in Bioinformatics</i> , 2011, 12, 614-625. | 6.5 | 15 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 8.9 | 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. | 3.4 | 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. | 2.9 | 69 |
| 1912 | SyMAP v3.4: a turnkey synteny system with application to plant genomes. <i>Nucleic Acids Research</i> , 2011, 39, e68-e68. | 14.5 | 304 |
| 1913 | piRNA profiling during specific stages of mouse spermatogenesis. <i>Rna</i> , 2011, 17, 1191-1203. | 3.5 | 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. | 2.2 | 29 |
| 1915 | Evolution of the V, D, and J gene segments used in the primate β 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. | 7.1 | 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. | 0.9 | 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. | 2.9 | 34 |
| 1918 | The evolution and expression of the snaR family of small non-coding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, 1485-1500. | 14.5 | 59 |
| 1919 | Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain H44/76. <i>Journal of Bacteriology</i> , 2011, 193, 2371-2372. | 2.2 | 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. | 14.5 | 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. | 5.5 | 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. | 5.5 | 100 |
| 1923 | Sequence Alignment as Hypothesis Testing. <i>Journal of Computational Biology</i> , 2011, 18, 677-691. | 1.6 | 8 |
| 1924 | The UCSC Genome Browser database: update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D876-D882. | 14.5 | 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. | 7.1 | 123 |
| 1926 | The Plant Cell Wall—Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765. | 12.6 | 512 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 1927 | A novel hybrid gene prediction method employing protein multiple sequence alignments. <i>Bioinformatics</i> , 2011, 27, 757-763. | 4.1 | 468 |
| 1928 | FR-HIT, a very fast program to recruit metagenomic reads to homologous reference genomes. <i>Bioinformatics</i> , 2011, 27, 1704-1705. | 4.1 | 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. | 5.6 | 271 |
| 1930 | MicroRNA-Driven Developmental Remodeling in the Brain Distinguishes Humans from Other Primates. <i>PLoS Biology</i> , 2011, 9, e1001214. | 5.6 | 198 |
| 1931 | MicroRNA Expression and Regulation in Human, Chimpanzee, and Macaque Brains. <i>PLoS Genetics</i> , 2011, 7, e1002327. | 3.5 | 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. | 3.0 | 86 |
| 1933 | Estimated Comparative Integration Hotspots Identify Different Behaviors of Retroviral Gene Transfer Vectors. <i>PLoS Computational Biology</i> , 2011, 7, e1002292. | 3.2 | 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. | 8.9 | 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. | 3.0 | 1 |
| 1936 | Narrowing a region on rat chromosome 13 that protects against hypertension in Dahl SS-13 ^{BN} congenic strains. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2011, 300, H1530-H1535. | 3.2 | 27 |
| 1937 | A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. <i>PLoS Genetics</i> , 2011, 7, e1002236. | 3.5 | 278 |
| 1938 | RNA-Seq Assembly “Are We There Yet?”. <i>Frontiers in Plant Science</i> , 2012, 3, 220. | 3.6 | 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. | 3.5 | 30 |
| 1940 | Virus Identification in Unknown Tropical Febrile Illness Cases Using Deep Sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1485. | 3.0 | 148 |
| 1941 | Joint Analysis of Multiple Metagenomic Samples. <i>PLoS Computational Biology</i> , 2012, 8, e1002373. | 3.2 | 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. | 4.7 | 118 |
| 1943 | Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. <i>Bioinformatics</i> , 2012, 28, 3232-3239. | 4.1 | 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 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1945 | A SEL1L Mutation Links a Canine Progressive Early-Onset Cerebellar Ataxia to the Endoplasmic Reticulumâ€Associated Protein Degradation (ERAD) Machinery. PLoS Genetics, 2012, 8, e1002759. | 3.5 | 52 |
| 1946 | A nucleosomal surface defines an integration hotspot for the <i>Saccharomyces cerevisiae</i> Ty1 retrotransposon. Genome Research, 2012, 22, 704-713. | 5.5 | 61 |
| 1947 | Tissue-Restricted Transcription from a Conserved Intragenic CpG Island in the Klf1 Gene in Mice1. Biology of Reproduction, 2012, 87, 108. | 2.7 | 9 |
| 1948 | Microarray Analysis of LTR Retrotransposon Silencing Identifies Hdac1 as a Regulator of Retrotransposon Expression in Mouse Embryonic Stem Cells. PLoS Computational Biology, 2012, 8, e1002486. | 3.2 | 64 |
| 1949 | Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. PLoS Genetics, 2012, 8, e1002692. | 3.5 | 80 |
| 1950 | A Novel Rhabdovirus Associated with Acute Hemorrhagic Fever in Central Africa. PLoS Pathogens, 2012, 8, e1002924. | 4.7 | 181 |
| 1951 | Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. PLoS Pathogens, 2012, 8, e1003037. | 4.7 | 595 |
| 1952 | The Paramecium Germline Genome Provides a Niche for Intragenic Parasitic DNA: Evolutionary Dynamics of Internal Eliminated Sequences. PLoS Genetics, 2012, 8, e1002984. | 3.5 | 154 |
| 1953 | Variants Affecting Exon Skipping Contribute to Complex Traits. PLoS Genetics, 2012, 8, e1002998. | 3.5 | 53 |
| 1954 | Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. PLoS Genetics, 2012, 8, e1003127. | 3.5 | 166 |
| 1955 | Hundreds of conserved non-coding genomic regions are independently lost in mammals. Nucleic Acids Research, 2012, 40, 11463-11476. | 14.5 | 48 |
| 1956 | Tachyon search speeds up retrieval of similar sequences by several orders of magnitude. Bioinformatics, 2012, 28, 1645-1646. | 4.1 | 12 |
| 1957 | High Levels of Sequence Diversity in the 5â€UTRs of Human-Specific L1 Elements. Comparative and Functional Genomics, 2012, 2012, 1-8. | 2.0 | 11 |
| 1958 | Tools for mapping high-throughput sequencing data. Bioinformatics, 2012, 28, 3169-3177. | 4.1 | 269 |
| 1959 | The genome of <i>Prunus mume</i> . Nature Communications, 2012, 3, 1318. | 12.8 | 441 |
| 1960 | Dr.VIS: a database of human disease-related viral integration sites. Nucleic Acids Research, 2012, 40, D1041-D1046. | 14.5 | 14 |
| 1961 | Complete Resequencing and Reannotation of the <i>Lactobacillus plantarum</i> WCFS1 Genome. Journal of Bacteriology, 2012, 194, 195-196. | 2.2 | 109 |
| 1962 | RAPSearch2: a fast and memory-efficient protein similarity search tool for next-generation sequencing data. Bioinformatics, 2012, 28, 125-126. | 4.1 | 386 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 1.8 | 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. | 3.5 | 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. | 2.9 | 27 |
| 1967 | GGRNA: an ultrafast, transcript-oriented search engine for genes and transcripts. <i>Nucleic Acids Research</i> , 2012, 40, W592-W596. | 14.5 | 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. | 14.5 | 39 |
| 1969 | Comment on "Widespread RNA and DNA Sequence Differences in the Human Transcriptome". <i>Science</i> , 2012, 335, 1302-1302. | 12.6 | 155 |
| 1970 | lobSTR: A short tandem repeat profiler for personal genomes. <i>Genome Research</i> , 2012, 22, 1154-1162. | 5.5 | 294 |
| 1971 | Copy number variation at 6q13 functions as a long-range regulator and is associated with pancreatic cancer risk. <i>Carcinogenesis</i> , 2012, 33, 94-100. | 2.8 | 34 |
| 1972 | Reverse engineering biomolecular systems using -omic data: challenges, progress and opportunities. <i>Briefings in Bioinformatics</i> , 2012, 13, 430-445. | 6.5 | 19 |
| 1973 | Ionising irradiation alters the dynamics of human long interspersed nuclear elements 1 (LINE1) retrotransposon. <i>Mutagenesis</i> , 2012, 27, 599-607. | 2.6 | 21 |
| 1974 | FoxO-Dependent Regulation of Diacylglycerol Kinase β Gene Expression. <i>Molecular and Cellular Biology</i> , 2012, 32, 4168-4180. | 2.3 | 32 |
| 1975 | Response to Comments on "Widespread RNA and DNA Sequence Differences in the Human Transcriptome". <i>Science</i> , 2012, 335, 1302-1302. | 12.6 | 98 |
| 1976 | Conditional CD8 ⁺ T Cell Escape during Acute Simian Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2012, 86, 605-609. | 3.4 | 29 |
| 1977 | Navigating the tip of the genomic iceberg: Next-generation sequencing for plant systematics. <i>American Journal of Botany</i> , 2012, 99, 349-364. | 1.7 | 558 |
| 1978 | YAHA: fast and flexible long-read alignment with optimal breakpoint detection. <i>Bioinformatics</i> , 2012, 28, 2417-2424. | 4.1 | 62 |
| 1979 | Double Digest RADseq: An Inexpensive Method for De Novo SNP Discovery and Genotyping in Model and Non-Model Species. <i>PLoS ONE</i> , 2012, 7, e37135. | 2.5 | 2,836 |
| 1980 | Genotypic and Phenotypic Evaluation of the Evolution of High-Level Daptomycin Nonsusceptibility in Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6051-6053. | 3.2 | 55 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 1981 | ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. <i>Nucleic Acids Research</i> , 2012, 41, D142-D151. | 14.5 | 47 |
| 1982 | Identification of allele-specific alternative mRNA processing via transcriptome sequencing. <i>Nucleic Acids Research</i> , 2012, 40, e104-e104. | 14.5 | 74 |
| 1983 | Genome Update of <i>Botrytis cinerea</i> Strains B05.10 and T4. <i>Eukaryotic Cell</i> , 2012, 11, 1413-1414. | 3.4 | 124 |
| 1984 | YOABS: yet other aligner of biological sequences—an efficient linearly scaling nucleotide aligner. <i>Bioinformatics</i> , 2012, 28, 1070-1077. | 4.1 | 11 |
| 1985 | Genome-Wide Selection on Codon Usage at the Population Level in the Fungal Model Organism <i>Neurospora crassa</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1975-1986. | 8.9 | 21 |
| 1986 | Accurate identification of A-to-I RNA editing in human by transcriptome sequencing. <i>Genome Research</i> , 2012, 22, 142-150. | 5.5 | 297 |
| 1987 | SCOREM: statistical consolidation of redundant expression measures. <i>Nucleic Acids Research</i> , 2012, 40, e46-e46. | 14.5 | 8 |
| 1988 | Dynamic Intra-Japonica Subspecies Variation and Resource Application. <i>Molecular Plant</i> , 2012, 5, 218-230. | 8.3 | 23 |
| 1989 | Spatio-temporal regulation of ADAR editing during development in porcine neural tissues. <i>RNA Biology</i> , 2012, 9, 1054-1065. | 3.1 | 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. <i>Plant Physiology</i> , 2012, 161, 252-265. | 4.8 | 113 |
| 1992 | A <i>Rickettsia</i> 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. | 2.2 | 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. | 3.4 | 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. | 5.5 | 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. | 1.5 | 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. | 3.4 | 51 |
| 1998 | SPLOOCE. <i>RNA Biology</i> , 2012, 9, 1339-1343. | 3.1 | 7 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. Nucleic Acids Research, 2012, 40, e83-e83. | 14.5 | 39 |
| 2001 | Evaluation of GPU-based Seed Generation for Computational Genomics Using Burrows-Wheeler Transform. , 2012, , . | | 7 |
| 2002 | Sex-Biased Transcriptome Evolution in Drosophila. Genome Biology and Evolution, 2012, 4, 1189-1200. | 2.5 | 159 |
| 2003 | SUITE OF TOOLS FOR STATISTICAL N-GRAM LANGUAGE MODELING FOR PATTERN MINING IN WHOLE GENOME SEQUENCES. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250016. | 0.8 | 3 |
| 2004 | Complementary Proteome and Transcriptome Profiling in Phosphate-deficient Arabidopsis Roots Reveals Multiple Levels of Gene Regulation. Molecular and Cellular Proteomics, 2012, 11, 1156-1166. | 3.8 | 266 |
| 2005 | Functional RNA Interference (RNAi) Screen Identifies System A Neutral Amino Acid Transporter 2 (SNAT2) as a Mediator of Arsenic-induced Endoplasmic Reticulum Stress. Journal of Biological Chemistry, 2012, 287, 6025-6034. | 3.4 | 29 |
| 2006 | Identification and Properties of 1,119 Candidate LincRNA Loci in the Drosophila melanogaster Genome. Genome Biology and Evolution, 2012, 4, 427-442. | 2.5 | 217 |
| 2007 | Conserved epigenetic sensitivity to early life experience in the rat and human hippocampus. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17266-17272. | 7.1 | 285 |
| 2008 | Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. Nucleic Acids Research, 2012, 40, D91-D97. | 14.5 | 179 |
| 2009 | PARALLEL ALGORITHMS FOR MAPPING SHORT DEGENERATE AND WEIGHTED DNA SEQUENCES TO A REFERENCE GENOME. International Journal of Foundations of Computer Science, 2012, 23, 249-259. | 1.1 | 1 |
| 2010 | Transcriptomic Evidence for the Expression of Horizontally Transferred Algal Nuclear Genes in the Photosynthetic Sea Slug, Elysia chlorotica. Molecular Biology and Evolution, 2012, 29, 1545-1556. | 8.9 | 54 |
| 2011 | Phenotype-specific effect of chromosome 1q21.1 rearrangements and GJA5 duplications in 2436 congenital heart disease patients and 6760 controls. Human Molecular Genetics, 2012, 21, 1513-1520. | 2.9 | 101 |
| 2012 | Strong signatures of selection in the domestic pig genome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19529-19536. | 7.1 | 548 |
| 2013 | Comparative Analysis of Genome Sequences Covering the Seven Cronobacter Species. PLoS ONE, 2012, 7, e49455. | 2.5 | 130 |
| 2014 | CADRE: the Central Aspergillus Data REpository 2012. Nucleic Acids Research, 2012, 40, D660-D666. | 14.5 | 55 |
| 2015 | Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. PLoS ONE, 2012, 7, e30087. | 2.5 | 360 |
| 2016 | Genome-Wide Analysis of DNA Methylation Differences in Muscle and Fat from Monozygotic Twins Discordant for Type 2 Diabetes. PLoS ONE, 2012, 7, e51302. | 2.5 | 171 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2017 | Novel domain combinations in proteins encoded by chimeric transcripts. <i>Bioinformatics</i> , 2012, 28, i67-i74. | 4.1 | 35 |
| 2018 | Regulated Expression of Chromobox Homolog 5 Revealed in Tumors of ApcMin/+ ROSA11 Gene Trap Mice. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 569-578. | 1.8 | 4 |
| 2019 | Rapid identification of non-human sequences in high-throughput sequencing datasets. <i>Bioinformatics</i> , 2012, 28, 1174-1175. | 4.1 | 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. | 3.4 | 16 |
| 2021 | Genomic Analysis of the Hydrocarbon-Producing, Cellulolytic, Endophytic Fungus <i>Ascocoryne sarcoides</i> . <i>PLoS Genetics</i> , 2012, 8, e1002558. | 3.5 | 76 |
| 2022 | RecountDB: a database of mapped and count corrected transcribed sequences. <i>Nucleic Acids Research</i> , 2012, 40, D1089-D1092. | 14.5 | 0 |
| 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. | 4.1 | 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. | 7.1 | 67 |
| 2025 | Dissect: detection and characterization of novel structural alterations in transcribed sequences. <i>Bioinformatics</i> , 2012, 28, i179-i187. | 4.1 | 13 |
| 2026 | Xenomeâ€”a tool for classifying reads from xenograft samples. <i>Bioinformatics</i> , 2012, 28, i172-i178. | 4.1 | 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. | 4.1 | 1 |
| 2028 | Transcriptome Analysis of a North American Songbird, <i>Melospiza melodia</i> . <i>DNA Research</i> , 2012, 19, 325-333. | 3.4 | 16 |
| 2029 | Elephant Transcriptome Provides Insights into the Evolution of Eutherian Placentation. <i>Genome Biology and Evolution</i> , 2012, 4, 713-725. | 2.5 | 27 |
| 2030 | RNASEQâ€”a streamlined and accurate RNA-seq sequence analysis program. <i>Nucleic Acids Research</i> , 2012, 40, e42-e42. | 14.5 | 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. | 14.5 | 67 |
| 2032 | Sequencing of the smallest Apicomplexan genome from the human pathogen <i>Babesia microti</i> . <i>Nucleic Acids Research</i> , 2012, 40, 9102-9114. | 14.5 | 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. | 3.6 | 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. | 14.5 | 114 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 0.7 | 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. | 1.6 | 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. | 0.9 | 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. | 2.6 | 2 |
| 2041 | Population Genomic Analysis of Model and Nonmodel Organisms Using Sequenced RAD Tags. <i>Methods in Molecular Biology</i> , 2012, 888, 235-260. | 0.9 | 56 |
| 2042 | Detection of Chromosomal Alterations in the Circulation of Cancer Patients with Whole-Genome Sequencing. <i>Science Translational Medicine</i> , 2012, 4, 162ra154. | 12.4 | 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. | 5.7 | 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. | 3.9 | 25 |
| 2045 | Lentiviral Hematopoietic Cell Gene Therapy for X-Linked Adrenoleukodystrophy. <i>Methods in Enzymology</i> , 2012, 507, 187-198. | 1.0 | 100 |
| 2046 | A <i>de novo</i> metagenomic assembly program for shotgun DNA reads. <i>Bioinformatics</i> , 2012, 28, 1455-1462. | 4.1 | 42 |
| 2047 | Genome-Wide Analysis Uncovers Regulation of Long Intergenic Noncoding RNAs in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 4333-4345. | 6.6 | 656 |
| 2048 | Targeted genome enrichment for efficient purification of endosymbiont DNA from host DNA. <i>Symbiosis</i> , 2012, 58, 201-207. | 2.3 | 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. | 14.5 | 25 |
| 2050 | Computational tools for viral metagenomics and their application in clinical research. <i>Virology</i> , 2012, 434, 162-174. | 2.4 | 59 |
| 2051 | Identification and Functional Analysis of Three Isoforms of Bovine BST-2. <i>PLoS ONE</i> , 2012, 7, e41483. | 2.5 | 18 |
| 2052 | The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. <i>Science</i> , 2012, 338, 1587-1593. | 12.6 | 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. | 8.9 | 36 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2054 | BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. <i>Bioinformatics</i> , 2012, 28, 1923-1924. | 4.1 | 54 |
| 2055 | Bioinformatics tools and databases for analysis of next-generation sequence data. <i>Briefings in Functional Genomics</i> , 2012, 11, 12-24. | 2.7 | 73 |
| 2056 | Chromosome conformation capture assays in bacteria. <i>Methods</i> , 2012, 58, 212-220. | 3.8 | 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. | 9.6 | 140 |
| 2058 | The GENCODE pseudogene resource. <i>Genome Biology</i> , 2012, 13, R51. | 9.6 | 273 |
| 2059 | Exploring the <i>Schistosoma mansoni</i> adult male transcriptome using RNA-seq. <i>Experimental Parasitology</i> , 2012, 132, 22-31. | 1.2 | 35 |
| 2060 | Characterisation of retroviruses in the horse genome and their transcriptional activity via transcriptome sequencing. <i>Virology</i> , 2012, 433, 55-63. | 2.4 | 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. | 1.8 | 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. | 2.9 | 1 |
| 2063 | Data Management Challenges in Next Generation Sequencing. <i>Datenbank-Spektrum</i> , 2012, 12, 161-171. | 1.3 | 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. | 1.4 | 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. | 2.2 | 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. | 6.6 | 198 |
| 2067 | Long noncoding RNAs are rarely translated in two human cell lines. <i>Genome Research</i> , 2012, 22, 1646-1657. | 5.5 | 346 |
| 2068 | Gene Assembly from Chipâ€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. | 8.9 | 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. | 3.0 | 28 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2072 | A multi-omic map of the lipid-producing yeast <i>Rhodospiridium toruloides</i> . <i>Nature Communications</i> , 2012, 3, 1112. | 12.8 | 324 |
| 2073 | Probabilistic Arithmetic Automata and Their Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1737-1750. | 3.0 | 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. | 14.5 | 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. | 3.0 | 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 |
| 2078 | Restricted Gene Flow among Hospital Subpopulations of <i>Enterococcus faecium</i> . <i>MBio</i> , 2012, 3, e00151-12. | 4.1 | 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. | 8.9 | 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. | 14.5 | 140 |
| 2081 | Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , 2012, 22, 1231-1242. | 5.5 | 143 |
| 2082 | Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. <i>Bioinformatics</i> , 2012, 28, 1086-1092. | 4.1 | 1,351 |
| 2083 | Ultrafast clustering algorithms for metagenomic sequence analysis. <i>Briefings in Bioinformatics</i> , 2012, 13, 656-668. | 6.5 | 403 |
| 2084 | Interactions Between Commensal Fungi and the C-Type Lectin Receptor Dectin-1 Influence Colitis. <i>Science</i> , 2012, 336, 1314-1317. | 12.6 | 886 |
| 2085 | A differential sequencing-based analysis of the <i>C. elegans</i> noncoding transcriptome. <i>Rna</i> , 2012, 18, 626-639. | 3.5 | 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. | 2.7 | 16 |
| 2087 | Mapsembler, targeted and micro assembly of large NGS datasets on a desktop computer. <i>BMC Bioinformatics</i> , 2012, 13, 48. | 2.6 | 31 |
| 2088 | OSA: a fast and accurate alignment tool for RNA-Seq. <i>Bioinformatics</i> , 2012, 28, 1933-1934. | 4.1 | 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. | 2.3 | 28 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2090 | Mapping single molecule sequencing reads using basic local alignment with successive refinement (BLASR): application and theory. BMC Bioinformatics, 2012, 13, 238. | 2.6 | 1,075 |
| 2091 | Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013. | 7.3 | 210 |
| 2092 | Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. Briefings in Bioinformatics, 2012, 13, 269-280. | 6.5 | 23 |
| 2093 | Classification of metagenomic sequences: methods and challenges. Briefings in Bioinformatics, 2012, 13, 669-681. | 6.5 | 184 |
| 2094 | MFEprimer-2.0: a fast thermodynamics-based program for checking PCR primer specificity. Nucleic Acids Research, 2012, 40, W205-W208. | 14.5 | 80 |
| 2095 | The genome of the xerotolerant mold <i>Wallemia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. Fungal Genetics and Biology, 2012, 49, 217-226. | 2.1 | 103 |
| 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. Cancer Genetics, 2012, 205, 295-303. | 0.4 | 10 |
| 2097 | Differential expression and intrachromosomal evolution of the <i>sgHc1q</i> genes in zebrafish (<i>Danio rerio</i>). Tj ETQq1 1 0.784314 rgBT /Overloc | 2.3 | 11 |
| 2098 | 6-10- pyrosequencing is a practical approach for whole prokaryote genome studies. Gene, 2012, 494, 57-64. | 2.2 | 10 |
| 2099 | CR1 retroposons provide a new insight into the phylogeny of Phasianidae species (Aves: Galliformes). Gene, 2012, 502, 125-132. | 2.2 | 16 |
| 2100 | KGBassembler: a karyotype-based genome assembler for Brassicaceae species. Bioinformatics, 2012, 28, 3141-3143. | 4.1 | 12 |
| 2101 | An Alu-Based Phylogeny of Gibbons (Hylobatidae). Molecular Biology and Evolution, 2012, 29, 3441-3450. | 8.9 | 41 |
| 2102 | CLIP-seq of eIF4AIII reveals transcriptome-wide mapping of the human exon junction complex. Nature Structural and Molecular Biology, 2012, 19, 1124-1131. | 8.2 | 197 |
| 2103 | Application of metatranscriptomics to soil environments. Journal of Microbiological Methods, 2012, 91, 246-251. | 1.6 | 142 |
| 2104 | A genome resource to address mechanisms of developmental programming: determination of the fetal sheep heart transcriptome. Journal of Physiology, 2012, 590, 2873-2884. | 2.9 | 15 |
| 2105 | The M5nr: a novel non-redundant database containing protein sequences and annotations from multiple sources and associated tools. BMC Bioinformatics, 2012, 13, 141. | 2.6 | 291 |
| 2106 | Short-read reading-frame predictors are not created equal: sequence error causes loss of signal. BMC Bioinformatics, 2012, 13, 183. | 2.6 | 39 |
| 2107 | CaPSID: A bioinformatics platform for computational pathogen sequence identification in human genomes and transcriptomes. BMC Bioinformatics, 2012, 13, 206. | 2.6 | 41 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2108 | AbsIDconvert: An absolute approach for converting genetic identifiers at different granularities. BMC Bioinformatics, 2012, 13, 229. | 2.6 | 8 |
| 2109 | ncRNAclassifier: a tool for detection and classification of transposable element sequences in RNA hairpins. BMC Bioinformatics, 2012, 13, 246. | 2.6 | 25 |
| 2110 | SIS: a program to generate draft genome sequence scaffolds for prokaryotes. BMC Bioinformatics, 2012, 13, 96. | 2.6 | 29 |
| 2111 | Separating the wheat from the chaff: mitigating the effects of noise in a plastome phylogenomic data set from <i>Pinus L.</i> (Pinaceae). BMC Evolutionary Biology, 2012, 12, 100. | 3.2 | 96 |
| 2112 | Comparative genomics of eukaryotic small nucleolar RNAs reveals deep evolutionary ancestry amidst ongoing intragenomic mobility. BMC Evolutionary Biology, 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. BMC Genetics, 2012, 13, 106. | 2.7 | 10 |
| 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. | 2.8 | 77 |
| 2115 | A framework genetic map for <i>Miscanthus sinensis</i> from RNAseq-based markers shows recent tetraploidy. BMC Genomics, 2012, 13, 142. | 2.8 | 87 |
| 2116 | A high-resolution map of the Nile tilapia genome: a resource for studying cichlids and other percomorphs. BMC Genomics, 2012, 13, 222. | 2.8 | 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. | 2.8 | 99 |
| 2118 | Comparative transcriptome analysis between planarian <i>Dugesia japonica</i> and other platyhelminth species. BMC Genomics, 2012, 13, 289. | 2.8 | 34 |
| 2119 | Oomycete transcriptomics database: A resource for oomycete transcriptomes. BMC Genomics, 2012, 13, 303. | 2.8 | 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. | 2.8 | 45 |
| 2121 | Optimizing de novo common wheat transcriptome assembly using short-read RNA-Seq data. BMC Genomics, 2012, 13, 392. | 2.8 | 104 |
| 2122 | Transcriptome-based exon capture enables highly cost-effective comparative genomic data collection at moderate evolutionary scales. BMC Genomics, 2012, 13, 403. | 2.8 | 253 |
| 2123 | Personal receptor repertoires: olfaction as a model. BMC Genomics, 2012, 13, 414. | 2.8 | 92 |
| 2124 | Identification and analysis of pig chimeric mRNAs using RNA sequencing data. BMC Genomics, 2012, 13, 429. | 2.8 | 15 |
| 2125 | Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosa</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. BMC Genomics, 2012, 13, 444. | 2.8 | 125 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2126 | Genome sequencing and genetic breeding of a bioethanol <i>Saccharomyces cerevisiae</i> strain YJS329. BMC Genomics, 2012, 13, 479. | 2.8 | 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. | 2.8 | 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. | 2.8 | 55 |
| 2129 | Identification, characterization and distribution of transposable elements in the flax (<i>Linum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj | 2.8 | 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. | 2.8 | 32 |
| 2131 | A genomic scale map of genetic diversity in <i>Trypanosoma cruzi</i> . BMC Genomics, 2012, 13, 736. | 2.8 | 16 |
| 2132 | Cutoffs and k-mers: implications from a transcriptome study in allopolyploid plants. BMC Genomics, 2012, 13, 92. | 2.8 | 52 |
| 2133 | RON is not a prognostic marker for resectable pancreatic cancer. BMC Cancer, 2012, 12, 395. | 2.6 | 17 |
| 2134 | Integrative transcriptome analysis suggest processing of a subset of long non-coding RNAs to small RNAs. Biology Direct, 2012, 7, 25. | 4.6 | 71 |
| 2135 | Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. BMC Medical Genomics, 2012, 5, 17. | 1.5 | 49 |
| 2136 | Bisquinolinium compounds induce quadruplex-specific transcriptome changes in HeLa S3 cell lines. BMC Research Notes, 2012, 5, 138. | 1.4 | 42 |
| 2137 | Evolutionary patterns of RNA-based gene duplicates in <i>Caenorhabditis</i> nematodes coincide with their genomic features. BMC Research Notes, 2012, 5, 398. | 1.4 | 7 |
| 2138 | Rapid phylogenetic and functional classification of short genomic fragments with signature peptides. BMC Research Notes, 2012, 5, 460. | 1.4 | 24 |
| 2139 | Next-generation sequencing coupled with a cell-free display technology for high-throughput production of reliable interactome data. Scientific Reports, 2012, 2, 691. | 3.3 | 25 |
| 2140 | Performance Comparison of Multiple Microarray Platforms for Gene Expression Profiling. Methods in Molecular Biology, 2012, 802, 141-155. | 0.9 | 13 |
| 2141 | The UCSC Genome Browser. Current Protocols in Bioinformatics, 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> lettuces (<i>Lactuca sativa</i>) achenes. New Phytologist, 2012, 196, 1060-1073. | 7.3 | 29 |
| 2144 | Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. Nature Biotechnology, 2012, 30, 83-89. | 17.5 | 788 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2145 | Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. Journal of Cystic Fibrosis, 2012, 11, 511-517. | 0.7 | 17 |
| 2146 | A randomized Numerical Aligner (rNA). Journal of Computer and System Sciences, 2012, 78, 1868-1882. | 1.2 | 7 |
| 2147 | A Survey of Copyâ€Number Variation Detection Tools Based on Highâ€Throughput Sequencing Data. Current Protocols in Human Genetics, 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. Current Topics in Developmental Biology, 2012, 99, 31-57. | 2.2 | 21 |
| 2151 | Gene Prediction. Methods in Molecular Biology, 2012, 855, 175-201. | 0.9 | 14 |
| 2152 | Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111. | 17.5 | 818 |
| 2154 | A Draft Genome Sequence of <i>Nicotiana benthamiana</i> to Enhance Molecular Plant-Microbe Biology Research. Molecular Plant-Microbe Interactions, 2012, 25, 1523-1530. | 2.6 | 411 |
| 2155 | Role of Genomics and RNA-seq in Studies of Fungal Virulence. Current Fungal Infection Reports, 2012, 6, 267-274. | 2.6 | 3 |
| 2156 | High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57. | | 0 |
| 2157 | Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427. | 27.8 | 1,204 |
| 2161 | Compressive genomics. Nature Biotechnology, 2012, 30, 627-630. | 17.5 | 99 |
| 2162 | Comparing Fungal Genomes: Insight into Functional and Evolutionary Processes. Methods in Molecular Biology, 2012, 835, 531-548. | 0.9 | 7 |
| 2163 | Genomic Variation in Natural Populations of <i>Drosophila melanogaster</i> . Genetics, 2012, 192, 533-598. | 2.9 | 325 |
| 2164 | Flexible and efficient genome tiling design with penalized uniqueness score. BMC Bioinformatics, 2012, 13, 323. | 2.6 | 2 |
| 2165 | Highly improved homopolymer aware nucleotide-protein alignments with 454 data. BMC Bioinformatics, 2012, 13, 230. | 2.6 | 7 |
| 2166 | The evolution of the class A scavenger receptors. BMC Evolutionary Biology, 2012, 12, 227. | 3.2 | 52 |
| 2167 | Newly evolved introns in human retrogenes provide novel insights into their evolutionary roles. BMC Evolutionary Biology, 2012, 12, 128. | 3.2 | 19 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2168 | Meta-analytical biomarker search of EST expression data reveals three differentially expressed candidates. BMC Genomics, 2012, 13, S12. | 2.8 | 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. BMC Genomics, 2012, 13, 711. | 2.8 | 28 |
| 2170 | Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse Escherichia coli genomes. BMC Genomics, 2012, 13, 577. | 2.8 | 205 |
| 2171 | Genetic structure of community acquired methicillin-resistant Staphylococcus aureus USA300. BMC Genomics, 2012, 13, 508. | 2.8 | 24 |
| 2172 | High-resolution genotyping and mapping of recombination and gene conversion in the protozoan Theileria parva using whole genome sequencing. BMC Genomics, 2012, 13, 503. | 2.8 | 41 |
| 2173 | Ultra-high resolution HLA genotyping and allele discovery by highly multiplexed cDNA amplicon pyrosequencing. BMC Genomics, 2012, 13, 378. | 2.8 | 38 |
| 2174 | Mutation spectrum of Drosophila CNVs revealed by breakpoint sequencing. Genome Biology, 2012, 13, R119. | 9.6 | 15 |
| 2175 | Orangutan Alu quiescence reveals possible source element: support for ancient backseat drivers. Mobile DNA, 2012, 3, 8. | 3.6 | 11 |
| 2176 | Activity-Dependent Human Brain Coding/Noncoding Gene Regulatory Networks. Genetics, 2012, 192, 1133-1148. | 2.9 | 175 |
| 2177 | Hospital and Community Ampicillin-Resistant Enterococcus faecium Are Evolutionarily Closely Linked but Have Diversified through Niche Adaptation. PLoS ONE, 2012, 7, e30319. | 2.5 | 45 |
| 2178 | CAPRG: Sequence Assembling Pipeline for Next Generation Sequencing of Non-Model Organisms. PLoS ONE, 2012, 7, e30370. | 2.5 | 4 |
| 2179 | Organizational Heterogeneity of Vertebrate Genomes. PLoS ONE, 2012, 7, e32076. | 2.5 | 7 |
| 2180 | Fast and Accurate Taxonomic Assignments of Metagenomic Sequences Using MetaBin. PLoS ONE, 2012, 7, e34030. | 2.5 | 27 |
| 2181 | Characterisation of Bovine Leukocyte Ig-like Receptors. PLoS ONE, 2012, 7, e34291. | 2.5 | 22 |
| 2182 | The Chlamydia psittaci Genome: A Comparative Analysis of Intracellular Pathogens. PLoS ONE, 2012, 7, e35097. | 2.5 | 87 |
| 2183 | Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS. PLoS ONE, 2012, 7, e35333. | 2.5 | 50 |
| 2184 | Experimental Verification of a Predicted Intronic MicroRNA in Human NGFR Gene with a Potential Pro-Apoptotic Function. PLoS ONE, 2012, 7, e35561. | 2.5 | 29 |
| 2185 | GHOSTM: A GPU-Accelerated Homology Search Tool for Metagenomics. PLoS ONE, 2012, 7, e36060. | 2.5 | 22 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2186 | Transcript Profiling Identifies Dynamic Gene Expression Patterns and an Important Role for Nrf2/Keap1 Pathway in the Developing Mouse Esophagus. PLoS ONE, 2012, 7, e36504. | 2.5 | 28 |
| 2187 | The Molecular Mechanism of Action of the CR6261-Azichromycin Combination Found through Computational Analysis. PLoS ONE, 2012, 7, e37790. | 2.5 | 1 |
| 2188 | Multi-Locus Phylogeographic and Population Genetic Analysis of <i>Anolis carolinensis</i> : Historical Demography of a Genomic Model Species. PLoS ONE, 2012, 7, e38474. | 2.5 | 40 |
| 2189 | Large-Scale Transcriptome Analysis of Retroelements in the Migratory Locust, <i>Locusta migratoria</i> . PLoS ONE, 2012, 7, e40532. | 2.5 | 30 |
| 2190 | The Natural History of Class I Primate Alcohol Dehydrogenases Includes Gene Duplication, Gene Loss, and Gene Conversion. PLoS ONE, 2012, 7, e41175. | 2.5 | 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. PLoS ONE, 2012, 7, e42371. | 2.5 | 43 |
| 2192 | Identification of 34 Novel Proinflammatory Proteins in a Genome-Wide Macrophage Functional Screen. PLoS ONE, 2012, 7, e42388. | 2.5 | 9 |
| 2193 | SAPâ€”A Sequence Mapping and Analyzing Program for Long Sequence Reads Alignment and Accurate Variants Discovery. PLoS ONE, 2012, 7, e42887. | 2.5 | 1 |
| 2194 | Ruler Arrays Reveal Haploid Genomic Structural Variation. PLoS ONE, 2012, 7, e43210. | 2.5 | 0 |
| 2195 | Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of <i>Salmonella Paratyphi A</i> . PLoS ONE, 2012, 7, e45346. | 2.5 | 26 |
| 2196 | A Fish-Specific Transposable Element Shapes the Repertoire of p53 Target Genes in Zebrafish. PLoS ONE, 2012, 7, e46642. | 2.5 | 17 |
| 2197 | Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213. | 2.5 | 61 |
| 2198 | Gene and Genome Parameters of Mammalian Liver Circadian Genes (LCGs). PLoS ONE, 2012, 7, e46961. | 2.5 | 10 |
| 2199 | A Hybrid Distance Measure for Clustering Expressed Sequence Tags Originating from the Same Gene Family. PLoS ONE, 2012, 7, e47216. | 2.5 | 5 |
| 2200 | A Streamlined Method for Detecting Structural Variants in Cancer Genomes by Short Read Paired-End Sequencing. PLoS ONE, 2012, 7, e48314. | 2.5 | 21 |
| 2201 | The Δ CstF-64 Polyadenylation Protein Controls Genome Expression in Testis. PLoS ONE, 2012, 7, e48373. | 2.5 | 26 |
| 2202 | Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (<i>Artibeus jamaicensis</i>). PLoS ONE, 2012, 7, e48472. | 2.5 | 77 |
| 2203 | Comprehensive Human Transcription Factor Binding Site Map for Combinatory Binding Motifs Discovery. PLoS ONE, 2012, 7, e49086. | 2.5 | 5 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2204 | Exploring Pandora's Box: Potential and Pitfalls of Low Coverage Genome Surveys for Evolutionary Biology. PLoS ONE, 2012, 7, e49202. | 2.5 | 31 |
| 2205 | Mutation at the Human D1S80 Minisatellite Locus. Scientific World Journal, The, 2012, 2012, 1-8. | 2.1 | 3 |
| 2206 | The Human Transcriptome: An Unfinished Story. Genes, 2012, 3, 344-360. | 2.4 | 121 |
| 2207 | On the Analysis of the Illumina 450k Array Data: Probes Ambiguously Mapped to the Human Genome. Frontiers in Genetics, 2012, 3, 73. | 2.3 | 45 |
| 2208 | Diversity of Antisense and Other Non-Coding RNAs in Archaea Revealed by Comparative Small RNA Sequencing in Four Pyrobaculum Species. Frontiers in Microbiology, 2012, 3, 231. | 3.5 | 46 |
| 2209 | Comparative genomic and transcriptional analyses of CRISPR systems across the genus Pyrobaculum. Frontiers in Microbiology, 2012, 3, 251. | 3.5 | 28 |
| 2210 | Characteristics of nucleosomes and linker DNA regions on the genome of the basidiomycete <i>Mixia osmundae</i> revealed by mono- and dinucleosome mapping. Open Biology, 2012, 2, 120043. | 3.6 | 11 |
| 2211 | A Transcriptome- and Marker-Based Systemic Analysis of Cervical Cancer. , 2012, , . | | 2 |
| 2213 | Evolutionary history of <i>εmyc</i> in teleosts and characterization of the duplicated <i>εmyc</i> genes in goldfish embryos. Molecular Reproduction and Development, 2012, 79, 85-96. | 2.0 | 20 |
| 2214 | Probe mapping across multiple microarray platforms. Briefings in Bioinformatics, 2012, 13, 547-554. | 6.5 | 25 |
| 2215 | Bioinformatic Clonality Analysis of Next-Generation Sequencing-Derived Viral Vector Integration Sites. Human Gene Therapy Methods, 2012, 23, 111-118. | 2.1 | 43 |
| 2216 | Extended Survival of Glioblastoma Patients After Chemoprotective HSC Gene Therapy. Science Translational Medicine, 2012, 4, 133ra57. | 12.4 | 91 |
| 2217 | A beginner's guide to eukaryotic genome annotation. Nature Reviews Genetics, 2012, 13, 329-342. | 16.3 | 553 |
| 2218 | Effect of Periodontal Pathogens on the Metatranscriptome of a Healthy Multispecies Biofilm Model. Journal of Bacteriology, 2012, 194, 2082-2095. | 2.2 | 85 |
| 2219 | The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. Nature, 2012, 488, 213-217. | 27.8 | 1,049 |
| 2220 | Functional assignment of metagenomic data: challenges and applications. Briefings in Bioinformatics, 2012, 13, 711-727. | 6.5 | 150 |
| 2221 | A Universal Method for the Study of CR1 Retroposons in Nonmodel Bird Genomes. Molecular Biology and Evolution, 2012, 29, 2899-2903. | 8.9 | 27 |
| 2222 | Proviral loads of human T-cell lymphotropic virus Type 1 in asymptomatic carriers with different infection routes. International Journal of Cancer, 2012, 130, 2318-2326. | 5.1 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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 ¹ . American Journal of Botany, 2012, 99, 257-266. | 1.7 | 192 |
| 2226 | Expressed Pseudogenes in the Transcriptional Landscape of Human Cancers. Cell, 2012, 149, 1622-1634. | 28.9 | 250 |
| 2227 | Meta-analysis of genetic association studies on bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 508-518. | 1.7 | 64 |
| 2228 | Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. Nature Biotechnology, 2012, 30, 549-554. | 17.5 | 636 |
| 2229 | Reference genome sequence of the model plant <i>Setaria</i> . Nature Biotechnology, 2012, 30, 555-561. | 17.5 | 864 |
| 2230 | SEQuel: improving the accuracy of genome assemblies. Bioinformatics, 2012, 28, i188-i196. | 4.1 | 56 |
| 2231 | Analysis of High-Throughput Ancient DNA Sequencing Data. Methods in Molecular Biology, 2012, 840, 197-228. | 0.9 | 177 |
| 2232 | Graph concordance of next-generation sequence assemblies. Bioinformatics, 2012, 28, 13-16. | 4.1 | 51 |
| 2233 | Hybrid error correction and de novo assembly of single-molecule sequencing reads. Nature Biotechnology, 2012, 30, 693-700. | 17.5 | 946 |
| 2234 | A tumour suppressor network relying on the polyamine-hypusine axis. Nature, 2012, 487, 244-248. | 27.8 | 133 |
| 2235 | Large-scale collection and annotation of gene models for date palm (<i>Phoenix dactylifera</i> , L.). Plant Molecular Biology, 2012, 79, 521-536. | 3.9 | 26 |
| 2236 | The chimpanzee GH locus: composition, organization, and evolution. Mammalian Genome, 2012, 23, 387-398. | 2.2 | 6 |
| 2237 | A pronounced evolutionary shift of the pseudoautosomal region boundary in house mice. Mammalian Genome, 2012, 23, 454-466. | 2.2 | 37 |
| 2238 | Polymorphic NumtS trace human population relationships. Human Genetics, 2012, 131, 757-771. | 3.8 | 40 |
| 2239 | Molecular cloning of large alternative transcripts based on comparative phylogenetic analysis and exploration of an EST database. Analytical Biochemistry, 2012, 424, 140-141. | 2.4 | 1 |
| 2240 | Hematopoietic stem cell expansion facilitates multilineage engraftment in a nonhuman primate cord blood transplantation model. Experimental Hematology, 2012, 40, 187-196. | 0.4 | 19 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2241 | The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. International Journal of Food Microbiology, 2012, 157, 202-209. | 4.7 | 102 |
| 2242 | From genomics to metagenomics. Current Opinion in Biotechnology, 2012, 23, 72-76. | 6.6 | 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. International Journal for Parasitology, 2012, 42, 39-48. | 3.1 | 30 |
| 2244 | CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus</i> (<i>Boophilus</i>) <i>microplus</i> . International Journal for Parasitology, 2012, 42, 161-169. | 3.1 | 55 |
| 2245 | Genome sequence of <i>Wickerhamomyces anomalus</i> DSM 6766 reveals genetic basis of biotechnologically important antimicrobial activities. FEMS Yeast Research, 2012, 12, 382-386. | 2.3 | 40 |
| 2246 | Characterizing complex structural variation in germline and somatic genomes. Trends in Genetics, 2012, 28, 43-53. | 6.7 | 93 |
| 2247 | Search for an aetiological virus candidate in chronic lymphocytic leukaemia by extensive transcriptome analysis. British Journal of Haematology, 2012, 157, 709-717. | 2.5 | 6 |
| 2248 | Plntron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. BMC Bioinformatics, 2012, 13, S2. | 2.6 | 8 |
| 2249 | KIS SPLICE: de-novo calling alternative splicing events from RNA-seq data. BMC Bioinformatics, 2012, 13, S5. | 2.6 | 85 |
| 2250 | A context-based approach to identify the most likely mapping for RNA-seq experiments. BMC Bioinformatics, 2012, 13, S9. | 2.6 | 14 |
| 2251 | A recurrent translocation is mediated by homologous recombination between HERV-H elements. Molecular Cytogenetics, 2012, 5, 6. | 0.9 | 25 |
| 2252 | A cost-effective and universal strategy for complete prokaryotic genomic sequencing proposed by computer simulation. BMC Research Notes, 2012, 5, 80. | 1.4 | 4 |
| 2253 | Metagenomics - a guide from sampling to data analysis. Microbial Informatics and Experimentation, 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. Genes Chromosomes and Cancer, 2012, 51, 590-597. | 2.8 | 80 |
| 2255 | Adrenal androgen production in catarrhine primates and the evolution of adrenarche. American Journal of Physical Anthropology, 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> . Journal of Plant Biology, 2012, 55, 33-42. | 2.1 | 5 |
| 2257 | Molecular mechanisms of EGF signaling-dependent regulation of <i>pipe</i> , a gene crucial for dorsoventral axis formation in <i>Drosophila</i> . Development Genes and Evolution, 2012, 222, 1-17. | 0.9 | 9 |
| 2258 | Genome-wide expression profiling of schizophrenia using a large combined cohort. Molecular Psychiatry, 2013, 18, 215-225. | 7.9 | 88 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2259 | Ratite Nonmonophyly: Independent Evidence from 40 Novel Loci. <i>Systematic Biology</i> , 2013, 62, 35-49. | 5.6 | 73 |
| 2260 | Epigenetics in the Human Brain. <i>Neuropsychopharmacology</i> , 2013, 38, 183-197. | 5.4 | 65 |
| 2261 | Microbial and viral metagenomes of a subtropical freshwater reservoir subject to climatic disturbances. <i>ISME Journal</i> , 2013, 7, 2374-2386. | 9.8 | 81 |
| 2262 | TNPO3 protects HIV-1 replication from CPSF6-mediated capsid stabilization in the host cell cytoplasm. <i>Retrovirology</i> , 2013, 10, 20. | 2.0 | 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. | 8.8 | 192 |
| 2265 | Mapping gene activity of <i>Arabidopsis</i> root hairs. <i>Genome Biology</i> , 2013, 14, R67. | 8.8 | 89 |
| 2266 | Integrated analysis of recurrent properties of cancer genes to identify novel drivers. <i>Genome Biology</i> , 2013, 14, R52. | 9.6 | 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. | 9.6 | 276 |
| 2268 | Retrotransposition of gene transcripts leads to structural variation in mammalian genomes. <i>Genome Biology</i> , 2013, 14, R22. | 9.6 | 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. | 9.6 | 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. | 3.9 | 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. | 8.2 | 306 |
| 2272 | <i>Populus euphratica</i> : the transcriptomic response to drought stress. <i>Plant Molecular Biology</i> , 2013, 83, 539-557. | 3.9 | 84 |
| 2273 | Transduction-Specific ATLAS Reveals a Cohort of Highly Active L1 Retrotransposons in Human Populations. <i>Human Mutation</i> , 2013, 34, 974-985. | 2.5 | 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. | 17.5 | 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. | 21.4 | 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. | 7.2 | 10 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2277 | Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. <i>Statistics in Biosciences</i> , 2013, 5, 3-25. | 1.2 | 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. | 2.6 | 16 |
| 2279 | A multispecies polyadenylation site model. <i>BMC Bioinformatics</i> , 2013, 14, S9. | 2.6 | 4 |
| 2280 | Mobilomics in <i>Saccharomyces cerevisiae</i> strains. <i>BMC Bioinformatics</i> , 2013, 14, 102. | 2.6 | 9 |
| 2281 | Genome sequence-based species delimitation with confidence intervals and improved distance functions. <i>BMC Bioinformatics</i> , 2013, 14, 60. | 2.6 | 5,139 |
| 2282 | Phylogenomics of stronglycentrotid sea urchins. <i>BMC Evolutionary Biology</i> , 2013, 13, 88. | 3.2 | 42 |
| 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. | 2.8 | 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. | 2.8 | 15 |
| 2285 | Phase-defined complete sequencing of the HLA genes by next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 355. | 2.8 | 121 |
| 2286 | Optimizing de novo assembly of short-read RNA-seq data for phylogenomics. <i>BMC Genomics</i> , 2013, 14, 328. | 2.8 | 189 |
| 2287 | TRACER: a resource to study the regulatory architecture of the mouse genome. <i>BMC Genomics</i> , 2013, 14, 215. | 2.8 | 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. | 2.8 | 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. | 2.8 | 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. | 2.8 | 31 |
| 2291 | Phylogenetic patterns of emergence of new genes support a model of frequent de novo evolution. <i>BMC Genomics</i> , 2013, 14, 117. | 2.8 | 218 |
| 2292 | Draft genome sequence of the rubber tree <i>Hevea brasiliensis</i> . <i>BMC Genomics</i> , 2013, 14, 75. | 2.8 | 222 |
| 2293 | Genome-wide identification, characterization, and expression analysis of lineage-specific genes within zebrafish. <i>BMC Genomics</i> , 2013, 14, 65. | 2.8 | 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. | 2.8 | 55 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2295 | HDAM: a resource of human disease associated mutations from next generation sequencing studies. BMC Medical Genomics, 2013, 6, S16. | 1.5 | 3 |
| 2296 | Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. Nature Biotechnology, 2013, 31, 240-246. | 17.5 | 1,049 |
| 2297 | MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. Human Genetics, 2013, 132, 1235-1243. | 3.8 | 68 |
| 2298 | Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. Human Genetics, 2013, 132, 899-911. | 3.8 | 13 |
| 2299 | Latent Regulatory Potential of Human-Specific Repetitive Elements. Molecular Cell, 2013, 49, 262-272. | 9.7 | 62 |
| 2300 | The first genetic map of the American cranberry: exploration of synteny conservation and quantitative trait loci. Theoretical and Applied Genetics, 2013, 126, 673-692. | 3.6 | 47 |
| 2301 | Directional RNA-seq reveals highly complex condition-dependent transcriptomes in <i>E. coli</i> K12 through accurate full-length transcripts assembling. BMC Genomics, 2013, 14, 520. | 2.8 | 31 |
| 2302 | Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. Nature Structural and Molecular Biology, 2013, 20, 1131-1139. | 8.2 | 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. Immunogenetics, 2013, 65, 749-762. | 2.4 | 19 |
| 2304 | Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. Nature Genetics, 2013, 45, 1232-1237. | 21.4 | 334 |
| 2305 | Resistance gene enrichment sequencing (<sc>R</sc>en<sc>S</sc>eq) enables reannotation of the <sc>NB</sc>â€<sc>LRR</sc> gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. Plant Journal, 2013, 76, 530-544. | 5.7 | 367 |
| 2306 | PECONPI: A novel software for uncovering pathogenic copy number variations in nonâ€syndromic sensorineural hearing loss and other genetically heterogeneous disorders. American Journal of Medical Genetics, Part A, 2013, 161, 2134-2147. | 1.2 | 5 |
| 2307 | Comparative study of de novo assembly and genome-guided assembly strategies for transcriptome reconstruction based on RNA-Seq. Science China Life Sciences, 2013, 56, 143-155. | 4.9 | 55 |
| 2308 | IDBA-MT: <i>De Novo</i> Assembler for Metatranscriptomic Data Generated from Next-Generation Sequencing Technology. Journal of Computational Biology, 2013, 20, 540-550. | 1.6 | 45 |
| 2309 | Transcriptional regulation of teleost Aicda genes. Part 1 â€ Suppressors of promiscuous promoters. Fish and Shellfish Immunology, 2013, 35, 1981-1987. | 3.6 | 4 |
| 2310 | Recessive Cancer Genes Engage in Negative Genetic Interactions with Their Functional Paralogs. Cell Reports, 2013, 5, 1519-1526. | 6.4 | 19 |
| 2311 | SSP: An interval integer linear programming for de novo transcriptome assembly and isoform discovery of RNA-seq reads. Genomics, 2013, 102, 507-514. | 2.9 | 11 |
| 2312 | No TAP63 promoter mutation is detected in bladder exstrophyâ€epispadias complex patients. Journal of Pediatric Surgery, 2013, 48, 2393-2400. | 1.6 | 3 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2313 | Nuclear Wave1 Is Required for Reprogramming Transcription in Oocytes and for Normal Development. Science, 2013, 341, 1002-1005. | 12.6 | 82 |
| 2314 | BRANCH: boosting RNA-Seq assemblies with partial or related genomic sequences. Bioinformatics, 2013, 29, 1250-1259. | 4.1 | 28 |
| 2315 | Conservation and Functional Element Discovery in 20 Angiosperm Plant Genomes. Molecular Biology and Evolution, 2013, 30, 1729-1744. | 8.9 | 60 |
| 2316 | Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. Nature Genetics, 2013, 45, 937-941. | 21.4 | 203 |
| 2317 | Large-scale detection of in vivo transcription errors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18584-18589. | 7.1 | 94 |
| 2318 | Sequencing Y Chromosomes Resolves Discrepancy in Time to Common Ancestor of Males Versus Females. Science, 2013, 341, 562-565. | 12.6 | 235 |
| 2319 | Reconstructing the Microbial Diversity and Function of Pre-Agricultural Tallgrass Prairie Soils in the United States. Science, 2013, 342, 621-624. | 12.6 | 480 |
| 2320 | Systematic evaluation of spliced alignment programs for RNA-seq data. Nature Methods, 2013, 10, 1185-1191. | 19.0 | 467 |
| 2321 | Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (Capra) Tj ETQq0 0 0 rgBT /Overlock 10 T | 17.5 | 479 |
| 2322 | Enrichment of processed pseudogene transcripts in L1-ribonucleoprotein particles. Human Molecular Genetics, 2013, 22, 3730-3748. | 2.9 | 50 |
| 2323 | The High Polyphenol Content of Grapevine Cultivar Tannat Berries Is Conferred Primarily by Genes That Are Not Shared with the Reference Genome. Plant Cell, 2013, 25, 4777-4788. | 6.6 | 138 |
| 2324 | Assembler for de novo assembly of large genomes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3417-24. | 7.1 | 41 |
| 2325 | BlastGraph: a comparative genomics tool based on BLAST and graph algorithms. Bioinformatics, 2013, 29, 3222-3224. | 4.1 | 10 |
| 2326 | RNAâ€DNA differences in human mitochondria restore ancestral form of 16S ribosomal RNA. Genome Research, 2013, 23, 1789-1796. | 5.5 | 49 |
| 2327 | Inference of Alternative Splicing from Tiling Array Data. Methods in Molecular Biology, 2013, 1067, 143-164. | 0.9 | 0 |
| 2328 | Comprehensive Analysis of Human Endogenous Retrovirus Group HERV-W Locus Transcription in Multiple Sclerosis Brain Lesions by High-Throughput Amplicon Sequencing. Journal of Virology, 2013, 87, 13837-13852. | 3.4 | 59 |
| 2329 | A heterozygous moth genome provides insights into herbivory and detoxification. Nature Genetics, 2013, 45, 220-225. | 21.4 | 472 |
| 2330 | Sex-specific expression, synthesis and localization of aromatase regulators in one-year-old Atlantic salmon ovaries and testes. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2013, 164, 236-246. | 1.6 | 21 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2331 | An integrative bioinformatics pipeline for the genomewide identification of novel porcine microRNA genes. <i>Journal of Genetics</i> , 2013, 92, 587-593. | 0.7 | 2 |
| 2332 | Environmental bio-monitoring with high-throughput sequencing. <i>Briefings in Bioinformatics</i> , 2013, 14, 575-588. | 6.5 | 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. | 1.4 | 31 |
| 2334 | Transparency tools in gene patenting for informing policy and practice. <i>Nature Biotechnology</i> , 2013, 31, 1086-1093. | 17.5 | 22 |
| 2335 | Transcriptome-wide identification of RNA binding sites by CLIP-seq. <i>Methods</i> , 2013, 63, 32-40. | 3.8 | 28 |
| 2336 | CruzDB: software for annotation of genomic intervals with UCSC genome-browser database. <i>Bioinformatics</i> , 2013, 29, 3003-3006. | 4.1 | 22 |
| 2337 | Genome-block expression-assisted association studies discover malaria resistance genes in <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20675-20680. | 7.1 | 37 |
| 2338 | An evaluation of the PacBio RS platform for sequencing and de novo assembly of a chloroplast genome. <i>BMC Genomics</i> , 2013, 14, 670. | 2.8 | 146 |
| 2339 | Construction of a high-density genetic map for sesame based on large scale marker development by specific length amplified fragment (SLAF) sequencing. <i>BMC Plant Biology</i> , 2013, 13, 141. | 3.6 | 256 |
| 2340 | Web Apollo: a web-based genomic annotation editing platform. <i>Genome Biology</i> , 2013, 14, R93. | 9.6 | 329 |
| 2341 | A SNP profiling panel for sample tracking in whole-exome sequencing studies. <i>Genome Medicine</i> , 2013, 5, 89. | 8.2 | 57 |
| 2342 | Transcriptome analyses of a Chinese hazelnut species <i>Corylus mandshurica</i> . <i>BMC Plant Biology</i> , 2013, 13, 152. | 3.6 | 24 |
| 2343 | HIV latency and integration site placement in five cell-based models. <i>Retrovirology</i> , 2013, 10, 90. | 2.0 | 104 |
| 2344 | Mena/VASP and β -Spectrin complexes regulate cytoplasmic actin networks in cardiomyocytes and protect from conduction abnormalities and dilated cardiomyopathy. <i>Cell Communication and Signaling</i> , 2013, 11, 56. | 6.5 | 38 |
| 2345 | L_RNA_scaffolder: scaffolding genomes with transcripts. <i>BMC Genomics</i> , 2013, 14, 604. | 2.8 | 129 |
| 2346 | Fine mapping of V(D)J recombinase mediated rearrangements in human lymphoid malignancies. <i>BMC Genomics</i> , 2013, 14, 565. | 2.8 | 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. <i>Mobile DNA</i> , 2013, 4, 19. | 3.6 | 18 |
| 2348 | Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013, 14, 550. | 2.8 | 12 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2349 | De novo transcriptome assembly of drought tolerant CAM plants, <i>Agave deserti</i> and <i>Agave tequilana</i> . BMC Genomics, 2013, 14, 563. | 2.8 | 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. | 9.6 | 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. | 2.8 | 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. | 3.3 | 26 |
| 2354 | Genome sequence and analysis of methylotrophic yeast <i>Hansenula polymorpha</i> DL1. BMC Genomics, 2013, 14, 837. | 2.8 | 81 |
| 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 <i>Miscanthus</i> genus reveals changes in the transcriptome associated with the rejuvenation of spring rhizomes. BMC Genomics, 2013, 14, 864. | 2.8 | 27 |
| 2358 | Spatial-temporal targeting of lung-specific mesenchyme by a <i>Tbx4</i> enhancer. BMC Biology, 2013, 11, 111. | 3.8 | 74 |
| 2359 | Exploration of the gene fusion landscape of glioblastoma using transcriptome sequencing and copy number data. BMC Genomics, 2013, 14, 818. | 2.8 | 72 |
| 2360 | Efficient cellular fractionation improves RNA sequencing analysis of mature and nascent transcripts from human tissues. BMC Biotechnology, 2013, 13, 99. | 3.3 | 47 |
| 2361 | Development of SSR markers by next-generation sequencing of Korean landraces of chamoe (<i>Cucumis</i>) Tj ETQq0 0.0 r gBT / Overlock 10 2.3 7 | 2.3 | 7 |
| 2362 | Genomic divergence between nine- and three-spined sticklebacks. BMC Genomics, 2013, 14, 756. | 2.8 | 42 |
| 2363 | A base composition analysis of natural patterns for the preprocessing of metagenome sequences. BMC Bioinformatics, 2013, 14, S5. | 2.6 | 4 |
| 2364 | The landscape of somatic mutations in Down syndrome-related myeloid disorders. Nature Genetics, 2013, 45, 1293-1299. | 21.4 | 324 |
| 2365 | A Metagenomics Portal for a Democratized Sequencing World. Methods in Enzymology, 2013, 531, 487-523. | 1.0 | 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. | 4.5 | 48 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2367 | A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. <i>Methods in Enzymology</i> , 2013, 531, 525-547. | 1.0 | 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. <i>FEMS Microbiology Letters</i> , 2013, 344, 179-185. | 1.8 | 47 |
| 2369 | Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444. | 1.0 | 553 |
| 2370 | Reliable Identification of Genomic Variants from RNA-Seq Data. <i>American Journal of Human Genetics</i> , 2013, 93, 641-651. | 6.2 | 319 |
| 2371 | De novo assembly methods for next generation sequencing data. <i>Tsinghua Science and Technology</i> , 2013, 18, 500-514. | 6.1 | 15 |
| 2374 | Human Analysts at Superhuman Scales: What Has Friendly Software To Do?. <i>Big Data</i> , 2013, 1, 227-236. | 3.4 | 1 |
| 2375 | The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408. | 5.5 | 832 |
| 2376 | WebAUGUSTUS--a web service for training AUGUSTUS and predicting genes in eukaryotes. <i>Nucleic Acids Research</i> , 2013, 41, W123-W128. | 14.5 | 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. | 2.1 | 17 |
| 2378 | The chemical interactome space between the human host and the genetically defined gut metabotypes. <i>ISME Journal</i> , 2013, 7, 730-742. | 9.8 | 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. | 2.5 | 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. | 4.1 | 233 |
| 2381 | Novel splicing events and post-transcriptional regulation of human estrogen receptor α E isoforms. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2013, 133, 120-128. | 2.5 | 15 |
| 2382 | gKaKs: the pipeline for genome-level Ka/Ks calculation. <i>Bioinformatics</i> , 2013, 29, 645-646. | 4.1 | 47 |
| 2383 | The UCSC genome browser and associated tools. <i>Briefings in Bioinformatics</i> , 2013, 14, 144-161. | 6.5 | 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. | 2.8 | 94 |
| 2385 | neXtProt: Organizing Protein Knowledge in the Context of Human Proteome Projects. <i>Journal of Proteome Research</i> , 2013, 12, 293-298. | 3.7 | 116 |
| 2386 | Discovery of cross-reactive probes and polymorphic CpGs in the Illumina Infinium HumanMethylation450 microarray. <i>Epigenetics</i> , 2013, 8, 203-209. | 2.7 | 1,276 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2387 | Current analysis platforms and methods for detecting copy number variation. <i>Physiological Genomics</i> , 2013, 45, 1-16. | 2.3 | 64 |
| 2388 | Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460. | 12.6 | 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. | 1.6 | 31 |
| 2391 | The SNPs in the human genetic blueprint era. <i>New Biotechnology</i> , 2013, 30, 475-484. | 4.4 | 10 |
| 2392 | Structural organization and classification of cytochrome P450 genes in flax (<i>Linum usitatissimum</i> L.). <i>Gene</i> , 2013, 513, 156-162. | 2.2 | 37 |
| 2393 | A guide to in silico vaccine discovery for eukaryotic pathogens. <i>Briefings in Bioinformatics</i> , 2013, 14, 753-774. | 6.5 | 29 |
| 2394 | Decominator: a tool for fast, efficient gene assignment in T-cell receptor sequences using a finite state machine. <i>Bioinformatics</i> , 2013, 29, 542-550. | 4.1 | 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. | 2.5 | 8 |
| 2396 | Mechanisms of Formation of Structural Variation in a Fully Sequenced Human Genome. <i>Human Mutation</i> , 2013, 34, 345-354. | 2.5 | 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. | 2.6 | 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. | 2.8 | 119 |
| 2399 | Genome-wide, whole mount in situ analysis of transcriptional regulators in zebrafish embryos. <i>Developmental Biology</i> , 2013, 380, 351-362. | 2.0 | 54 |
| 2400 | Exploring the utility of human DNA methylation arrays for profiling mouse genomic DNA. <i>Genomics</i> , 2013, 102, 38-46. | 2.9 | 36 |
| 2401 | Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. <i>Cell Reports</i> , 2013, 5, 1469-1478. | 6.4 | 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. | 3.8 | 93 |
| 2403 | Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2013, 45, 1431-1438. | 21.4 | 472 |
| 2404 | Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial β 5 Integrin. <i>Cancer Research</i> , 2013, 73, 4579-4590. | 0.9 | 97 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2405 | A Computational Workflow to Identify Allele-specific Expression and Epigenetic Modification in Maize. Genomics, Proteomics and Bioinformatics, 2013, 11, 247-252. | 6.9 | 10 |
| 2406 | Building a Genome Analysis Pipeline to Predict Disease Risk and Prevent Disease. Journal of Molecular Biology, 2013, 425, 3993-4005. | 4.2 | 31 |
| 2407 | Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. American Journal of Human Genetics, 2013, 93, 876-890. | 6.2 | 330 |
| 2408 | The plasmidome of a Salmonella enterica serovar Derby isolated from pork meat. Plasmid, 2013, 69, 202-210. | 1.4 | 20 |
| 2409 | Hoxa-5 acts in segmented somites to regulate cervical vertebral morphology. Mechanisms of Development, 2013, 130, 226-240. | 1.7 | 20 |
| 2410 | Genomic Pathology of SLE-Associated Copy-Number Variation at the FCGR2C/FCGR3B/FCGR2B Locus. American Journal of Human Genetics, 2013, 92, 28-40. | 6.2 | 63 |
| 2411 | Whole genome association of SNP with newborn calf cannon bone length. Livestock Science, 2013, 155, 186-196. | 1.6 | 10 |
| 2412 | Exome sequencing reveals a homozygous mutation in TWINKLE as the cause of multisystemic failure including renal tubulopathy in three siblings. Molecular Genetics and Metabolism, 2013, 108, 190-194. | 1.1 | 22 |
| 2413 | A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. Nature Methods, 2013, 10, 122-124. | 19.0 | 66 |
| 2414 | Alternative Polyadenylation in Glioblastoma Multiforme and Changes in Predicted RNA Binding Protein Profiles. OMICS A Journal of Integrative Biology, 2013, 17, 136-149. | 2.0 | 14 |
| 2415 | A specific family of interspersed repeats (SINEs) facilitates meiotic synapsis in mammals. Molecular Cytogenetics, 2013, 6, 1. | 0.9 | 17 |
| 2416 | Delimiting species in recent radiations with low levels of morphological divergence: A case study in Australian Gehyra geckos. Molecular Phylogenetics and Evolution, 2013, 68, 135-143. | 2.7 | 33 |
| 2417 | The Coding and the Non-coding Transcriptome. , 2013, , 27-41. | | 3 |
| 2418 | Beyond an <scp>AFLP</scp> genome scan towards the identification of immune genes involved in plague resistance in <i>Rattus rattus</i> from Madagascar. Molecular Ecology, 2013, 22, 354-367. | 3.9 | 11 |
| 2419 | Untangling the transcriptome from fungus-infected plant tissues. Gene, 2013, 519, 238-244. | 2.2 | 6 |
| 2420 | Saccharinae Bioinformatics Resources. , 2013, , 303-330. | | 0 |
| 2421 | Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. Nature Genetics, 2013, 45, 12-17. | 21.4 | 374 |
| 2422 | Comparative Analysis of MicroRNA Promoters in <i>Arabidopsis</i> and Rice. Genomics, Proteomics and Bioinformatics, 2013, 11, 56-60. | 6.9 | 21 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2423 | Transcriptome analysis of Inbred Long Sleep and Inbred Short Sleep mice. <i>Genes, Brain and Behavior</i> , 2013, 12, 263-274. | 2.2 | 15 |
| 2424 | Circular RNAs are a large class of animal RNAs with regulatory potency. <i>Nature</i> , 2013, 495, 333-338. | 27.8 | 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. | 4.0 | 147 |
| 2426 | MosaicFinder: identification of fused gene families in sequence similarity networks. <i>Bioinformatics</i> , 2013, 29, 837-844. | 4.1 | 29 |
| 2427 | Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. <i>Science</i> , 2013, 339, 1063-1067. | 12.6 | 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. | 3.9 | 53 |
| 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. | 4.8 | 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. | 11.1 | 224 |
| 2431 | Computational solutions for omics data. <i>Nature Reviews Genetics</i> , 2013, 14, 333-346. | 16.3 | 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. | 7.0 | 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. | 2.9 | 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. | 2.4 | 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. | 3.4 | 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. | 21.4 | 409 |
| 2437 | Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663. | 21.4 | 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. | 1.7 | 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. | 21.4 | 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>G3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63. | 1.8 | 167 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.5 | 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. | 0.9 | 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. | 4.5 | 41 |
| 2444 | Reversal of an ancient sex chromosome to an autosome in <i>Drosophila</i> . <i>Nature</i> , 2013, 499, 332-335. | 27.8 | 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. | 3.8 | 13 |
| 2447 | Ground tit genome reveals avian adaptation to living at high altitudes in the Tibetan plateau. <i>Nature Communications</i> , 2013, 4, 2071. | 12.8 | 229 |
| 2448 | Integrated molecular analysis of clear-cell renal cell carcinoma. <i>Nature Genetics</i> , 2013, 45, 860-867. | 21.4 | 955 |
| 2449 | Somatic Alterations Contributing to Metastasis of a Castration-Resistant Prostate Cancer. <i>Human Mutation</i> , 2013, 34, 1231-1241. | 2.5 | 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. | 5.7 | 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. | 8.2 | 9 |
| 2452 | Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013, 45, 767-775. | 21.4 | 176 |
| 2453 | Clinical and cytogenetic features of a Potocki-Lupski syndrome with the shortest 0.25Mb microduplication in 17p11.2 including <i>RAI1</i> . <i>Brain and Development</i> , 2013, 35, 681-685. | 1.1 | 13 |
| 2454 | Better spaced seeds using Quadratic Residues. <i>Journal of Computer and System Sciences</i> , 2013, 79, 1144-1155. | 1.2 | 17 |
| 2455 | Analysis of western lowland gorilla (<i>Gorilla gorilla gorilla</i>) specific Alu repeats. <i>Mobile DNA</i> , 2013, 4, 26. | 3.6 | 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. | 1.8 | 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. | 3.4 | 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. | 21.4 | 251 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.5 | 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. | 7.1 | 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. | 3.1 | 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. | 2.1 | 15 |
| 2463 | STAR: ultrafast universal RNA-seq aligner. <i>Bioinformatics</i> , 2013, 29, 15-21. | 4.1 | 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. | 0.9 | 4 |
| 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. | 1.8 | 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. | 1.8 | 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. | 2.8 | 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, . | 4.1 | 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. | 14.5 | 29 |
| 2471 | Insertional Mutagenesis Using <i>Tnt1</i> Retrotransposon in Potato. <i>Plant Physiology</i> , 2013, 163, 21-29. | 4.8 | 30 |
| 2472 | Microbiome in Human Health and Disease. <i>Science Progress</i> , 2013, 96, 153-170. | 1.9 | 18 |
| 2473 | Activity-regulated RNA editing in select neuronal subfields in hippocampus. <i>Nucleic Acids Research</i> , 2013, 41, 1124-1134. | 14.5 | 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. | 3.5 | 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. | 14.5 | 58 |
| 2476 | Substantial Loss of Conserved and Gain of Novel MicroRNA Families in Flatworms. <i>Molecular Biology and Evolution</i> , 2013, 30, 2619-2628. | 8.9 | 84 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2477 | Inferring the choreography of parental genomes during fertilization from ultralarge-scale whole-transcriptome analysis. <i>Genes and Development</i> , 2013, 27, 2736-2748. | 5.9 | 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. | 5.5 | 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. | 14.5 | 115 |
| 2480 | Low-Bandwidth and Non-Compute Intensive Remote Identification of Microbes from Raw Sequencing Reads. <i>PLoS ONE</i> , 2013, 8, e83784. | 2.5 | 5 |
| 2481 | Henipavirus Pathogenesis in Human Respiratory Epithelial Cells. <i>Journal of Virology</i> , 2013, 87, 3284-3294. | 3.4 | 46 |
| 2482 | nhmmer: DNA homology search with profile HMMs. <i>Bioinformatics</i> , 2013, 29, 2487-2489. | 4.1 | 735 |
| 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. | 8.9 | 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. | 3.4 | 68 |
| 2485 | ASPic-GenelD: A Lightweight Pipeline for Gene Prediction and Alternative Isoforms Detection. <i>BioMed Research International</i> , 2013, 2013, 1-11. | 1.9 | 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. | 3.5 | 574 |
| 2487 | The transcriptional response of Arabidopsis leaves to Fe deficiency. <i>Frontiers in Plant Science</i> , 2013, 4, 276. | 3.6 | 152 |
| 2488 | Evolutionary Dynamics of Sex-Biased Genes in a Hermaphrodite Fungus. <i>Molecular Biology and Evolution</i> , 2013, 30, 2435-2446. | 8.9 | 27 |
| 2489 | Probabilistic Inference of Biochemical Reactions in Microbial Communities from Metagenomic Sequences. <i>PLoS Computational Biology</i> , 2013, 9, e1002981. | 3.2 | 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. | 2.8 | 65 |
| 2491 | Genetic Genomic Replication to Identify Candidate Mouse Atherosclerosis Modifier Genes. <i>Journal of the American Heart Association</i> , 2013, 2, e005421. | 3.7 | 16 |
| 2492 | The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46. | 3.6 | 198 |
| 2493 | ToPS: A Framework to Manipulate Probabilistic Models of Sequence Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003234. | 3.2 | 6 |
| 2494 | Genome-Wide Analysis Reveals Origin of Transfer RNA Genes from tRNA Halves. <i>Molecular Biology and Evolution</i> , 2013, 30, 2087-2098. | 8.9 | 20 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2495 | The <i>Oxytricha trifallax</i> Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. <i>PLoS Biology</i> , 2013, 11, e1001473. | 5.6 | 198 |
| 2496 | Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003242. | 3.5 | 88 |
| 2497 | Microhomology-Mediated Mechanisms Underlie Non-Recurrent Disease-Causing Microdeletions of the <i>FOXL2</i> Gene or Its Regulatory Domain. <i>PLoS Genetics</i> , 2013, 9, e1003358. | 3.5 | 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. | 8.9 | 15 |
| 2499 | Systems Approaches to Modeling Chronic Mucosal Inflammation. <i>BioMed Research International</i> , 2013, 2013, 1-17. | 1.9 | 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. | 4.1 | 1 |
| 2501 | MGMT expression: insights into its regulation. 2. Single nucleotide polymorphisms. <i>Biopolymers and Cell</i> , 2013, 29, 367-374. | 0.4 | 1 |
| 2502 | Comparative Sex Chromosome Genomics in Snakes: Differentiation, Evolutionary Strata, and Lack of Global Dosage Compensation. <i>PLoS Biology</i> , 2013, 11, e1001643. | 5.6 | 270 |
| 2503 | Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233. | 3.5 | 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. | 2.5 | 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. | 4.1 | 8 |
| 2506 | Dual Host-Virus Arms Races Shape an Essential Housekeeping Protein. <i>PLoS Biology</i> , 2013, 11, e1001571. | 5.6 | 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. | 3.5 | 110 |
| 2508 | Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. <i>PLoS Pathogens</i> , 2013, 9, e1003196. | 4.7 | 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. | 3.4 | 17 |
| 2510 | Identification of Biologically Relevant Enhancers in Human Erythroid Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 8433-8444. | 3.4 | 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. | 4.8 | 212 |
| 2512 | Genome-Wide Detection of Condition-Sensitive Alternative Splicing in <i>Arabidopsis</i> Roots. <i>Plant Physiology</i> , 2013, 162, 1750-1763. | 4.8 | 113 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.0 | 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. | 2.2 | 20 |
| 2515 | Hominoid fission of chromosome 14/15 and the role of segmental duplications. <i>Genome Research</i> , 2013, 23, 1763-1773. | 5.5 | 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. | 14.5 | 54 |
| 2517 | OLego: fast and sensitive mapping of spliced mRNA-Seq reads using small seeds. <i>Nucleic Acids Research</i> , 2013, 41, 5149-5163. | 14.5 | 116 |
| 2518 | An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e89-e89. | 14.5 | 177 |
| 2519 | WebScipio: reconstructing alternative splice variants of eukaryotic proteins. <i>Nucleic Acids Research</i> , 2013, 41, W504-W509. | 14.5 | 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. | 7.1 | 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. | 14.5 | 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. | 1.8 | 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. | 2.5 | 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. | 2.5 | 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 & 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. | 12.4 | 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. | 2.5 | 27 |
| 2528 | MGAvviewer: a desktop visualization tool for analysis of metagenomics alignment data. <i>Bioinformatics</i> , 2013, 29, 122-123. | 4.1 | 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. | 2.5 | 29 |
| 2530 | TrueSight: a new algorithm for splice junction detection using RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e51-e51. | 14.5 | 31 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2531 | Reprever: resolving low-copy duplicated sequences using template driven assembly. <i>Nucleic Acids Research</i> , 2013, 41, e128-e128. | 14.5 | 7 |
| 2532 | Boosting the Detection of Transposable Elements Using Machine Learning. <i>Advances in Intelligent Systems and Computing</i> , 2013, , 85-91. | 0.6 | 8 |
| 2533 | ReviSTER: an automated pipeline to revise misaligned reads to simple tandem repeats. <i>Bioinformatics</i> , 2013, 29, 1734-1741. | 4.1 | 21 |
| 2534 | GnplS: 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. | 3.0 | 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. | 2.5 | 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. | 2.5 | 139 |
| 2537 | Genome sequence of ground tit <i>Pseudopodoces humilis</i> and its adaptation to high altitude. <i>Genome Biology</i> , 2013, 14, R29. | 9.6 | 81 |
| 2538 | Separating homeologs by phasing in the tetraploid wheat transcriptome. <i>Genome Biology</i> , 2013, 14, R66. | 8.8 | 126 |
| 2539 | The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89. | 9.6 | 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. | 9.6 | 89 |
| 2541 | rDNA-directed integration by an HIV-1 integrase- Ψ I-Ppol fusion protein. <i>Nucleic Acids Research</i> , 2013, 41, e61-e61. | 14.5 | 20 |
| 2542 | TriageTools: tools for partitioning and prioritizing analysis of high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e86-e86. | 14.5 | 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. | 3.2 | 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. | 3.4 | 16 |
| 2545 | A Guide to Bioinformatics for Immunologists. <i>Frontiers in Immunology</i> , 2013, 4, 416. | 4.8 | 10 |
| 2546 | Probabilistic error correction for RNA sequencing. <i>Nucleic Acids Research</i> , 2013, 41, e109-e109. | 14.5 | 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. | 12.8 | 229 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 3.5 | 19 |
| 2550 | Lack of evidence for existence of noncanonical RNA editing. <i>Nature Biotechnology</i> , 2013, 31, 19-20. | 17.5 | 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. | 3.1 | 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. | 3.1 | 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. | 3.1 | 51 |
| 2554 | Building localized bioinformatics platform based on Galaxy and high performance computing cluster. , 2013, , . | | 1 |
| 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. | 2.5 | 55 |
| 2557 | RCpedia: a database of retrocopied genes. <i>Bioinformatics</i> , 2013, 29, 1235-1237. | 4.1 | 32 |
| 2558 | Using Chimaeric Expression Sequence Tag as the Reference to Identify Three-Dimensional Chromosome Contacts. <i>DNA Research</i> , 2013, 20, 45-53. | 3.4 | 2 |
| 2559 | The shared genomic architecture of human nucleolar organizer regions. <i>Genome Research</i> , 2013, 23, 2003-2012. | 5.5 | 107 |
| 2560 | Draft genome of the kiwifruit <i>Actinidia chinensis</i> . <i>Nature Communications</i> , 2013, 4, 2640. | 12.8 | 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. | 3.4 | 187 |
| 2562 | Inactivation of the RB family prevents thymus involution and promotes thymic function by direct control of Foxn1 expression. <i>Journal of Experimental Medicine</i> , 2013, 210, 1087-1097. | 8.5 | 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. | 5.4 | 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. | 21.4 | 173 |
| 2566 | The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013, 4, 2433. | 12.8 | 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. | 2.5 | 19 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 3.1 | 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. | 14.5 | 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. | 3.3 | 44 |
| 2571 | Phenotypic Plasticity, CYP19A1 Pleiotropy, and Maladaptive Selection in Developmental Disorders. <i>SAGE Open</i> , 2013, 3, 215824401348447. | 1.7 | 0 |
| 2572 | Combined methylation mapping of 5mC and 5hmC during early embryonic stages in bovine. <i>BMC Genomics</i> , 2013, 14, 406. | 2.8 | 15 |
| 2573 | Data compression for sequencing data. <i>Algorithms for Molecular Biology</i> , 2013, 8, 25. | 1.2 | 82 |
| 2574 | Answering biological questions by querying k-mer databases. <i>Concurrency Computation Practice and Experience</i> , 2013, 25, 497-509. | 2.2 | 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. | 8.8 | 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. | 3.0 | 17 |
| 2577 | Global regulation of alternative splicing by adenosine deaminase acting on RNA (ADAR). <i>Rna</i> , 2013, 19, 591-604. | 3.5 | 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. | 1.5 | 47 |
| 2579 | Deep Sequencing of RNA from Ancient Maize Kernels. <i>PLoS ONE</i> , 2013, 8, e50961. | 2.5 | 38 |
| 2580 | Cloning, Annotation and Developmental Expression of the Chicken Intestinal MUC2 Gene. <i>PLoS ONE</i> , 2013, 8, e53781. | 2.5 | 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. | 2.5 | 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. | 2.5 | 28 |
| 2583 | Analysis of Metagenomic Data Containing High Biodiversity Levels. <i>PLoS ONE</i> , 2013, 8, e58118. | 2.5 | 12 |
| 2584 | PSimScan: Algorithm and Utility for Fast Protein Similarity Search. <i>PLoS ONE</i> , 2013, 8, e58505. | 2.5 | 7 |
| 2585 | Contradiction between Plastid Gene Transcription and Function Due to Complex Posttranscriptional Splicing: An Exemplary Study of <i>ycf15</i> Function and Evolution in Angiosperms. <i>PLoS ONE</i> , 2013, 8, e59620. | 2.5 | 55 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2586 | Construction of Customized Sub-Databases from NCBI-nr Database for Rapid Annotation of Huge Metagenomic Datasets Using a Combined BLAST and MEGAN Approach. PLoS ONE, 2013, 8, e59831. | 2.5 | 49 |
| 2587 | Transcriptome Analysis of the Differentially Expressed Genes in the Male and Female Shrub Willows (<i>Salix suchowensis</i>). PLoS ONE, 2013, 8, e60181. | 2.5 | 38 |
| 2588 | Overexpression of Full-Length Centrobin Rescues Limb Malformation but Not Male Fertility of the Hypodactylous (hd) Rats. PLoS ONE, 2013, 8, e60859. | 2.5 | 7 |
| 2589 | Mechanisms of Intron Loss and Gain in the Fission Yeast <i>Schizosaccharomyces</i> . PLoS ONE, 2013, 8, e61683. | 2.5 | 27 |
| 2590 | Simultaneous Transcriptome Analysis of <i>Sorghum</i> and <i>Bipolaris sorghicola</i> by Using RNA-seq in Combination with De Novo Transcriptome Assembly. PLoS ONE, 2013, 8, e62460. | 2.5 | 79 |
| 2591 | High-Throughput miRNA and mRNA Sequencing of Paired Colorectal Normal, Tumor and Metastasis Tissues and Bioinformatic Modeling of miRNA-1 Therapeutic Applications. PLoS ONE, 2013, 8, e67461. | 2.5 | 53 |
| 2592 | Complete Genome Analysis of a <i>Haemophilus parasuis</i> Serovar 12 Strain from China. PLoS ONE, 2013, 8, e68350. | 2.5 | 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. | 2.5 | 26 |
| 2594 | Genomic Treasure Troves: Complete Genome Sequencing of Herbarium and Insect Museum Specimens. PLoS ONE, 2013, 8, e69189. | 2.5 | 215 |
| 2595 | Analysis of Unannotated Equine Transcripts Identified by mRNA Sequencing. PLoS ONE, 2013, 8, e70125. | 2.5 | 16 |
| 2596 | Comprehensive Genomic Characterization of <i>Campylobacter</i> Genus Reveals Some Underlying Mechanisms for its Genomic Diversification. PLoS ONE, 2013, 8, e70241. | 2.5 | 16 |
| 2597 | RNA-Seq Reveals Infection-Related Gene Expression Changes in <i>Phytophthora capsici</i> . PLoS ONE, 2013, 8, e74588. | 2.5 | 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 | 2.5 | 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. | 2.5 | 18 |
| 2600 | Evaluation of Alignment Algorithms for Discovery and Identification of Pathogens Using RNA-Seq. PLoS ONE, 2013, 8, e76935. | 2.5 | 37 |
| 2601 | Optimal Scaling of Digital Transcriptomes. PLoS ONE, 2013, 8, e77885. | 2.5 | 44 |
| 2602 | Cross-Platform Prediction of Gene Expression Signatures. PLoS ONE, 2013, 8, e79228. | 2.5 | 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. | 2.5 | 94 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2604 | Genome-Wide Survey of Cold Stress Regulated Alternative Splicing in <i>Arabidopsis thaliana</i> with Tiling Microarray. PLoS ONE, 2013, 8, e66511. | 2.5 | 64 |
| 2605 | Development of Peptide Nucleic Acid Probes for Detection of the HER2 Oncogene. PLoS ONE, 2013, 8, e58870. | 2.5 | 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. | 2.5 | 791 |
| 2607 | MATCHCLIP: locate precise breakpoints for copy number variation using CIGAR string by matching soft clipped reads. Frontiers in Genetics, 2013, 4, 157. | 2.3 | 16 |
| 2608 | Sense-antisense gene pairs: sequence, transcription, and structure are not conserved between human and mouse. Frontiers in Genetics, 2013, 4, 183. | 2.3 | 46 |
| 2609 | The spliced leader trans-splicing mechanism in different organisms: molecular details and possible biological roles. Frontiers in Genetics, 2013, 4, 199. | 2.3 | 29 |
| 2610 | A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. Frontiers in Genetics, 2013, 4, 209. | 2.3 | 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. Frontiers in Microbiology, 2013, 4, 63. | 3.5 | 42 |
| 2612 | Monocular inhibition reveals temporal and spatial changes in gene expression in the primary visual cortex of marmoset. Frontiers in Neural Circuits, 2013, 7, 43. | 2.8 | 15 |
| 2613 | Trapping DNA Replication Origins from the Human Genome. Genes, 2013, 4, 198-225. | 2.4 | 0 |
| 2614 | Shared and Unique Proteins in Human, Mouse and Rat Saliva Proteomes: Footprints of Functional Adaptation. Proteomes, 2013, 1, 275-289. | 3.5 | 16 |
| 2615 | Comprehensive Analysis of Alternative Splicing in <i>Digitalis purpurea</i> by Strand-Specific RNA-Seq. PLoS ONE, 2014, 9, e106001. | 2.5 | 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. PLoS ONE, 2014, 9, e86399. | 2.5 | 38 |
| 2617 | Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. PLoS ONE, 2014, 9, e85568. | 2.5 | 57 |
| 2618 | C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. PLoS ONE, 2014, 9, e86476. | 2.5 | 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> . PLoS ONE, 2014, 9, e89398. | 2.5 | 29 |
| 2620 | The Impacts of Read Length and Transcriptome Complexity for De Novo Assembly: A Simulation Study. PLoS ONE, 2014, 9, e94825. | 2.5 | 32 |
| 2621 | A Method for Detecting Long Non-Coding RNAs with Tiled RNA Expression Microarrays. PLoS ONE, 2014, 9, e99899. | 2.5 | 12 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 2622 | Repair of Oxidative DNA Base Damage in the Host Genome Influences the HIV Integration Site Sequence Preference. PLoS ONE, 2014, 9, e103164. | 2.5 | 12 |
| 2623 | SNP Identification by Transcriptome Sequencing and Candidate Gene-Based Association Analysis for Heat Tolerance in the Bay Scallop <i>Argopecten irradians</i> . PLoS ONE, 2014, 9, e104960. | 2.5 | 20 |
| 2624 | LncRBase: An Enriched Resource for lncRNA Information. PLoS ONE, 2014, 9, e108010. | 2.5 | 60 |
| 2625 | NSIT: Novel Sequence Identification Tool. PLoS ONE, 2014, 9, e108011. | 2.5 | 1 |
| 2626 | Effective Extraction and Assembly Methods for Simultaneously Obtaining Plastid and Mitochondrial Genomes. PLoS ONE, 2014, 9, e108291. | 2.5 | 13 |
| 2627 | Evaluation of a Hybrid Approach Using UBLAST and BLASTX for Metagenomic Sequences Annotation of Specific Functional Genes. PLoS ONE, 2014, 9, e110947. | 2.5 | 36 |
| 2628 | RADIA: RNA and DNA Integrated Analysis for Somatic Mutation Detection. PLoS ONE, 2014, 9, e111516. | 2.5 | 90 |
| 2629 | Detection Theory in Identification of RNA-DNA Sequence Differences Using RNA-Sequencing. PLoS ONE, 2014, 9, e112040. | 2.5 | 7 |
| 2630 | Comparative Genomic Analysis Shows That Avian Pathogenic <i>Escherichia coli</i> Isolate IMT5155 (O2:K1:H5;) Tj ETQq0 0 0 rgBT /Overlock . PLoS ONE, 2014, 9, e112048. | 2.5 | 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. | 2.5 | 79 |
| 2632 | Transcriptional Consequence and Impaired Gametogenesis with High-Grade Aneuploidy in <i>Arabidopsis thaliana</i> . PLoS ONE, 2014, 9, e114617. | 2.5 | 6 |
| 2633 | Comparative Genome Analyses Reveal Distinct Structure in the Saltwater Crocodile MHC. PLoS ONE, 2014, 9, e114631. | 2.5 | 22 |
| 2634 | BLAT-Based Comparative Analysis for Transposable Elements: BLATCAT. BioMed Research International, 2014, 2014, 1-7. | 1.9 | 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. | 2.4 | 76 |
| 2637 | Genome-wide mapping in a house mouse hybrid zone reveals hybrid sterility loci and Dobzhansky-Muller interactions. ELife, 2014, 3, . | 6.0 | 107 |
| 2638 | Suppression of cell wall-related genes associated with stunting of <i>Oryza glaberrima</i> infected with Rice tungro spherical virus. Frontiers in Microbiology, 2014, 5, 26. | 3.5 | 26 |
| 2639 | The role of photorespiration during the evolution of C4 photosynthesis in the genus <i>Flaveria</i> . ELife, 2014, 3, e02478. | 6.0 | 182 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 2.5 | 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 <i>Saitoella complicata</i> has three histone deacetylases belonging to the Clr6, Hos2, and Rpd3 lineages. Journal of General and Applied Microbiology, 2014, 60, 7-12. | 0.7 | 5 |
| 2643 | A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38. | 1.8 | 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. | 4.7 | 46 |
| 2646 | Genome Sequence of <i>Fusarium graminearum</i> Isolate CS3005. Genome Announcements, 2014, 2, . | 0.8 | 32 |
| 2647 | A comprehensive survey of non-canonical splice sites in the human transcriptome. Nucleic Acids Research, 2014, 42, 10564-10578. | 14.5 | 109 |
| 2649 | Fungal Genomics. Advances in Botanical Research, 2014, , 1-52. | 1.1 | 25 |
| 2650 | Whole-Genome Sequencing for Rapid and Accurate Identification of Bacterial Transmission Pathways. Methods in Microbiology, 2014, 41, 123-152. | 0.8 | 4 |
| 2651 | Highly Variable Recombinational Landscape Modulates Efficacy of Natural Selection in Birds. Genome Biology and Evolution, 2014, 6, 2061-2075. | 2.5 | 36 |
| 2652 | The nuclear hormone receptor family member NR5A2 controls aspects of multipotent progenitor cell formation and acinar differentiation during pancreatic organogenesis. Development (Cambridge), 2014, 141, 3123-3133. | 2.5 | 92 |
| 2653 | Transcriptome sequencing and analysis of <i>Plasmodium gallinaceum</i> reveals polymorphisms and selection on the apical membrane antigen-1. Malaria Journal, 2014, 13, 382. | 2.3 | 25 |
| 2654 | Dynamic evolution of the alpha (\hat{I}_1) and beta (\hat{I}_2) keratins has accompanied integument diversification and the adaptation of birds into novel lifestyles. BMC Evolutionary Biology, 2014, 14, 249. | 3.2 | 84 |
| 2655 | Tangram: a comprehensive toolbox for mobile element insertion detection. BMC Genomics, 2014, 15, 795. | 2.8 | 54 |
| 2656 | Unfixed Endogenous Retroviral Insertions in the Human Population. Journal of Virology, 2014, 88, 9529-9537. | 3.4 | 118 |
| 2657 | Estimating overannotation across prokaryotic genomes using BLAST+, UBLAST, LAST and BLAT. BMC Research Notes, 2014, 7, 651. | 1.4 | 6 |
| 2658 | Host and viral determinants for MxB restriction of HIV-1 infection. Retrovirology, 2014, 11, 90. | 2.0 | 89 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2659 | Conserved syntenic clusters of protein coding genes are missing in birds. <i>Genome Biology</i> , 2014, 15, 565. | 8.8 | 123 |
| 2660 | Evaluation of de novo transcriptome assemblies from RNA-Seq data. <i>Genome Biology</i> , 2014, 15, 553. | 8.8 | 256 |
| 2661 | A PTCH1 Homolog Transcriptionally Activated by p53 Suppresses Hedgehog Signaling. <i>Journal of Biological Chemistry</i> , 2014, 289, 33020-33031. | 3.4 | 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. | 3.4 | 20 |
| 2663 | Definition of the Cattle Killer Cell Igα-like Receptor Gene Family: Comparison with Aurochs and Human Counterparts. <i>Journal of Immunology</i> , 2014, 193, 6016-6030. | 0.8 | 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. | 4.8 | 30 |
| 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. | 1.8 | 17 |
| 2666 | Piecing the puzzle together: a revisit to transcript reconstruction problem in RNA-seq. <i>BMC Bioinformatics</i> , 2014, 15, S3. | 2.6 | 1 |
| 2667 | Population history and genomic signatures for high-altitude adaptation in Tibetan pigs. <i>BMC Genomics</i> , 2014, 15, 834. | 2.8 | 140 |
| 2668 | A naturally occurring, noncanonical GTP aptamer made of simple tandem repeats. <i>RNA Biology</i> , 2014, 11, 682-692. | 3.1 | 9 |
| 2669 | MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. <i>Nucleic Acids Research</i> , 2014, 42, e73-e73. | 14.5 | 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. | 2.5 | 11 |
| 2671 | Genomic Organization, Transcriptomic Analysis, and Functional Characterization of Avian β - and β 2-Keratins in Diverse Feather Forms. <i>Genome Biology and Evolution</i> , 2014, 6, 2258-2273. | 2.5 | 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. | 14.5 | 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. | 3.6 | 55 |
| 2674 | Postzygotic single-nucleotide mosaicisms in whole-genome sequences of clinically unremarkable individuals. <i>Cell Research</i> , 2014, 24, 1311-1327. | 12.0 | 54 |
| 2675 | Haploinsufficiency of Sf3b1 leads to compromised stem cell function but not to myelodysplasia. <i>Leukemia</i> , 2014, 28, 1844-1850. | 7.2 | 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. | 4.1 | 15 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 2677 | Methods to Study Splicing from High-Throughput RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2014, 1126, 357-397. | 0.9 | 68 |
| 2678 | Gene-based SNP discovery and genetic mapping in pea. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2225-2241. | 3.6 | 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. | 2.5 | 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. | 0.6 | 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. | 4.8 | 19 |
| 2683 | A Genome-Wide Analysis of Genetic Diversity in <i>Trypanosoma cruzi</i> Intergenic Regions. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2839. | 3.0 | 8 |
| 2684 | Functional Divergence and Evolutionary Turnover in Mammalian Phosphoproteomes. <i>PLoS Genetics</i> , 2014, 10, e1004062. | 3.5 | 41 |
| 2685 | Genomic Networks of Hybrid Sterility. <i>PLoS Genetics</i> , 2014, 10, e1004162. | 3.5 | 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. | 2.3 | 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. | 3.5 | 59 |
| 2690 | Neutral nuclear variation in <i>Baboons</i> (genus <i>Protopithecus</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. | 3.1 | 13 |
| 2692 | HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. <i>Bioinformatics</i> , 2014, 30, 3302-3309. | 4.1 | 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. | 2.9 | 23 |
| 2694 | Sequence Analysis of Industrially Important Genes from <i>Trichoderma</i> . , 2014, , 377-392. | | 11 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 2695 | New MicroRNAs in <i>Drosophila</i> —Birth, Death and Cycles of Adaptive Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004096. | 3.5 | 53 |
| 2696 | NCYM, a Cis-Antisense Gene of MYCN, Encodes a De Novo Evolved Protein That Inhibits GSK3 β Resulting in the Stabilization of MYCN in Human Neuroblastomas. <i>PLoS Genetics</i> , 2014, 10, e1003996. | 3.5 | 83 |
| 2697 | A comprehensive set of transcript sequences of the heavy metal hyperaccumulator <i>Noccaea caerulea</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 261. | 3.6 | 32 |
| 2698 | P2Y ₁₂ Receptor on the Verge of a Neuroinflammatory Breakdown. <i>Mediators of Inflammation</i> , 2014, 2014, 1-15. | 3.0 | 65 |
| 2699 | Toxoplasma Effector MAF1 Mediates Recruitment of Host Mitochondria and Impacts the Host Response. <i>PLoS Biology</i> , 2014, 12, e1001845. | 5.6 | 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. | 3.5 | 66 |
| 2701 | CDKN2D-WDFY2 Is a Cancer-Specific Fusion Gene Recurrent in High-Grade Serous Ovarian Carcinoma. <i>PLoS Genetics</i> , 2014, 10, e1004216. | 3.5 | 41 |
| 2702 | Widespread Use of Non-productive Alternative Splice Sites in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004249. | 3.5 | 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. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2014, 27, 1397-1408. | 1.5 | 25 |
| 2704 | Type I Interferon Regulates the Expression of Long Non-Coding RNAs. <i>Frontiers in Immunology</i> , 2014, 5, 548. | 4.8 | 54 |
| 2705 | A Practical Approach to a Viral Detection Pipeline Using Existing Viral and Non-Viral Sequence Resources. <i>PDA Journal of Pharmaceutical Science and Technology</i> , 2014, 68, 595-601. | 0.5 | 1 |
| 2706 | AlignGraph: algorithm for secondary <i>de novo</i> genome assembly guided by closely related references. <i>Bioinformatics</i> , 2014, 30, i319-i328. | 4.1 | 61 |
| 2707 | Lambda: the local aligner for massive biological data. <i>Bioinformatics</i> , 2014, 30, i349-i355. | 4.1 | 60 |
| 2708 | Comparative Metagenomic Analysis of Human Gut Microbiome Composition Using Two Different Bioinformatic Pipelines. <i>BioMed Research International</i> , 2014, 2014, 1-10. | 1.9 | 68 |
| 2709 | Shotgun metagenomics reveals a wide array of antibiotic resistance genes and mobile elements in a polluted lake in India. <i>Frontiers in Microbiology</i> , 2014, 5, 648. | 3.5 | 193 |
| 2710 | IDBA-MTP: A Hybrid MetaTranscriptomic Assembler Based on Protein Information. <i>Lecture Notes in Computer Science</i> , 2014, , 160-172. | 1.3 | 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. <i>PLoS Genetics</i> , 2014, 10, e1004261. | 3.5 | 336 |
| 2712 | Forty-Four Novel Protein-Coding Loci Discovered Using a Proteomics Informed by Transcriptomics (PIT) Approach in Rat Male Germ Cells. <i>Biology of Reproduction</i> , 2014, 91, 123. | 2.7 | 20 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 3.4 | 149 |
| 2717 | Complete genome assembly and characterization of an outbreak strain of the causative agent of swine erysipelas â€“ Erysipelothrix rhusiopathiae SY1027. BMC Microbiology, 2014, 14, 176. | 3.3 | 36 |
| 2718 | AlgaePath: comprehensive analysis of metabolic pathways using transcript abundance data from next-generation sequencing in green algae. BMC Genomics, 2014, 15, 196. | 2.8 | 36 |
| 2719 | Genome sequencing of four Aureobasidium pullulans varieties: biotechnological potential, stress tolerance, and description of new species. BMC Genomics, 2014, 15, 549. | 2.8 | 262 |
| 2720 | Towards computational improvement of DNA database indexing and short DNA query searching. Biotechnology and Biotechnological Equipment, 2014, 28, 958-967. | 1.3 | 1 |
| 2721 | The discrepancies in the results of bioinformatics tools for genomic structural annotation. Proceedings of SPIE, 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. Development (Cambridge), 2014, 141, 4018-4030. | 2.5 | 26 |
| 2723 | Diversification of bacterial genome content through distinct mechanisms over different timescales. Nature Communications, 2014, 5, 5471. | 12.8 | 173 |
| 2724 | Gene Prediction and Annotation in <i>Penstemon</i> (Plantaginaceae): A Workflow for Marker Development from Extremely Low-Coverage Genome Sequencing. Applications in Plant Sciences, 2014, 2, 1400044. | 2.1 | 15 |
| 2725 | Genome-wide eQTLs and heritability for gene expression traits in unrelated individuals. BMC Genomics, 2014, 15, 13. | 2.8 | 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. Genome Announcements, 2014, 2, . | 0.8 | 16 |
| 2727 | Complete Genome Sequences of IncI1 Plasmids Carrying Extended-Spectrum β -Lactamase Genes. Genome Announcements, 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. MBio, 2014, 5, e01464-14. | 4.1 | 126 |
| 2729 | IRBIS: a systematic search for conserved complementarity. Rna, 2014, 20, 1519-1531. | 3.5 | 16 |
| 2730 | Differential Locus Expansion Distinguishes <i>Toxoplasmatinae</i> Species and Closely Related Strains of <i>Toxoplasma gondii</i> . MBio, 2014, 5, e01003-13. | 4.1 | 22 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2731 | The <i>Cryptococcus neoformans</i> Transcriptome at the Site of Human Meningitis. <i>MBio</i> , 2014, 5, e01087-13. | 4.1 | 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. | 3.0 | 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 LpxA. <i>BMC Microbiology</i> , 2014, 14, 336. | 3.3 | 6 |
| 2735 | Genetic dysregulation in recurrent respiratory papillomatosis. <i>Laryngoscope</i> , 2014, 124, E320-5. | 2.0 | 8 |
| 2736 | HybSeq: Combining target enrichment and genome skimming for plant phylogenomics. <i>Applications in Plant Sciences</i> , 2014, 2, 1400042. | 2.1 | 405 |
| 2737 | Anti-centrosome antibodies in breast cancer are the expression of autoimmunity. <i>Immunologic Research</i> , 2014, 60, 339-347. | 2.9 | 11 |
| 2738 | Approximate k -Mer Matching Using Fuzzy Hash Maps. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 258-264. | 3.0 | 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. | 5.7 | 18 |
| 2740 | The <i>GATA</i> transcription factor/ <i>MTA</i> homolog <i>egl</i> promotes longevity and stress resistance in <i>C. elegans</i> . <i>Aging Cell</i> , 2014, 13, 329-339. | 6.7 | 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. | 1.2 | 29 |
| 2742 | Symbiotic adaptations in the fungal cultivar of leaf-cutting ants. <i>Nature Communications</i> , 2014, 5, 5675. | 12.8 | 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. | 5.7 | 38 |
| 2744 | Haploinsufficiency of insulin gene enhancer protein 1 (<i>ISL1</i>) is associated with Δ transposition of the great arteries. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 341-351. | 1.2 | 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. | 3.9 | 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. | 0.6 | 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. | 4.8 | 18 |
| 2748 | Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331. | 12.6 | 1,583 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2749 | Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320. | 12.6 | 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. | 14.5 | 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. | 3.4 | 33 |
| 2752 | <i>zolla</i> domestication towards a biobased economy?. <i>New Phytologist</i> , 2014, 202, 1069-1082. | 7.3 | 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. | 7.1 | 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. | 6.9 | 4 |
| 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. | 2.5 | 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. | 11.1 | 67 |
| 2758 | Bayesian Estimation of Nonsynonymous/Synonymous Rate Ratios for Pairwise Sequence Comparisons. <i>Molecular Biology and Evolution</i> , 2014, 31, 1902-1913. | 8.9 | 13 |
| 2759 | Orione, a web-based framework for NGS analysis in microbiology. <i>Bioinformatics</i> , 2014, 30, 1928-1929. | 4.1 | 139 |
| 2760 | Genetic analysis of a consanguineous Pakistani family with Leber congenital amaurosis identifies a novel mutation in <i>GUCY2D</i> gene. <i>Journal of Genetics</i> , 2014, 93, 527-530. | 0.7 | 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. | 14.5 | 71 |
| 2762 | Alignment-Annotator web server: rendering and annotating sequence alignments. <i>Nucleic Acids Research</i> , 2014, 42, W3-W6. | 14.5 | 56 |
| 2763 | Comparative genomics reveals molecular features unique to the songbird lineage. <i>BMC Genomics</i> , 2014, 15, 1082. | 2.8 | 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. | 2.8 | 134 |
| 2765 | Genome-wide analysis of alternative splicing in <i>Volvox carteri</i> . <i>BMC Genomics</i> , 2014, 15, 1117. | 2.8 | 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. | 2.8 | 111 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2767 | Variable recombination dynamics during the emergence, transmission and “disarming” of a multidrug-resistant pneumococcal clone. <i>BMC Biology</i> , 2014, 12, 49. | 3.8 | 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. | 2.0 | 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. | 1.4 | 14 |
| 2770 | CLAST: CUDA implemented large-scale alignment search tool. <i>BMC Bioinformatics</i> , 2014, 15, 406. | 2.6 | 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. | 3.6 | 15 |
| 2773 | GWIPS-viz: development of a ribo-seq genome browser. <i>Nucleic Acids Research</i> , 2014, 42, D859-D864. | 14.5 | 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. | 2.5 | 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. | 2.1 | 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. | 2.5 | 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. | 3.4 | 67 |
| 2778 | Assessing the State of Substitution Models Describing Noncoding RNA Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 65-75. | 2.5 | 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. | 3.6 | 15 |
| 2780 | RBPmap: a web server for mapping binding sites of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2014, 42, W361-W367. | 14.5 | 409 |
| 2781 | Amplification and thrifty single-molecule sequencing of recurrent somatic structural variations. <i>Genome Research</i> , 2014, 24, 318-328. | 5.5 | 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. | 3.5 | 68 |
| 2783 | Gene Therapy for Wiskott-Aldrich Syndrome—Long-Term Efficacy and Genotoxicity. <i>Science Translational Medicine</i> , 2014, 6, 227ra33. | 12.4 | 460 |
| 2784 | Potential for genomic instability associated with retrotranspositionally-incompetent L1 loci. <i>Nucleic Acids Research</i> , 2014, 42, 10488-10502. | 14.5 | 44 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 2785 | A bioinformatician's guide to the forefront of suffix array construction algorithms. Briefings in Bioinformatics, 2014, 15, 138-154. | 6.5 | 29 |
| 2786 | Systematic design and functional analysis of artificial microRNAs. Nucleic Acids Research, 2014, 42, 6064-6077. | 14.5 | 14 |
| 2787 | TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317. | 5.5 | 81 |
| 2788 | Discovery of Invariant T Cells by Next-Generation Sequencing of the Human TCR α -Chain Repertoire. Journal of Immunology, 2014, 193, 5338-5344. | 0.8 | 23 |
| 2789 | UnSplicer: mapping spliced RNA-seq reads in compact genomes and filtering noisy splicing. Nucleic Acids Research, 2014, 42, e25-e25. | 14.5 | 3 |
| 2790 | A genome-wide map of hyper-edited RNA reveals numerous new sites. Nature Communications, 2014, 5, 4726. | 12.8 | 193 |
| 2791 | Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067. | 2.5 | 153 |
| 2792 | Characterization of Genetic Diversity in the Nematode <i>Pristionchus pacificus</i> from Population-Scale Resequencing Data. Genetics, 2014, 196, 1153-1165. | 2.9 | 79 |
| 2793 | Current Challenges in the Bioinformatics of Single Cell Genomics. Frontiers in Oncology, 2014, 4, 7. | 2.8 | 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. | 3.0 | 64 |
| 2795 | MetaGeniE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing. PLoS ONE, 2014, 9, e110915. | 2.5 | 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. | 8.9 | 60 |
| 2798 | Improved search heuristics find 20 000 new alignments between human and mouse genomes. Nucleic Acids Research, 2014, 42, e59-e59. | 14.5 | 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. | 4.8 | 17 |
| 2800 | Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. Genome Biology, 2014, 15, R48. | 9.6 | 37 |
| 2801 | Estimating differential expression from multiple indicators. Nucleic Acids Research, 2014, 42, e72-e72. | 14.5 | 13 |
| 2802 | MorusDB: a resource for mulberry genomics and genome biology. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau054-bau054. | 3.0 | 40 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2803 | Comparative Genomics of <i>Taphrina</i> Fungi Causing Varying Degrees of Tumorous Deformity in Plants. <i>Genome Biology and Evolution</i> , 2014, 6, 861-872. | 2.5 | 33 |
| 2804 | Evolutionary Origin and Methylation Status of Human Intronic CpG Islands that Are Not Present in Mouse. <i>Genome Biology and Evolution</i> , 2014, 6, 1579-1588. | 2.5 | 16 |
| 2805 | Admixture mapping of prostate cancer in African Americans participating in the North Carolina–Louisiana Prostate Cancer Project (PCaP). <i>Prostate</i> , 2014, 74, 1-9. | 2.3 | 24 |
| 2806 | Detection of Gene Rearrangements in Targeted Clinical Next-Generation Sequencing. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 405-417. | 2.8 | 65 |
| 2807 | Transcriptome de novo assembly sequencing and analysis of the toxic dinoflagellate <i>Alexandrium catenella</i> using the Illumina platform. <i>Gene</i> , 2014, 537, 285-293. | 2.2 | 53 |
| 2808 | A tool for mapping Single Nucleotide Polymorphisms using Graphics Processing Units. <i>BMC Bioinformatics</i> , 2014, 15, S10. | 2.6 | 5 |
| 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. | 1.6 | 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. | 2.2 | 10 |
| 2811 | Sequence capture using <sc>PCR</sc>-generated probes: a cost-effective method of targeted high-throughput sequencing for nonmodel organisms. <i>Molecular Ecology Resources</i> , 2014, 14, 1000-1010. | 4.8 | 89 |
| 2812 | Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , 2014, 24, 885-895. | 5.5 | 200 |
| 2813 | A whole-genome <sc>SNP</sc> array (<sc>RICE6K</sc>) for genomic breeding in rice. <i>Plant Biotechnology Journal</i> , 2014, 12, 28-37. | 8.3 | 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. | 1.7 | 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. | 1.4 | 50 |
| 2816 | doublesex is a mimicry supergene. <i>Nature</i> , 2014, 507, 229-232. | 27.8 | 320 |
| 2817 | Identification of sex-specific molecular markers using restriction site-associated <sc>DNA</sc> sequencing. <i>Molecular Ecology Resources</i> , 2014, 14, 902-913. | 4.8 | 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. | 2.8 | 12 |
| 2820 | Evolution of primate β and δ defensins revealed by analysis of genomes. <i>Molecular Biology Reports</i> , 2014, 41, 3859-3866. | 2.3 | 22 |
| 2821 | Molecular Evolution and Functional Divergence of the Metallothionein Gene Family in Vertebrates. <i>Journal of Molecular Evolution</i> , 2014, 78, 217-233. | 1.8 | 17 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2822 | Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86. | 2.8 | 375 |
| 2823 | Genotyping of BCL11A and HBS1L-MYB SNPs associated with fetal haemoglobin levels: a SNaPshot minisequencing approach. <i>BMC Genomics</i> , 2014, 15, 108. | 2.8 | 25 |
| 2824 | Endogenous viral elements in algal genomes. <i>Acta Oceanologica Sinica</i> , 2014, 33, 102-107. | 1.0 | 11 |
| 2825 | Genome sequencing of high-penicillin producing industrial strain of <i>Penicillium chrysogenum</i> . <i>BMC Genomics</i> , 2014, 15, S11. | 2.8 | 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. | 2.8 | 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. | 3.9 | 42 |
| 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. | 6.2 | 42 |
| 2829 | The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates. <i>Nature Communications</i> , 2014, 5, 3657. | 12.8 | 814 |
| 2830 | Origins and functional evolution of Y chromosomes across mammals. <i>Nature</i> , 2014, 508, 488-493. | 27.8 | 448 |
| 2831 | The advantages of going large: genome-wide <scp>SNP</scp>s clarify the complex population history and systematics of the threatened western pond turtle. <i>Molecular Ecology</i> , 2014, 23, 2228-2241. | 3.9 | 56 |
| 2832 | Current impact and future directions of high throughput sequencing in plant virus diagnostics. <i>Virus Research</i> , 2014, 188, 90-96. | 2.2 | 196 |
| 2833 | Development of fluorescent double-strand probes labeled with 8-(p-CF3-cinnamyl)-adenosine for the detection of cyclin D1 breast cancer marker. <i>European Journal of Medicinal Chemistry</i> , 2014, 79, 77-88. | 5.5 | 5 |
| 2834 | The tobacco genome sequence and its comparison with those of tomato and potato. <i>Nature Communications</i> , 2014, 5, 3833. | 12.8 | 503 |
| 2835 | DICER1 is essential for survival of postmitotic rod photoreceptor cells in mice. <i>FASEB Journal</i> , 2014, 28, 3780-3791. | 0.5 | 54 |
| 2836 | Resources for systems biology in rice. <i>Journal of Plant Biology</i> , 2014, 57, 80-92. | 2.1 | 34 |
| 2837 | Detection and correction of assembly errors of rice <scp>N</scp>ipponbare reference sequence. <i>Plant Biology</i> , 2014, 16, 643-650. | 3.8 | 11 |
| 2838 | The ctenophore genome and the evolutionary origins of neural systems. <i>Nature</i> , 2014, 510, 109-114. | 27.8 | 606 |
| 2839 | Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913. | 12.6 | 124 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2840 | GenomeVISTA“an integrated software package for whole-genome alignment and visualization. <i>Bioinformatics</i> , 2014, 30, 2654-2655. | 4.1 | 27 |
| 2841 | The three major types of CRISPR-Cas systems function independently in CRISPR RNA biogenesis in <i>S. treptococcus thermophilus</i> . <i>Molecular Microbiology</i> , 2014, 93, 98-112. | 2.5 | 81 |
| 2842 | Ensembl Genomes 2013: scaling up access to genome-wide data. <i>Nucleic Acids Research</i> , 2014, 42, D546-D552. | 14.5 | 205 |
| 2843 | Comparative BAC-based physical mapping of <i>Oryza sativa</i> ssp. <i>indica</i> var. 9311 and evaluation of the two rice reference sequence assemblies. <i>Plant Journal</i> , 2014, 77, 795-805. | 5.7 | 16 |
| 2844 | Genomic adaptations of the halophilic Dead Sea filamentous fungus <i>Eurotium rubrum</i> . <i>Nature Communications</i> , 2014, 5, 3745. | 12.8 | 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. | 4.0 | 23 |
| 2846 | Genome-wide analysis of HPV integration in human cancers reveals recurrent, focal genomic instability. <i>Genome Research</i> , 2014, 24, 185-199. | 5.5 | 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. | 2.7 | 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. | 3.0 | 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. | 3.1 | 131 |
| 2850 | Alignment-free genetic sequence comparisons: a review of recent approaches by word analysis. <i>Briefings in Bioinformatics</i> , 2014, 15, 890-905. | 6.5 | 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. | 21.4 | 417 |
| 2852 | Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 171-175. | 21.4 | 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. | 8.2 | 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. | 21.4 | 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. | 2.2 | 14 |
| 2856 | Rhizosphere microbiome assemblage is affected by plant development. <i>ISME Journal</i> , 2014, 8, 790-803. | 9.8 | 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. | 16.2 | 304 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2858 | Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014, 46, 88-92. | 21.4 | 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. | 3.8 | 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. | 4.8 | 101 |
| 2861 | ABRA: improved coding indel detection via assembly-based realignment. <i>Bioinformatics</i> , 2014, 30, 2813-2815. | 4.1 | 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. | 7.1 | 164 |
| 2863 | Integrative transcriptome sequencing identifies <i>trans</i> -splicing events with important roles in human embryonic stem cell pluripotency. <i>Genome Research</i> , 2014, 24, 25-36. | 5.5 | 91 |
| 2864 | MEGANTE: A Web-Based System for Integrated Plant Genome Annotation. <i>Plant and Cell Physiology</i> , 2014, 55, e2-e2. | 3.1 | 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. | 4.8 | 102 |
| 2866 | Anchored multiplex PCR for targeted next-generation sequencing. <i>Nature Medicine</i> , 2014, 20, 1479-1484. | 30.7 | 705 |
| 2867 | Disease variants in genomes of 44 centenarians. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 438-450. | 1.2 | 58 |
| 2868 | exonsampler: 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. | 4.8 | 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. | 6.5 | 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. | 2.4 | 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. | 3.9 | 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. | 2.1 | 3 |
| 2873 | Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. <i>Nature Communications</i> , 2014, 5, 4784. | 12.8 | 118 |
| 2874 | Preparation and Evaluation of ^{99m} 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. | 5.0 | 15 |
| 2875 | Genomic resources and genetic diversity of captive lesser kudu (<i>Tragelaphus imberbis</i>). <i>Zoo Biology</i> , 2014, 33, 440-445. | 1.2 | 4 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 1.8 | 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. | 1.9 | 21 |
| 2879 | Merging of multi-string BWTs with applications. <i>Bioinformatics</i> , 2014, 30, 3524-3531. | 4.1 | 36 |
| 2880 | A Rapid Profiling Assay for Avian Leukosis Virus Subgroup E Proviruses in Chickens. <i>Avian Diseases</i> , 2014, 58, 34-38. | 1.0 | 2 |
| 2881 | RepARK de novo creation of repeat libraries from whole-genome NGS reads. <i>Nucleic Acids Research</i> , 2014, 42, e80-e80. | 14.5 | 67 |
| 2882 | Estimating the Population Mutation Rate from a de novo Assembled Bactrian Camel Genome and Cross-Species Comparison with Dromedary ESTs. <i>Journal of Heredity</i> , 2014, 105, 933-940. | 2.4 | 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. | 6.6 | 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. | 2.7 | 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. | 2.7 | 63 |
| 2886 | Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014, 46, 701-706. | 21.4 | 93 |
| 2887 | Analysis Considerations for Utilizing RNA-Seq to Characterize the Brain Transcriptome. <i>International Review of Neurobiology</i> , 2014, 116, 21-54. | 2.0 | 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. | 1.7 | 483 |
| 2889 | Evidence for the persistence of an active endogenous retrovirus (ERVE) in humans. <i>Genetica</i> , 2014, 142, 451-460. | 1.1 | 10 |
| 2890 | The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184. | 12.6 | 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. | 5.5 | 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. | 3.4 | 106 |
| 2893 | A survey of tools for variant analysis of next-generation genome sequencing data. <i>Briefings in Bioinformatics</i> , 2014, 15, 256-278. | 6.5 | 480 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2894 | Alternative splicing of the sheep MITF gene: Novel transcripts detectable in skin. <i>Gene</i> , 2014, 552, 165-175. | 2.2 | 21 |
| 2895 | De novo assembly and characterization of the complete chloroplast genome of radish (<i>Raphanus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock | 2.2 | 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. | 0.2 | 14 |
| 2897 | megaTALs: a rare-cleaving nuclease architecture for therapeutic genome engineering. <i>Nucleic Acids Research</i> , 2014, 42, 2591-2601. | 14.5 | 151 |
| 2898 | Evolution of the mir-181 microRNA family. <i>Computers in Biology and Medicine</i> , 2014, 52, 82-87. | 7.0 | 31 |
| 2899 | RNA-Seq for the identification of novel Mediator transcripts in endothelial progenitor cells. <i>Gene</i> , 2014, 547, 98-105. | 2.2 | 10 |
| 2900 | The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857. | 21.4 | 225 |
| 2901 | Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343. | 12.6 | 348 |
| 2902 | The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362. | 27.8 | 725 |
| 2903 | Efficient de novo assembly of highly heterozygous genomes from whole-genome shotgun short reads. <i>Genome Research</i> , 2014, 24, 1384-1395. | 5.5 | 1,000 |
| 2904 | <i>CYP1B1</i> Gene Mutations Causing Primary Congenital Glaucoma in Tunisia. <i>Annals of Human Genetics</i> , 2014, 78, 255-263. | 0.8 | 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. | 6.2 | 54 |
| 2906 | Proliferation of cells with HIV integrated into cancer genes contributes to persistent infection. <i>Science</i> , 2014, 345, 570-573. | 12.6 | 573 |
| 2907 | circBase: a database for circular RNAs. <i>Rna</i> , 2014, 20, 1666-1670. | 3.5 | 1,417 |
| 2908 | An integrated algorithm for local sequence alignment. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2014, 3, 1. | 2.1 | 5 |
| 2909 | MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. <i>BMC Bioinformatics</i> , 2014, 15, 224. | 2.6 | 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. | 2.6 | 55 |
| 2911 | Synthesis of 53 tissue and cell line expression QTL datasets reveals master eQTLs. <i>BMC Genomics</i> , 2014, 15, 532. | 2.8 | 49 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2912 | A comprehensive analysis of piRNAs from adult human testis and their relationship with genes and mobile elements. BMC Genomics, 2014, 15, 545. | 2.8 | 105 |
| 2913 | An integrated genomic and metabolomic framework for cell wall biology in rice. BMC Genomics, 2014, 15, 596. | 2.8 | 26 |
| 2914 | A Bead-based Normalization for Uniform Sequencing depth (BeNUS) protocol for multi-samples sequencing exemplified by HLA-B. BMC Genomics, 2014, 15, 645. | 2.8 | 29 |
| 2915 | The Babesia bovis gene and promoter model: an update from full-length EST analysis. BMC Genomics, 2014, 15, 678. | 2.8 | 8 |
| 2916 | The American cranberry: first insights into the whole genome of a species adapted to bog habitat. BMC Plant Biology, 2014, 14, 165. | 3.6 | 105 |
| 2917 | Identification of G protein-coupled receptors in Schistosoma haematobium and S. mansoni by comparative genomics. Parasites and Vectors, 2014, 7, 242. | 2.5 | 37 |
| 2918 | De novo transcriptome sequencing and sequence analysis of the malaria vector Anopheles sinensis (Diptera: Culicidae). Parasites and Vectors, 2014, 7, 314. | 2.5 | 29 |
| 2919 | Corset: enabling differential gene expression analysis for de novoassembled transcriptomes. Genome Biology, 2014, 15, 410. | 8.8 | 427 |
| 2920 | A genome-wide CNV analysis of schizophrenia reveals a potential role for a multiple-hit model. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 619-626. | 1.7 | 25 |
| 2921 | The Architecture of a Scrambled Genome Reveals Massive Levels of Genomic Rearrangement during Development. Cell, 2014, 158, 1187-1198. | 28.9 | 152 |
| 2922 | Genome-wide transcriptional changes of ramie (Boehmeria nivea L. Gaud) in response to root-lesion nematode infection. Gene, 2014, 552, 67-74. | 2.2 | 30 |
| 2923 | Characterizing regions in the human genome unmappable by next-generation-sequencing at the read length of 1000 bases. Computational Biology and Chemistry, 2014, 53, 108-117. | 2.3 | 16 |
| 2924 | Heterochromatin Controls $\text{H}^3\text{H}2\text{A}$ Localization in Neurospora crassa. Eukaryotic Cell, 2014, 13, 990-1000. | 3.4 | 26 |
| 2925 | Multiple Groups of Endogenous Epsilon-Like Retroviruses Conserved across Primates. Journal of Virology, 2014, 88, 12464-12471. | 3.4 | 15 |
| 2926 | Hi-C Analysis in Arabidopsis Identifies the KNOT, a Structure with Similarities to the flamenco Locus of Drosophila. Molecular Cell, 2014, 55, 678-693. | 9.7 | 264 |
| 2927 | CEM-Designer: Design of custom expression microarrays in the post-ENCODE Era. Journal of Biotechnology, 2014, 189, 154-156. | 3.8 | 2 |
| 2928 | Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. Science, 2014, 346, 251-256. | 12.6 | 962 |
| 2929 | Development and characterization of a new 12-plex ChrX miniSTR system. International Journal of Legal Medicine, 2014, 128, 595-598. | 2.2 | 8 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2930 | Plant systems biology: insights, advances and challenges. <i>Planta</i> , 2014, 240, 33-54. | 3.2 | 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. | 1.2 | 2 |
| 2932 | A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788. | 12.6 | 1,479 |
| 2933 | Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721. | 12.6 | 542 |
| 2934 | A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. <i>Genome Biology</i> , 2014, 15, R34. | 9.6 | 242 |
| 2935 | Multicilin drives centriole biogenesis via E2f proteins. <i>Genes and Development</i> , 2014, 28, 1461-1471. | 5.9 | 130 |
| 2936 | Lacking alignments? The next-generation sequencing mapper segemehl revisited. <i>Bioinformatics</i> , 2014, 30, 1837-1843. | 4.1 | 105 |
| 2937 | Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539. | 3.9 | 241 |
| 2938 | The Chlamydomonas genome project: a decade on. <i>Trends in Plant Science</i> , 2014, 19, 672-680. | 8.8 | 145 |
| 2939 | An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841. | 17.5 | 1,664 |
| 2940 | Genome editing assessment using CRISPR Genome Analyzer (CRISPR-GA). <i>Bioinformatics</i> , 2014, 30, 2968-2970. | 4.1 | 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. | 8.9 | 15 |
| 2942 | Rewiring Host Lipid Metabolism by Large Viruses Determines the Fate of <i>Emiliana huxleyi</i> , a Bloom-Forming Alga in the Ocean. <i>Plant Cell</i> , 2014, 26, 2689-2707. | 6.6 | 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. | 2.8 | 5 |
| 2944 | RNA-seq analysis identifies an intricate regulatory network controlling cluster root development in white lupin. <i>BMC Genomics</i> , 2014, 15, 230. | 2.8 | 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. | 2.8 | 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. | 2.8 | 12 |
| 2947 | XSAnno: a framework for building ortholog models in cross-species transcriptome comparisons. <i>BMC Genomics</i> , 2014, 15, 343. | 2.8 | 27 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 2948 | GAP-Seq: a method for identification of DNA palindromes. BMC Genomics, 2014, 15, 394. | 2.8 | 10 |
| 2949 | Predicting the fungal CUG codon translation with Bagheera. BMC Genomics, 2014, 15, 411. | 2.8 | 18 |
| 2950 | A novel approach to identify driver genes involved in androgen-independent prostate cancer. Molecular Cancer, 2014, 13, 120. | 19.2 | 53 |
| 2951 | Novel principles of gamma-retroviral insertional transcription activation in murine leukemia virus-induced end-stage tumors. Retrovirology, 2014, 11, 36. | 2.0 | 21 |
| 2952 | Aptaligner: Automated Software for Aligning Pseudorandom DNA X-Aptamers from Next-Generation Sequencing Data. Biochemistry, 2014, 53, 3523-3525. | 2.5 | 19 |
| 2953 | Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. Environmental Microbiology Reports, 2014, 6, 640-655. | 2.4 | 36 |
| 2954 | Novel galanin receptors in teleost fish: Identification, expression and regulation by sex steroids. General and Comparative Endocrinology, 2014, 205, 109-120. | 1.8 | 24 |
| 2955 | Sequencing of the chloroplast genomes of cytoplasmic male-sterile and male-fertile lines of soybean and identification of polymorphic markers. Plant Science, 2014, 229, 208-214. | 3.6 | 12 |
| 2956 | Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. Science, 2014, 345, 950-953. | 12.6 | 2,089 |
| 2957 | Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. DNA Research, 2014, 21, 169-181. | 3.4 | 201 |
| 2958 | Loss of oncogenic Notch1 with resistance to a PI3K inhibitor in T-cell leukaemia. Nature, 2014, 513, 512-516. | 27.8 | 60 |
| 2959 | Get your high-quality low-cost genome sequence. Trends in Plant Science, 2014, 19, 288-291. | 8.8 | 33 |
| 2960 | The heterothallic sugarbeet pathogen <i>Cercospora beticola</i> contains exon fragments of both MAT genes that are homogenized by concerted evolution. Fungal Genetics and Biology, 2014, 62, 43-54. | 2.1 | 15 |
| 2961 | Molecular characterization and expression analysis of the small GTPase ROP members expressed in laticifers of the rubber tree (<i>Hevea brasiliensis</i>). Plant Physiology and Biochemistry, 2014, 74, 193-204. | 5.8 | 4 |
| 2962 | No evidence of clonal dominance after transplant of HOXB4-expanded cord blood cells in a nonhuman primate model. Experimental Hematology, 2014, 42, 497-504. | 0.4 | 2 |
| 2963 | Angiosperm Phylogeny Based on 18S/26S rDNA Sequence Data: Constructing a Large Data Set Using Next-Generation Sequence Data. International Journal of Plant Sciences, 2014, 175, 613-650. | 1.3 | 24 |
| 2964 | Genome-Wide Analysis of Heat-Sensitive Alternative Splicing in <i>Physcomitrella patens</i> . Plant Physiology, 2014, 165, 826-840. | 4.8 | 119 |
| 2965 | A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713. | 21.4 | 1,159 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 2966 | Compressive biological sequence analysis and archival in the era of high-throughput sequencing technologies. <i>Briefings in Bioinformatics</i> , 2014, 15, 390-406. | 6.5 | 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. | 2.9 | 207 |
| 2968 | Improving transcriptome construction in non-model organisms: integrating manual and automated gene definition in <i>Emiliania huxleyi</i> . <i>BMC Genomics</i> , 2014, 15, 148. | 2.8 | 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. | 5.7 | 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. | 3.6 | 13 |
| 2971 | BIMA V3: an aligner customized for mate pair library sequencing. <i>Bioinformatics</i> , 2014, 30, 1627-1629. | 4.1 | 80 |
| 2972 | The development of specific SNP markers for chromosome 14 in cotton using next-generation sequencing. <i>Plant Breeding</i> , 2014, 133, 256-261. | 1.9 | 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. | 1.8 | 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. | 8.5 | 21 |
| 2975 | Gene duplication followed by exon structure divergence substitutes for alternative splicing in zebrafish. <i>Gene</i> , 2014, 546, 271-276. | 2.2 | 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 | 3.8 | 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. | 2.5 | 87 |
| 2978 | Integrative workflows for metagenomic analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 70. | 3.7 | 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. | 2.3 | 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. | 0.5 | 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. | 2.8 | 15 |
| 2983 | Jitterbug: somatic and germline transposon insertion detection at single-nucleotide resolution. <i>BMC Genomics</i> , 2015, 16, 768. | 2.8 | 31 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 2984 | High performance computing of a fusion gene detection pipeline on the K computer. , 2015, , . | | 3 |
| 2985 | Linkage disequilibrium network analysis (<scp>LD</scp>na) gives a global view of chromosomal inversions, local adaptation and geographic structure. Molecular Ecology Resources, 2015, 15, 1031-1045. | 4.8 | 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 <i>Blattabacterium cuenoti&i> Inhabiting the Fat Bodies of Cockroaches. Microbes and Environments, 2015, 30, 208-220. | 1.6 | 14 |
| 2988 | ImmuSort, a database on gene plasticity and electronic sorting for immune cells. Scientific Reports, 2015, 5, 10370. | 3.3 | 36 |
| 2989 | Mutational spectrum of myeloid malignancies with inv(3)/t(3;3) reveals a predominant involvement of RAS/RTK signaling pathways. Blood, 2015, 125, 133-139. | 1.4 | 86 |
| 2990 | Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. Npj Biofilms and Microbiomes, 2015, 1, 15007. | 6.4 | 82 |
| 2991 | Living without DAT: Loss and compensation of the dopamine transporter gene in sauropsids (birds and) Tj ETQq1 1.0,784314,rgBT /Ove | 3.3 | 10 |
| 2992 | Entropy-Scaling Search of Massive Biological Data. Cell Systems, 2015, 1, 130-140. | 6.2 | 64 |
| 2993 | Lactococcus garvieae: a small bacteria and a big data world. Health Information Science and Systems, 2015, 3, S5. | 5.2 | 8 |
| 2994 | The fate of recent duplicated genes following a fourth-round whole genome duplication in a tetraploid fish, common carp (Cyprinus carpio). Scientific Reports, 2015, 5, 8199. | 3.3 | 60 |
| 2995 | Phylogenetic and genomic diversity in isolates from the globally distributed Acinetobacter baumannii ST25 lineage. Scientific Reports, 2015, 5, 15188. | 3.3 | 93 |
| 2996 | Red clover (Trifolium pratense L.) draft genome provides a platform for trait improvement. Scientific Reports, 2015, 5, 17394. | 3.3 | 136 |
| 2997 | Population genomic datasets describing the post-vaccine evolutionary epidemiology of Streptococcus pneumoniae. Scientific Data, 2015, 2, 150058. | 5.3 | 67 |
| 2998 | Southernâ€œSequencing: A Robust Screening Approach for Molecular Characterization of Genetically Modified Crops. Plant Genome, 2015, 8, eplantgenome2014.08.0037. | 2.8 | 65 |
| 2999 | RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. Scientific Reports, 2015, 5, 8365. | 3.3 | 2,080 |
| 3000 | Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, Hypothenemus hampei. Scientific Reports, 2015, 5, 12525. | 3.3 | 60 |
| 3001 | Generation and Analysis of Microbial Metatranscriptomes. , 2015, , 2.4.5-1-2.4.5-19. | | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3002 | Defining the Schistosoma haematobium kinome enables the prediction of essential kinases as anti-schistosome drug targets. Scientific Reports, 2015, 5, 17759. | 3.3 | 37 |
| 3003 | Sequencing of plant genomes – a review. Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 2015, 39, 361-376. | 2.1 | 20 |
| 3004 | Comprehensive assembly of novel transcripts from unmapped human RNA-seq data and their association with cancer. Molecular Systems Biology, 2015, 11, 826. | 7.2 | 18 |
| 3005 | TRUFA: A User-Friendly Web Server for <i>de novo</i> RNA-seq Analysis Using Cluster Computing. Evolutionary Bioinformatics, 2015, 11, EBO.S23873. | 1.2 | 37 |
| 3006 | Transcriptome Analysis in Domesticated Species: Challenges and Strategies. Bioinformatics and Biology Insights, 2015, 9S4, BBI.S29334. | 2.0 | 17 |
| 3007 | Advanced Applications of RNA Sequencing and Challenges. Bioinformatics and Biology Insights, 2015, 9s1, BBI.S28991. | 2.0 | 178 |
| 3008 | Resequencing of the common marmoset genome improves genome assemblies and gene-coding sequence analysis. Scientific Reports, 2015, 5, 16894. | 3.3 | 32 |
| 3009 | No association between HPV positive breast cancer and expression of human papilloma viral transcripts. Scientific Reports, 2015, 5, 18081. | 3.3 | 21 |
| 3010 | Data in support of genome-wide identification of lineage-specific genes within Caenorhabditis elegans. Data in Brief, 2015, 4, 595-601. | 1.0 | 3 |
| 3011 | Evolutionary conservation and function of the human embryonic stem cell specific miR-302/367 cluster. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 16, 83-98. | 1.0 | 20 |
| 3012 | Transcriptional profiling of predator-induced phenotypic plasticity in Daphnia pulex. Frontiers in Zoology, 2015, 12, 18. | 2.0 | 32 |
| 3013 | The Haemonchus contortus kinome - a resource for fundamental molecular investigations and drug discovery. Parasites and Vectors, 2015, 8, 623. | 2.5 | 14 |
| 3014 | Discovery and characterization of <i>Alu</i> repeat sequences via precise local read assembly. Nucleic Acids Research, 2015, 43, gkv1089. | 14.5 | 31 |
| 3015 | Sequence Analysis and Characterization of Active Human <i>Alu</i> subfamilies Based on the 1000 Genomes Pilot Project. Genome Biology and Evolution, 2015, 7, evv167. | 2.5 | 60 |
| 3016 | Fusion transcript loci share many genomic features with non-fusion loci. BMC Genomics, 2015, 16, 1021. | 2.8 | 16 |
| 3017 | A human 3'UTR clone collection to study post-transcriptional gene regulation. BMC Genomics, 2015, 16, 1036. | 2.8 | 7 |
| 3018 | LOTUS-DB: an integrative and interactive database for Nelumbo nucifera study. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav023. | 3.0 | 18 |
| 3019 | dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav052-bav052. | 3.0 | 13 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 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. | 2.3 | 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. | 1.2 | 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. | 2.3 | 88 |
| 3023 | Eco-genomic analysis of the poleward range expansion of the wasp spider <i>A. rigoiebruennichi</i> shows rapid adaptation and genomic admixture. <i>Global Change Biology</i> , 2015, 21, 4320-4332. | 9.5 | 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. | 3.9 | 20 |
| 3025 | Regulation of flowering time by the histone deacetylase <i>HDA5</i> in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 82, 925-936. | 5.7 | 94 |
| 3026 | A host plant genome (<i>Zizania latifolia</i>) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609. | 5.7 | 67 |
| 3027 | Exploring the tertiary gene pool of bread wheat: sequence assembly and analysis of chromosome 5M ^g of <i>Aegilops geniculata</i> . <i>Plant Journal</i> , 2015, 84, 733-746. | 5.7 | 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. | 2.8 | 11 |
| 3029 | misFinder: identify mis-assemblies in an unbiased manner using reference and paired-end reads. <i>BMC Bioinformatics</i> , 2015, 16, 386. | 2.6 | 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. | 2.8 | 206 |
| 3032 | Generation of a de novo transcriptome from equine lamellar tissue. <i>BMC Genomics</i> , 2015, 16, 739. | 2.8 | 14 |
| 3033 | Characterization and fine mapping of a novel barley Stage Green-Revertible Albino Gene (HvSGRA) by Bulk Segregant Analysis based on SSR assay and Specific Length Amplified Fragment Sequencing. <i>BMC Genomics</i> , 2015, 16, 838. | 2.8 | 44 |
| 3034 | Functionally conserved enhancers with divergent sequences in distant vertebrates. <i>BMC Genomics</i> , 2015, 16, 882. | 2.8 | 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. | 2.8 | 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. | 2.8 | 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. | 3.6 | 51 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3038 | Differential expression analysis of human endogenous retroviruses based on ENCODE RNA-seq data. BMC Medical Genomics, 2015, 8, 71. | 1.5 | 20 |
| 3039 | Gene activity in primary T cells infected with HIV89.6: intron retention and induction of genomic repeats. Retrovirology, 2015, 12, 79. | 2.0 | 40 |
| 3040 | Comparative genomics of <i>Steinernema</i> reveals deeply conserved gene regulatory networks. Genome Biology, 2015, 16, 200. | 8.8 | 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. Biotechnology for Biofuels, 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. Epigenetics and Chromatin, 2015, 8, 32. | 3.9 | 55 |
| 3043 | JAFFA: High sensitivity transcriptome-focused fusion gene detection. Genome Medicine, 2015, 7, 43. | 8.2 | 132 |
| 3044 | Dp412e: a novel human embryonic dystrophin isoform induced by BMP4 in early differentiated cells. Skeletal Muscle, 2015, 5, 40. | 4.2 | 28 |
| 3045 | Strong spurious transcription likely contributes to DNA insert bias in typical metagenomic clone libraries. Microbiome, 2015, 3, 22. | 11.1 | 25 |
| 3046 | Draft Genome Sequence of <i>Mycobacterium neworleansense</i> Strain ATCC 49404 T. Genome Announcements, 2015, 3, . | 0.8 | 0 |
| 3047 | High-throughput monitoring of integration site clonality in preclinical and clinical gene therapy studies. Molecular Therapy - Methods and Clinical Development, 2015, 2, 14061. | 4.1 | 8 |
| 3048 | Discovering All Transcriptome Single-Nucleotide Polymorphisms and Scanning for Selection Signatures in Ducks (<i>Anas platyrhynchos</i>). Evolutionary Bioinformatics, 2015, 11s1, EBO.S21545. | 1.2 | 5 |
| 3049 | Identification and Expression Analysis of Ribosome Biogenesis Factor Co-orthologs in <i>Solanum lycopersicum</i> . Bioinformatics and Biology Insights, 2015, 9, BBI.S20751. | 2.0 | 62 |
| 3050 | The sequenced rat brain transcriptome – its use in identifying networks predisposing alcohol consumption. FEBS Journal, 2015, 282, 3556-3578. | 4.7 | 52 |
| 3051 | Acid sensitivity of the spinal dorsal root ganglia C-fiber nociceptors innervating the guinea pig esophagus. Neurogastroenterology and Motility, 2015, 27, 865-874. | 3.0 | 15 |
| 3052 | GraP: platform for functional genomics analysis of <i>Gossypium raimondii</i> . Database: the Journal of Biological Databases and Curation, 2015, 2015, bav047. | 3.0 | 14 |
| 3053 | Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. G3: Genes, Genomes, Genetics, 2015, 5, 629-638. | 1.8 | 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. Journal of Fish Biology, 2015, 87, 360-370. | 1.6 | 15 |
| 3055 | FARE-CAFE: a database of functional and regulatory elements of cancer-associated fusion events. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav086. | 3.0 | 11 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3056 | A synteny-based draft genome sequence of the forage grass <i>Lolium perenne</i> . Plant Journal, 2015, 84, 816-826. | 5.7 | 166 |
| 3057 | Draft Genome Sequence of Mycobacterium lentiflavum CSUR P1491. Genome Announcements, 2015, 3, . | 0.8 | 1 |
| 3058 | Kiwifruit Information Resource (KIR): a comparative platform for kiwifruit genomics. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav113. | 3.0 | 14 |
| 3059 | An Introduction to Genome Annotation. Current Protocols in Bioinformatics, 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. Cancers, 2015, 7, 2217-2235. | 3.7 | 27 |
| 3061 | Transcriptome Sequencing of Lima Bean (Phaseolus lunatus) to Identify Putative Positive Selection in Phaseolus and Legumes. International Journal of Molecular Sciences, 2015, 16, 15172-15187. | 4.1 | 13 |
| 3062 | Analysis of pollen-specific alternative splicing in <i>Arabidopsis thaliana</i> via semi-quantitative PCR. PeerJ, 2015, 3, e919. | 2.0 | 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. | 0.2 | 41 |
| 3064 | Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. Plant Genome, 2015, 8, eplantgenome2015.06.0045. | 2.8 | 10 |
| 3065 | Identification of Ramie Genes in Response to Pratylenchus coffeae Infection Challenge by Digital Gene Expression Analysis. International Journal of Molecular Sciences, 2015, 16, 21989-22007. | 4.1 | 26 |
| 3066 | Diversity of acid stress resistant variants of Listeria monocytogenes and the potential role of ribosomal protein S21 encoded by rpsU. Frontiers in Microbiology, 2015, 6, 422. | 3.5 | 35 |
| 3067 | Spatial and temporal dynamics of virus occurrence in two freshwater lakes captured through metagenomic analysis. Frontiers in Microbiology, 2015, 6, 960. | 3.5 | 69 |
| 3068 | The role of biofilms as environmental reservoirs of antibiotic resistance. Frontiers in Microbiology, 2015, 6, 1216. | 3.5 | 321 |
| 3069 | Integrated Omics™, Targeted Metabolite and Single-cell Analyses of Arctic Snow Algae Functionality and Adaptability. Frontiers in Microbiology, 2015, 6, 1323. | 3.5 | 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. | 1.9 | 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. | 2.5 | 19 |
| 3073 | Developmental Genetic Mechanisms of C4 Syndrome Based on Transcriptome Analysis of C3 Cotyledons and C4 Assimilating Shoots in Haloxylon ammodendron. PLoS ONE, 2015, 10, e0117175. | 2.5 | 38 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 3074 | De Novo Origin of VCY2 from Autosome to Y-Transposed Amplicon. PLoS ONE, 2015, 10, e0119651. | 2.5 | 5 |
| 3075 | Transcriptome Assembly, Gene Annotation and Tissue Gene Expression Atlas of the Rainbow Trout. PLoS ONE, 2015, 10, e0121778. | 2.5 | 53 |
| 3076 | Genome-Wide Identification, Characterization and Evolutionary Analysis of Long Intergenic Noncoding RNAs in Cucumber. PLoS ONE, 2015, 10, e0121800. | 2.5 | 98 |
| 3077 | Identification and Functional Analysis of Genome Mutations in a Fluoride-Resistant <i>Streptococcus mutans</i> Strain. PLoS ONE, 2015, 10, e0122630. | 2.5 | 52 |
| 3078 | Influence of a Non-Hospital Medical Care Facility on Antimicrobial Resistance in Wastewater. PLoS ONE, 2015, 10, e0122635. | 2.5 | 36 |
| 3079 | Comparative Genome Analyses of <i>Serratia marcescens</i> FS14 Reveals Its High Antagonistic Potential. PLoS ONE, 2015, 10, e0123061. | 2.5 | 51 |
| 3080 | ALDB: A Domestic-Animal Long Noncoding RNA Database. PLoS ONE, 2015, 10, e0124003. | 2.5 | 90 |
| 3081 | Annotation of the Protein Coding Regions of the Equine Genome. PLoS ONE, 2015, 10, e0124375. | 2.5 | 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. | 2.5 | 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. | 2.5 | 6 |
| 3084 | Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274. | 3.2 | 83 |
| 3085 | Nmf9 Encodes a Highly Conserved Protein Important to Neurological Function in Mice and Flies. PLoS Genetics, 2015, 11, e1005344. | 3.5 | 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. | 3.5 | 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. | 3.0 | 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. | 3.0 | 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. | 2.5 | 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. | 2.5 | 36 |
| 3091 | BCD: A Database of Bat Genomes. PLoS ONE, 2015, 10, e0131296. | 2.5 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 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. | 2.5 | 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. | 2.5 | 45 |
| 3094 | Improving the Annotation of <i>Arabidopsis lyrata</i> Using RNA-Seq Data. PLoS ONE, 2015, 10, e0137391. | 2.5 | 82 |
| 3095 | Whole Blood Gene Expression Profiles of Patients with a Past Aneurysmal Subarachnoid Hemorrhage. PLoS ONE, 2015, 10, e0139352. | 2.5 | 11 |
| 3096 | Small RNA Sequencing Uncovers New miRNAs and moRNAs Differentially Expressed in Normal and Primary Myelofibrosis CD34+ Cells. PLoS ONE, 2015, 10, e0140445. | 2.5 | 20 |
| 3097 | A catalogue of novel bovine long noncoding RNA across 18 tissues. PLoS ONE, 2015, 10, e0141225. | 2.5 | 130 |
| 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. PLoS ONE, 2015, 10, e0143665. | 2.5 | 29 |
| 3099 | Using Next Generation Sequencing for Multiplexed Trait-Linked Markers in Wheat. PLoS ONE, 2015, 10, e0143890. | 2.5 | 28 |
| 3100 | Investigation of a Quadruplex-Forming Repeat Sequence Highly Enriched in <i>Xanthomonas</i> and <i>Nostoc</i> sp.. PLoS ONE, 2015, 10, e0144275. | 2.5 | 12 |
| 3101 | Transcript Quantification by RNA-Seq Reveals Differentially Expressed Genes in the Red and Yellow Fruits of <i>Fragaria vesca</i> . PLoS ONE, 2015, 10, e0144356. | 2.5 | 46 |
| 3102 | Application of a Novel "Pan-Genome"-Based Strategy for Assigning RNAseq Transcript Reads to <i>Staphylococcus aureus</i> Strains. PLoS ONE, 2015, 10, e0145861. | 2.5 | 9 |
| 3103 | Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy. PLoS ONE, 2015, 10, e0145176. | 2.5 | 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. | 3.6 | 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. | 3.6 | 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. | 3.6 | 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 | 0.2 | 15 |
| 3108 | Long Read Alignment with Parallel MapReduce Cloud Platform. <i>BioMed Research International</i> , 2015, 2015, 1-13. | 1.9 | 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. | 1.9 | 26 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3110 | Evaluation and Application of the Strand-Specific Protocol for Next-Generation Sequencing. BioMed Research International, 2015, 2015, 1-8. | 1.9 | 11 |
| 3111 | <i>De Novo</i> Transcriptome Sequencing of the Orange-Fleshed Sweet Potato and Analysis of Differentially Expressed Genes Related to Carotenoid Biosynthesis. International Journal of Genomics, 2015, 2015, 1-10. | 1.6 | 27 |
| 3112 | A Complex Genome-MicroRNA Interplay in Human Mitochondria. BioMed Research International, 2015, 2015, 1-13. | 1.9 | 37 |
| 3113 | Novel RNA variants in colorectal cancers. Oncotarget, 2015, 6, 36587-36602. | 1.8 | 15 |
| 3114 | Identification of an AVP-NPII mutation within the AVP moiety in a family with neurohypophyseal diabetes insipidus: review of the literature. Hormones, 2015, 14, 442-6. | 1.9 | 2 |
| 3115 | A Unified Single Nucleotide Polymorphism Map of Sunflower (<i>Helianthus annuus</i> L.) Derived from Current Genomic Resources. Crop Science, 2015, 55, 1696-1702. | 1.8 | 16 |
| 3116 | Structural variation discovery in the cancer genome using next generation sequencing: Computational solutions and perspectives. Oncotarget, 2015, 6, 5477-5489. | 1.8 | 33 |
| 3117 | Comprehensive analyses of genomes, transcriptomes and metabolites of neem tree. PeerJ, 2015, 3, e1066. | 2.0 | 35 |
| 3118 | The exonuclease Nibbler regulates age-associated traits and modulates piRNA length in <i>Drosophila</i> . Aging Cell, 2015, 14, 443-452. | 6.7 | 58 |
| 3119 | Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. MBio, 2015, 6, e00306-15. | 4.1 | 380 |
| 3120 | TUT 7 controls the fate of precursor microRNAs by using three different uridylation mechanisms. EMBO Journal, 2015, 34, 1801-1815. | 7.8 | 97 |
| 3121 | Development of a high-resolution NGS-based HLA-typing and analysis pipeline. Nucleic Acids Research, 2015, 43, e70-e70. | 14.5 | 77 |
| 3122 | Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. Bioinformatics and Biology Insights, 2015, 9, BBI.S12462. | 2.0 | 317 |
| 3123 | Structural basis for retroviral integration into nucleosomes. Nature, 2015, 523, 366-369. | 27.8 | 133 |
| 3124 | A Comprehensive Transcriptomic and Proteomic Analysis of Hydra Head Regeneration. Molecular Biology and Evolution, 2015, 32, 1928-1947. | 8.9 | 106 |
| 3125 | Recurrent somatic mutations in regulatory regions of human cancer genomes. Nature Genetics, 2015, 47, 710-716. | 21.4 | 225 |
| 3126 | Secondary structure-based analysis of mouse brain small RNA sequences obtained by using next-generation sequencing. Genomics, 2015, 106, 122-128. | 2.9 | 5 |
| 3127 | Oxytocin receptor gene sequences in owl monkeys and other primates show remarkable interspecific regulatory and protein coding variation. Molecular Phylogenetics and Evolution, 2015, 91, 160-177. | 2.7 | 11 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3128 | Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. <i>Nature Communications</i> , 2015, 6, 7256. | 12.8 | 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. | 8.9 | 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. | 2.5 | 49 |
| 3131 | Inferring bona fide transfrags in RNA-Seq derived-transcriptome assemblies of non-model organisms. <i>BMC Bioinformatics</i> , 2015, 16, 58. | 2.6 | 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. | 2.8 | 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. | 2.0 | 26 |
| 3134 | A Python package for parsing, validating, mapping and formatting sequence variants using HGVS nomenclature. <i>Bioinformatics</i> , 2015, 31, 268-270. | 4.1 | 74 |
| 3135 | Selecting Specific PCR Primers with MFEprimer. <i>Methods in Molecular Biology</i> , 2015, 1275, 201-213. | 0.9 | 20 |
| 3136 | RNA-Seq: Improving Our Understanding of Retinal Biology and Disease. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a017152. | 6.2 | 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. | 2.5 | 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. | 1.1 | 85 |
| 3139 | BatAlign: an incremental method for accurate alignment of sequencing reads. <i>Nucleic Acids Research</i> , 2015, 43, e107-e107. | 14.5 | 9 |
| 3140 | Transposable element detection from whole genome sequence data. <i>Mobile DNA</i> , 2015, 6, 24. | 3.6 | 139 |
| 3141 | Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. <i>Genome Biology and Evolution</i> , 2015, 7, evv172. | 2.5 | 22 |
| 3142 | The molecular evolution of spiggin nesting glue in sticklebacks. <i>Molecular Ecology</i> , 2015, 24, 4474-4488. | 3.9 | 9 |
| 3143 | The Genome of the "Great Speciator" Provides Insights into Bird Diversification. <i>Genome Biology and Evolution</i> , 2015, 7, 2680-2691. | 2.5 | 55 |
| 3144 | SuRankCo: supervised ranking of contigs in de novo assemblies. <i>BMC Bioinformatics</i> , 2015, 16, 240. | 2.6 | 13 |
| 3145 | Scrutinizing the immune defence inventory of <i>Camponotus floridanus</i> applying total transcriptome sequencing. <i>BMC Genomics</i> , 2015, 16, 540. | 2.8 | 33 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3146 | The complete mitochondrial genome sequence of the green microalga <i>Lobosphaera</i> (<i>Parietochloris</i>) <i>incisa</i> reveals a new type of palindromic repetitive repeat. <i>BMC Genomics</i> , 2015, 16, 580. | 2.8 | 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. | 2.8 | 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. | 3.6 | 80 |
| 3149 | Exploiting single-molecule transcript sequencing for eukaryotic gene prediction. <i>Genome Biology</i> , 2015, 16, 184. | 8.8 | 148 |
| 3150 | Spatio-temporal regulation of circular RNA expression during porcine embryonic brain development. <i>Genome Biology</i> , 2015, 16, 245. | 8.8 | 422 |
| 3151 | Global Diversity Linesâ€œA Five-Continent Reference Panel of Sequenced <i>Drosophila melanogaster</i> Strains. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 593-603. | 1.8 | 124 |
| 3152 | Endogenous Small RNA Mediates Meiotic Silencing of a Novel DNA Transposon. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1949-1960. | 1.8 | 34 |
| 3153 | Unique transposon landscapes are pervasive across <i>Drosophila melanogaster</i> genomes. <i>Nucleic Acids Research</i> , 2015, 43, 10655-10672. | 14.5 | 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. | 7.1 | 329 |
| 3155 | A thesaurus of genetic variation for interrogation of repetitive genomic regions. <i>Nucleic Acids Research</i> , 2015, 43, e68-e68. | 14.5 | 5 |
| 3156 | The ReproGenomics Viewer: an integrative cross-species toolbox for the reproductive science community. <i>Nucleic Acids Research</i> , 2015, 43, W109-W116. | 14.5 | 46 |
| 3157 | High speed BLASTN: an accelerated MegaBLAST search tool. <i>Nucleic Acids Research</i> , 2015, 43, 7762-7768. | 14.5 | 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. | 1.3 | 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. | 2.5 | 45 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3164 | ScanIndel: a hybrid framework for indel detection via gapped alignment, split reads and de novo assembly. <i>Genome Medicine</i> , 2015, 7, 127. | 8.2 | 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. | 2.3 | 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. | 2.5 | 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. | 2.8 | 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 <i>Cryptocaryon irritans</i> . <i>Gene</i> , 2015, 556, 98-105. | 2.2 | 20 |
| 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. | 2.8 | 22 |
| 3171 | Genome assembly and annotation of a <i>Drosophila simulans</i> strain from Madagascar. <i>Molecular Ecology Resources</i> , 2015, 15, 372-381. | 4.8 | 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. | 3.9 | 13 |
| 3173 | Online Resources for Genomic Analysis Using High-Throughput Sequencing. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.top083667. | 0.3 | 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. | 2.1 | 141 |
| 3175 | Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2015, 9, 1928-1940. | 9.8 | 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. | 2.9 | 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. | 5.7 | 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. | 12.8 | 178 |
| 3179 | HIV-1 Integration Landscape during Latent and Active Infection. <i>Cell</i> , 2015, 160, 420-432. | 28.9 | 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. | 6.2 | 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. | 8.9 | 70 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 3.3 | 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. | 7.1 | 147 |
| 3184 | Studying Genome Heterogeneity within the Arbuscular Mycorrhizal Fungal Cytoplasm. <i>Genome Biology and Evolution</i> , 2015, 7, 505-521. | 2.5 | 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. | 4.8 | 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. | 3.6 | 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. | 5.7 | 149 |
| 3188 | Polymerase chain reaction-based serotyping of pathogenic bacteria in food. <i>Journal of Microbiological Methods</i> , 2015, 110, 18-26. | 1.6 | 25 |
| 3189 | Sustained Heterozygosity Across a Self-Incompatibility Locus in an Inbred Ascidian. <i>Molecular Biology and Evolution</i> , 2015, 32, 81-90. | 8.9 | 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. | 7.1 | 363 |
| 3191 | AmpliVar: Mutation Detection in High-Throughput Sequence from Amplicon-Based Libraries. <i>Human Mutation</i> , 2015, 36, 411-418. | 2.5 | 7 |
| 3192 | Nicotinic receptors in non-human primates: Analysis of genetic and functional conservation with humans. <i>Neuropharmacology</i> , 2015, 96, 263-273. | 4.1 | 14 |
| 3193 | A CRISPR/Cas9 Vector System for Tissue-Specific Gene Disruption in Zebrafish. <i>Developmental Cell</i> , 2015, 32, 756-764. | 7.0 | 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. | 2.9 | 25 |
| 3195 | Expression and regulation of long noncoding RNAs in TLR4 signaling in mouse macrophages. <i>BMC Genomics</i> , 2015, 16, 45. | 2.8 | 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. | 0.8 | 2 |
| 3197 | Single-nucleotide polymorphism identification and genotyping in <i>Camelina sativa</i> . <i>Molecular Breeding</i> , 2015, 35, 35. | 2.1 | 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. | 21.4 | 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. | 6.2 | 150 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3200 | Genome-wide characterization of developmental stage- and tissue-specific transcription factors in wheat. <i>BMC Genomics</i> , 2015, 16, 125. | 2.8 | 19 |
| 3201 | Gut microbiome development along the colorectal adenoma–carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528. | 12.8 | 1,062 |
| 3202 | Bridger: a new framework for de novo transcriptome assembly using RNA-seq data. <i>Genome Biology</i> , 2015, 16, 30. | 8.8 | 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. | 2.2 | 8 |
| 3204 | PAIDB v2.0: exploration and analysis of pathogenicity and resistance islands. <i>Nucleic Acids Research</i> , 2015, 43, D624-D630. | 14.5 | 139 |
| 3205 | A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. <i>PLoS Genetics</i> , 2015, 11, e1004850. | 3.5 | 76 |
| 3206 | Sex-Biased Expression of Young Genes in <i>Xenopus laevis</i> . <i>Cytogenetic and Genome Research</i> , 2015, 145, 265-277. | 1.1 | 4 |
| 3207 | Design and bioinformatics analysis of genome-wide CLIP experiments. <i>Nucleic Acids Research</i> , 2015, 43, 5263-5274. | 14.5 | 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>). <i>Plant Science</i> , 2015, 238, 188-197. | 3.6 | 14 |
| 3210 | Genetic Regulation of Bone Metabolism in the Chicken: Similarities and Differences to Mammalian Systems. <i>PLoS Genetics</i> , 2015, 11, e1005250. | 3.5 | 47 |
| 3211 | Quantitative Measurement of Immunoglobulins and Free Light Chains Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 8268-8274. | 6.5 | 27 |
| 3212 | Single-cell RNA-seq transcriptome analysis of linear and circular RNAs in mouse preimplantation embryos. <i>Genome Biology</i> , 2015, 16, 148. | 9.6 | 369 |
| 3213 | The barber's pole worm CAP protein superfamily – A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , 2015, 33, 1744-1754. | 11.7 | 16 |
| 3214 | Cypiripi: exact genotyping of <i>CYP2D6</i> using high-throughput sequencing data. <i>Bioinformatics</i> , 2015, 31, i27-i34. | 4.1 | 37 |
| 3215 | A high-density genetic map for P genome of <i>Agropyron Gaertn.</i> based on specific-locus amplified fragment sequencing (SLAF-seq). <i>Planta</i> , 2015, 242, 1335-1347. | 3.2 | 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 (Cetartiodactyla). <i>Gene</i> , 2015, 571, 271-278. | 2.2 | 8 |
| 3217 | Incl shufflons: Assembly issues in the next-generation sequencing era. <i>Plasmid</i> , 2015, 80, 111-117. | 1.4 | 30 |
| 3218 | A Revised Genome Assembly of the Region 5â² to Canine <i>SOX9</i> ; Includes the <i>RevSex</i> Orthologous Region. <i>Sexual Development</i> , 2015, 9, 155-161. | 2.0 | 10 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3219 | The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015, 21, 895-905. | 30.7 | 1,306 |
| 3220 | A piRNA-like small RNA interacts with and modulates p-ERM proteins in human somatic cells. <i>Nature Communications</i> , 2015, 6, 7316. | 12.8 | 88 |
| 3222 | Can We Identify Genes with Increased Phylogenetic Reliability?. <i>Systematic Biology</i> , 2015, 64, 824-837. | 5.6 | 80 |
| 3223 | Chromosome-Specific Painting in <i>Cucumis</i> Species Using Bulk Oligonucleotides. <i>Genetics</i> , 2015, 200, 771-779. | 2.9 | 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. <i>Cell Cycle</i> , 2015, 14, 2619-2633. | 2.6 | 16 |
| 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. | 2.5 | 67 |
| 3227 | Natural variation of the expression pattern of the segmentation gene even-skipped in melanogaster. <i>Developmental Biology</i> , 2015, 405, 173-181. | 2.0 | 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. | 3.5 | 29 |
| 3230 | Identification of agonists for a group of human odorant receptors. <i>Frontiers in Pharmacology</i> , 2015, 6, 35. | 3.5 | 37 |
| 3231 | Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327. | 2.8 | 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. | 2.1 | 22 |
| 3233 | Genome-wide identification of lineage-specific genes within <i>Caenorhabditis elegans</i> . <i>Genomics</i> , 2015, 106, 242-248. | 2.9 | 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. | 2.4 | 189 |
| 3235 | Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. <i>Scientific Reports</i> , 2015, 5, 11534. | 3.3 | 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. | 1.9 | 32 |
| 3237 | The radish genome and comprehensive gene expression profile of tuberous root formation and development. <i>Scientific Reports</i> , 2015, 5, 10835. | 3.3 | 154 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3238 | Numerous Transitions of Sex Chromosomes in Diptera. <i>PLoS Biology</i> , 2015, 13, e1002078. | 5.6 | 279 |
| 3239 | Biosequence Timeâ€“Frequency Processing: Pathogen Detection and Identification. <i>Applied and Numerical Harmonic Analysis</i> , 2015, , 65-85. | 0.3 | 0 |
| 3240 | A RESTful API for Accessing Microbial Community Data for MG-RAST. <i>PLoS Computational Biology</i> , 2015, 11, e1004008. | 3.2 | 83 |
| 3241 | Novel Transcription Factor Variants through RNA-Sequencing: The Importance of Being â€œAlternativeâ€. <i>International Journal of Molecular Sciences</i> , 2015, 16, 1755-1771. | 4.1 | 8 |
| 3242 | G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. <i>Nature Methods</i> , 2015, 12, 519-522. | 19.0 | 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. | 2.9 | 36 |
| 3244 | Haploinsufficiency of the miR-873/miR-876 microRNA cluster is associated with craniofacial abnormalities. <i>Gene</i> , 2015, 561, 95-100. | 2.2 | 15 |
| 3245 | The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76. | 8.8 | 330 |
| 3246 | Proteogenomic Analysis of <i>Trichophyton rubrum</i> Aided by RNA Sequencing. <i>Journal of Proteome Research</i> , 2015, 14, 2207-2218. | 3.7 | 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. | 17.5 | 1,064 |
| 3248 | Comparative transcriptome of rhizome and leaf in <i>Ligusticum Chuanxiong</i> . <i>Plant Systematics and Evolution</i> , 2015, 301, 2073-2085. | 0.9 | 9 |
| 3249 | Potassium stress growth characteristics and energetics in the haloarchaeon <i>Haloarcula marismortui</i> . <i>Extremophiles</i> , 2015, 19, 315-325. | 2.3 | 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. | 3.0 | 44 |
| 3251 | DRESS: dimensionality reduction for efficient sequence search. <i>Data Mining and Knowledge Discovery</i> , 2015, 29, 1280-1311. | 3.7 | 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. | 1.6 | 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. | 0.8 | 3 |
| 3254 | Cigarette smoke mediates epigenetic repression of miR-217 during esophageal adenocarcinogenesis. <i>Oncogene</i> , 2015, 34, 5548-5559. | 5.9 | 32 |
| 3255 | Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660. | 28.9 | 482 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3256 | Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <i>Salsola vermiculata</i> and tanshinone biosynthesis. Plant Journal, 2015, 82, 951-961. | 5.7 | 337 |
| 3257 | RIEMS: a software pipeline for sensitive and comprehensive taxonomic classification of reads from metagenomics datasets. BMC Bioinformatics, 2015, 16, 69. | 2.6 | 73 |
| 3258 | The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. BMC Genomics, 2015, 16, 143. | 2.8 | 9 |
| 3259 | Transcriptome characterization of three wild Chinese Vitis uncovers a large number of distinct disease related genes. BMC Genomics, 2015, 16, 223. | 2.8 | 23 |
| 3260 | Identification of novel fusion genes in lung cancer using breakpoint assembly of transcriptome sequencing data. Genome Biology, 2015, 16, 7. | 8.8 | 44 |
| 3261 | A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. Genome Biology, 2015, 16, 48. | 8.8 | 216 |
| 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. BMC Evolutionary Biology, 2015, 15, 62. | 3.2 | 57 |
| 3263 | BAP1 mutation is a frequent somatic event in peritoneal malignant mesothelioma. Journal of Translational Medicine, 2015, 13, 122. | 4.4 | 69 |
| 3264 | Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143. | 12.6 | 357 |
| 3265 | Dynamics of gene expression patterns during early development of the European seabass (<i>Dicentrarchus labrax</i>). Physiological Genomics, 2015, 47, 158-169. | 2.3 | 23 |
| 3266 | Genome sequence-independent identification of RNA editing sites. Nature Methods, 2015, 12, 347-350. | 19.0 | 102 |
| 3267 | Scrim: designing primers from transcriptome data. Molecular Ecology Resources, 2015, 15, 1415-1420. | 4.8 | 6 |
| 3268 | <i>Drosophila</i> Muller F Elements Maintain a Distinct Set of Genomic Properties Over 40 Million Years of Evolution. G3: Genes, Genomes, Genetics, 2015, 5, 719-740. | 1.8 | 84 |
| 3269 | Implications of <i>miR166</i> and <i>miR159</i> induction to the basal response mechanisms of an <i>Solanum tuberosum</i> subsp. <i>andigena</i> to salinity stress, predicted from network models in <i>Arabidopsis</i> . Genome, 2015, 58, 13-24. | 2.0 | 38 |
| 3270 | Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824. | 5.5 | 69 |
| 3271 | Elucidating the composition and conservation of the autophagy pathway in photosynthetic eukaryotes. Autophagy, 2015, 11, 701-715. | 9.1 | 79 |
| 3272 | Gender-specific postnatal demethylation and establishment of epigenetic memory. Genes and Development, 2015, 29, 923-933. | 5.9 | 83 |
| 3273 | Identification of a gene controlling variation in the salt tolerance of rapeseed (<i>Brassica napus</i> L.). Planta, 2015, 242, 313-326. | 3.2 | 45 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3274 | Faster sequence homology searches by clustering subsequences. <i>Bioinformatics</i> , 2015, 31, 1183-1190. | 4.1 | 64 |
| 3275 | BreakMer: detection of structural variation in targeted massively parallel sequencing data using kmers. <i>Nucleic Acids Research</i> , 2015, 43, e19-e19. | 14.5 | 161 |
| 3276 | CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. <i>BMC Genomics</i> , 2015, 16, 236. | 2.8 | 514 |
| 3277 | Diverse chitinases are invoked during the activity-dormancy transition in spruce. <i>Tree Genetics and Genomes</i> , 2015, 11, 1. | 1.6 | 16 |
| 3278 | The variation game: Cracking complex genetic disorders with NGS and omics data. <i>Methods</i> , 2015, 79-80, 18-31. | 3.8 | 22 |
| 3279 | HAlign: Fast multiple similar DNA/RNA sequence alignment based on the centre star strategy. <i>Bioinformatics</i> , 2015, 31, 2475-2481. | 4.1 | 136 |
| 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. | 14.5 | 61 |
| 3281 | Triticeae Resources in Ensembl Plants. <i>Plant and Cell Physiology</i> , 2015, 56, e3-e3. | 3.1 | 59 |
| 3282 | SNPfisher: tools for probing genetic variation in laboratory-reared zebrafish. <i>Development (Cambridge)</i> , 2015, 142, 1542-52. | 2.5 | 39 |
| 3283 | The BRAF Pseudogene Functions as a Competitive Endogenous RNA and Induces Lymphoma In Vivo. <i>Cell</i> , 2015, 161, 319-332. | 28.9 | 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. | 2.9 | 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. | 3.6 | 79 |
| 3286 | Transcriptome-wide identification of adenosine-to-inosine editing using the ICE-seq method. <i>Nature Protocols</i> , 2015, 10, 715-732. | 12.0 | 67 |
| 3287 | IDBA-MTP: A Hybrid Metatranscriptomic Assembler Based on Protein Information. <i>Journal of Computational Biology</i> , 2015, 22, 367-376. | 1.6 | 19 |
| 3288 | Woods: A fast and accurate functional annotator and classifier of genomic and metagenomic sequences. <i>Genomics</i> , 2015, 106, 1-6. | 2.9 | 34 |
| 3289 | Germline and somatic imprinting in the nonhuman primate highlights species differences in oocyte methylation. <i>Genome Research</i> , 2015, 25, 611-623. | 5.5 | 25 |
| 3290 | The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681. | 14.5 | 891 |
| 3291 | Identification of a Recently Active Mammalian SINE Derived from Ribosomal RNA. <i>Genome Biology and Evolution</i> , 2015, 7, 775-788. | 2.5 | 12 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 3.1 | 11 |
| 3293 | A novel locus of resistance to severe malaria in a region of ancient balancing selection. <i>Nature</i> , 2015, 526, 253-257. | 27.8 | 182 |
| 3294 | Viral metagenomics in drug-naïve, first-onset schizophrenia patients with prominent negative symptoms. <i>Psychiatry Research</i> , 2015, 229, 678-684. | 3.3 | 2 |
| 3295 | Gene panels and primers for next generation sequencing studies on neurodegenerative disorders. <i>Molecular and Cellular Toxicology</i> , 2015, 11, 89-143. | 1.7 | 32 |
| 3296 | Human Mpn1 promotes post-transcriptional processing and stability of U6atac. <i>FEBS Letters</i> , 2015, 589, 2417-2423. | 2.8 | 16 |
| 3297 | A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108. | 17.5 | 422 |
| 3298 | VISA - Vector Integration Site Analysis server: a web-based server to rapidly identify retroviral integration sites from next-generation sequencing. <i>BMC Bioinformatics</i> , 2015, 16, 212. | 2.6 | 37 |
| 3299 | The distribution and evolution of <i>Arabidopsis thaliana</i> cis natural antisense transcripts. <i>BMC Genomics</i> , 2015, 16, 444. | 2.8 | 8 |
| 3300 | MG-RAST, a Metagenomics Service for the Analysis of Microbial Community Structure and Function. <i>Springer Protocols</i> , 2015, , 69-87. | 0.3 | 4 |
| 3301 | Genetic mapping uncovers cis-regulatory landscape of RNA editing. <i>Nature Communications</i> , 2015, 6, 8194. | 12.8 | 76 |
| 3302 | microDuMIP: target-enrichment technique for microarray-based duplex molecular inversion probes. <i>Nucleic Acids Research</i> , 2015, 43, e28-e28. | 14.5 | 11 |
| 3303 | Discovering new biology through RNA-Seq. <i>Plant Physiology</i> , 2015, 169, pp.01081.2015. | 4.8 | 28 |
| 3304 | Rapid evolution of chemosensory receptor genes in a pair of sibling species of orchid bees (Apidae:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> | 3.2 | 56 |
| 3305 | Unravelling the genome of Holy basil: an "incomparable" "elixir of life" of traditional Indian medicine. <i>BMC Genomics</i> , 2015, 16, 413. | 2.8 | 60 |
| 3306 | The Evolution of Bony Vertebrate Enhancers at Odds with Their Coding Sequence Landscape. <i>Genome Biology and Evolution</i> , 2015, 7, 2333-2343. | 2.5 | 9 |
| 3307 | The essential gene set of a photosynthetic organism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6634-43. | 7.1 | 166 |
| 3308 | Comparative genome analysis of <i>Mycoplasma pneumoniae</i> . <i>BMC Genomics</i> , 2015, 16, 610. | 2.8 | 59 |
| 3309 | Metagenomic analysis of planktonic microbial consortia from a non-tidal urban-impacted segment of James River. <i>Standards in Genomic Sciences</i> , 2015, 10, 65. | 1.5 | 24 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3310 | GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. Conservation Genetics Resources, 2015, 7, 851-857. | 0.8 | 5 |
| 3311 | The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. Science, 2015, 350, 691-694. | 12.6 | 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 (<i>capra aegagrus</i>) and sequencing of goat breeds provide insight into genic basis of goat domestication. BMC Genomics, 2015, 16, 431. | 2.8 | 103 |
| 3314 | Transcriptional profiling provides insights into metronomic cyclophosphamide-activated, innate immune-dependent regression of brain tumor xenografts. BMC Cancer, 2015, 15, 375. | 2.6 | 18 |
| 3315 | Structural basis of head to head polyketide fusion by CorB. Chemical Science, 2015, 6, 6525-6536. | 7.4 | 20 |
| 3316 | BSPAT: a fast online tool for DNA methylation co-occurrence pattern analysis based on high-throughput bisulfite sequencing data. BMC Bioinformatics, 2015, 16, 220. | 2.6 | 28 |
| 3317 | Transcriptome sequencing and annotation of the polychaete <i>Hermodice carunculata</i> (Annelida,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 | 2.8 | 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. BMC Genomics, 2015, 16, 514. | 2.8 | 36 |
| 3319 | Identification and analysis of retrogenes in the East Asian nematode <i>Caenorhabditis</i> sp. 5 genome. Genome, 2015, 58, 349-355. | 2.0 | 2 |
| 3320 | Spider Transcriptomes Identify Ancient Large-Scale Gene Duplication Event Potentially Important in Silk Gland Evolution. Genome Biology and Evolution, 2015, 7, 1856-1870. | 2.5 | 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. Theoretical and Applied Genetics, 2015, 128, 1725-1738. | 3.6 | 10 |
| 3322 | Read count-based method for high-throughput allelic genotyping of transposable elements and structural variants. BMC Genomics, 2015, 16, 508. | 2.8 | 0 |
| 3323 | Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. Environmental Science & Technology, 2015, 49, 12628-12640. | 10.0 | 72 |
| 3324 | SANSparallel: interactive homology search against Uniprot. Nucleic Acids Research, 2015, 43, W24-W29. | 14.5 | 38 |
| 3325 | Complete Genome Sequence of <i>Streptococcus thermophilus</i> SMQ-301, a Model Strain for Phage-Host Interactions. Genome Announcements, 2015, 3, . | 0.8 | 33 |
| 3326 | RNA-Seq based phylogeny recapitulates previous phylogeny of the genus <i>Flaveria</i> (Asteraceae) with some modifications. BMC Evolutionary Biology, 2015, 15, 116. | 3.2 | 46 |
| 3327 | Assessing Recent Selection and Functionality at Long Noncoding RNA Loci in the Mouse Genome. Genome Biology and Evolution, 2015, 7, 2432-2444. | 2.5 | 12 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3328 | GESPA: classifying nsSNPs to predict disease association. BMC Bioinformatics, 2015, 16, 228. | 2.6 | 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). Human Molecular Genetics, 2015, 24, 3143-3154. | 2.9 | 117 |
| 3330 | Local sequence assembly reveals a high-resolution profile of somatic structural variations in 97 cancer genomes. Nucleic Acids Research, 2015, 43, 8146-8156. | 14.5 | 22 |
| 3331 | Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10967-10972. | 7.1 | 1,023 |
| 3332 | Identification and Characterization of Androgen-Responsive Genes in Zebrafish Embryos. Environmental Science & Technology, 2015, 49, 11789-11798. | 10.0 | 42 |
| 3333 | Tentacle: distributed quantification of genes in metagenomes. GigaScience, 2015, 4, 40. | 6.4 | 10 |
| 3334 | The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). Genome Research, 2015, 25, 1921-1933. | 5.5 | 114 |
| 3335 | High-resolution analysis of the human T-cell receptor repertoire. Nature Communications, 2015, 6, 8081. | 12.8 | 123 |
| 3336 | RASER: reads aligner for SNPs and editing sites of RNA. Bioinformatics, 2015, 31, 3906-3913. | 4.1 | 21 |
| 3337 | Identification, Phylogeny, and Function of fabp2 Paralogs in Two Non-Model Teleost Fish Species. Marine Biotechnology, 2015, 17, 663-677. | 2.4 | 7 |
| 3338 | Accelerated rates of protein evolution in barley grain and pistil biased genes might be legacy of domestication. Plant Molecular Biology, 2015, 89, 253-261. | 3.9 | 6 |
| 3339 | Genome wide polymorphisms and yield heterosis in rice (<i>Oryza sativa</i> subsp. indica). Tropical Plant Biology, 2015, 8, 117-125. | 1.9 | 2 |
| 3340 | Detecting protein complexes using connectivity among nodes in a PPI Network. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1. | 2.1 | 2 |
| 3341 | Rare k-mer DNA: Identification of sequence motifs and prediction of CpG island and promoter. Journal of Theoretical Biology, 2015, 387, 88-100. | 1.7 | 13 |
| 3342 | ICRmax: An optimized approach to detect tumor-specific interchromosomal rearrangements for clinical application. Genomics, 2015, 105, 265-272. | 2.9 | 4 |
| 3343 | Stable recombination hotspots in birds. Science, 2015, 350, 928-932. | 12.6 | 280 |
| 3344 | Comparative genomics of grass EST libraries reveals previously uncharacterized splicing events in crop plants. BMC Plant Biology, 2015, 15, 39. | 3.6 | 3 |
| 3345 | piRNA-like small RNAs mark extended 3' UTRs present in germ and somatic cells. BMC Genomics, 2015, 16, 462. | 2.8 | 14 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3346 | Genetic signatures of adaptation revealed from transcriptome sequencing of Arctic and red foxes. BMC Genomics, 2015, 16, 585. | 2.8 | 22 |
| 3347 | Prokaryotic Metatranscriptomics. Springer Protocols, 2015, , 69-98. | 0.3 | 1 |
| 3348 | E-MEM: efficient computation of maximal exact matches for very large genomes. Bioinformatics, 2015, 31, 509-514. | 4.1 | 26 |
| 3349 | Identification of a new maize inflorescence meristem mutant and association analysis using SLAF-seq method. Euphytica, 2015, 202, 35-44. | 1.2 | 33 |
| 3350 | Profiling the RNA editomes of wild-type <i>C. elegans</i> and ADAR mutants. Genome Research, 2015, 25, 66-75. | 5.5 | 70 |
| 3351 | Chemokine receptors in Atlantic salmon. Developmental and Comparative Immunology, 2015, 49, 79-95. | 2.3 | 37 |
| 3352 | Comparing the effectiveness of metagenomics and metabarcoding for diet analysis of a leaf-feeding monkey (<i>Presbytis nemaeus</i>). Molecular Ecology Resources, 2015, 15, 250-261. | 4.8 | 119 |
| 3353 | Intron evolution in <i>Neurospora</i> : the role of mutational bias and selection. Genome Research, 2015, 25, 100-110. | 5.5 | 9 |
| 3354 | The genome sequence of the orchid <i>Phalaenopsis equestris</i> . Nature Genetics, 2015, 47, 65-72. | 21.4 | 413 |
| 3355 | The Mutational Landscape in Pediatric Acute Lymphoblastic Leukemia Deciphered by Whole Genome Sequencing. Human Mutation, 2015, 36, 118-128. | 2.5 | 38 |
| 3356 | RNA-seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. Plant Biotechnology Journal, 2015, 13, 613-624. | 8.3 | 202 |
| 3357 | A phylogenomic analysis of turtles. Molecular Phylogenetics and Evolution, 2015, 83, 250-257. | 2.7 | 244 |
| 3358 | Off-target assessment of CRISPR-Cas9 guiding RNAs in human iPS and mouse ES cells. Genesis, 2015, 53, 225-236. | 1.6 | 55 |
| 3359 | High-resolution genetic maps of <i>Eucalyptus</i> improve <i>Eucalyptus grandis</i> genome assembly. New Phytologist, 2015, 206, 1283-1296. | 7.3 | 90 |
| 3360 | Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669. | 14.5 | 1,145 |
| 3361 | Performance evaluation of Warshall algorithm and dynamic programming for Markov chain in local sequence alignment. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 78-81. | 3.6 | 4 |
| 3362 | Fast and sensitive protein alignment using DIAMOND. Nature Methods, 2015, 12, 59-60. | 19.0 | 8,761 |
| 3363 | Species-Specific Exon Loss in Human Transcriptomes. Molecular Biology and Evolution, 2015, 32, 481-494. | 8.9 | 7 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 3364 | Thiamine Pyrophosphate Riboswitch in Some Representative Plant Species: A Bioinformatics Study. <i>Journal of Computational Biology</i> , 2015, 22, 1-9. | 1.6 | 13 |
| 3365 | Improved rat genome gene prediction by integration of ESTs with RNA-Seq information. <i>Bioinformatics</i> , 2015, 31, 25-32. | 4.1 | 6 |
| 3366 | A near complete snapshot of the Zea mays seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519. | 3.3 | 28 |
| 3367 | Classification of cytochrome P450s in common bean (<i>Phaseolus vulgaris</i> L.). <i>Plant Systematics and Evolution</i> , 2015, 301, 211-216. | 0.9 | 8 |
| 3368 | Preliminary genomic survey and sequence analysis of the complement system in non-eutherian mammals. <i>Australian Mammalogy</i> , 2016, 38, 80. | 1.1 | 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. | 1.2 | 20 |
| 3370 | Genomics Study of <i>Mycobacterium tuberculosis</i> Strains from Different Ethnic Populations in Taiwan. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S40152. | 1.2 | 2 |
| 3371 | [Letter to the Editor] Many commercial hot-start polymerases demonstrate activity prior to thermal activation. <i>BioTechniques</i> , 2016, 61, 293-296. | 1.8 | 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. | 2.8 | 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. | 2.8 | 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. | 1.7 | 18 |
| 3377 | Genome Sequence and Analysis of <i>Peptoclostridium difficile</i> Strain ZJCDC-S82. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S32476. | 1.2 | 9 |
| 3378 | Comparative Analysis of Human B Cell Epitopes Based on BCG Genomes. <i>BioMed Research International</i> , 2016, 2016, 1-5. | 1.9 | 2 |
| 3379 | Identifying Cancer Driver Genes Using Replication-Incompetent Retroviral Vectors. <i>Cancers</i> , 2016, 8, 99. | 3.7 | 4 |
| 3380 | Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. <i>Frontiers in Genetics</i> , 2016, 7, 5. | 2.3 | 4 |
| 3381 | Bacterioplankton Dynamics within a Large Anthropogenically Impacted Urban Estuary. <i>Frontiers in Microbiology</i> , 2015, 6, 1438. | 3.5 | 98 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 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. | 3.5 | 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. | 3.5 | 103 |
| 3384 | Expression of a Novel D4 Dopamine Receptor in the Lamprey Brain. Evolutionary Considerations about Dopamine Receptors. <i>Frontiers in Neuroanatomy</i> , 2016, 9, 165. | 1.7 | 11 |
| 3385 | BBBomics-Human Blood Brain Barrier Transcriptomics Hub. <i>Frontiers in Neuroscience</i> , 2016, 10, 71. | 2.8 | 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. | 4.1 | 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. | 4.1 | 5 |
| 3388 | Endogenous Multiple Exon Skipping and Back-Splicing at the DMD Mutation Hotspot. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1722. | 4.1 | 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. | 3.8 | 9 |
| 3390 | BinPacker: Packing-Based De Novo Transcriptome Assembly from RNA-seq Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004772. | 3.2 | 116 |
| 3391 | H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. <i>PLoS Genetics</i> , 2016, 12, e1005796. | 3.5 | 25 |
| 3392 | Mitochondrial Genome and Nuclear Markers Provide New Insight into the Evolutionary History of Macaques. <i>PLoS ONE</i> , 2016, 11, e0154665. | 2.5 | 25 |
| 3393 | Hotair Is Dispensable for Mouse Development. <i>PLoS Genetics</i> , 2016, 12, e1006232. | 3.5 | 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. | 3.5 | 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. | 3.0 | 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. | 2.5 | 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. | 2.5 | 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. | 2.5 | 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</i> L. (Orobanchaceae). <i>PLoS ONE</i> , 2016, 11, e0148203. | 2.5 | 70 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 3400 | TOPORS, a Dual E3 Ubiquitin and Sumo1 Ligase, Interacts with 26 S Protease Regulatory Subunit 4, Encoded by the PSMC1 Gene. PLoS ONE, 2016, 11, e0148678. | 2.5 | 10 |
| 3401 | Identification of Targets of CUG-BP, Elav-Like Family Member 1 (CELF1) Regulation in Embryonic Heart Muscle. PLoS ONE, 2016, 11, e0149061. | 2.5 | 30 |
| 3402 | Population Structure and Antimicrobial Resistance Profiles of Streptococcus suis Serotype 2 Sequence Type 25 Strains. PLoS ONE, 2016, 11, e0150908. | 2.5 | 32 |
| 3403 | Mapping of a Novel Race Specific Resistance Gene to Phytophthora Root Rot of Pepper (Capsicum) Tj ETQq1 1 0.784314 rgBT /Overlook Sequencing Strategy. PLoS ONE, 2016, 11, e0151401. | 2.5 | 49 |
| 3404 | Using Synthetic Mouse Spike-In Transcripts to Evaluate RNA-Seq Analysis Tools. PLoS ONE, 2016, 11, e0153782. | 2.5 | 13 |
| 3405 | Characterisation of Candida within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients. PLoS ONE, 2016, 11, e0155033. | 2.5 | 45 |
| 3406 | BLAT2DOLite: An Online System for Identifying Significant Relationships between Genetic Sequences and Diseases. PLoS ONE, 2016, 11, e0157274. | 2.5 | 2 |
| 3407 | Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks (Quercus L. sect. Quercus). PLoS ONE, 2016, 11, e0158221. | 2.5 | 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. | 2.5 | 5 |
| 3409 | Differing Alterations of Two Esca Associated Fungi, Phaeoacremonium aleophilum and Phaeomoniella chlamydospora on Transcriptomic Level, to Co-Cultured Vitis vinifera L. calli. PLoS ONE, 2016, 11, e0163344. | 2.5 | 7 |
| 3410 | The Phenotypic and Genetic Underpinnings of Flower Size in Polemoniaceae. Frontiers in Plant Science, 2015, 6, 1144. | 3.6 | 21 |
| 3411 | High-Density Genetic Mapping Identifies New Major Loci for Tolerance to Low-Phosphorus Stress in Soybean. Frontiers in Plant Science, 2016, 7, 372. | 3.6 | 57 |
| 3412 | Targeted Capture Sequencing in Whitebark Pine Reveals Range-Wide Demographic and Adaptive Patterns Despite Challenges of a Large, Repetitive Genome. Frontiers in Plant Science, 2016, 7, 484. | 3.6 | 38 |
| 3413 | Natural Allelic Variations in Highly Polyploidy Saccharum Complex. Frontiers in Plant Science, 2016, 7, 804. | 3.6 | 40 |
| 3414 | Transcriptome Profiling of Huanglongbing (HLB) Tolerant and Susceptible Citrus Plants Reveals the Role of Basal Resistance in HLB Tolerance. Frontiers in Plant Science, 2016, 7, 933. | 3.6 | 75 |
| 3415 | Cloning and Characterization of TaTGW-7A Gene Associated with Grain Weight in Wheat via SLAF-seq-BSA. Frontiers in Plant Science, 2016, 7, 1902. | 3.6 | 75 |
| 3416 | TRPM8 genetic variations associated with COPD risk in the Chinese Han population. International Journal of COPD, 2016, Volume 11, 2563-2571. | 2.3 | 18 |
| 3417 | An Analysis of Adenovirus Genomes Using Whole Genome Software Tools. Bioinformation, 2016, 12, 301-310. | 0.5 | 3 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3418 | Circular RNAs and their associations with breast cancer subtypes. <i>Oncotarget</i> , 2016, 7, 80967-80979. | 1.8 | 140 |
| 3419 | Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016, 5, . | 6.0 | 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. | 4.8 | 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. | 2.3 | 25 |
| 3422 | CrisprVariants charts the mutation spectrum of genome engineering experiments. <i>Nature Biotechnology</i> , 2016, 34, 701-702. | 17.5 | 149 |
| 3423 | Structure and evolution of the gorilla and orangutan growth hormone loci. <i>Mammalian Genome</i> , 2016, 27, 511-523. | 2.2 | 3 |
| 3424 | Lentiviral vector-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. | 2.7 | 37 |
| 3425 | The complete genome of a viable archaeum isolated from 123-million-year-old rock salt. <i>Environmental Microbiology</i> , 2016, 18, 565-579. | 3.8 | 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. | 2.5 | 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. | 5.6 | 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. | 1.8 | 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. | 3.6 | 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. | 3.4 | 12 |
| 3431 | A local alignment approach to similarity analysis of industrial alarm flood sequences. <i>Control Engineering Practice</i> , 2016, 55, 13-25. | 5.5 | 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. | 4.8 | 101 |
| 3433 | Identification of <i>CR1</i> retroposons in <i>Arborophila rufipectus</i> and their application to <i>P</i> -hasianidae phylogeny. <i>Molecular Ecology Resources</i> , 2016, 16, 1037-1049. | 4.8 | 1 |
| 3434 | High-throughput RNA sequencing reveals structural differences of orthologous brain-expressed genes between western lowland gorillas and humans. <i>Journal of Comparative Neurology</i> , 2016, 524, 288-308. | 1.6 | 2 |
| 3435 | Anthropogenic effects on bacterial diversity and function along a river-to-estuary gradient in Northwest Greece revealed by metagenomics. <i>Environmental Microbiology</i> , 2016, 18, 4640-4652. | 3.8 | 58 |

| | | | |
|------|--|------|-----|
| 3437 | Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. Poultry Science, 2016, 95, 2250-2258. | 3.4 | 11 |
| 3438 | Studying RNA Homology and Conservation with Infernal: From Single Sequences to RNA Families. Current Protocols in Bioinformatics, 2016, 54, 12.13.1-12.13.25. | 25.8 | 21 |
| 3439 | <scp>SCR</scp>96, a small cysteineâ€rich secretory protein of <scp><i>P</i></scp><i>hytophthora cactorum</i></sup>, can trigger cell death in the Solanaceae and is important for pathogenicity and oxidative stress tolerance. Molecular Plant Pathology, 2016, 17, 577-587. | 4.2 | 42 |
| 3440 | Curation of the genome annotation of<i>Pichia pastoris</i></sup> (<i>Komagataella phaffii</i></sup>) CBS7435 from gene level to protein function. FEMS Yeast Research, 2016, 16, fow051. | 2.3 | 69 |
| 3441 | A Distinct Class of Chromoanagenesis Events Characterized by Focal Copy Number Gains. Human Mutation, 2016, 37, 661-668. | 2.5 | 30 |
| 3442 | Molecular analysis of complex cases of alphaâ€and betaâ€thalassemia in Mexican mestizo patients with microcytosis and hypochromia reveals two novel alpha⁰</sup>â€thalassemia deletions â€•â€sup>Mex1</sup> and â€•â€sup>Mex2</sup>. International Journal of Laboratory Hematology, 2016, 38, 535-542. | 1.3 | 6 |
| 3443 | A genetic delineation of Patchouli (<i>Pogostemon cablin</i></sup>) revealed by specificâ€locus amplified fragment sequencing. Journal of Systematics and Evolution, 2016, 54, 491-501. | 3.1 | 16 |
| 3444 | Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096. | 3.0 | 344 |
| 3445 | Distinct interacting core taxa in co-occurrence networks enable discrimination of polymicrobial oral diseases with similar symptoms. Scientific Reports, 2016, 6, 30997. | 3.3 | 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. | 3.3 | 12 |
| 3447 | Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. Nature Communications, 2016, 7, 12797. | 12.8 | 190 |
| 3448 | OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D626-D634. | 14.5 | 308 |
| 3449 | The mitochondrial genome map of Nelumbo nucifera reveals ancient evolutionary features. Scientific Reports, 2016, 6, 30158. | 3.3 | 40 |
| 3450 | Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: Phaffia rhodozyma. BMC Genomics, 2016, 17, 901. | 2.8 | 35 |
| 3451 | New insights into the Plasmodium vivax transcriptome using RNA-Seq. Scientific Reports, 2016, 6, 20498. | 3.3 | 65 |
| 3452 | Roar: detecting alternative polyadenylation with standard mRNA sequencing libraries. BMC Bioinformatics, 2016, 17, 423. | 2.6 | 64 |
| 3453 | Computational workflow for the fine-grained analysis of metagenomic samples. BMC Genomics, 2016, 17, 802. | 2.8 | 6 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3454 | A chromosome-level genome assembly of the Asian arowana, <i>Scleropages formosus</i> . <i>Scientific Data</i> , 2016, 3, 160105. | 5.3 | 13 |
| 3455 | Kmerind. , 2016, , . | | 11 |
| 3456 | Genome-Wide Analysis of Transposon and Retroviral Insertions Reveals Preferential Integrations in Regions of DNA Flexibility. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 805-817. | 1.8 | 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. <i>BMC Genomics</i> , 2016, 17, 915. | 2.8 | 63 |
| 3458 | SARVAVID. , 2016, , . | | 14 |
| 3459 | Possible mechanisms of acquisition of herpesvirus virokinases. <i>Biochemistry (Moscow)</i> , 2016, 81, 1350-1357. | 1.5 | 1 |
| 3460 | Acquired RAS or EGFR mutations and duration of response to EGFR blockade in colorectal cancer. <i>Nature Communications</i> , 2016, 7, 13665. | 12.8 | 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. | 4.7 | 48 |
| 3462 | A pipeline for local assembly of minisatellite alleles from single-molecule sequencing data. <i>Bioinformatics</i> , 2017, 33, 650-653. | 4.1 | 2 |
| 3463 | SeqLib: a C++ API for rapid BAM manipulation, sequence alignment and sequence assembly. <i>Bioinformatics</i> , 2017, 33, 751-753. | 4.1 | 12 |
| 3464 | Genome-wide characterization of microsatellites in Triticeae species: abundance, distribution and evolution. <i>Scientific Reports</i> , 2016, 6, 32224. | 3.3 | 30 |
| 3465 | The intron-enriched HERV-K(HML-10) family suppresses apoptosis, an indicator of malignant transformation. <i>Mobile DNA</i> , 2016, 7, 25. | 3.6 | 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. | 3.4 | 73 |
| 3467 | Comparative metagenomics reveals taxonomically idiosyncratic yet functionally congruent communities in periodontitis. <i>Scientific Reports</i> , 2016, 6, 38993. | 3.3 | 89 |
| 3468 | The seahorse genome and the evolution of its specialized morphology. <i>Nature</i> , 2016, 540, 395-399. | 27.8 | 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. | 2.5 | 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. | 3.3 | 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. | 1.8 | 6 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3472 | A comprehensive benchmark of RNAâ€“RNA interaction prediction tools for all domains of life. <i>Bioinformatics</i> , 2017, 33, 988-996. | 4.1 | 54 |
| 3473 | Is the Evolution of <i>Salmonella enterica</i> subsp. <i>enterica</i> Linked to Restriction-Modification Systems?. <i>MSystems</i> , 2016, 1, . | 3.8 | 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. | 2.5 | 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. | 3.3 | 33 |
| 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. <i>BMC Genomics</i> , 2016, 17, 708. | 2.8 | 134 |
| 3480 | The Next Generation Sequencing and Applications in Clinical Research. <i>Translational Bioinformatics</i> , 2016, , 83-113. | 0.0 | 0 |
| 3481 | Genome wide identification and functional prediction of long non-coding RNAs in <i>Brassica rapa</i> . <i>Genes and Genomics</i> , 2016, 38, 547-555. | 1.4 | 5 |
| 3482 | Identification of a novel fusion transcript between human relaxin-1 (RLN1) and human relaxin-2 (RLN2) in prostate cancer. <i>Molecular and Cellular Endocrinology</i> , 2016, 420, 159-168. | 3.2 | 18 |
| 3483 | Germline Chromothripsis Driven by L1-Mediated Retrotransposition and Alu/Alu Homologous Recombination. <i>Human Mutation</i> , 2016, 37, 385-395. | 2.5 | 50 |
| 3484 | Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344. | 12.6 | 368 |
| 3485 | JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 2309-2320. | 3.7 | 76 |
| 3486 | Navigating highly homologous genes in a molecular diagnostic setting: a resource for clinical next-generation sequencing. <i>Genetics in Medicine</i> , 2016, 18, 1282-1289. | 2.4 | 170 |
| 3487 | Identification of polymorphic and off-target probe binding sites on the Illumina Infinium MethylationEPIC BeadChip. <i>Genomics Data</i> , 2016, 9, 22-24. | 1.3 | 264 |
| 3488 | Next-generation biology: Sequencing and data analysis approaches for non-model organisms. <i>Marine Genomics</i> , 2016, 30, 3-13. | 1.1 | 164 |
| 3489 | Identification of human RNA editing sites: A historical perspective. <i>Methods</i> , 2016, 107, 42-47. | 3.8 | 66 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3490 | Aberrant PD-L1 expression through 3' UTR disruption in multiple cancers. <i>Nature</i> , 2016, 534, 402-406. | 27.8 | 536 |
| 3491 | Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267. | 2.8 | 74 |
| 3492 | A time- and cost-effective strategy to sequence mammalian Y Chromosomes: an application to the de novo assembly of gorilla Y. <i>Genome Research</i> , 2016, 26, 530-540. | 5.5 | 99 |
| 3493 | Stress-induced gene expression and behavior are controlled by DNA methylation and methyl donor availability in the dentate gyrus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4830-4835. | 7.1 | 100 |
| 3494 | RNA-seq analysis in forest tree species: bioinformatic problems and solutions. <i>Tree Genetics and Genomes</i> , 2016, 12, 1. | 1.6 | 25 |
| 3495 | A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. <i>Nature Genetics</i> , 2016, 48, 657-666. | 21.4 | 432 |
| 3496 | Bacterial Genomic Data Analysis in the Next-Generation Sequencing Era. <i>Methods in Molecular Biology</i> , 2016, 1415, 407-422. | 0.9 | 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. | 4.8 | 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. | 0.5 | 0 |
| 3499 | Redundans: an assembly pipeline for highly heterozygous genomes. <i>Nucleic Acids Research</i> , 2016, 44, e113-e113. | 14.5 | 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. | 2.3 | 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. | 3.7 | 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. | 4.8 | 148 |
| 3503 | DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. <i>Genome Biology</i> , 2016, 17, 92. | 8.8 | 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. | 2.2 | 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. | 2.0 | 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. | 6.4 | 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. | 14.5 | 66 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 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. | 6.5 | 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. | 2.8 | 12 |
| 3510 | Four novel polymorphisms of buffalo <i>INSIG2</i> gene are associated with milk production traits in Chinese buffaloes. <i>Molecular and Cellular Probes</i> , 2016, 30, 294-299. | 2.1 | 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. | 2.3 | 41 |
| 3512 | A <i>Bacillus anthracis</i> Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. <i>MBio</i> , 2016, 7, . | 4.1 | 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. | 1.6 | 9 |
| 3514 | Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. <i>Genome Biology</i> , 2016, 17, 208. | 8.8 | 912 |
| 3515 | Deciphering the Wisent Demographic and Adaptive Histories from Individual Whole-Genome Sequences. <i>Molecular Biology and Evolution</i> , 2016, 33, 2801-2814. | 8.9 | 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. | 3.4 | 35 |
| 3517 | Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. <i>Bioinformatics</i> , 2016, 32, 3058-3064. | 4.1 | 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. | 2.2 | 8 |
| 3519 | Proline coordination with fatty acid synthesis and redox metabolism of chloroplast and mitochondria. <i>Plant Physiology</i> , 2016, 172, pp.01097.2016. | 4.8 | 60 |
| 3520 | Identification and Correction of Erroneous Protein Sequences in Public Databases. <i>Methods in Molecular Biology</i> , 2016, 1415, 179-192. | 0.9 | 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. | 3.9 | 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. | 7.2 | 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. | 1.7 | 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. | 4.8 | 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. | 1.7 | 31 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3526 | Utility of next-generation <sc>RNA</sc>-sequencing in identifying chimeric transcription involving human endogenous retroviruses. <i>Apmis</i> , 2016, 124, 127-139. | 2.0 | 10 |
| 3527 | Characterization of the T-cell receptor beta chain repertoire in tumor-infiltrating lymphocytes. <i>Cancer Medicine</i> , 2016, 5, 2513-2521. | 2.8 | 17 |
| 3528 | TALEN-Mediated Mutagenesis and Genome Editing. <i>Methods in Molecular Biology</i> , 2016, 1451, 17-30. | 0.9 | 22 |
| 3529 | Identification of Coilin Mutants in a Screen for Enhanced Expression of an Alternatively Spliced <i>GFP</i> Reporter Gene in <i>Arabidopsis thaliana</i>. <i>Genetics</i> , 2016, 203, 1709-1720. | 2.9 | 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. | 0.3 | 14 |
| 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. | 0.7 | 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>. <i>Rna</i> , 2016, 22, 1522-1534. | 3.5 | 32 |
| 3535 | Uncovering Earth's virome. <i>Nature</i> , 2016, 536, 425-430. | 27.8 | 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. | 7.1 | 211 |
| 3537 | Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830. | 12.6 | 241 |
| 3538 | AnnoLnc: a web server for systematically annotating novel human lncRNAs. <i>BMC Genomics</i> , 2016, 17, 931. | 2.8 | 51 |
| 3539 | Prevalence and Abundance of Florfenicol and Linezolid Resistance Genes in Soils Adjacent to Swine Feedlots. <i>Scientific Reports</i> , 2016, 6, 32192. | 3.3 | 70 |
| 3540 | Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. <i>Nature Communications</i> , 2016, 7, 12233. | 12.8 | 106 |
| 3541 | Draft genome of the living fossil <i>Ginkgo biloba</i> . <i>GigaScience</i> , 2016, 5, 49. | 6.4 | 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. | 3.9 | 33 |
| 3544 | Genome Analysis of Plants. , 2016, , 1-27. | | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 1.2 | 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. | 7.1 | 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. | 0.9 | 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. | 2.9 | 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. | 3.6 | 21 |
| 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. | 3.4 | 24 |
| 3552 | Microbiota Dysbiosis Controls the Neuroinflammatory Response after Stroke. <i>Journal of Neuroscience</i> , 2016, 36, 7428-7440. | 3.6 | 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. | 1.6 | 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. | 12.8 | 69 |
| 3555 | A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161. | 13.3 | 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. | 3.3 | 143 |
| 3557 | High expression of new genes in trochophore enlightening the ontogeny and evolution of trochozoans. <i>Scientific Reports</i> , 2016, 6, 34664. | 3.3 | 32 |
| 3558 | An evaluation of the accuracy and speed of metagenome analysis tools. <i>Scientific Reports</i> , 2016, 6, 19233. | 3.3 | 278 |
| 3559 | A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232. | 8.8 | 12 |
| 3560 | LSCplus: a fast solution for improving long read accuracy by short read alignment. <i>BMC Bioinformatics</i> , 2016, 17, 451. | 2.6 | 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. | 2.8 | 61 |
| 3562 | The genome of the miuiy croaker reveals well-developed innate immune and sensory systems. <i>Scientific Reports</i> , 2016, 6, 21902. | 3.3 | 67 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3563 | Exploring the transcriptome of <i>Staphylococcus aureus</i> in its natural niche. <i>Scientific Reports</i> , 2016, 6, 33174. | 3.3 | 52 |
| 3564 | Feralisation targets different genomic loci to domestication in the chicken. <i>Nature Communications</i> , 2016, 7, 12950. | 12.8 | 60 |
| 3565 | The endotracheal tube microbiome associated with <i>Pseudomonas aeruginosa</i> or <i>Staphylococcus epidermidis</i> . <i>Scientific Reports</i> , 2016, 6, 36507. | 3.3 | 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. | 3.0 | 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. | 3.3 | 17 |
| 3568 | RNA editing generates cellular subsets with diverse sequence within populations. <i>Nature Communications</i> , 2016, 7, 12145. | 12.8 | 48 |
| 3569 | Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032. | 13.3 | 207 |
| 3570 | Comparative assessment of methods for the fusion transcripts detection from RNA-Seq data. <i>Scientific Reports</i> , 2016, 6, 21597. | 3.3 | 123 |
| 3571 | Morphological and Transcriptomic Analysis of a Beetle Chemosensory System Reveals a Gnathal Olfactory Center. <i>BMC Biology</i> , 2016, 14, 90. | 3.8 | 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. | 12.8 | 49 |
| 3573 | Expansion and stress responses of AP2/EREBP superfamily in <i>Brachypodium distachyon</i> . <i>Scientific Reports</i> , 2016, 6, 21623. | 3.3 | 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. | 0.7 | 3 |
| 3575 | Mechanical cell competition kills cells via induction of lethal p53 levels. <i>Nature Communications</i> , 2016, 7, 11373. | 12.8 | 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. | 2.1 | 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. | 3.3 | 100 |
| 3579 | LTR-mediated retroposition as a mechanism of RNA-based duplication in metazoans. <i>Genome Research</i> , 2016, 26, 1663-1675. | 5.5 | 42 |
| 3580 | The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, . | 4.1 | 49 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3581 | RES-Scanner: a software package for genome-wide identification of RNA-editing sites. GigaScience, 2016, 5, 37. | 6.4 | 55 |
| 3582 | The Simple Chordate <i>Ciona intestinalis</i> Has a Reduced Complement of Genes Associated with Fanconi Anemia. Evolutionary Bioinformatics, 2016, 12, EBO.S37920. | 1.2 | 6 |
| 3583 | Draft Genome Sequence of Mycobacterium houstonense Strain ATCC 49403 T. Genome Announcements, 2016, 4, . | 0.8 | 4 |
| 3584 | Draft Genome Sequence of Mycobacterium interjectum Strain ATCC 51457 T. Genome Announcements, 2016, 4, . | 0.8 | 0 |
| 3585 | The multicellularity genes of dictyostelid social amoebas. Nature Communications, 2016, 7, 12085. | 12.8 | 63 |
| 3586 | LINE-1-like retrotransposons contribute to RNA-based gene duplication in dicots. Scientific Reports, 2016, 6, 24755. | 3.3 | 13 |
| 3587 | Assembling the Setaria italica L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. Scientific Reports, 2016, 6, 35076. | 3.3 | 10 |
| 3588 | Amplification, Next-generation Sequencing, and Genomic DNA Mapping of Retroviral Integration Sites. Journal of Visualized Experiments, 2016, , . | 0.3 | 36 |
| 3589 | Contribution of type W human endogenous retroviruses to the human genome: characterization of HERV-W proviral insertions and processed pseudogenes. Retrovirology, 2016, 13, 67. | 2.0 | 62 |
| 3590 | Complete genome sequence of thermophilic Bacillus smithii type strain DSM 4216T. Standards in Genomic Sciences, 2016, 11, 52. | 1.5 | 13 |
| 3591 | RNA-Sequencing for profiling goat milk transcriptome in colostrum and mature milk. BMC Veterinary Research, 2016, 12, 264. | 1.9 | 71 |
| 3592 | Retrozymes are a unique family of non-autonomous retrotransposons with hammerhead ribozymes that propagate in plants through circular RNAs. Genome Biology, 2016, 17, 135. | 8.8 | 39 |
| 3593 | High-quality genome assembly of channel catfish, Ictalurus punctatus. GigaScience, 2016, 5, 39. | 6.4 | 45 |
| 3594 | Complete plastid genome of Eriobotrya japonica (Thunb.) Lindl and comparative analysis in Rosaceae. SpringerPlus, 2016, 5, 2036. | 1.2 | 13 |
| 3595 | Pinpointing the vesper bat transposon revolution using the Miniopterus natalensis genome. Mobile DNA, 2016, 7, 12. | 3.6 | 23 |
| 3596 | Evidence for L1-associated DNA rearrangements and negligible L1 retrotransposition in glioblastoma multiforme. Mobile DNA, 2016, 7, 21. | 3.6 | 32 |
| 3597 | Molecular analysis of the Sydney rock oyster (Saccostrea glomerata) CO2 stress response. Climate Change Responses, 2016, 3, . | 2.6 | 9 |
| 3599 | PGD: a pangolin genome hub for the research community. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw063. | 3.0 | 5 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3600 | gEVE: a genome-based endogenous viral element database provides comprehensive viral protein-coding sequences in mammalian genomes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw087. | 3.0 | 56 |
| 3601 | Unlocking the genetic diversity of Creole wheats. Scientific Reports, 2016, 6, 23092. | 3.3 | 75 |
| 3602 | Mitogenome assembly from genomic multiplex libraries: comparison of strategies and novel mitogenomes for five species of frogs. Molecular Ecology Resources, 2016, 16, 686-693. | 4.8 | 21 |
| 3603 | Characterization of the teosinte transcriptome reveals adaptive sequence divergence during maize domestication. Molecular Ecology Resources, 2016, 16, 1465-1477. | 4.8 | 7 |
| 3604 | Novel mutations in the genes <i>TGM1</i> and <i>ALOXE3</i> underlying autosomal recessive congenital ichthyosis. International Journal of Dermatology, 2016, 55, 524-530. | 1.0 | 6 |
| 3605 | Whole genome duplication in coast redwood (<i>Sequoia sempervirens</i>) and its implications for explaining the rarity of polyploidy in conifers. New Phytologist, 2016, 211, 186-193. | 7.3 | 49 |
| 3606 | PTESFinder: a computational method to identify post-transcriptional exon shuffling (PTES) events. BMC Bioinformatics, 2016, 17, 31. | 2.6 | 45 |
| 3607 | UNDR ROVER - a fast and accurate variant caller for targeted DNA sequencing. BMC Bioinformatics, 2016, 17, 165. | 2.6 | 3 |
| 3608 | Multivariate models from RNA-Seq SNVs yield candidate molecular targets for biomarker discovery: SNV-DA. BMC Genomics, 2016, 17, 263. | 2.8 | 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. | 2.4 | 9 |
| 3610 | Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. BMC Genomics, 2016, 17, 180. | 2.8 | 71 |
| 3611 | Next-generation sequencing-based detection of germline L1-mediated transductions. BMC Genomics, 2016, 17, 342. | 2.8 | 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. | 3.5 | 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. | 1.8 | 41 |
| 3615 | Informed <i>k</i> -mer selection for <i>de novo</i> transcriptome assembly. Bioinformatics, 2016, 32, 1670-1677. | 4.1 | 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. | 2.5 | 54 |
| 3617 | The MG-RAST metagenomics database and portal in 2015. Nucleic Acids Research, 2016, 44, D590-D594. | 14.5 | 187 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3618 | TBR1 regulates autism risk genes in the developing neocortex. <i>Genome Research</i> , 2016, 26, 1013-1022. | 5.5 | 71 |
| 3619 | RapMap: a rapid, sensitive and accurate tool for mapping RNA-seq reads to transcriptomes. <i>Bioinformatics</i> , 2016, 32, i192-i200. | 4.1 | 99 |
| 3620 | Evolutionary direction of processed pseudogenes. <i>Science China Life Sciences</i> , 2016, 59, 839-849. | 4.9 | 5 |
| 3621 | Human C-terminally truncated ERÎ± variants resulting from the use of alternative exons in the ligand-binding domain. <i>Molecular and Cellular Endocrinology</i> , 2016, 425, 111-122. | 3.2 | 16 |
| 3622 | Noncontiguous finished genome sequence and description of <i>Paenibacillus ihumii</i> sp. nov. strain AT5. <i>New Microbes and New Infections</i> , 2016, 10, 142-150. | 1.6 | 17 |
| 3623 | Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. <i>Epigenetics</i> , 2016, 11, 501-516. | 2.7 | 65 |
| 3624 | Sequence and partial functional analysis of canine Bcl-2 family proteins. <i>Research in Veterinary Science</i> , 2016, 104, 126-135. | 1.9 | 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. | 2.8 | 114 |
| 3627 | Identification of mRNA isoform switching in breast cancer. <i>BMC Genomics</i> , 2016, 17, 181. | 2.8 | 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. | 3.6 | 36 |
| 3629 | Bitpacking techniques for indexing genomes: I. Hash tables. <i>Algorithms for Molecular Biology</i> , 2016, 11, 5. | 1.2 | 3 |
| 3630 | Landscape and evolutionary dynamics of terminal repeat retrotransposons in miniature in plant genomes. <i>Genome Biology</i> , 2016, 17, 7. | 8.8 | 50 |
| 3631 | Reconstruction of the insulin-like signalling pathway of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2016, 9, 64. | 2.5 | 12 |
| 3632 | Genome ARTIST: a robust, high-accuracy aligner tool for mapping transposon insertions and self-insertions. <i>Mobile DNA</i> , 2016, 7, 3. | 3.6 | 11 |
| 3633 | Genomic analysis of mouse VL30 retrotransposons. <i>Mobile DNA</i> , 2016, 7, 10. | 3.6 | 21 |
| 3634 | Metatranscriptomic analysis of diverse microbial communities reveals core metabolic pathways and microbiome-specific functionality. <i>Microbiome</i> , 2016, 4, 2. | 11.1 | 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. | 2.5 | 45 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 2.1 | 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. | 1.3 | 8 |
| 3639 | Transcriptome asymmetry in synthetic and natural allotetraploid wheats, revealed by <i>scRNA-seq</i> . <i>New Phytologist</i> , 2016, 209, 1264-1277. | 7.3 | 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. | 3.4 | 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. | 8.9 | 28 |
| 3642 | Complete chloroplast genomes of <i>Saccharum spontaneum</i> and <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. | 1.2 | 34 |
| 3643 | PEP_scaffolder: using (homologous) proteins to scaffold genomes. <i>Bioinformatics</i> , 2016, 32, 3193-3195. | 4.1 | 14 |
| 3644 | Crystallins of the chicken lens: remnants of an ancient vertebrate gene family in birds. <i>FEBS Journal</i> , 2016, 283, 1516-1530. | 4.7 | 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. | 12.1 | 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. | 2.1 | 8 |
| 3647 | SIENA: Efficient Compilation of Selective Protein Binding Site Ensembles. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 248-259. | 5.4 | 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. | 4.1 | 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. | 0.9 | 371 |
| 3650 | MEPD: medaka expression pattern database, genes and more. <i>Nucleic Acids Research</i> , 2016, 44, D819-D821. | 14.5 | 11 |
| 3651 | Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , 2016, 6, 166-175. | 9.4 | 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. | 1.3 | 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. | 14.5 | 152 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3654 | RiboFR-Seq: a novel approach to linking 16S rRNA amplicon profiles to metagenomes. <i>Nucleic Acids Research</i> , 2016, 44, e99-e99. | 14.5 | 24 |
| 3655 | Minimap and miniiasm: fast mapping and de novo assembly for noisy long sequences. <i>Bioinformatics</i> , 2016, 32, 2103-2110. | 4.1 | 1,082 |
| 3656 | The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725. | 14.5 | 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. | 1.9 | 7 |
| 3658 | Efficient privacy-preserving string search and an application in genomics. <i>Bioinformatics</i> , 2016, 32, 1652-1661. | 4.1 | 46 |
| 3659 | The real cost of sequencing: scaling computation to keep pace with data generation. <i>Genome Biology</i> , 2016, 17, 53. | 8.8 | 264 |
| 3660 | GMAP and GSNAP for Genomic Sequence Alignment: Enhancements to Speed, Accuracy, and Functionality. <i>Methods in Molecular Biology</i> , 2016, 1418, 283-334. | 0.9 | 354 |
| 3661 | <i>Microvirga massiliensis</i> sp. nov., the human commensal with the largest genome. <i>MicrobiologyOpen</i> , 2016, 5, 307-322. | 3.0 | 27 |
| 3662 | An Exon-Capture System for the Entire Class Ophiuroidea. <i>Molecular Biology and Evolution</i> , 2016, 33, 281-294. | 8.9 | 90 |
| 3663 | Organellar Genomes of White Spruce (<i>Picea glauca</i>): Assembly and Annotation. <i>Genome Biology and Evolution</i> , 2016, 8, 29-41. | 2.5 | 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. | 3.6 | 82 |
| 3665 | Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600. | 18.8 | 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. | 2.8 | 34 |
| 3667 | Haplotyping germline and cancer genomes with high-throughput linked-read sequencing. <i>Nature Biotechnology</i> , 2016, 34, 303-311. | 17.5 | 617 |
| 3668 | Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476. | 12.8 | 189 |
| 3669 | Discovery of a new repeat family in the <i>Callithrix jacchus</i> genome. <i>Genome Research</i> , 2016, 26, 649-659. | 5.5 | 11 |
| 3670 | Genetic features of <i>Mycobacterium tuberculosis</i> modern Beijing sublineage. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8. | 6.5 | 35 |
| 3671 | Organizational Heterogeneity of the Human Genome: Significant Variation of Recombination Rate of 100 kbp Sequences within GC Ranges. , 2016, , . | | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 3.4 | 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. | 2.9 | 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. | 4.6 | 44 |
| 3675 | TheVignaGenome Server, â€˜VigGSâ€™: A Genomic Knowledge Base of the GenusVignaBased on High-Quality, Annotated Genome Sequence of the Azuki Bean,Vigna angularis(Willd.) Ohwi & Ohashi. <i>Plant and Cell Physiology</i> , 2016, 57, e2-e2. | 3.1 | 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. | 2.7 | 16 |
| 3677 | Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016, 13, 177-183. | 19.0 | 274 |
| 3678 | Genome-wide identification and characterization of transcription start sites and promoters in the tunicateCiona intestinalis. <i>Genome Research</i> , 2016, 26, 140-150. | 5.5 | 13 |
| 3679 | Genetical Genomics of Behavior: A Novel Chicken Genomic Model for Anxiety Behavior. <i>Genetics</i> , 2016, 202, 327-340. | 2.9 | 51 |
| 3680 | Characterization of Ambra1 in asexual cycle of a non-vertebrate chordate, the colonial tunicate Botryllus schlosseri, and phylogenetic analysis of the protein group in Bilateria. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 46-57. | 2.7 | 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. | 14.5 | 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. | 14.5 | 60 |
| 3683 | Comparative genomics analysis of decapod shrimps in the Pancrustacea clade. <i>Biochemical Systematics and Ecology</i> , 2016, 64, 111-121. | 1.3 | 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. | 2.5 | 87 |
| 3685 | Hypomorphic mutations in <i>TRNT1</i> cause retinitis pigmentosa with erythrocytic microcytosis. <i>Human Molecular Genetics</i> , 2016, 25, 44-56. | 2.9 | 64 |
| 3686 | Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomics Data. <i>Methods in Molecular Biology</i> , 2016, 1374, 115-140. | 0.9 | 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. | 3.2 | 49 |
| 3688 | The complement of family M1 aminopeptidases of Haemonchus contortus â€” Biotechnological implications. <i>Biotechnology Advances</i> , 2016, 34, 65-76. | 11.7 | 8 |
| 3689 | Rapid Short-Read Sequencing and Aneuploidy Detection Using MinION Nanopore Technology. <i>Genetics</i> , 2016, 202, 37-44. | 2.9 | 32 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3690 | Fecal Recovery of Ingested Cellular DNA: Implications for Noninvasive Detection of Upper Gastrointestinal Neoplasms. Digestive Diseases and Sciences, 2016, 61, 117-125. | 2.3 | 5 |
| 3691 | Transposition burst of mariner-like elements in the sequenced genome of <i>Rhodnius prolixus</i> . Insect Biochemistry and Molecular Biology, 2016, 69, 14-24. | 2.7 | 11 |
| 3692 | SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. Bioinformatics, 2016, 32, 354-361. | 4.1 | 161 |
| 3693 | NCLscan: accurate identification of non-co-linear transcripts (fusion, <i>trans</i> -splicing and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T e29-e29. | 14.5 | 98 |
| 3694 | Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. Applied and Environmental Microbiology, 2016, 82, 157-166. | 3.1 | 73 |
| 3695 | Will solid-state drives accelerate your bioinformatics? In-depth profiling, performance analysis and beyond. Briefings in Bioinformatics, 2016, 17, 713-727. | 6.5 | 12 |
| 3696 | Transcriptional dynamics of <i>Phytophthora infestans</i> during sequential stages of hemibiotrophic infection of tomato. Molecular Plant Pathology, 2016, 17, 29-41. | 4.2 | 77 |
| 3697 | Analysis of the tomato leaf transcriptome during successive hemibiotrophic stages of a compatible interaction with the oomycete pathogen <i>Phytophthora infestans</i> . Molecular Plant Pathology, 2016, 17, 42-54. | 4.2 | 55 |
| 3698 | cuBLASTP: Fine-Grained Parallelization of Protein Sequence Search on CPU+GPU. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 830-843. | 3.0 | 19 |
| 3699 | Short Read Mapping: An Algorithmic Tour. Proceedings of the IEEE, 2017, 105, 436-458. | 21.3 | 63 |
| 3700 | Characterizing and annotating the genome using RNA-seq data. Science China Life Sciences, 2017, 60, 116-125. | 4.9 | 35 |
| 3701 | Identification of misexpressed genetic elements in hybrids between <i>Drosophila</i> -related species. Scientific Reports, 2017, 7, 40618. | 3.3 | 49 |
| 3702 | Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . Nature Microbiology, 2017, 2, 16263. | 13.3 | 124 |
| 3703 | GENE-IS: Time-Efficient and Accurate Analysis of Viral Integration Events in Large-Scale Gene Therapy Data. Molecular Therapy - Nucleic Acids, 2017, 6, 133-139. | 5.1 | 21 |
| 3704 | A second generation SNP and SSR integrated linkage map and QTL mapping for the Chinese mitten crab <i>Eriocheir sinensis</i> . Scientific Reports, 2017, 7, 39826. | 3.3 | 38 |
| 3705 | Cytosine methylation at CpCpG sites triggers accumulation of non-CpG methylation in gene bodies. Nucleic Acids Research, 2017, 45, gkw1330. | 14.5 | 26 |
| 3706 | Integrating genomic resources of flatfish (<i>Pleuronectiformes</i>) to boost aquaculture production. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 21, 41-55. | 1.0 | 21 |
| 3707 | Accurate clinical genetic testing for autoinflammatory diseases using the next-generation sequencing platform MiSeq. Biochemistry and Biophysics Reports, 2017, 9, 146-152. | 1.3 | 17 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.3 | 1 |
| 3709 | Transcriptome profiles reveal gene regulation of peanut (<i>Arachis hypogaea</i> L.) nodulation. <i>Scientific Reports</i> , 2017, 7, 40066. | 3.3 | 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. | 14.5 | 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. | 0.8 | 7 |
| 3713 | Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540. | 27.8 | 332 |
| 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. | 3.9 | 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. | 7.1 | 31 |
| 3716 | A user guide to the Brassica 60K Illumina Infinium [®] SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2017, 130, 621-633. | 3.6 | 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. | 2.1 | 63 |
| 3718 | Convergent Evolution of the Osmoregulation System in Decapod Shrimps. <i>Marine Biotechnology</i> , 2017, 19, 76-88. | 2.4 | 13 |
| 3719 | The evolution and population diversity of human-specific segmental duplications. <i>Nature Ecology and Evolution</i> , 2017, 1, 69. | 7.8 | 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. | 3.4 | 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. | 8.8 | 159 |
| 3722 | Aboriginal mitogenomes reveal 50,000 years of regionalism in Australia. <i>Nature</i> , 2017, 544, 180-184. | 27.8 | 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. | 3.3 | 46 |
| 3724 | An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. <i>BMC Genomics</i> , 2017, 18, 95. | 2.8 | 153 |
| 3725 | Mutational landscape reflects the biological continuum of plasma cell dyscrasias. <i>Blood Cancer Journal</i> , 2017, 7, e537-e537. | 6.2 | 32 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3726 | An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204. | 27.8 | 898 |
| 3727 | MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580. | 14.5 | 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. | 2.0 | 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. | 8.5 | 30 |
| 3730 | Genomic Rearrangements in <i>Arabidopsis</i> Considered as Quantitative Traits. <i>Genetics</i> , 2017, 205, 1425-1441. | 2.9 | 21 |
| 3733 | Identification of some main <i>Streptococcus iniae</i> associated proteins: relationship. <i>Veterinary Research Communications</i> , 2017, 41, 85-95. | 1.6 | 1 |
| 3734 | Evolutionary mechanism and biological functions of 8-mers containing CG dinucleotide in yeast. <i>Chromosome Research</i> , 2017, 25, 173-189. | 2.2 | 6 |
| 3735 | Molecular characteristics of two new waxy mutations in China waxy maize. <i>Molecular Breeding</i> , 2017, 37, 1. | 2.1 | 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. | 3.4 | 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. | 2.6 | 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. | 2.8 | 9 |
| 3740 | Small genomic insertions form enhancers that misregulate oncogenes. <i>Nature Communications</i> , 2017, 8, 14385. | 12.8 | 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. | 3.3 | 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. | 4.0 | 51 |
| 3743 | Genomics and evolution of protein phosphatases. <i>Science Signaling</i> , 2017, 10, . | 3.6 | 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. | 3.5 | 20 |
| 3745 | Typing and Characterization of Bacteria Using Bottom-up Tandem Mass Spectrometry Proteomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1052-1063. | 3.8 | 66 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3746 | Large-scale collection of full-length cDNA and transcriptome analysis in <i>Hevea brasiliensis</i> . DNA Research, 2017, 24, dsw056. | 3.4 | 18 |
| 3747 | Comparative studies of vertebrate iduronate 2-sulfatase (IDS) genes and proteins: evolution of A mammalian X-linked gene. 3 Biotech, 2017, 7, 22. | 2.2 | 12 |
| 3748 | Contrasting evolutionary genome dynamics between domesticated and wild yeasts. Nature Genetics, 2017, 49, 913-924. | 21.4 | 340 |
| 3749 | Squamate Conserved Loci (Sq<scp>CL</scp>): A unified set of conserved loci for phylogenomics and population genetics of squamate reptiles. Molecular Ecology Resources, 2017, 17, e12-e24. | 4.8 | 36 |
| 3750 | Pneumococcal prophages are diverse, but not without structure or history. Scientific Reports, 2017, 7, 42976. | 3.3 | 62 |
| 3751 | GeSeq“ versatile and accurate annotation of organelle genomes. Nucleic Acids Research, 2017, 45, W6-W11. | 14.5 | 1,964 |
| 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. BMC Genomics, 2017, 18, 355. | 2.8 | 46 |
| 3753 | Expansion of the redox-sensitive proteome coincides with the plastid endosymbiosis. Nature Plants, 2017, 3, 17066. | 9.3 | 26 |
| 3754 | Transposable Element Misregulation Is Linked to the Divergence between Parental piRNA Pathways in Drosophila Hybrids. Genome Biology and Evolution, 2017, 9, 1450-1470. | 2.5 | 26 |
| 3755 | From data to knowledge: The future of multi-omics data analysis for the rhizosphere. Rhizosphere, 2017, 3, 222-229. | 3.0 | 30 |
| 3756 | Draft genome sequence of the Tibetan medicinal herb <i>Rhodiola crenulata</i> . GigaScience, 2017, 6, 1-5. | 6.4 | 33 |
| 3757 | Targeted Enrichment for Pathogen Detection and Characterization in Three Felid Species. Journal of Clinical Microbiology, 2017, 55, 1658-1670. | 3.9 | 25 |
| 3758 | Detection of viromes of RNA viruses using the next generation sequencing libraries prepared by three methods. Virus Research, 2017, 237, 22-26. | 2.2 | 8 |
| 3759 | Chromosome-level genome assembly and transcriptome of the green alga <i>Chromochloris zofingiensis</i> illuminates astaxanthin production. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4296-E4305. | 7.1 | 131 |
| 3760 | Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes. Briefings in Bioinformatics, 2018, 19, 1415-1429. | 6.5 | 34 |
| 3761 | Heritable L1 retrotransposition in the mouse primordial germline and early embryo. Genome Research, 2017, 27, 1395-1405. | 5.5 | 90 |
| 3762 | Target enrichment sequencing in cultivated peanut (<i>Arachis hypogaea</i> L.) using probes designed from transcript sequences. Molecular Genetics and Genomics, 2017, 292, 955-965. | 2.1 | 17 |
| 3763 | Overexpression of hsa-miR-939 follows by NGFR down-regulation and apoptosis reduction. Journal of Biosciences, 2017, 42, 23-30. | 1.1 | 5 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3764 | Integrated high-density consensus genetic map of <i>Pyrus</i> and anchoring of the ‘Bartlett’™ v1.0 (<i>Pyrus communis</i>) genome. DNA Research, 2017, 24, dsw063. | 3.4 | 28 |
| 3765 | An Agile Functional Analysis of Metagenomic Data Using SUPER-FOCUS. Methods in Molecular Biology, 2017, 1611, 35-44. | 0.9 | 2 |
| 3766 | A-to-I RNA Editing in the Earliest-Diverging Eumetazoan Phyla. Molecular Biology and Evolution, 2017, 34, 1890-1901. | 8.9 | 45 |
| 3767 | Mutational screening of SLC39A5, LEPREL1 and LRPAP1 in a cohort of 187 high myopia patients. Scientific Reports, 2017, 7, 1120. | 3.3 | 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. | 2.7 | 13 |
| 3769 | Whole genome sequencing predicts novel human disease models in rhesus macaques. Genomics, 2017, 109, 214-220. | 2.9 | 28 |
| 3770 | Whole exome association of rare deletions in multiplex oral cleft families. Genetic Epidemiology, 2017, 41, 61-69. | 1.3 | 10 |
| 3771 | Inferring Function from Homology. Methods in Molecular Biology, 2017, 1526, 23-40. | 0.9 | 5 |
| 3772 | A human microprotein that interacts with the mRNA decapping complex. Nature Chemical Biology, 2017, 13, 174-180. | 8.0 | 212 |
| 3774 | Genomic Database Searching. Methods in Molecular Biology, 2017, 1525, 225-269. | 0.9 | 2 |
| 3775 | Large-Scale Sequence Comparison. Methods in Molecular Biology, 2017, 1525, 191-224. | 0.9 | 3 |
| 3776 | CRISPR-STOP: gene silencing through base-editing-induced nonsense mutations. Nature Methods, 2017, 14, 710-712. | 19.0 | 290 |
| 3777 | Application of the cghRA framework to the genomic characterization of Diffuse Large B-Cell Lymphoma. Bioinformatics, 2017, 33, 2977-2985. | 4.1 | 3 |
| 3778 | Sexual Dimorphism and Retinal Mosaic Diversification following the Evolution of a Violet Receptor in Butterflies. Molecular Biology and Evolution, 2017, 34, 2271-2284. | 8.9 | 46 |
| 3779 | HALC: High throughput algorithm for long read error correction. BMC Bioinformatics, 2017, 18, 204. | 2.6 | 55 |
| 3780 | High-throughput sequencing of transposable element insertions suggests adaptive evolution of the invasive Asian tiger mosquito towards temperate environments. Molecular Ecology, 2017, 26, 3968-3981. | 3.9 | 34 |
| 3781 | Identification of Sex-determining Loci in Pacific White Shrimp <i>Litopenaeus vannamei</i> Using Linkage and Association Analysis. Marine Biotechnology, 2017, 19, 277-286. | 2.4 | 60 |
| 3782 | Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5671-5676. | 7.1 | 49 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3783 | Bioinformatics Tools for Genome-Wide Epigenetic Research. <i>Advances in Experimental Medicine and Biology</i> , 2017, 978, 489-512. | 1.6 | 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. | 1.3 | 4 |
| 3785 | <i>MET</i> Exon 14 Mutation Encodes an Actionable Therapeutic Target in Lung Adenocarcinoma. <i>Cancer Research</i> , 2017, 77, 4498-4505. | 0.9 | 57 |
| 3786 | Reading <scp>LINE</scp>s within the cocaine addicted brain. <i>Brain and Behavior</i> , 2017, 7, e00678. | 2.2 | 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. | 1.2 | 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. | 4.1 | 13 |
| 3789 | The genome sequence of <i>Barbarea vulgaris</i> facilitates the study of ecological biochemistry. <i>Scientific Reports</i> , 2017, 7, 40728. | 3.3 | 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. | 3.1 | 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. | 12.8 | 58 |
| 3792 | Analysis of LINE-1 Elements in DNA from Postmortem Brains of Individuals with Schizophrenia. <i>Neuropsychopharmacology</i> , 2017, 42, 2602-2611. | 5.4 | 60 |
| 3793 | Analysis of Copy Number Variation in the Abp Gene Regions of Two House Mouse Subspecies Suggests Divergence during the Gene Family Expansions. <i>Genome Biology and Evolution</i> , 2017, 9, . | 2.5 | 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. | 6.4 | 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. | 2.3 | 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. | 4.0 | 75 |
| 3797 | Androgen receptor and miR-206 regulation in prostate cancer. <i>Transcription</i> , 2017, 8, 313-327. | 3.1 | 15 |
| 3798 | Repeated divergent selection on pigmentation genes in a rapid finch radiation. <i>Science Advances</i> , 2017, 3, e1602404. | 10.3 | 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. | 8.3 | 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. | 3.3 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 3.3 | 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. | 6.4 | 49 |
| 3803 | The Limitations of Existing Approaches in Improving MicroRNA Target Prediction Accuracy. <i>Methods in Molecular Biology</i> , 2017, 1617, 133-158. | 0.9 | 16 |
| 3804 | Exploring structural variation and gene family architecture with De Novo assemblies of 15 Medicago genomes. <i>BMC Genomics</i> , 2017, 18, 261. | 2.8 | 87 |
| 3805 | Whipworm kinomes reflect a unique biology and adaptation to the host animal. <i>International Journal for Parasitology</i> , 2017, 47, 857-866. | 3.1 | 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. | 3.9 | 16 |
| 3807 | Live birth derived from oocyte spindle transfer to prevent mitochondrial disease. <i>Reproductive BioMedicine Online</i> , 2017, 34, 361-368. | 2.4 | 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. | 19.0 | 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. | 2.7 | 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. | 3.9 | 16 |
| 3811 | Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017, 1, 120. | 7.8 | 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. | 1.2 | 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. | 6.4 | 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. | 2.7 | 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. | 1.4 | 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. | 6.9 | 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. | 8.3 | 32 |
| 3818 | Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. <i>Nature Communications</i> , 2017, 8, 14742. | 12.8 | 96 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 3819 | Kart: a divide-and-conquer algorithm for NGS read alignment. <i>Bioinformatics</i> , 2017, 33, 2281-2287. | 4.1 | 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. | 2.9 | 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. | 2.8 | 49 |
| 3822 | A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 109-117. | 1.8 | 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. | 3.9 | 28 |
| 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. | 2.8 | 342 |
| 3827 | The birth of a human-specific neural gene by incomplete duplication and gene fusion. <i>Genome Biology</i> , 2017, 18, 49. | 8.8 | 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. | 2.9 | 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. | 2.2 | 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. | 4.8 | 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. | 3.3 | 156 |
| 3832 | Bioinformatic tools for analysis of CLIP ribonucleoprotein data. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1404. | 6.4 | 9 |
| 3833 | â€ Candidatus Dichloromethanomonas elyunquensisâ€™ gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the Peptococcaceae family. <i>Systematic and Applied Microbiology</i> , 2017, 40, 150-159. | 2.8 | 50 |
| 3834 | Evolution of transcript modification by N ⁶ -methyladenosine in primates. <i>Genome Research</i> , 2017, 27, 385-392. | 5.5 | 49 |
| 3835 | Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. <i>Methods in Molecular Biology</i> , 2017, 1533, 1-31. | 0.9 | 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. | 4.1 | 106 |
| 3837 | Identification and characterization of protein coding genes in monsonia (Monsonia burkeana Planch.) Tj ETQq1 1 0.784314 rgBT /Overl | 1.4 | 4 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3838 | Level of genetic differentiation affects relative performances of expressed sequence tag and genomic SSRs. <i>Molecular Ecology Resources</i> , 2017, 17, 893-903. | 4.8 | 11 |
| 3839 | The genome draft of coconut (<i>Cocos nucifera</i>). <i>GigaScience</i> , 2017, 6, 1-11. | 6.4 | 96 |
| 3840 | Spontaneous circadian rhythms in a cold-adapted natural isolate of <i>Aureobasidium pullulans</i> . <i>Scientific Reports</i> , 2017, 7, 13837. | 3.3 | 15 |
| 3841 | sRNAAnalyzer—a flexible and customizable small RNA sequencing data analysis pipeline. <i>Nucleic Acids Research</i> , 2017, 45, 12140-12151. | 14.5 | 76 |
| 3842 | Keeping it complicated: Mitochondrial genome plasticity across diplomonads. <i>Scientific Reports</i> , 2017, 7, 14166. | 3.3 | 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 |
| 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. | 2.9 | 28 |
| 3845 | A distinct hematopoietic stem cell population for rapid multilineage engraftment in nonhuman primates. <i>Science Translational Medicine</i> , 2017, 9, . | 12.4 | 97 |
| 3846 | Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15. | 28.9 | 973 |
| 3847 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25. | 28.9 | 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. | 3.3 | 40 |
| 3849 | Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254. | 27.8 | 495 |
| 3850 | DNA sequencing at 40: past, present and future. <i>Nature</i> , 2017, 550, 345-353. | 27.8 | 729 |
| 3851 | SoyBase: A Comprehensive Database for Soybean Genetic and Genomic Data. <i>Compendium of Plant Genomes</i> , 2017, , 193-211. | 0.5 | 2 |
| 3852 | Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960. | 7.8 | 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. | 7.1 | 35 |
| 3854 | Metatranscriptomic and metagenomic description of the bacterial nitrogen metabolism in waste water wet oxidation effluents. <i>Heliyon</i> , 2017, 3, e00427. | 3.2 | 12 |
| 3855 | An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878. | 17.5 | 456 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 3856 | Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23. | 3.8 | 84 |
| 3857 | Regulation of the activity of the promoter of RNA-induced silencing, C3PO. Protein Science, 2017, 26, 1807-1818. | 7.6 | 12 |
| 3858 | The high-quality genome of <i>Brassica napus</i> cultivar 'ZS11' reveals the introgression history in semi-winter morphotype. Plant Journal, 2017, 92, 452-468. | 5.7 | 233 |
| 3859 | The draft genome assembly of <i>Rhododendron delavayi</i> Franch. var. <i>delavayi</i> . GigaScience, 2017, 6, 1-11. | 6.4 | 64 |
| 3860 | Genomic structure and evolution of the mating type locus in the green seaweed <i>Ulva partita</i> . Scientific Reports, 2017, 7, 11679. | 3.3 | 25 |
| 3861 | Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. Nature Biotechnology, 2017, 35, 969-976. | 17.5 | 356 |
| 3862 | Comprehensive analysis of lncRNAs and mRNAs in skeletal muscle of rainbow trout (<i>Oncorhynchus mykiss</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 8.3 | 9 |
| 3863 | Evaluation of single-cell genomics to address evolutionary questions using three SAGs of the choanoflagellate <i>Monosiga brevicollis</i> . Scientific Reports, 2017, 7, 11025. | 3.3 | 19 |
| 3864 | Acidophilic green algal genome provides insights into adaptation to an acidic environment. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8304-E8313. | 7.1 | 93 |
| 3865 | Identification and functional prediction of stress responsive AP2/ERF transcription factors in <i>Brassica napus</i> by genome-wide analysis. Computational Biology and Chemistry, 2017, 71, 32-56. | 2.3 | 24 |
| 3866 | On the application of reverse vaccinology to parasitic diseases: a perspective on feature selection and ranking of vaccine candidates. International Journal for Parasitology, 2017, 47, 779-790. | 3.1 | 13 |
| 3867 | Assessment of T-cell receptor repertoire and clonal expansion in peripheral T-cell lymphoma using RNA-seq data. Scientific Reports, 2017, 7, 11301. | 3.3 | 27 |
| 3868 | Single nucleotide polymorphisms for DNA typing in the domestic horse. Animal Genetics, 2017, 48, 669-676. | 1.7 | 20 |
| 3869 | Metagenomics for Monitoring Environmental Biodiversity: Challenges, Progress, and Opportunities. Health Information Science, 2017, , 73-87. | 0.4 | 2 |
| 3870 | Molecular analysis of three <i>Clostridium difficile</i> strain genomes isolated from pig farm-related samples. Anaerobe, 2017, 48, 224-231. | 2.1 | 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. Scientific Reports, 2017, 7, 7648. | 3.3 | 125 |
| 3873 | Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. Scientific Reports, 2017, 7, 8859. | 3.3 | 50 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3874 | Multi-omics Analyses of Starvation Responses Reveal a Central Role for Lipoprotein Metabolism in Acute Starvation Survival in <i>C.Âelegans</i> . <i>Cell Systems</i> , 2017, 5, 38-52.e4. | 6.2 | 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. | 12.8 | 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. | 2.0 | 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. | 2.4 | 62 |
| 3878 | Differentiating Botulinum Neurotoxin-Producing Clostridia with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , 2017, 83, . | 3.1 | 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. | 2.3 | 30 |
| 3880 | <i>KIT</i> mutations and <i>CD</i> 117 overexpression are markers of better progression-free survival in vulvar melanomas. <i>British Journal of Dermatology</i> , 2017, 177, 1376-1384. | 1.5 | 16 |
| 3881 | Splicing Activation by Rbfox Requires Self-Aggregation through Its Tyrosine-Rich Domain. <i>Cell</i> , 2017, 170, 312-323.e10. | 28.9 | 102 |
| 3882 | Development of Insertion and Deletion Markers for Bottle Gourd Based on Restriction Site-associated DNA Sequencing Data. <i>Horticultural Plant Journal</i> , 2017, 3, 13-16. | 5.0 | 9 |
| 3883 | Whole-Genome Sequencing and Concordance Between Antimicrobial Susceptibility Genotypes and Phenotypes of Bacterial Isolates Associated with Bovine Respiratory Disease. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3059-3071. | 1.8 | 19 |
| 3884 | GCN2 phosphorylates HIV-1 integrase and decreases HIV-1 replication by limiting viral integration. <i>Scientific Reports</i> , 2017, 7, 2283. | 3.3 | 17 |
| 3885 | High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. <i>Scientific Reports</i> , 2017, 7, 7106. | 3.3 | 56 |
| 3886 | A systems approach to a spatio-temporal understanding of the drought stress response in maize. <i>Scientific Reports</i> , 2017, 7, 6590. | 3.3 | 68 |
| 3887 | Quantitative metagenomics reveals unique gut microbiome biomarkers in ankylosing spondylitis. <i>Genome Biology</i> , 2017, 18, 142. | 8.8 | 268 |
| 3888 | A review of existing whole genome data suggests lichen mycelia may be haploid or diploid. <i>Bryologist</i> , 2017, 120, 302-310. | 0.6 | 14 |
| 3889 | Elevated auxin biosynthesis and transport underlie high vein density in <i>C</i> ⁴ leaves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6884-E6891. | 7.1 | 34 |
| 3890 | Presence of a Shared 5â€²-Leader Sequence in Ancestral Human and Mammalian Retroviruses and Its Transduction into Feline Leukemia Virus. <i>Journal of Virology</i> , 2017, 91, . | 3.4 | 9 |
| 3891 | Transcriptome Association Identifies Regulators of Wheat Spike Architecture. <i>Plant Physiology</i> , 2017, 175, 746-757. | 4.8 | 94 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3892 | Recombinant Origins of Pathogenic and Nonpathogenic Mouse Gammaretroviruses with Polytopic Host Range. <i>Journal of Virology</i> , 2017, 91, . | 3.4 | 14 |
| 3893 | Age, estrogen, and immune response in breast adenocarcinoma and adjacent normal tissue. <i>OncotImmunology</i> , 2017, 6, e1356142. | 4.6 | 34 |
| 3894 | MinIONâ„¢ nanopore sequencing of environmental metagenomes: a synthetic approach. <i>GigaScience</i> , 2017, 6, 1-10. | 6.4 | 111 |
| 3895 | Oncogenic Role of THOR, a Conserved Cancer/Testis Long Non-coding RNA. <i>Cell</i> , 2017, 171, 1559-1572.e20. | 28.9 | 200 |
| 3896 | Efficient transgenesis and annotated genome sequence of the regenerative flatworm model <i>Macrostomum lignano</i> . <i>Nature Communications</i> , 2017, 8, 2120. | 12.8 | 60 |
| 3897 | Genome Analysis. <i>Compendium of Plant Genomes</i> , 2017, , 3-19. | 0.5 | 0 |
| 3898 | A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017, 171, 1437-1452.e17. | 28.9 | 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. | 12.8 | 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. | 12.8 | 87 |
| 3901 | Convergent evolution of Y chromosome gene content in flies. <i>Nature Communications</i> , 2017, 8, 785. | 12.8 | 59 |
| 3902 | Genome-wide discovery of long intergenic noncoding RNAs and their epigenetic signatures in the rat. <i>Scientific Reports</i> , 2017, 7, 14817. | 3.3 | 3 |
| 3903 | Variant Review with the Integrative Genomics Viewer. <i>Cancer Research</i> , 2017, 77, e31-e34. | 0.9 | 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. | 2.0 | 22 |
| 3906 | Indoleacrylic Acid Produced by Commensal <i>Peptostreptococcus</i> Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6. | 11.0 | 523 |
| 3907 | Soft Sweeps Are the Dominant Mode of Adaptation in the Human Genome. <i>Molecular Biology and Evolution</i> , 2017, 34, 1863-1877. | 8.9 | 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. | 5.4 | 24 |
| 3909 | Personalized RNA mutanome vaccines mobilize poly-specific therapeutic immunity against cancer. <i>Nature</i> , 2017, 547, 222-226. | 27.8 | 1,806 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 3910 | Customized workflow development and data modularization concepts for RNA-Sequencing and metatranscriptome experiments. <i>Journal of Biotechnology</i> , 2017, 261, 85-96. | 3.8 | 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. | 21.4 | 693 |
| 3912 | A massively parallel strategy for STR marker development, capture, and genotyping. <i>Nucleic Acids Research</i> , 2017, 45, e142-e142. | 14.5 | 8 |
| 3913 | The pomegranate (<i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. <i>Plant Journal</i> , 2017, 91, 1108-1128. | 5.7 | 109 |
| 3914 | ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. <i>BMC Genomics</i> , 2017, 18, 7. | 2.8 | 30 |
| 3915 | Improved annotation with de novo transcriptome assembly in four social amoeba species. <i>BMC Genomics</i> , 2017, 18, 120. | 2.8 | 7 |
| 3916 | Comparative genomic identification and validation of β -defensin genes in the <i>Ovis aries</i> genome. <i>BMC Genomics</i> , 2017, 18, 278. | 2.8 | 14 |
| 3917 | A comprehensive hybridization model allows whole HERV transcriptome profiling using high density microarray. <i>BMC Genomics</i> , 2017, 18, 286. | 2.8 | 29 |
| 3918 | HirBin: high-resolution identification of differentially abundant functions in metagenomes. <i>BMC Genomics</i> , 2017, 18, 316. | 2.8 | 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. | 2.8 | 29 |
| 3920 | A simple and economical method for improving whole genome alignment. <i>BMC Genomics</i> , 2017, 18, 362. | 2.8 | 3 |
| 3921 | CottonFGD: an integrated functional genomics database for cotton. <i>BMC Plant Biology</i> , 2017, 17, 101. | 3.6 | 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. | 1.9 | 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. | 2.5 | 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. | 2.5 | 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. | 3.9 | 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. | 1.8 | 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. | 2.4 | 15 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 3928 | Distinct biogeographical patterns of marine bacterial taxonomy and functional genes. <i>Global Ecology and Biogeography</i> , 2017, 26, 177-190. | 5.8 | 65 |
| 3929 | Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. <i>Indian Journal of Microbiology</i> , 2017, 57, 23-38. | 2.7 | 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. | 2.5 | 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. | 3.8 | 43 |
| 3932 | Draft genome of the American Eel (<i>Anguilla rostrata</i>). <i>Molecular Ecology Resources</i> , 2017, 17, 806-811. | 4.8 | 21 |
| 3933 | Genomic Basis of Adaptive Evolution: The Survival of Amur Ide (<i>Leuciscus waleckii</i>) in an Extremely Alkaline Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 145-159. | 8.9 | 66 |
| 3934 | Satellite DNA content illuminates the ancestry of a supernumerary (B) chromosome. <i>Chromosoma</i> , 2017, 126, 487-500. | 2.2 | 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. | 1.3 | 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. | 1.8 | 19 |
| 3937 | A Bloom filter based semi-index on <i>q</i> -grams. <i>Software - Practice and Experience</i> , 2017, 47, 799-811. | 3.6 | 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. | 4.8 | 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, . | 3.1 | 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. | 1.0 | 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. | 6.4 | 26 |
| 3942 | Whole-genome sequencing and SNV genotyping of "Nebbiolo" (<i>Vitis vinifera</i> L.) clones. <i>Scientific Reports</i> , 2017, 7, 17294. | 3.3 | 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. | 0.5 | 0 |
| 3945 | Long-read sequence assembly of the firefly <i>Pyrocoelia pectoralis</i> genome. <i>GigaScience</i> , 2017, 6, 1-7. | 6.4 | 32 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 3946 | Draft genome of the lined seahorse, <i>Hippocampus erectus</i> . GigaScience, 2017, 6, 1-6. | 6.4 | 38 |
| 3947 | CNVcaller: highly efficient and widely applicable software for detecting copy number variations in large populations. GigaScience, 2017, 6, 1-12. | 6.4 | 101 |
| 3948 | Root transcriptomic responses of grafted grapevines to heterogeneous nitrogen availability depend on rootstock genotype. Journal of Experimental Botany, 2017, 68, 4339-4355. | 4.8 | 42 |
| 3949 | Genome-wide analysis of SSR and ILP markers in trees: diversity profiling, alternate distribution, and applications in duplication. Scientific Reports, 2017, 7, 17902. | 3.3 | 20 |
| 3950 | Genomics Resources for Peanut Improvement. Compendium of Plant Genomes, 2017, , 69-91. | 0.5 | 7 |
| 3951 | A SNP-enabled assessment of genetic diversity, evolutionary relationships and the identification of candidate genes in chrysanthemum. Genome Biology and Evolution, 2017, 8, eww270. | 2.5 | 38 |
| 3952 | Transcriptome assembly in <i>Suaeda aralocaspica</i> to reveal the distinct temporal gene/miRNA alterations between the dimorphic seeds during germination. BMC Genomics, 2017, 18, 806. | 2.8 | 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> . EvoDevo, 2017, 8, 16. | 3.2 | 4 |
| 3954 | Scaling bioinformatics applications on HPC. BMC Bioinformatics, 2017, 18, 501. | 2.6 | 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. BMC Genomics, 2017, 18, 558. | 2.8 | 35 |
| 3957 | The draft genome of <i>Ruellia speciosa</i> (Beautiful Wild Petunia: Acanthaceae). DNA Research, 2017, 24, dsw054. | 3.4 | 31 |
| 3958 | Evolution of Alu Subfamily Structure in the Saimiri Lineage of New World Monkeys. Genome Biology and Evolution, 2017, 9, 2365-2376. | 2.5 | 16 |
| 3959 | An Annotated Draft Genome for <i>Radix auricularia</i> (Gastropoda, Mollusca). Genome Biology and Evolution, 2017, 9, 585-592. | 2.5 | 57 |
| 3960 | Detecting large deletions at base pair level by combining split read and paired read data. BMC Bioinformatics, 2017, 18, 413. | 2.6 | 2 |
| 3961 | Gapless genome assembly of <i>Colletotrichum higginsianum</i> reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. BMC Genomics, 2017, 18, 667. | 2.8 | 111 |
| 3962 | The coding and noncoding transcriptome of <i>Neurospora crassa</i> . BMC Genomics, 2017, 18, 978. | 2.8 | 26 |
| 3963 | Establishment of a genome-wide and quantitative protocol for assessment of transcriptional activity at human retrotransposon L1 antisense promoters. Genes and Genetic Systems, 2017, 92, 243-249. | 0.7 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 3964 | Global transcriptional landscape and promoter mapping of the gut commensal <i>Bifidobacterium breve</i> UCC2003. <i>BMC Genomics</i> , 2017, 18, 991. | 2.8 | 24 |
| 3965 | Photosynthesis in <i>C₃</i> â€C ₄ intermediate <i>Moricandia</i> species. <i>Journal of Experimental Botany</i> , 2017, 68, 191-206. | 4.8 | 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. | 3.1 | 33 |
| 3967 | Optimal choice of word length when comparing two Markov sequences using a χ^2 -statistic. <i>BMC Genomics</i> , 2017, 18, 732. | 2.8 | 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. | 3.6 | 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. | 3.6 | 65 |
| 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. | 3.6 | 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. | 3.6 | 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. | 3.6 | 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. | 3.6 | 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. | 2.8 | 54 |
| 3975 | Reliable Detection of Herpes Simplex Virus Sequence Variation by High-Throughput Resequencing. <i>Viruses</i> , 2017, 9, 226. | 3.3 | 9 |
| 3976 | Interpreting whole genome and exome sequencing data of individual gastric cancer samples. <i>BMC Genomics</i> , 2017, 18, 517. | 2.8 | 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. | 2.0 | 19 |
| 3978 | A Massively Parallel Sequence Similarity Search for Metagenomic Sequencing Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2124. | 4.1 | 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. | 4.6 | 52 |
| 3980 | Transcriptomic Complexity of <i>Aspergillus terreus</i> Velvet Gene Family under the Influence of Butyrolactone I. <i>Microorganisms</i> , 2017, 5, 12. | 3.6 | 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. | 2.6 | 30 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 3982 | LTR-Retrotransposons from Bdelloid Rotifers Capture Additional ORFs Shared between Highly Diverse Retroelement Types. <i>Viruses</i> , 2017, 9, 78. | 3.3 | 10 |
| 3983 | Contrasting patterns of evolutionary constraint and novelty revealed by comparative sperm proteomic analysis in Lepidoptera. <i>BMC Genomics</i> , 2017, 18, 931. | 2.8 | 18 |
| 3984 | A Frameshift Mutation in KIT Is Associated with White Spotting in the Arabian Camel. <i>Genes</i> , 2017, 8, 1024. | 2.4 | 33 |
| 3985 | Dynamics of genomic innovation in the unicellular ancestry of animals. <i>ELife</i> , 2017, 6, . | 6.0 | 121 |
| 3986 | A Glimpse into the Satellite DNA Library in Characidae Fish (Teleostei, Characiformes). <i>Frontiers in Genetics</i> , 2017, 8, 103. | 2.3 | 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. | 4.8 | 20 |
| 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. | 3.5 | 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. | 3.5 | 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. | 1.9 | 3 |
| 3991 | PALADIN: protein alignment for functional profiling whole metagenome shotgun data. <i>Bioinformatics</i> , 2017, 33, 1473-1478. | 4.1 | 38 |
| 3992 | A Review on Recent Computational Methods for Predicting Noncoding RNAs. <i>BioMed Research International</i> , 2017, 2017, 1-14. | 1.9 | 25 |
| 3993 | Describing Genomic and Epigenomic Traits Underpinning Emerging Fungal Pathogens. <i>Advances in Genetics</i> , 2017, 100, 73-140. | 1.8 | 17 |
| 3994 | HLA genotyping by next-generation sequencing of complementary DNA. <i>BMC Genomics</i> , 2017, 18, 914. | 2.8 | 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. | 2.5 | 39 |
| 3996 | MIPE: A metagenome-based community structure explorer and SSU primer evaluation tool. <i>PLoS ONE</i> , 2017, 12, e0174609. | 2.5 | 7 |
| 3997 | The Agassiz's desert tortoise genome provides a resource for the conservation of a threatened species. <i>PLoS ONE</i> , 2017, 12, e0177708. | 2.5 | 33 |
| 3998 | The effects of sampling on the efficiency and accuracy of k-mer indexes: Theoretical and empirical comparisons using the human genome. <i>PLoS ONE</i> , 2017, 12, e0179046. | 2.5 | 1 |
| 3999 | Microbiome overview in swine lungs. <i>PLoS ONE</i> , 2017, 12, e0181503. | 2.5 | 33 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 4000 | Comprehensive benchmarking of SNV callers for highly admixed tumor data. PLoS ONE, 2017, 12, e0186175. | 2.5 | 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. PLoS ONE, 2017, 12, e0189785. | 2.5 | 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. PLoS Genetics, 2017, 13, e1006823. | 3.5 | 118 |
| 4003 | A comprehensive overview and evaluation of circular RNA detection tools. PLoS Computational Biology, 2017, 13, e1005420. | 3.2 | 313 |
| 4004 | An independent component analysis confounding factor correction framework for identifying broad impact expression quantitative trait loci. PLoS Computational Biology, 2017, 13, e1005537. | 3.2 | 12 |
| 4005 | Rfx2 Stabilizes Foxj1 Binding at Chromatin Loops to Enable Multiciliated Cell Gene Expression. PLoS Genetics, 2017, 13, e1006538. | 3.5 | 68 |
| 4006 | Genomic introgression mapping of field-derived multiple-anthelmintic resistance in <i>Teladorsagia circumcincta</i> . PLoS Genetics, 2017, 13, e1006857. | 3.5 | 67 |
| 4007 | Flavivirus and Filovirus EvoPrinters: New alignment tools for the comparative analysis of viral evolution. PLoS Neglected Tropical Diseases, 2017, 11, e0005673. | 3.0 | 3 |
| 4008 | A miRNA catalogue and ncRNA annotation of the short-living fish <i>Nothobranchius furzeri</i> . BMC Genomics, 2017, 18, 693. | 2.8 | 18 |
| 4009 | Evaluating allopolyploid origins in strawberries (<i>Fragaria</i>) using haplotypes generated from target capture sequencing. BMC Evolutionary Biology, 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. BMC Evolutionary Biology, 2017, 17, 224. | 3.2 | 18 |
| 4011 | Gene expression patterns of chicken neuregulin 3 in association with copy number variation and frameshift deletion. BMC Genetics, 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). BMC Genetics, 2017, 18, 119. | 2.7 | 27 |
| 4013 | The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC Biology, 2017, 15, 62. | 3.8 | 286 |
| 4014 | Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur (<i>Microcebus murinus</i>). BMC Biology, 2017, 15, 110. | 3.8 | 53 |
| 4015 | De novo assembly and characterization of breast cancer transcriptomes identifies large numbers of novel fusion-gene transcripts of potential functional significance. BMC Medical Genomics, 2017, 10, 53. | 1.5 | 10 |
| 4016 | HAlign-II: efficient ultra-large multiple sequence alignment and phylogenetic tree reconstruction with distributed and parallel computing. Algorithms for Molecular Biology, 2017, 12, 25. | 1.2 | 30 |
| 4017 | SuperTranscripts: a data driven reference for analysis and visualisation of transcriptomes. Genome Biology, 2017, 18, 148. | 8.8 | 79 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4018 | Consideration of non-canonical splice sites improves gene prediction on the Arabidopsis thaliana Niederzenz-1 genome sequence. BMC Research Notes, 2017, 10, 667. | 1.4 | 24 |
| 4019 | Stress amplifies sex differences in primate prefrontal profiles of gene expression. Biology of Sex Differences, 2017, 8, 36. | 4.1 | 7 |
| 4020 | Perilipin-2 modulates dietary fat-induced microbial global gene expression profiles in the mouse intestine. Microbiome, 2017, 5, 117. | 11.1 | 17 |
| 4021 | Comparative Transcriptome and DNA methylation analyses of the molecular mechanisms underlying skin color variations in Crucian carp (<i>Carassius carassius</i> L.). BMC Genetics, 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. BMC Bioinformatics, 2017, 18, 467. | 2.6 | 17 |
| 4023 | Similarity Projection: A Geometric Measure for Comparison of Biological Sequences. , 2017, , . | | 0 |
| 4024 | Transcriptome analysis reveals the host selection fitness mechanisms of the Rhizoctonia solani AG11A pathogen. Scientific Reports, 2017, 7, 10120. | 3.3 | 43 |
| 4025 | MPD: multiplex primer design for next-generation targeted sequencing. BMC Bioinformatics, 2017, 18, 14. | 2.6 | 23 |
| 4026 | Detection and quantification of mitochondrial DNA deletions from next-generation sequence data. BMC Bioinformatics, 2017, 18, 407. | 2.6 | 29 |
| 4027 | VISMapper: ultra-fast exhaustive cartography of viral insertion sites for gene therapy. BMC Bioinformatics, 2017, 18, 421. | 2.6 | 1 |
| 4028 | An optimized approach for annotation of large eukaryotic genomic sequences using genetic algorithm. BMC Bioinformatics, 2017, 18, 460. | 2.6 | 2 |
| 4029 | Fast batch searching for protein homology based on compression and clustering. BMC Bioinformatics, 2017, 18, 508. | 2.6 | 6 |
| 4030 | Overexpressed HSF1 cancer signature genes cluster in human chromosome 8q. Human Genomics, 2017, 11, 35. | 2.9 | 17 |
| 4031 | Draft de novo transcriptome assembly and proteome characterization of the electric lobe of Tetronarce californica: a molecular tool for the study of cholinergic neurotransmission in the electric organ. BMC Genomics, 2017, 18, 611. | 2.8 | 7 |
| 4032 | C ³ cotyledons are followed by C ⁴ leaves: intra-individual transcriptome analysis of <i>Salsola soda</i> (Chenopodiaceae). Journal of Experimental Botany, 2017, 68, 161-176. | 4.8 | 29 |
| 4033 | Transcriptome Analysis for Non-Model Organism: Current Status and Best-Practices. , 0, , . | | 10 |
| 4034 | RetrogeneDB—a database of plant and animal retrocopies. Database: the Journal of Biological Databases and Curation, 2017, 2017, . | 3.0 | 30 |
| 4035 | Identification of Proteases and Protease Inhibitors in Allergenic and Non-Allergenic Pollen. International Journal of Molecular Sciences, 2017, 18, 1199. | 4.1 | 19 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 2.0 | 53 |
| 4037 | Efficient Genome-wide Association in Biobanks Using Topic Modeling Identifies Multiple Novel Disease Loci. <i>Molecular Medicine</i> , 2017, 23, 285-294. | 4.4 | 19 |
| 4038 | Approaches for in silico finishing of microbial genome sequences. <i>Genetics and Molecular Biology</i> , 2017, 40, 553-576. | 1.3 | 17 |
| 4039 | Cooptio 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. | 7.1 | 25 |
| 4040 | Site-specificity of serine integrase demonstrated by the <i>attB</i> sequence preference of <i>Escherichia coli</i> integrase. <i>FEBS Letters</i> , 2018, 592, 1389-1399. | 2.8 | 3 |
| 4041 | Analysis of RNA Editing Sites from RNA-Seq Data Using GIREMI. <i>Methods in Molecular Biology</i> , 2018, 1751, 101-108. | 0.9 | 7 |
| 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. | 2.5 | 10 |
| 4044 | A translational silencing function of MCP1/Regnase-1 specified by the target site context. <i>Nucleic Acids Research</i> , 2018, 46, 4256-4270. | 14.5 | 20 |
| 4045 | Evolution of pyrrolizidine alkaloid biosynthesis in Apocynaceae: revisiting the defence de-escalation hypothesis. <i>New Phytologist</i> , 2018, 218, 762-773. | 7.3 | 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. | 2.9 | 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. | 1.5 | 11 |
| 4048 | Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. <i>Nature</i> , 2018, 555, 371-376. | 27.8 | 649 |
| 4049 | Discovery of coding regions in the human genome by integrated proteogenomics analysis workflow. <i>Nature Communications</i> , 2018, 9, 903. | 12.8 | 108 |
| 4050 | Landscape of the spliced leader trans-splicing mechanism in <i>Schistosoma mansoni</i> . <i>Scientific Reports</i> , 2018, 8, 3877. | 3.3 | 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. | 2.7 | 49 |
| 4052 | Gain-of-function analysis of cis-acting diversification elements in <i>DT40</i> cells. <i>Immunology and Cell Biology</i> , 2018, 96, 948-957. | 2.3 | 1 |
| 4053 | Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335. | 12.6 | 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. | 10.3 | 48 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4055 | A Blast implementation in Hadoop MapReduce using low cost commodity hardware. <i>Procedia Computer Science</i> , 2018, 127, 69-75. | 2.0 | 5 |
| 4056 | Chromosome-scale assembly of the <i>Monopterus</i> genome. <i>GigaScience</i> , 2018, 7, . | 6.4 | 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. | 5.6 | 71 |
| 4058 | De novo draft assembly of the <i>Botryllodes leachii</i> genome provides further insight into tunicate evolution. <i>Scientific Reports</i> , 2018, 8, 5518. | 3.3 | 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. | 3.8 | 33 |
| 4060 | Improved de novo genomic assembly for the domestic donkey. <i>Science Advances</i> , 2018, 4, eaaq0392. | 10.3 | 46 |
| 4061 | G-Anchor: a novel approach for whole-genome comparative mapping utilizing evolutionary conserved DNA sequences. <i>GigaScience</i> , 2018, 7, . | 6.4 | 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. | 1.0 | 39 |
| 4063 | Draft genome of the Peruvian scallop <i>Argopecten purpuratus</i> . <i>GigaScience</i> , 2018, 7, . | 6.4 | 60 |
| 4064 | The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. <i>Cancer Cell</i> , 2018, 33, 607-619.e15. | 16.8 | 88 |
| 4065 | L1 retrotransposition is a common feature of mammalian hepatocarcinogenesis. <i>Genome Research</i> , 2018, 28, 639-653. | 5.5 | 79 |
| 4066 | HNRNPA1 promotes recognition of splice site decoys by U2AF2 in vivo. <i>Genome Research</i> , 2018, 28, 689-698. | 5.5 | 28 |
| 4067 | Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668. | 7.8 | 124 |
| 4068 | Genomic Analyses Yield Markers for Identifying Agronomically Important Genes in Potato. <i>Molecular Plant</i> , 2018, 11, 473-484. | 8.3 | 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. | 2.7 | 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. | 3.3 | 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. | 28.9 | 189 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4073 | Whole-genome assembly of the coral reef Pearlscale Pygmy Angelfish (<i>Centropyge vrolikii</i>). Scientific Reports, 2018, 8, 1498. | 3.3 | 13 |
| 4074 | Contribution of transposable elements and distal enhancers to evolution of human-specific features of interphase chromatin architecture in embryonic stem cells. Chromosome Research, 2018, 26, 61-84. | 2.2 | 28 |
| 4075 | Identification of an (AC) _n microsatellite in the Six1 gene promoter and its effect on production traits in Pietrain × Duroc × Landrace × Yorkshire pigs1. Journal of Animal Science, 2018, 96, 17-26. | 0.5 | 3 |
| 4076 | 5-Azacytidine prevents relapse and produces long-term complete remissions in leukemia xenografts treated with Moxetumomab pasudotox. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1867-E1875. | 7.1 | 12 |
| 4077 | ZNF462 and KLF12 are disrupted by a de novo translocation in a patient with syndromic intellectual disability and autism spectrum disorder. European Journal of Medical Genetics, 2018, 61, 376-383. | 1.3 | 13 |
| 4078 | Novel FR-900493 Analogues That Inhibit the Outgrowth of <i>Clostridium difficile</i> Spores. ACS Omega, 2018, 3, 1726-1739. | 3.5 | 21 |
| 4079 | The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10. | 16.8 | 270 |
| 4080 | Genome sequence and description of <i>Haloferax massiliense</i> sp. nov., a new halophilic archaeon isolated from the human gut. Extremophiles, 2018, 22, 485-498. | 2.3 | 14 |
| 4081 | SLAF-based high-density genetic map construction and QTL mapping for major economic traits in sea urchin <i>Strongylocentrotus intermedius</i> . Scientific Reports, 2018, 8, 820. | 3.3 | 33 |
| 4082 | Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. Nucleic Acids Research, 2018, 46, e38-e38. | 14.5 | 116 |
| 4083 | Draft genome and reference transcriptomic resources for the urticating pine defoliator <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). Molecular Ecology Resources, 2018, 18, 602-619. | 4.8 | 23 |
| 4084 | Genome assembly of the Pink Ipê ^a (<i>Handroanthus impetiginosus</i> , Bignoniaceae), a highly valued, ecologically keystone Neotropical timber forest tree. GigaScience, 2018, 7, 1-16. | 6.4 | 23 |
| 4085 | Uncovering Genomic Regions Associated with <i>Trypanosoma</i> Infections in Wild Populations of the Tsetse Fly <i>Glossina fuscipes</i> . G3: Genes, Genomes, Genetics, 2018, 8, 887-897. | 1.8 | 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. Journal of Biotechnology, 2018, 267, 12-18. | 3.8 | 13 |
| 4087 | <i>MYRF</i> is associated with encephalopathy with reversible myelin vacuolization. Annals of Neurology, 2018, 83, 98-106. | 5.3 | 35 |
| 4088 | Detection of de novo single nucleotide variants in offspring of atomic-bomb survivors close to the hypocenter by whole-genome sequencing. Journal of Human Genetics, 2018, 63, 357-363. | 2.3 | 20 |
| 4089 | The Hidden Genomic and Transcriptomic Plasticity of Giant Marker Chromosomes in Cancer. Genetics, 2018, 208, 951-961. | 2.9 | 13 |
| 4090 | Duplicated membrane estrogen receptors in the European sea bass (<i>Dicentrarchus labrax</i>): Phylogeny, expression and regulation throughout the reproductive cycle. Journal of Steroid Biochemistry and Molecular Biology, 2018, 178, 234-242. | 2.5 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4091 | Transcription profiling and identification of infection-related genes in <i>Phytophthora cactorum</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 541-555. | 2.1 | 23 |
| 4092 | Computational Strategies for Exploring Circular RNAs. <i>Trends in Genetics</i> , 2018, 34, 389-400. | 6.7 | 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. | 7.2 | 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. | 6.4 | 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. | 2.5 | 33 |
| 4096 | POU6f1 Mediates Neuropeptide-Dependent Plasticity in the Adult Brain. <i>Journal of Neuroscience</i> , 2018, 38, 1443-1461. | 3.6 | 20 |
| 4097 | DNAAF1 links heart laterality with the AAA+ ATPase RUVBL1 and ciliary intraflagellar transport. <i>Human Molecular Genetics</i> , 2018, 27, 529-545. | 2.9 | 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. | 2.5 | 61 |
| 4099 | Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. <i>Science</i> , 2018, 359, 55-61. | 12.6 | 102 |
| 4100 | Multiplexed gene synthesis in emulsions for exploring protein functional landscapes. <i>Science</i> , 2018, 359, 343-347. | 12.6 | 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. | 2.8 | 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. | 2.8 | 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. | 2.8 | 56 |
| 4105 | FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. <i>Genome Biology</i> , 2018, 19, 38. | 8.8 | 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. | 3.6 | 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. | 2.8 | 10 |
| 4108 | Alignment-Free Sequence Analysis and Applications. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 93-114. | 6.5 | 78 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4109 | A new strategy to infer circularity applied to four new complete frog mitogenomes. Ecology and Evolution, 2018, 8, 4011-4018. | 1.9 | 15 |
| 4110 | Partially Local Multi-way Alignments. Mathematics in Computer Science, 2018, 12, 207-234. | 0.4 | 4 |
| 4111 | Necklace: combining reference and assembled transcriptomes for more comprehensive RNA-Seq analysis. GigaScience, 2018, 7, . | 6.4 | 9 |
| 4112 | Targeting legume loci: A comparison of three methods for target enrichment bait design in Leguminosae phylogenomics. Applications in Plant Sciences, 2018, 6, e1036. | 2.1 | 64 |
| 4113 | The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . Nature Communications, 2018, 9, 1702. | 12.8 | 73 |
| 4114 | Piercing the dark matter: bioinformatics of long-range sequencing and mapping. Nature Reviews Genetics, 2018, 19, 329-346. | 16.3 | 395 |
| 4115 | DNA Conformation Induces Adaptable Binding by Tandem Zinc Finger Proteins. Cell, 2018, 173, 221-233.e12. | 28.9 | 52 |
| 4116 | HybPhyloMaker: Target Enrichment Data Analysis From Raw Reads to Species Trees. Evolutionary Bioinformatics, 2018, 14, 117693431774261. | 1.2 | 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> . G3: Genes, Genomes, Genetics, 2018, 8, 1367-1377. | 1.8 | 15 |
| 4118 | Genomic insight into the taxonomy of <i>Rhizobium</i> genospecies that nodulate <i>Phaseolus vulgaris</i> . Systematic and Applied Microbiology, 2018, 41, 300-310. | 2.8 | 44 |
| 4119 | High-density genetic map construction and comparative genome analysis in asparagus bean. Scientific Reports, 2018, 8, 4836. | 3.3 | 16 |
| 4120 | Deep learning improves antimicrobial peptide recognition. Bioinformatics, 2018, 34, 2740-2747. | 4.1 | 282 |
| 4121 | HOXB7 overexpression in lung cancer is a hallmark of acquired stem-like phenotype. Oncogene, 2018, 37, 3575-3588. | 5.9 | 29 |
| 4122 | Darwin. , 2018, , . | | 66 |
| 4123 | Rapid Multiplex Small DNA Sequencing on the MinION Nanopore Sequencing Platform. G3: Genes, Genomes, Genetics, 2018, 8, 1649-1657. | 1.8 | 25 |
| 4124 | High-throughput analysis of satellite DNA in the grasshopper <i>Pyrgomorpha conica</i> reveals abundance of homologous and heterologous higher-order repeats. Chromosoma, 2018, 127, 323-340. | 2.2 | 29 |
| 4125 | Phylogenomic evidence for a recent and rapid radiation of lizards in the Patagonian <i>Liolaemus fitzingerii</i> species group. Molecular Phylogenetics and Evolution, 2018, 125, 243-254. | 2.7 | 25 |
| 4126 | Genome-wide association identifies a novel locus for delirium risk. Neurobiology of Aging, 2018, 68, 160.e9-160.e14. | 3.1 | 14 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4127 | Identification and characterization of evolutionarily conserved alternative splicing events in a mangrove genus <i>Sonneratia</i> . <i>Scientific Reports</i> , 2018, 8, 4425. | 3.3 | 5 |
| 4128 | EumicrobeDBLite: a lightweight genomic resource and analytic platform for draft oomycete genomes. <i>Molecular Plant Pathology</i> , 2018, 19, 227-237. | 4.2 | 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. | 3.0 | 1 |
| 4130 | LINE-1 Hypermethylation in Serum Cell-Free DNA of Relapsing Remitting Multiple Sclerosis Patients. <i>Molecular Neurobiology</i> , 2018, 55, 4681-4688. | 4.0 | 24 |
| 4131 | Genome structure of <i>Rosa multiflora</i> , a wild ancestor of cultivated roses. <i>DNA Research</i> , 2018, 25, 113-121. | 3.4 | 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. | 8.2 | 1 |
| 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. | 1.1 | 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. | 0.9 | 21 |
| 4135 | Intelligent mining of large-scale bio-data: Bioinformatics applications. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 10-29. | 1.3 | 29 |
| 4136 | Quantitative sequence characterization for repetitive DNA content in the supernumerary chromosome of the migratory locust. <i>Chromosoma</i> , 2018, 127, 45-57. | 2.2 | 25 |
| 4137 | qPrimerDB: a thermodynamics-based gene-specific qPCR primer database for 147 organisms. <i>Nucleic Acids Research</i> , 2018, 46, D1229-D1236. | 14.5 | 115 |
| 4138 | <i>ABCA4</i> midgenes reveal the full splice spectrum of all reported noncanonical splice site variants in Stargardt disease. <i>Genome Research</i> , 2018, 28, 100-110. | 5.5 | 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. | 3.8 | 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. | 0.9 | 4 |
| 4141 | The Hardy Rubber Tree Genome Provides Insights into the Evolution of Polyisoprene Biosynthesis. <i>Molecular Plant</i> , 2018, 11, 429-442. | 8.3 | 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. | 5.5 | 81 |
| 4143 | The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533. | 5.7 | 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. | 8.3 | 50 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 4145 | Voluntary exposure to a toxin: the genetic influence on ethanol consumption. <i>Mammalian Genome</i> , 2018, 29, 128-140. | 2.2 | 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. | 1.5 | 7 |
| 4147 | Conservation analysis of long non-coding RNAs in plants. <i>Science China Life Sciences</i> , 2018, 61, 190-198. | 4.9 | 83 |
| 4148 | Stable Core Gut Microbiota across the Freshwater-to-Saltwater Transition for Farmed Atlantic Salmon. <i>Applied and Environmental Microbiology</i> , 2018, 84, . | 3.1 | 90 |
| 4149 | Microhaplotypes provide increased power from short-read DNA sequences for relationship inference. <i>Molecular Ecology Resources</i> , 2018, 18, 296-305. | 4.8 | 101 |
| 4150 | Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. <i>New Phytologist</i> , 2018, 217, 1292-1306. | 7.3 | 92 |
| 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. | 2.8 | 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. | 4.8 | 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. | 2.9 | 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. | 3.3 | 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. | 3.4 | 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. | 3.3 | 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. | 3.3 | 9 |
| 4160 | A benchmark study of sequence alignment methods for protein clustering. <i>BMC Bioinformatics</i> , 2018, 19, 529. | 2.6 | 26 |
| 4161 | Replication-incompetent gammaretroviral and lentiviral vector-based insertional mutagenesis screens identify prostate cancer progression genes. <i>Oncotarget</i> , 2018, 9, 15451-15463. | 1.8 | 18 |
| 4162 | Inference of Sequence Homology by BLAST visualization of Influenza Genome set. , 2018, , . | | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. International Journal of Molecular Sciences, 2018, 19, 3201. | 4.1 | 29 |
| 4165 | Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. Cell Reports, 2018, 25, 2617-2633. | 6.4 | 74 |
| 4166 | Predicting Genes in Single Genomes with AUGUSTUS. Current Protocols in Bioinformatics, 2019, 65, e57. | 25.8 | 225 |
| 4167 | Whole genome sequencing of Trypanosoma cruzi field isolates reveals extensive genomic variability and complex aneuploidy patterns within TcII DTU. BMC Genomics, 2018, 19, 816. | 2.8 | 45 |
| 4168 | Wingless promotes EGFR signaling in follicle stem cells to maintain self-renewal. Development (Cambridge), 2018, 145, dev168716. | 2.5 | 26 |
| 4169 | Mobile elements contribute to the uniqueness of human genome with 15,000 human-specific insertions and 14Âmbp sequence increase. DNA Research, 2018, 25, 521-533. | 3.4 | 45 |
| 4170 | Regulatory processes that control haploid expression of salmon sperm mRNAs. BMC Research Notes, 2018, 11, 639. | 1.4 | 1 |
| 4171 | Transcriptome reprogramming during severe dehydration contributes to physiological and metabolic changes in the resurrection plant Haberlea rhodopensis. BMC Plant Biology, 2018, 18, 351. | 3.6 | 40 |
| 4172 | Comparative genetic and genomic analysis of the novel fusellovirus Sulfolobus spindle-shaped virus 10. Virus Evolution, 2018, 4, vey022. | 4.9 | 20 |
| 4173 | A Method for RNA Structure Prediction Shows Evidence for Structure in lncRNAs. Frontiers in Molecular Biosciences, 2018, 5, 111. | 3.5 | 16 |
| 4174 | RGAAT: A Reference-based Genome Assembly and Annotation Tool for New Genomes and Upgrade of Known Genomes. Genomics, Proteomics and Bioinformatics, 2018, 16, 373-381. | 6.9 | 15 |
| 4175 | Assessing the impact of exact reads on reducing the error rate of read mapping. BMC Bioinformatics, 2018, 19, 406. | 2.6 | 2 |
| 4176 | The genomic landscape of molecular responses to natural drought stress in Panicum hallii. Nature Communications, 2018, 9, 5213. | 12.8 | 101 |
| 4177 | Comparative genomics of 84 Pectobacterium genomes reveals the variations related to a pathogenic lifestyle. BMC Genomics, 2018, 19, 889. | 2.8 | 53 |
| 4178 | Full Shotgun DNA Metagenomics. Learning Materials in Biosciences, 2018, , 163-175. | 0.4 | 1 |
| 4179 | High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. Nature Communications, 2018, 9, 5114. | 12.8 | 2,816 |
| 4180 | The transcriptomic landscape of yaks reveals molecular pathways for high altitude adaptation. Genome Biology and Evolution, 2019, 11, 72-85. | 2.5 | 41 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.3 | 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. | 2.3 | 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. | 6.6 | 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. | 2.5 | 17 |
| 4185 | Progress of analytical tools and techniques for human gut microbiome research. <i>Journal of Microbiology</i> , 2018, 56, 693-705. | 2.8 | 49 |
| 4186 | High-Throughput Genotyping of CRISPR/Cas Edited Cells in 96-Well Plates. <i>Methods and Protocols</i> , 2018, 1, 29. | 2.0 | 6 |
| 4187 | Roquin targets mRNAs in a 3' UTR-specific manner by different modes of regulation. <i>Nature Communications</i> , 2018, 9, 3810. | 12.8 | 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. | 2.5 | 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. | 3.6 | 35 |
| 4190 | Considerations for Optimization of High-Throughput Sequencing Bioinformatics Pipelines for Virus Detection. <i>Viruses</i> , 2018, 10, 528. | 3.3 | 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. | 1.6 | 13 |
| 4192 | MetaPGN: a pipeline for construction and graphical visualization of annotated pangenome networks. <i>GigaScience</i> , 2018, 7, . | 6.4 | 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. | 3.5 | 34 |
| 4194 | Repurposing of promoters and enhancers during mammalian evolution. <i>Nature Communications</i> , 2018, 9, 4066. | 12.8 | 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. | 7.1 | 18 |
| 4196 | Genome-wide Surveillance of Transcription Errors in Eukaryotic Organisms. <i>Journal of Visualized Experiments</i> , 2018, . | 0.3 | 5 |
| 4197 | Rapid preimplantation genetic screening using a handheld, nanopore-based DNA sequencer. <i>Fertility and Sterility</i> , 2018, 110, 910-916.e2. | 1.0 | 18 |
| 4198 | Single-step Precision Genome Editing in Yeast Using CRISPR-Cas9. <i>Bio-protocol</i> , 2018, 8, . | 0.4 | 45 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4199 | Unicellular Origin of the Animal MicroRNA Machinery. <i>Current Biology</i> , 2018, 28, 3288-3295.e5. | 3.9 | 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. | 2.5 | 1 |
| 4201 | Deciphering Genome Organization of the Polyploid <i>Brassica napus</i> . <i>Compendium of Plant Genomes</i> , 2018, , 87-97. | 0.5 | 0 |
| 4202 | Fine Mapping of Lobed Leaf Genes in Two <i>Brassica napus</i> Lines Using SLAF Sequencing. <i>Crop Science</i> , 2018, 58, 1684-1692. | 1.8 | 1 |
| 4203 | Genomic distribution of a novel <i>Pyrenophora tritici-repentis</i> ToxA insertion element. <i>PLoS ONE</i> , 2018, 13, e0206586. | 2.5 | 16 |
| 4204 | Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. <i>Nature Plants</i> , 2018, 4, 879-887. | 9.3 | 316 |
| 4205 | Firefly genomes illuminate parallel origins of bioluminescence in beetles. <i>ELife</i> , 2018, 7, . | 6.0 | 108 |
| 4206 | UM-HACC-2A: MYB-NFIB fusion-positive human adenoid cystic carcinoma cell line. <i>Oral Oncology</i> , 2018, 87, 21-28. | 1.5 | 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. | 4.1 | 27 |
| 4208 | Classifying Protein Specific Residue Structures Based on Graph Mining. <i>IEEE Access</i> , 2018, 6, 55828-55837. | 4.2 | 3 |
| 4209 | The somatic piRNA pathway controls germline transposition over generations. <i>Nucleic Acids Research</i> , 2018, 46, 9524-9536. | 14.5 | 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. | 2.4 | 30 |
| 4211 | A Comparative Assessment of Human and Chimpanzee iPSC-derived Cardiomyocytes with Primary Heart Tissues. <i>Scientific Reports</i> , 2018, 8, 15312. | 3.3 | 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. | 3.3 | 0 |
| 4213 | Homology Search and Multiple Alignment. <i>Computational Biology</i> , 2018, , 325-360. | 0.2 | 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. | 5.7 | 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. | 2.5 | 27 |
| 4216 | Xenotropic Mouse Gammaretroviruses Isolated from Pre-Leukemic Tissues Include a Recombinant. <i>Viruses</i> , 2018, 10, 418. | 3.3 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4217 | Evolutionary conservation of Y Chromosome ampliconic gene families despite extensive structural variation. <i>Genome Research</i> , 2018, 28, 1841-1851. | 5.5 | 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. | 3.6 | 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. | 3.0 | 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. | 2.5 | 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. | 2.5 | 1 |
| 4222 | Development of Species-Specific InDel Markers in Citrus. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 653-662. | 1.8 | 9 |
| 4223 | Genome Annotation of a Model Diatom <i>Phaeodactylum tricornutum</i> Using an Integrated Proteogenomic Pipeline. <i>Molecular Plant</i> , 2018, 11, 1292-1307. | 8.3 | 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. | 2.5 | 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. | 3.9 | 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. | 1.5 | 12 |
| 4227 | The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018, 562, 373-379. | 27.8 | 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. | 7.1 | 180 |
| 4229 | Comparative genomics and transcriptomics of <i>Chrysolophus</i> provide insights into the evolution of complex plumage colouration. <i>GigaScience</i> , 2018, 7, . | 6.4 | 14 |
| 4230 | From Short Reads to Chromosome-Scale Genome Assemblies. <i>Methods in Molecular Biology</i> , 2018, 1848, 151-197. | 0.9 | 7 |
| 4231 | Repeated translocation of a gene cassette drives sex-chromosome turnover in strawberries. <i>PLoS Biology</i> , 2018, 16, e2006062. | 5.6 | 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. | 3.3 | 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. | 1.3 | 38 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4235 | The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769. | 14.5 | 476 |
| 4236 | Chromosome Yâ€‘encoded antigens associate with acute graft-versus-host disease in sex-mismatched stem cell transplant. <i>Blood Advances</i> , 2018, 2, 2419-2429. | 5.2 | 11 |
| 4237 | Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018, 9, 2054. | 12.8 | 68 |
| 4238 | Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509. | 27.8 | 433 |
| 4239 | The Eukaryotic Proteome Is Shaped by E3Â‘Ubiquitin Ligases Targeting C-Terminal Degrons. <i>Cell</i> , 2018, 173, 1622-1635.e14. | 28.9 | 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. | 6.2 | 147 |
| 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. | 0.9 | 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. | 14.5 | 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. | 14.5 | 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. | 14.5 | 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. | 1.7 | 87 |
| 4246 | The Ensembl Genome Browser: Strategies for Accessing Eukaryotic Genome Data. <i>Methods in Molecular Biology</i> , 2018, 1757, 115-139. | 0.9 | 13 |
| 4247 | Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, . | 6.4 | 38 |
| 4248 | Metagenomics reveal triclosan-induced changes in the antibiotic resistome of anaerobic digesters. <i>Environmental Pollution</i> , 2018, 241, 1182-1190. | 7.5 | 28 |
| 4249 | De Novo Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. <i>Neuron</i> , 2018, 99, 302-314.e4. | 8.1 | 112 |
| 4250 | Efficient and precise editing of endogenous transcripts with SNAP-tagged ADARs. <i>Nature Methods</i> , 2018, 15, 535-538. | 19.0 | 113 |
| 4251 | Association mapping from sequencing reads using k-mers. <i>ELife</i> , 2018, 7, . | 6.0 | 88 |
| 4252 | Comparative genomics of bdelloid rotifers: Insights from desiccating and nondesiccating species. <i>PLoS Biology</i> , 2018, 16, e2004830. | 5.6 | 78 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4254 | Molecular Cytogenetics Guides Massively Parallel Sequencing of a Radiation-Induced Chromosome Translocation in Human Cells. <i>Radiation Research</i> , 2018, 190, 88. | 1.5 | 11 |
| 4255 | Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, . | 6.0 | 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. | 5.7 | 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. | 2.8 | 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, . | 6.4 | 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. | 2.7 | 53 |
| 4260 | Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295. | 21.4 | 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. | 3.6 | 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. | 4.1 | 22 |
| 4263 | No Evidence for Recent Selection at FOXP2 among Diverse Human Populations. <i>Cell</i> , 2018, 174, 1424-1435.e15. | 28.9 | 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. | 3.8 | 26 |
| 4265 | Blazing Signature Filter: a library for fast pairwise similarity comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 221. | 2.6 | 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. | 2.8 | 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. | 1.4 | 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. | 3.6 | 38 |
| 4270 | The habu genome reveals accelerated evolution of venom protein genes. <i>Scientific Reports</i> , 2018, 8, 11300. | 3.3 | 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. | 3.1 | 35 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.8 | 19 |
| 4273 | Coinfections identified from metagenomic analysis of cervical lymph nodes from tularemia patients. <i>BMC Infectious Diseases</i> , 2018, 18, 319. | 2.9 | 8 |
| 4274 | Combining RNA-seq data and homology-based gene prediction for plants, animals and fungi. <i>BMC Bioinformatics</i> , 2018, 19, 189. | 2.6 | 192 |
| 4275 | Comparative Genomics of <i>Escherichia coli</i> Sequence Type 219 Clones From the Same Patient: Evolution of the Inc11 blaCMY-Carrying Plasmid in Vivo. <i>Frontiers in Microbiology</i> , 2018, 9, 1518. | 3.5 | 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. | 12.8 | 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. | 3.5 | 9 |
| 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. | 10.8 | 47 |
| 4279 | SNP hot-spots in the clam parasite QPX. <i>BMC Genomics</i> , 2018, 19, 486. | 2.8 | 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. | 3.5 | 54 |
| 4281 | Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680. | 3.5 | 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. | 3.5 | 21 |
| 4283 | Hydrogen-Fueled Microbial Pathways in Biogas Upgrading Systems Revealed by Genome-Centric Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1079. | 3.5 | 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. | 2.9 | 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. | 2.4 | 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. | 2.4 | 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. | 2.4 | 30 |
| 4288 | REXTAL: Regional Extension of Assemblies Using Linked-Reads. <i>Lecture Notes in Computer Science</i> , 2018, 10847, 63-78. | 1.3 | 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. | 2.5 | 25 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4290 | Long Non-Coding RNAs Responsive to Salt and Boron Stress in the Hyper-Arid Lluta Maize from Atacama Desert. <i>Genes</i> , 2018, 9, 170. | 2.4 | 53 |
| 4291 | miR-196b target screen reveals mechanisms maintaining leukemia stemness with therapeutic potential. <i>Journal of Experimental Medicine</i> , 2018, 215, 2115-2136. | 8.5 | 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. | 28.9 | 420 |
| 4294 | Genomic analysis of MHC-based mate choice in the monogamous California mouse. <i>Behavioral Ecology</i> , 2018, 29, 1167-1180. | 2.2 | 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. | 2.8 | 24 |
| 4296 | P_RNA_scaffolder: a fast and accurate genome scaffolder using paired-end RNA-sequencing reads. <i>BMC Genomics</i> , 2018, 19, 175. | 2.8 | 49 |
| 4297 | Bioinformatics analyses and in vitro evidence for five and six stacked G-quadruplex forming sequences. <i>Biochimie</i> , 2018, 150, 70-75. | 2.6 | 17 |
| 4298 | Cigarette smoke and chewing tobacco alter expression of different sets of miRNAs in oral keratinocytes. <i>Scientific Reports</i> , 2018, 8, 7040. | 3.3 | 34 |
| 4299 | Population size may shape the accumulation of functional mutations following domestication. <i>BMC Evolutionary Biology</i> , 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. <i>BMC Evolutionary Biology</i> , 2018, 18, 6. | 3.2 | 26 |
| 4301 | Reconstruction of a replication-competent ancestral murine endogenous retrovirus-L. <i>Retrovirology</i> , 2018, 15, 34. | 2.0 | 11 |
| 4302 | seq-seq-pan: building a computational pan-genome data structure on whole genome alignment. <i>BMC Genomics</i> , 2018, 19, 47. | 2.8 | 25 |
| 4303 | CAS-viewer: web-based tool for splicing-guided integrative analysis of multi-omics cancer data. <i>BMC Medical Genomics</i> , 2018, 11, 25. | 1.5 | 17 |
| 4304 | Recently integrated Alu insertions in the squirrel monkey (<i>Saimiri</i>) lineage and application for population analyses. <i>Mobile DNA</i> , 2018, 9, 9. | 3.6 | 6 |
| 4305 | Sequencing Plant Genomes. <i>Progress in Botany Fortschritte Der Botanik</i> , 2018, , 109-193. | 0.3 | 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. <i>Scientific Reports</i> , 2018, 8, 6808. | 3.3 | 10 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4309 | Unsupervised, Statistically Based Systems Biology Approach for Unraveling the Genetics of Complex Traits: A Demonstration with Ethanol Metabolism. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 1177-1191. | 2.4 | 7 |
| 4310 | NvERTx: A gene expression database to compare embryogenesis and regeneration in the sea anemone <i>Nematostella vectensis</i> . <i>Development (Cambridge)</i> , 2018, 145, . | 2.5 | 47 |
| 4311 | Genome sequence of the progenitor of wheat A subgenome <i>Triticum urartu</i> . <i>Nature</i> , 2018, 557, 424-428. | 27.8 | 354 |
| 4312 | Applications and efficiencies of the first cat 63K DNA array. <i>Scientific Reports</i> , 2018, 8, 7024. | 3.3 | 38 |
| 4313 | Contrasting duplication patterns reflect functional diversities of <i>ubiquitin</i> and <i>ubiquitin</i> -like protein modifiers in plants. <i>Plant Journal</i> , 2018, 95, 296-311. | 5.7 | 11 |
| 4314 | Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in <i>Agave</i> . <i>BMC Genomics</i> , 2018, 19, 588. | 2.8 | 64 |
| 4315 | Genome Plasticity in Cultured <i>Leishmania donovani</i> : Comparison of Early and Late Passages. <i>Frontiers in Microbiology</i> , 2018, 9, 1279. | 3.5 | 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. | 2.5 | 11 |
| 4318 | Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. <i>Forensic Science International: Genetics</i> , 2018, 37, 162-171. | 3.1 | 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. | 2.3 | 31 |
| 4320 | Genetical genomics of growth in a chicken model. <i>BMC Genomics</i> , 2018, 19, 72. | 2.8 | 31 |
| 4321 | The chromosome-level genome assemblies of two rattans (<i>Calamus simplicifolius</i> and <i>Daemonorops</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 6.4 | 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. | 2.8 | 39 |
| 4323 | The landscape of the A-to-I RNA editome from 462 human genomes. <i>Scientific Reports</i> , 2018, 8, 12069. | 3.3 | 15 |
| 4324 | Draft genome of <i>Glyptosternon maculatum</i> , an endemic fish from Tibet Plateau. <i>GigaScience</i> , 2018, 7, . | 6.4 | 18 |
| 4325 | The Genetics of a Behavioral Speciation Phenotype in an Island System. <i>Genes</i> , 2018, 9, 346. | 2.4 | 16 |
| 4326 | phylotaR: An Automated Pipeline for Retrieving Orthologous DNA Sequences from GenBank in R. <i>Life</i> , 2018, 8, 20. | 2.4 | 26 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 2.5 | 27 |
| 4328 | The small RNA complement of adult <i>Schistosoma haematobium</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006535. | 3.0 | 17 |
| 4329 | Ancient convergent losses of <i>Paraoxonase 1</i> yield potential risks for modern marine mammals. <i>Science</i> , 2018, 361, 591-594. | 12.6 | 79 |
| 4330 | Developmental barcoding of whole mouse via homing CRISPR. <i>Science</i> , 2018, 361, . | 12.6 | 263 |
| 4331 | Evolutionary stability of topologically associating domains is associated with conserved gene regulation. <i>BMC Biology</i> , 2018, 16, 87. | 3.8 | 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. | 1.4 | 0 |
| 4333 | Characterization of the β -defensin genes in giant panda. <i>Scientific Reports</i> , 2018, 8, 12308. | 3.3 | 7 |
| 4334 | <i>Trichoplax</i> genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. <i>Scientific Reports</i> , 2018, 8, 11168. | 3.3 | 36 |
| 4335 | Genome-wide mapping of large deletions and their population-genetic properties in dairy cattle. <i>DNA Research</i> , 2018, 25, 49-59. | 3.4 | 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. | 1.1 | 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. | 3.3 | 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. | 1.8 | 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. | 3.4 | 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, . | 6.4 | 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. | 2.5 | 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. | 2.5 | 6 |
| 4346 | Fungal Genome Annotation. <i>Methods in Molecular Biology</i> , 2018, 1775, 171-184. | 0.9 | 14 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.9 | 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. | 5.0 | 15 |
| 4349 | A high-quality genome sequence of <i>Rosa chinensis</i> to elucidate ornamental traits. <i>Nature Plants</i> , 2018, 4, 473-484. | 9.3 | 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. | 1.8 | 33 |
| 4351 | Long-lived rodents reveal signatures of positive selection in genes associated with lifespan. <i>PLoS Genetics</i> , 2018, 14, e1007272. | 3.5 | 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. | 2.5 | 27 |
| 4353 | Urinary cell-free DNA is a versatile analyte for monitoring infections of the urinary tract. <i>Nature Communications</i> , 2018, 9, 2412. | 12.8 | 121 |
| 4354 | <i>In silico</i> read normalization using set multi-cover optimization. <i>Bioinformatics</i> , 2018, 34, 3273-3280. | 4.1 | 8 |
| 4355 | Long-read sequencing and de novo genome assembly of <i>Ammopiptanthus nanus</i> , a desert shrub. <i>GigaScience</i> , 2018, 7, . | 6.4 | 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. | 5.2 | 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. | 8.3 | 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. | 2.0 | 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. | 2.6 | 59 |
| 4364 | Prediction of Coding and Non-Coding RNA. , 2019, , 230-240. | | 4 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 1.2 | 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. | 0.4 | 1 |
| 4368 | Uncovering missed indels by leveraging unmapped reads. <i>Scientific Reports</i> , 2019, 9, 11093. | 3.3 | 8 |
| 4369 | Transposable elements contribute to dynamic genome content in maize. <i>Plant Journal</i> , 2019, 100, 1052-1065. | 5.7 | 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. | 3.4 | 17 |
| 4371 | BART-Seq: cost-effective massively parallelized targeted sequencing for genomics, transcriptomics, and single-cell analysis. <i>Genome Biology</i> , 2019, 20, 155. | 8.8 | 19 |
| 4372 | Dicyemid Mesozoans: A Unique Parasitic Lifestyle and a Reduced Genome. <i>Genome Biology and Evolution</i> , 2019, 11, 2232-2243. | 2.5 | 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. | 3.5 | 16 |
| 4374 | Performance of gene expression analyses using <i>de novo</i> assembled transcripts in polyploid species. <i>Bioinformatics</i> , 2019, 35, 4314-4320. | 4.1 | 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. | 2.5 | 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. | 3.1 | 26 |
| 4377 | A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. <i>Scientific Reports</i> , 2019, 9, 11769. | 3.3 | 179 |
| 4378 | Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147. | 8.8 | 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. | 0.4 | 4 |
| 4380 | Endogenous Retrovirus-Derived Long Noncoding RNA Enhances Innate Immune Responses via Derepressing RELA Expression. <i>MBio</i> , 2019, 10, . | 4.1 | 39 |
| 4381 | Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. <i>Nature Biotechnology</i> , 2019, 37, 907-915. | 17.5 | 6,567 |
| 4382 | Metagenomics analysis of cocoa bean fermentation microbiome identifying species diversity and putative functional capabilities. <i>Heliyon</i> , 2019, 5, e02170. | 3.2 | 56 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4383 | Exploring the molecular basis of neuronal excitability in a vocal learner. BMC Genomics, 2019, 20, 629. | 2.8 | 12 |
| 4384 | Conserved Pseudoknots in lncRNA MEG3 Are Essential for Stimulation of the p53 Pathway. Molecular Cell, 2019, 75, 982-995.e9. | 9.7 | 138 |
| 4385 | Construction and comparison of three reference-quality genome assemblies for soybean. Plant Journal, 2019, 100, 1066-1082. | 5.7 | 113 |
| 4386 | The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data. Scientific Data, 2019, 6, 122. | 5.3 | 29 |
| 4387 | Whole-Genome Alignment. Methods in Molecular Biology, 2019, 1910, 121-147. | 0.9 | 5 |
| 4388 | A high-quality genome of Eragrostis curvula grass provides insights into Poaceae evolution and supports new strategies to enhance forage quality. Scientific Reports, 2019, 9, 10250. | 3.3 | 27 |
| 4389 | Centromere Satellite Repeats Have Undergone Rapid Changes in Polyploid Wheat Subgenomes. Plant Cell, 2019, 31, 2035-2051. | 6.6 | 56 |
| 4390 | Instability of the Pseudoautosomal Boundary in House Mice. Genetics, 2019, 212, 469-487. | 2.9 | 15 |
| 4391 | Arctic charr brain transcriptome strongly affected by summer seasonal growth but only subtly by feed deprivation. BMC Genomics, 2019, 20, 529. | 2.8 | 6 |
| 4392 | Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. BMC Medical Genomics, 2019, 12, 104. | 1.5 | 10 |
| 4393 | Closing target trimming and CTTdocker programs for discovering hidden superfamily loci in genomes. PLoS ONE, 2019, 14, e0209468. | 2.5 | 7 |
| 4394 | Stress, novel sex genes, and epigenetic reprogramming orchestrate socially controlled sex change. Science Advances, 2019, 5, eaaw7006. | 10.3 | 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. Bladder Cancer, 2019, 5, 147-157. | 0.4 | 2 |
| 4396 | Ecological speciation in sympatric palms: 3. Genetic map reveals genomic islands underlying species divergence in <i>Howea</i> . Evolution; International Journal of Organic Evolution, 2019, 73, 1986-1995. | 2.3 | 13 |
| 4397 | Musa balbisiana genome reveals subgenome evolution and functional divergence. Nature Plants, 2019, 5, 810-821. | 9.3 | 132 |
| 4398 | Chromosome-Level Alpaca Reference Genome VicPac3.1 Improves Genomic Insight Into the Biology of New World Camelids. Frontiers in Genetics, 2019, 10, 586. | 2.3 | 19 |
| 4399 | De novo genome assembly of the endangered Acer yangbiense, a plant species with extremely small populations endemic to Yunnan Province, China. GigaScience, 2019, 8, . | 6.4 | 42 |
| 4400 | Transposable Elements: Classification, Identification, and Their Use As a Tool For Comparative Genomics. Methods in Molecular Biology, 2019, 1910, 177-207. | 0.9 | 74 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4401 | Curing cytoplasmic male sterility via TALEN-mediated mitochondrial genome editing. <i>Nature Plants</i> , 2019, 5, 722-730. | 9.3 | 126 |
| 4402 | The Methodology Behind Network Thinking: Graphs to Analyze Microbial Complexity and Evolution. <i>Methods in Molecular Biology</i> , 2019, 1910, 271-308. | 0.9 | 4 |
| 4403 | The genome assembly of asparagus bean, <i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i> . <i>Scientific Data</i> , 2019, 6, 124. | 5.3 | 18 |
| 4404 | Genome and transcriptome characterization of the glycoengineered <i>Nicotiana benthamiana</i> line Î”XT/FT. <i>BMC Genomics</i> , 2019, 20, 594. | 2.8 | 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. | 21.4 | 265 |
| 4406 | Impact of sequencing depth and technology on de novo RNA-Seq assembly. <i>BMC Genomics</i> , 2019, 20, 604. | 2.8 | 40 |
| 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. | 2.5 | 4 |
| 4408 | Large-scale potential <scp>RNA</scp> editing profiling in different adult chicken tissues. <i>Animal Genetics</i> , 2019, 50, 460-474. | 1.7 | 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. | 10.3 | 41 |
| 4410 | The genome assembly and annotation of yellowhorn (<i>Xanthoceras sorbifolium</i> Bunge). <i>GigaScience</i> , 2019, 8, . | 6.4 | 37 |
| 4411 | HLA alleles and haplotypes observed in 263 US families. <i>Human Immunology</i> , 2019, 80, 644-660. | 2.4 | 18 |
| 4412 | Major natural genetic variation contributes to waterlogging tolerance in maize seedlings. <i>Molecular Breeding</i> , 2019, 39, 1. | 2.1 | 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. | 12.8 | 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. | 1.9 | 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, . | 6.4 | 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. | 2.4 | 24 |
| 4417 | Extensive intraspecific gene order and gene structural variations in upland cotton cultivars. <i>Nature Communications</i> , 2019, 10, 2989. | 12.8 | 144 |
| 4418 | Chromosome-level genome assembly of golden pompano (<i>Trachinotus ovatus</i>) in the family Carangidae. <i>Scientific Data</i> , 2019, 6, 216. | 5.3 | 42 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 2.5 | 9 |
| 4420 | A new species in the major malaria vector complex sheds light on reticulated species evolution. <i>Scientific Reports</i> , 2019, 9, 14753. | 3.3 | 56 |
| 4421 | Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019, 10, 4680. | 12.8 | 75 |
| 4422 | Profiling the Functional Diversity of Termite Mound Soil Bacteria as Revealed by Shotgun Sequencing. <i>Genes</i> , 2019, 10, 637. | 2.4 | 24 |
| 4423 | The Structure, Evolution, and Gene Expression Within the Caprine Leukocyte Receptor Complex. <i>Frontiers in Immunology</i> , 2019, 10, 2302. | 4.8 | 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. | 2.1 | 12 |
| 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. | 3.1 | 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. | 2.5 | 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. | 3.4 | 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. | 2.3 | 1 |
| 4429 | Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681. | 14.5 | 18 |
| 4430 | pblat: a multithread blat algorithm speeding up aligning sequences to genomes. <i>BMC Bioinformatics</i> , 2019, 20, 28. | 2.6 | 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. | 3.3 | 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. | 14.5 | 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. | 2.5 | 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. | 8.2 | 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. | 2.4 | 1 |
| 4436 | Genetic Variations of Ultraconserved Elements in the Human Genome. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 549-559. | 2.0 | 13 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4437 | UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761. | 14.5 | 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. | 0.7 | 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. | 3.3 | 4 |
| 4440 | Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019, 179, 1057-1067.e14. | 28.9 | 320 |
| 4441 | Adaptive Radiation Genomics of Two Ecologically Divergent Hawaiian Honeycreepers: The <i>Âkaiapohou</i> and the <i>Amakihi</i> . <i>Journal of Heredity</i> , 2020, 111, 21-32. | 2.4 | 6 |
| 4442 | MitoMut. , 2019, , . | | 0 |
| 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. | 2.6 | 7 |
| 4444 | SwiftOrtho: A fast, memory-efficient, multiple genome orthology classifier. <i>GigaScience</i> , 2019, 8, . | 6.4 | 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. | 3.6 | 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. | 2.5 | 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. | 2.5 | 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. | 3.4 | 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. | 4.2 | 4 |
| 4450 | NCLcomparator: systematically post-screening non-co-linear transcripts (circular, trans-spliced, or Tj ETQq1 1 0.784314 rgBT / Overlook | 2.6 | 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. | 8.8 | 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. | 8.9 | 30 |
| 4453 | An expanded landscape of human long noncoding RNA. <i>Nucleic Acids Research</i> , 2019, 47, 7842-7856. | 14.5 | 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. | 2.3 | 25 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 4455 | Rapidly evolving protointrons in <i>Saccharomyces</i> genomes revealed by a hungry spliceosome. <i>PLoS Genetics</i> , 2019, 15, e1008249. | 3.5 | 16 |
| 4456 | Hi-Plex2: a simple and robust approach to targeted sequencing-based genetic screening. <i>BioTechniques</i> , 2019, 67, 118-122. | 1.8 | 11 |
| 4457 | Chinese Fir Breeding in the High-Throughput Sequencing Era: Insights from SNPs. <i>Forests</i> , 2019, 10, 681. | 2.1 | 10 |
| 4458 | A high-quality genome assembly for the endangered golden snub-nosed monkey (<i>Rhinopithecus</i>) TJ ETQq1 1 0.784314 rgBT /Overlock 1 | 6.4 | 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. | 3.6 | 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. | 3.1 | 15 |
| 4461 | CNER: A toolkit for exploring extreme noncoding conservation. <i>PLoS Computational Biology</i> , 2019, 15, e1006940. | 3.2 | 17 |
| 4462 | Novel Locus Associated with Symmetrical Lupoid Onychodystrophy in the Bearded Collie. <i>Genes</i> , 2019, 10, 635. | 2.4 | 1 |
| 4463 | BREAK, MAKE and TAKE: an information retrieval approach. <i>Sadhana - Academy Proceedings in Engineering Sciences</i> , 2019, 44, 1. | 1.3 | 0 |
| 4464 | <i>Burkholderia pseudomallei</i> , the causative agent of melioidosis, is rare but ecologically established and widely dispersed in the environment in Puerto Rico. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007727. | 3.0 | 26 |
| 4465 | Dietary Energy Level Promotes Rumen Microbial Protein Synthesis by Improving the Energy Productivity of the Ruminal Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 847. | 3.5 | 43 |
| 4466 | The evolution study on <i>Oryza rufipogon</i> . dw by whole-genome sequencing. <i>Journal of Genetics</i> , 2019, 98, 1. | 0.7 | 3 |
| 4467 | Srrm234, but not canonical SR and hnRNP proteins, drive inclusion of <i>Dscam</i> exon 9 variable exons. <i>Rna</i> , 2019, 25, 1353-1365. | 3.5 | 16 |
| 4468 | Long noncoding RNAs are involved in multiple immunological pathways in response to vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17121-17126. | 7.1 | 58 |
| 4469 | Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. <i>Clinica Chimica Acta</i> , 2019, 498, 38-46. | 1.1 | 38 |
| 4470 | The Tannat genome: Unravelling its unique characteristics. <i>BIO Web of Conferences</i> , 2019, 12, 01016. | 0.2 | 1 |
| 4471 | The population genetics of structural variants in grapevine domestication. <i>Nature Plants</i> , 2019, 5, 965-979. | 9.3 | 229 |
| 4472 | Horizontally transmitted symbiont populations in deep-sea mussels are genetically isolated. <i>ISME Journal</i> , 2019, 13, 2954-2968. | 9.8 | 42 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4473 | Gene expression vs. sequence divergence: comparative transcriptome sequencing among natural <i>Rhinolophus ferrumequinum</i> populations with different acoustic phenotypes. <i>Frontiers in Zoology</i> , 2019, 16, 37. | 2.0 | 13 |
| 4474 | Dosage regulation, and variation in gene expression and copy number of human Y chromosome ampliconic genes. <i>PLoS Genetics</i> , 2019, 15, e1008369. | 3.5 | 19 |
| 4475 | Transcriptome profiling reveals insights into the molecular mechanism of drought tolerance in sweetpotato. <i>Journal of Integrative Agriculture</i> , 2019, 18, 9-23. | 3.5 | 33 |
| 4476 | The statistical power of k-mer based aggregative statistics for alignment-free detection of horizontal gene transfer. <i>Synthetic and Systems Biotechnology</i> , 2019, 4, 150-156. | 3.7 | 5 |
| 4477 | DNA Sequencing Technologies. <i>ACM Computing Surveys</i> , 2020, 52, 1-30. | 23.0 | 8 |
| 4478 | Transcription analysis of the response of the porcine adrenal cortex to a single subclinical dose of lipopolysaccharide from <i>Salmonella Enteritidis</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 141, 1228-1245. | 7.5 | 5 |
| 4479 | A purely bioinformatic pipeline for the prediction of mammalian odorant receptor gene enhancers. <i>BMC Bioinformatics</i> , 2019, 20, 474. | 2.6 | 6 |
| 4480 | The Epigenetic Signature of Colonizing New Environments in <i>Anolis</i> Lizards. <i>Molecular Biology and Evolution</i> , 2019, 36, 2165-2170. | 8.9 | 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. | 2.5 | 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. | 5.3 | 50 |
| 4483 | Pedigree-based estimation of human mobile element retrotransposition rates. <i>Genome Research</i> , 2019, 29, 1567-1577. | 5.5 | 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. | 5.3 | 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. | 2.5 | 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. | 4.1 | 4 |
| 4487 | The Biodiversity and Geochemistry of Cryoconite Holes in Queen Maud Land, East Antarctica. <i>Microorganisms</i> , 2019, 7, 160. | 3.6 | 21 |
| 4488 | Realizing the potential of full-length transcriptome sequencing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190097. | 4.0 | 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. | 2.8 | 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. | 3.3 | 23 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 3.2 | 25 |
| 4492 | A Sequence-Based Novel Approach for Quality Evaluation of Third-Generation Sequencing Reads. <i>Genes</i> , 2019, 10, 44. | 2.4 | 3 |
| 4493 | Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54. | 2.4 | 8 |
| 4494 | Inflammation in Traumatic Brain Injury: Roles for Toxic A1 Astrocytes and Microglialâ€‘Astrocytic Crosstalk. <i>Neurochemical Research</i> , 2019, 44, 1410-1424. | 3.3 | 82 |
| 4495 | Defective Epsteinâ€‘Barr virus in chronic active infection and haematological malignancy. <i>Nature Microbiology</i> , 2019, 4, 404-413. | 13.3 | 152 |
| 4496 | Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, . | 6.4 | 36 |
| 4497 | Genome structure and evolution of <i>Antirrhinum majus</i> L. <i>Nature Plants</i> , 2019, 5, 174-183. | 9.3 | 85 |
| 4498 | Precise RNA editing by recruiting endogenous ADARs with antisense oligonucleotides. <i>Nature Biotechnology</i> , 2019, 37, 133-138. | 17.5 | 186 |
| 4499 | Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. <i>Cell</i> , 2019, 176, 1222-1237.e22. | 28.9 | 347 |
| 4500 | Aligning optical maps to de Bruijn graphs. <i>Bioinformatics</i> , 2019, 35, 3250-3256. | 4.1 | 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, . | 6.4 | 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. | 3.8 | 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. | 1.8 | 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. | 8.8 | 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. | 8.9 | 43 |
| 4506 | Prediction of functional microRNA targets by integrative modeling of microRNA binding and target expression data. <i>Genome Biology</i> , 2019, 20, 18. | 8.8 | 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. | 11.1 | 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. | 2.2 | 10 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4509 | Environmental filtering of bacterial functional diversity along an aridity gradient. <i>Scientific Reports</i> , 2019, 9, 866. | 3.3 | 33 |
| 4510 | Gene editing of the multi-copy H2A.B gene and its importance for fertility. <i>Genome Biology</i> , 2019, 20, 23. | 8.8 | 29 |
| 4511 | De novo assembly of white poplar genome and genetic diversity of white poplar population in Irtysh River basin in China. <i>Science China Life Sciences</i> , 2019, 62, 609-618. | 4.9 | 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. | 2.0 | 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, . | 2.2 | 8 |
| 4514 | Pairwise alignment of nucleotide sequences using maximal exact matches. <i>BMC Bioinformatics</i> , 2019, 20, 261. | 2.6 | 4 |
| 4515 | Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918. | 2.9 | 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. | 2.5 | 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. | 4.8 | 1 |
| 4518 | Transcriptome Changes during Major Developmental Transitions Accompanied with Little Alteration of DNA Methylation in Two <i>Pleurotus</i> Species. <i>Genes</i> , 2019, 10, 465. | 2.4 | 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. | 3.3 | 104 |
| 4520 | MammaPrint and Blueprint Molecular Diagnostics Using Targeted RNA Next-Generation Sequencing Technology. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 808-823. | 2.8 | 15 |
| 4521 | Factors other than hTau overexpression that contribute to tauopathy-like phenotype in rTg4510 mice. <i>Nature Communications</i> , 2019, 10, 2479. | 12.8 | 117 |
| 4522 | Genome sequencing provides insights into the evolution and antioxidant activity of Chinese bayberry. <i>BMC Genomics</i> , 2019, 20, 458. | 2.8 | 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. | 2.3 | 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. | 8.0 | 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. | 2.6 | 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. | 2.8 | 73 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4527 | Microhomologies are prevalent at Cas9-induced larger deletions. <i>Nucleic Acids Research</i> , 2019, 47, 7402-7417. | 14.5 | 100 |
| 4528 | Chromosomal and Genomic Dynamics of Satellite DNAs in Characidae (Characiformes, Teleostei) Species. <i>Zebrafish</i> , 2019, 16, 408-414. | 1.1 | 2 |
| 4529 | Phylogenomic Approaches to DNA Barcoding of Herbal Medicines: Developing Clade-Specific Diagnostic Characters for Berberis. <i>Frontiers in Plant Science</i> , 2019, 10, 586. | 3.6 | 28 |
| 4530 | Leaf Transcriptome Assembly of <i>Protium copal</i> (Burseraceae) and Annotation of Terpene Biosynthetic Genes. <i>Genes</i> , 2019, 10, 392. | 2.4 | 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. | 21.4 | 202 |
| 4532 | Darwin-WGA: A Co-processor Provides Increased Sensitivity in Whole Genome Alignments with High Speedup. , 2019, , . | | 17 |
| 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. | 6.1 | 65 |
| 4534 | Altered microRNA expression profiles in large offspring syndrome and Beckwith-Wiedemann syndrome. <i>Epigenetics</i> , 2019, 14, 850-876. | 2.7 | 32 |
| 4535 | Comment on "A comprehensive overview and evaluation of circular RNA detection tools". <i>PLoS Computational Biology</i> , 2019, 15, e1006158. | 3.2 | 15 |
| 4536 | HNCDDB: An Integrated Gene and Drug Database for Head and Neck Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 371. | 2.8 | 7 |
| 4537 | BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433. | 2.4 | 25 |
| 4538 | Draft genome of the big-headed turtle <i>Platysternon megacephalum</i> . <i>Scientific Data</i> , 2019, 6, 60. | 5.3 | 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. | 4.8 | 19 |
| 4540 | Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. <i>Genome Biology</i> , 2019, 20, 97. | 8.8 | 122 |
| 4541 | Retrotransposons evolution and impact on lncRNA and protein coding genes in pigs. <i>Mobile DNA</i> , 2019, 10, 19. | 3.6 | 22 |
| 4542 | Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. <i>PLoS Genetics</i> , 2019, 15, e1008119. | 3.5 | 70 |
| 4543 | Mitochondrial autoimmunity and MNRR1 in breast carcinogenesis. <i>BMC Cancer</i> , 2019, 19, 411. | 2.6 | 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. | 28.9 | 293 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.2 | 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. | 5.7 | 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. | 3.6 | 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. | 3.3 | 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.) | 0.0 | 0 |
| 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. | 4.1 | 25 |
| 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. | 3.9 | 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. | 0.6 | 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. | 2.5 | 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. | 2.7 | 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. | 4.8 | 44 |
| 4556 | Genomic changes in the biological control agent <i>Cryptolaemus montrouzieri</i> associated with introduction. <i>Evolutionary Applications</i> , 2019, 12, 989-1000. | 3.1 | 9 |
| 4557 | Local protein synthesis is a ubiquitous feature of neuronal pre- and postsynaptic compartments. <i>Science</i> , 2019, 364, . | 12.6 | 285 |
| 4558 | Islands of retroelements are major components of <i>Drosophila</i> centromeres. <i>PLoS Biology</i> , 2019, 17, e3000241. | 5.6 | 124 |
| 4559 | CiliaCarta: An integrated and validated compendium of ciliary genes. <i>PLoS ONE</i> , 2019, 14, e0216705. | 2.5 | 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. | 3.3 | 27 |
| 4561 | The complete chloroplast genome sequence of <i>Pyrus phaeocarpa</i> Rehd.. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1370-1371. | 0.4 | 2 |
| 4562 | Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. <i>Genome Biology</i> , 2019, 20, 79. | 8.8 | 81 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 3.5 | 69 |
| 4564 | BHap: a novel approach for bacterial haplotype reconstruction. <i>Bioinformatics</i> , 2019, 35, 4624-4631. | 4.1 | 18 |
| 4565 | Dauer signalling pathway model for <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2019, 12, 187. | 2.5 | 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. | 7.8 | 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. | 14.5 | 15 |
| 4568 | The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, . | 6.4 | 88 |
| 4569 | Insertion of a chimeric retrotransposon sequence in mouse <i>Axin1</i> locus causes metastable kinky tail phenotype. <i>Mobile DNA</i> , 2019, 10, 17. | 3.6 | 11 |
| 4570 | Analysis of Subtelomeric REXTAL Assemblies Using QUASt. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1. | 3.0 | 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. | 3.0 | 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. | 7.1 | 68 |
| 4573 | Methanethiol and Dimethylsulfide Cycling in Stiffkey Saltmarsh. <i>Frontiers in Microbiology</i> , 2019, 10, 1040. | 3.5 | 23 |
| 4574 | Linkage-based genome assembly improvement of oil palm (<i>Elaeis guineensis</i>). <i>Scientific Reports</i> , 2019, 9, 6619. | 3.3 | 16 |
| 4575 | A Transmissible RNA Pathway in Honey Bees. <i>Cell Reports</i> , 2019, 27, 1949-1959.e6. | 6.4 | 44 |
| 4576 | Amplification Dynamics of Platy-1 Retrotransposons in the Cebidae Platyrrhine Lineage. <i>Genome Biology and Evolution</i> , 2019, 11, 1105-1116. | 2.5 | 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. | 3.8 | 8 |
| 4578 | A Modifying Autoantigen in Graves's Disease. <i>Endocrinology</i> , 2019, 160, 1008-1020. | 2.8 | 11 |
| 4579 | Subtype classification and functional annotation of L1Md retrotransposon promoters. <i>Mobile DNA</i> , 2019, 10, 14. | 3.6 | 18 |
| 4580 | TransLiG: a de novo transcriptome assembler that uses line graph iteration. <i>Genome Biology</i> , 2019, 20, 81. | 8.8 | 30 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4581 | Details in the evaluation of circular RNA detection tools: Reply to Chen and Chuang. PLoS Computational Biology, 2019, 15, e1006916. | 3.2 | 8 |
| 4582 | Chromosome-Level Assembly of the Chinese Seabass (<i>Lateolabrax maculatus</i>) Genome. Frontiers in Genetics, 2019, 10, 275. | 2.3 | 33 |
| 4583 | Shedding Light on a Secretive Tertiary Urodelean Relict: Hynobiid Salamanders (<i>Paradactylodon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 Genes, 2019, 10, 306. | 2.4 | 4 |
| 4584 | Predicting Genes in Closely Related Species with Scipio and WebScipio. Methods in Molecular Biology, 2019, 1962, 193-206. | 0.9 | 0 |
| 4585 | Structural and Functional Annotation of Eukaryotic Genomes with GenSAS. Methods in Molecular Biology, 2019, 1962, 29-51. | 0.9 | 66 |
| 4586 | Accurate high throughput alignment via line sweep-based seed processing. Nature Communications, 2019, 10, 1939. | 12.8 | 11 |
| 4587 | Divergent Fine-Scale Recombination Landscapes between a Freshwater and Marine Population of Threespine Stickleback Fish. Genome Biology and Evolution, 2019, 11, 1552-1572. | 2.5 | 44 |
| 4588 | Agricultural Origins of a Highly Persistent Lineage of Vancomycin-Resistant <i>Enterococcus faecalis</i> in New Zealand. Applied and Environmental Microbiology, 2019, 85, . | 3.1 | 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. BMC Genomics, 2019, 20, 223. | 2.8 | 15 |
| 4590 | Cryo-EM structure of a light chain-derived amyloid fibril from a patient with systemic AL amyloidosis. Nature Communications, 2019, 10, 1103. | 12.8 | 120 |
| 4591 | Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. Nature Communications, 2019, 10, 1338. | 12.8 | 38 |
| 4592 | <i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. Nature Genetics, 2019, 51, 739-748. | 21.4 | 568 |
| 4593 | Molecular spectrum of somaclonal variation in PLB-regenerated <i>Oncidium</i> revealed by SLAF-seq. Plant Cell, Tissue and Organ Culture, 2019, 137, 541-552. | 2.3 | 8 |
| 4594 | Evolution-guided evaluation of the inverted terminal repeats of the synthetic transposon Sleeping Beauty. Scientific Reports, 2019, 9, 1171. | 3.3 | 5 |
| 4595 | Genome-wide analysis reveals the genomic features of the turkey vulture (<i>Cathartes aura</i>) as a scavenger. Molecular Genetics and Genomics, 2019, 294, 679-692. | 2.1 | 10 |
| 4596 | The transcriptome of the veiled chameleon (<i>Chamaeleo calytratus</i>): A resource for studying the evolution and development of vertebrates. Developmental Dynamics, 2019, 248, 702-708. | 1.8 | 26 |
| 4597 | Dicer1 is required for pigment cell and craniofacial development in zebrafish. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 472-485. | 1.9 | 12 |
| 4598 | A Genomic Analysis Workflow for Colorectal Cancer Precision Oncology. Clinical Colorectal Cancer, 2019, 18, 91-101.e3. | 2.3 | 29 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4599 | RNA sequencing discloses the genome-wide profile of long noncoding RNAs in dilated cardiomyopathy. <i>Molecular Medicine Reports</i> , 2019, 19, 2569-2580. | 2.4 | 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. | 1.3 | 196 |
| 4601 | Genome Sequence of Flavor-Producing Yeast <i>Saprochaete suaveolens</i> NRRL Y-17571. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.6 | 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. | 4.9 | 21 |
| 4603 | Deep-learning augmented RNA-seq analysis of transcript splicing. <i>Nature Methods</i> , 2019, 16, 307-310. | 19.0 | 74 |
| 4604 | Improving in-silico normalization using read weights. <i>Scientific Reports</i> , 2019, 9, 5133. | 3.3 | 9 |
| 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. | 0.8 | 5 |
| 4606 | ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline. <i>Bioinformatics</i> , 2019, 35, 4156-4158. | 4.1 | 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. | 3.9 | 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. | 8.3 | 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. | 7.8 | 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, . | 3.0 | 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. | 1.8 | 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. | 2.5 | 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. | 2.1 | 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. | 1.6 | 18 |
| 4615 | A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216. | 12.8 | 183 |
| 4616 | Characterization of mammalian Lipocalin UTRs in silico: Predictions for their role in post-transcriptional regulation. <i>PLoS ONE</i> , 2019, 14, e0213206. | 2.5 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4617 | Memory and relatedness of transcriptional activity in mammalian cell lineages. <i>Nature Communications</i> , 2019, 10, 1208. | 12.8 | 34 |
| 4618 | Chromothripsis during telomere crisis is independent of NHEJ, and consistent with a replicative origin. <i>Genome Research</i> , 2019, 29, 737-749. | 5.5 | 47 |
| 4619 | Circular RNAs in human and vertebrate neural retinas. <i>RNA Biology</i> , 2019, 16, 821-829. | 3.1 | 26 |
| 4620 | Genomic analysis of marker-associated fiber development genes in upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Qve | 1.2 | 5 |
| 4621 | Carbapenem-Susceptible OXA-23-Producing <i>Proteus mirabilis</i> in the French Community. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, . | 3.2 | 10 |
| 4622 | A quick guide for student-driven community genome annotation. <i>PLoS Computational Biology</i> , 2019, 15, e1006682. | 3.2 | 33 |
| 4623 | iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. <i>Nature Communications</i> , 2019, 10, 1636. | 12.8 | 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. <i>Genome Biology and Evolution</i> , 2019, 11, 1440-1450. | 2.5 | 26 |
| 4625 | Genome Sequence of an Arthroconidial Yeast, <i>Saprochaete fungicola</i> CBS 625.85. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.6 | 1 |
| 4626 | SplicedFamAlign: CDS-to-gene spliced alignment and identification of transcript orthology groups. <i>BMC Bioinformatics</i> , 2019, 20, 133. | 2.6 | 8 |
| 4627 | MGS-Fast: Metagenomic shotgun data fast annotation using microbial gene catalogs. <i>GigaScience</i> , 2019, 8, . | 6.4 | 15 |
| 4628 | Whole genome sequencing reveals complexity in both HPV sequences present and HPV integrations in HPV-positive oropharyngeal squamous cell carcinomas. <i>BMC Cancer</i> , 2019, 19, 352. | 2.6 | 26 |
| 4629 | Analysis of 100 high-coverage genomes from a pedigreed captive baboon colony. <i>Genome Research</i> , 2019, 29, 848-856. | 5.5 | 27 |
| 4630 | Placenta Transcriptome Profiling in Intrauterine Growth Restriction (IUGR). <i>International Journal of Molecular Sciences</i> , 2019, 20, 1510. | 4.1 | 53 |
| 4631 | Tools and Methods in the Analysis of Simple Sequences. , 2019, , 127-153. | | 0 |
| 4632 | High-throughput methods in aptamer discovery and analysis. <i>Methods in Enzymology</i> , 2019, 621, 329-346. | 1.0 | 8 |
| 4633 | Low-cost assembly of a cacao crop genome is able to resolve complex heterozygous bubbles. <i>Horticulture Research</i> , 2019, 6, 44. | 6.3 | 5 |
| 4634 | Chromosomal inversions in the Atlantic cod genome: Implications for management of Canadaâ€™s Northern cod stock. <i>Fisheries Research</i> , 2019, 216, 29-40. | 1.7 | 12 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4635 | Dynamic evolutionary history and gene content of sex chromosomes across diverse songbirds. <i>Nature Ecology and Evolution</i> , 2019, 3, 834-844. | 7.8 | 68 |
| 4636 | Genome-wide de novo L1 Retrotransposition Connects Endonuclease Activity with Replication. <i>Cell</i> , 2019, 177, 837-851.e28. | 28.9 | 88 |
| 4637 | scRNAAss: a single-cell RNA-seq assembler via imputing dropouts and combing junctions. <i>Bioinformatics</i> , 2019, 35, 4264-4271. | 4.1 | 7 |
| 4638 | Evolutionary Implications of the microRNA- and piRNA Complement of <i>Lepidodermella squamata</i> (Gastrotricha). <i>Non-coding RNA</i> , 2019, 5, 19. | 2.6 | 5 |
| 4639 | Widespread and Functional RNA Circularization in Localized Prostate Cancer. <i>Cell</i> , 2019, 176, 831-843.e22. | 28.9 | 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. <i>PLoS ONE</i> , 2019, 14, e0210792. | 2.5 | 37 |
| 4641 | Resolving the backbone of the Brassicaceae phylogeny for investigating trait diversity. <i>New Phytologist</i> , 2019, 222, 1638-1651. | 7.3 | 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. | 2.1 | 14 |
| 4643 | Comprehensive structural variation genome map of individuals carrying complex chromosomal rearrangements. <i>PLoS Genetics</i> , 2019, 15, e1007858. | 3.5 | 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. | 3.6 | 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. | 3.1 | 29 |
| 4646 | Genomewide Association Study of Fracture Nonunion Using Electronic Health Records. <i>JBMR Plus</i> , 2019, 3, 23-28. | 2.7 | 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. | 6.4 | 8 |
| 4648 | Draft genome of the river water buffalo. <i>Ecology and Evolution</i> , 2019, 9, 3378-3388. | 1.9 | 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. | 6.4 | 103 |
| 4650 | Unraveling the complex genome of <i>Saccharum spontaneum</i> using Polyploid Gene Assembler. <i>DNA Research</i> , 2019, 26, 205-216. | 3.4 | 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. | 12.8 | 42 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 4653 | Ribosomal DNA harbors an evolutionarily conserved clock of biological aging. <i>Genome Research</i> , 2019, 29, 325-333. | 5.5 | 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. | 6.6 | 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, . | 2.0 | 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, . | 3.8 | 28 |
| 4658 | Predisposition to childhood acute lymphoblastic leukemia caused by a constitutional translocation disrupting ETV6. <i>Blood Advances</i> , 2019, 3, 2722-2731. | 5.2 | 10 |
| 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, . | 2.5 | 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. | 1.8 | 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. | 7.1 | 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. | 1.8 | 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. | 2.1 | 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. | 1.9 | 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, . | 3.4 | 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. | 3.3 | 20 |
| 4669 | Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905. | 2.8 | 59 |
| 4670 | deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. <i>Genome Biology</i> , 2019, 20, 274. | 8.8 | 41 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4671 | Pseudo-chromosomeâ€‘length genome assembly of a double haploid â€œBartlettâ€‘pear (<i>Pyrus communis</i> L.). GigaScience, 2019, 8, . | 6.4 | 76 |
| 4672 | Atypical chromosome 22q11.2 deletions are complex rearrangements and have different mechanistic origins. Human Molecular Genetics, 2019, 28, 3724-3733. | 2.9 | 7 |
| 4673 | Annotated Draft Genomes of Two Caddisfly Species <i>Plectrocnemia conspersa</i> CURTIS and <i>Hydropsyche tenuis</i> NAVAS (Insecta: Trichoptera). Genome Biology and Evolution, 2019, 11, 3445-3451. | 2.5 | 21 |
| 4674 | Programmed DNA elimination of germline development genes in songbirds. Nature Communications, 2019, 10, 5468. | 12.8 | 66 |
| 4675 | Retroelement Insertion in a CRISPR/Cas9 Editing Site in the Early Embryo Intensifies Genetic Mosaicism. Frontiers in Cell and Developmental Biology, 2019, 7, 273. | 3.7 | 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. GigaScience, 2019, 8, . | 6.4 | 106 |
| 4677 | Comparative genomics of <i>Mycoplasma pneumoniae</i> isolated from children with pneumonia: South Korea, 2010â€‘2016. BMC Genomics, 2019, 20, 910. | 2.8 | 7 |
| 4678 | Environmental transcriptomes of invasive <i>dreissena</i> , a model species in ecotoxicology and invasion biology. Scientific Data, 2019, 6, 234. | 5.3 | 6 |
| 4679 | Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . Communications Biology, 2019, 2, 428. | 4.4 | 19 |
| 4680 | Minimal <i>in vivo</i> requirements for developmentally regulated cardiac long intergenic non-coding RNAs. Development (Cambridge), 2019, 146, . | 2.5 | 19 |
| 4681 | Towards Improved Molecular Identification Tools in Fine Fescue (<i>Festuca</i> L., Poaceae) Turfgrasses: Nuclear Genome Size, Ploidy, and Chloroplast Genome Sequencing. Frontiers in Genetics, 2019, 10, 1223. | 2.3 | 14 |
| 4682 | Discovery of genomic variations by whole-genome resequencing of the North American Araucana chicken. PLoS ONE, 2019, 14, e0225834. | 2.5 | 8 |
| 4683 | SGID: a comprehensive and interactive database of the silkworm. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 3.0 | 12 |
| 4684 | ReVac: a reverse vaccinology computational pipeline for prioritization of prokaryotic protein vaccine candidates. BMC Genomics, 2019, 20, 981. | 2.8 | 18 |
| 4685 | Alu insertion polymorphisms shared by <i>Papio</i> baboons and <i>Theropithecus gelada</i> reveal an intertwined common ancestry. Mobile DNA, 2019, 10, 46. | 3.6 | 11 |
| 4686 | Evolution of the new head by gradual acquisition of neural crest regulatory circuits. Nature, 2019, 574, 675-678. | 27.8 | 74 |
| 4687 | QTL identification for seed weight and size based on a high-density SLAF-seq genetic map in peanut (<i>Arachis hypogaea</i> L.). BMC Plant Biology, 2019, 19, 537. | 3.6 | 54 |
| 4688 | Genetic Diversity and Signatures of Selection in 15 Chinese Indigenous Dog Breeds Revealed by Genome-Wide SNPs. Frontiers in Genetics, 2019, 10, 1174. | 2.3 | 12 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4689 | Functional metagenomics: a tool to gain knowledge for agronomic and veterinary sciences. <i>Biotechnology and Genetic Engineering Reviews</i> , 2019, 35, 69-91. | 6.2 | 6 |
| 4690 | Multiple forms of selection shape reproductive isolation in a primate hybrid zone. <i>Molecular Ecology</i> , 2019, 28, 1056-1069. | 3.9 | 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. | 2.4 | 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. | 14.5 | 70 |
| 4693 | Actively personalized vaccination trial for newly diagnosed glioblastoma. <i>Nature</i> , 2019, 565, 240-245. | 27.8 | 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. | 1.8 | 11 |
| 4695 | Analysis of chromosome microstructures in products of conception associated with recurrent miscarriage. <i>Reproductive BioMedicine Online</i> , 2019, 38, 787-795. | 2.4 | 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. | 4.8 | 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. | 7.1 | 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. | 5.7 | 26 |
| 4699 | RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229. | 14.5 | 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. | 8.5 | 25 |
| 4701 | Modelling of zero-inflation improves inference of metagenomic gene count data. <i>Statistical Methods in Medical Research</i> , 2019, 28, 3712-3728. | 1.5 | 10 |
| 4702 | The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858. | 14.5 | 699 |
| 4703 | Defining TP53 pioneering capabilities with competitive nucleosome binding assays. <i>Genome Research</i> , 2019, 29, 107-115. | 5.5 | 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. | 5.5 | 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. | 2.9 | 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. | 4.0 | 13 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 5.6 | 20 |
| 4708 | DNA Methylation as a Biomarker in Environmental Epidemiology. , 2019, , 173-189. | | 1 |
| 4709 | SQUIRE reveals locus-specific regulation of interspersed repeat expression. <i>Nucleic Acids Research</i> , 2019, 47, e27-e27. | 14.5 | 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. | 2.4 | 34 |
| 4711 | Evaluation and application of RNA-Seq by MinION. <i>DNA Research</i> , 2019, 26, 55-65. | 3.4 | 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. | 2.5 | 15 |
| 4713 | Improved Genome Sequence of Wild Emmer Wheat Zavitan with the Aid of Optical Maps. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 619-624. | 1.8 | 64 |
| 4714 | Genome-Wide Copy Number Variation Detection Using NGS: Data Analysis and Interpretation. <i>Methods in Molecular Biology</i> , 2019, 1908, 113-124. | 0.9 | 17 |
| 4715 | Identifying loci controlling fiber composition in polyploid sugarcane (<i>Saccharum</i> spp.) through genome-wide association study. <i>Industrial Crops and Products</i> , 2019, 130, 598-605. | 5.2 | 16 |
| 4716 | Phylogenetic and expression analysis of histone acetyltransferases in <i>Brachypodium distachyon</i> . <i>Genomics</i> , 2019, 111, 1966-1976. | 2.9 | 5 |
| 4717 | Simulation of heterogeneous tumour genomes with HeteroGenesis and in silico whole exome sequencing. <i>Bioinformatics</i> , 2019, 35, 2850-2852. | 4.1 | 3 |
| 4718 | Chromosome level comparative analysis of Brassica genomes. <i>Plant Molecular Biology</i> , 2019, 99, 237-249. | 3.9 | 14 |
| 4719 | Morphometric differentiation and gene flow in emerald shiners (<i>Notropis atherinoides</i>) from the lower Great Lakes and the Niagara River. <i>Journal of Great Lakes Research</i> , 2019, 45, 324-332. | 1.9 | 3 |
| 4720 | Convergent evolution misled taxonomy in schizothoracine fishes (Cypriniformes: Cyprinidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 323-337. | 2.7 | 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. <i>Industrial Crops and Products</i> , 2019, 128, 566-571. | 5.2 | 4 |
| 4722 | REDfly: the transcriptional regulatory element database for <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2019, 47, D828-D834. | 14.5 | 59 |
| 4723 | Targeted RNA sequencing: A routine ancillary technique in the diagnosis of bone and soft tissue neoplasms. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 75-87. | 2.8 | 38 |
| 4724 | Resveratrol decreases the expression of genes involved in inflammation through transcriptional regulation. <i>Free Radical Biology and Medicine</i> , 2019, 130, 8-22. | 2.9 | 37 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 2.9 | 20 |
| 4726 | Whole-Genome Alignment and Comparative Annotation. Annual Review of Animal Biosciences, 2019, 7, 41-64. | 7.4 | 62 |
| 4727 | Identification of Mutated Cancer Driver Genes in Unpaired RNA-Seq Samples. Methods in Molecular Biology, 2019, 1878, 95-108. | 0.9 | 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. | 1.1 | 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. | 9.8 | 40 |
| 4730 | Methylation pattern and mutational status of BRCA1 in canine mammary tumors in a Brazilian population. Comparative Clinical Pathology, 2019, 28, 63-67. | 0.7 | 1 |
| 4731 | The heart of an acrobatic bird. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2019, 228, 9-17. | 1.8 | 8 |
| 4732 | Intensive allochthonous inputs along the Ganges River and their effect on microbial community composition and dynamics. Environmental Microbiology, 2019, 21, 182-196. | 3.8 | 40 |
| 4733 | Off- and on-target effects of genome editing in mouse embryos. Journal of Reproduction and Development, 2019, 65, 1-5. | 1.4 | 24 |
| 4734 | The draft genomes of five agriculturally important African orphan crops. GigaScience, 2019, 8, . | 6.4 | 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. ISME Journal, 2019, 13, 523-536. | 9.8 | 35 |
| 4737 | <i>De novo</i> clustering of long reads by gene from transcriptomics data. Nucleic Acids Research, 2019, 47, e2-e2. | 14.5 | 29 |
| 4738 | Structure and evolution of double minutes in diagnosis and relapse brain tumors. Acta Neuropathologica, 2019, 137, 123-137. | 7.7 | 63 |
| 4739 | A Nanopore Sequencing-Based Assay for Rapid Detection of Gene Fusions. Journal of Molecular Diagnostics, 2019, 21, 58-69. | 2.8 | 34 |
| 4740 | CRISPRInc: a manually curated database of validated sgRNAs for lncRNAs. Nucleic Acids Research, 2019, 47, D63-D68. | 14.5 | 37 |
| 4741 | MG-RAST version 4 lessons learned from a decade of low-budget ultra-high-throughput metagenome analysis. Briefings in Bioinformatics, 2019, 20, 1151-1159. | 6.5 | 98 |
| 4742 | Kmerind: A Flexible Parallel Library for K-mer Indexing of Biological Sequences on Distributed Memory Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1117-1131. | 3.0 | 10 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 4743 | Federation in genomics pipelines: techniques and challenges. Briefings in Bioinformatics, 2019, 20, 235-244. | 6.5 | 18 |
| 4744 | Chromosomal inversions promote genomic islands of concerted evolution of <i>Hsp70</i> genes in the <i>Drosophila subobscura</i> species subgroup. Molecular Ecology, 2019, 28, 1316-1332. | 3.9 | 16 |
| 4745 | The complete chloroplast genome sequence annotation for <i>Malania oleifera</i> , a critically endangered and important bioresource tree. Conservation Genetics Resources, 2019, 11, 271-274. | 0.8 | 10 |
| 4746 | VA-Store: A Virtual Approximate Store Approach to Supporting Repetitive Big Data in Genome Sequence Analyses. IEEE Transactions on Knowledge and Data Engineering, 2020, 32, 602-616. | 5.7 | 4 |
| 4747 | OBSOLETE: Bioinformatic Platforms for Metagenomics. , 2020, , . | | 0 |
| 4748 | Comparative assessment of long-read error correction software applied to Nanopore RNA-sequencing data. Briefings in Bioinformatics, 2020, 21, 1164-1181. | 6.5 | 33 |
| 4749 | Validation of a Next-Generation Sequencing Assay Targeting RNA for the Multiplexed Detection of Fusion Transcripts and Oncogenic Isoforms. Archives of Pathology and Laboratory Medicine, 2020, 144, 90-98. | 2.5 | 18 |
| 4750 | Insight into the epigenetic landscape of a currently endogenizing gammaretrovirus in mule deer (<i>Odocoileus hemionus</i>). Genomics, 2020, 112, 886-896. | 2.9 | 2 |
| 4751 | Satellite DNA content of B chromosomes in the characid fish <i>Characidium gomesi</i> supports their origin from sex chromosomes. Molecular Genetics and Genomics, 2020, 295, 195-207. | 2.1 | 22 |
| 4752 | A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i> . Molecular Ecology Resources, 2020, 20, 268-282. | 4.8 | 51 |
| 4753 | A chromosome-level genome assembly of <i>Pyropia haitanensis</i> (Bangiales, Rhodophyta). Molecular Ecology Resources, 2020, 20, 216-227. | 4.8 | 37 |
| 4754 | RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. Bioinformatics, 2020, 36, 1382-1390. | 4.1 | 12 |
| 4755 | Building a sequence map of the pig pan-genome from multiple de novo assemblies and Hi-C data. Science China Life Sciences, 2020, 63, 750-763. | 4.9 | 47 |
| 4756 | Large miRNA survival analysis reveals a prognostic four-biomarker signature for triple negative breast cancer. Genetics and Molecular Biology, 2020, 43, e20180269. | 1.3 | 16 |
| 4757 | Metataxonomics of Tunisian phosphogypsum based on five bioinformatics pipelines: Insights for bioremediation. Genomics, 2020, 112, 981-989. | 2.9 | 18 |
| 4758 | Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. International Journal of Biological Macromolecules, 2020, 145, 1189-1198. | 7.5 | 3 |
| 4759 | A pseudomolecule-scale genome assembly of the liverwort <i>Marchantia polymorpha</i> . Plant Journal, 2020, 101, 1378-1396. | 5.7 | 35 |
| 4760 | Preventive antibiotic treatment of calves: emergence of dysbiosis causing propagation of obese state-associated and mobile multidrug resistance-carrying bacteria. Microbial Biotechnology, 2020, 13, 669-682. | 4.2 | 18 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 8.3 | 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. | 5.7 | 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. | 2.6 | 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. | 2.8 | 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. | 3.3 | 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. | 9.5 | 32 |
| 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. | 0.5 | 6 |
| 4768 | SWAV: a web-based visualization browser for sliding window analysis. <i>Scientific Reports</i> , 2020, 10, 149. | 3.3 | 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. | 3.4 | 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. | 12.8 | 55 |
| 4771 | Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (<i>Portunus trituberculatus</i>). <i>GigaScience</i> , 2020, 9, . | 6.4 | 44 |
| 4772 | ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. <i>Nature Genetics</i> , 2020, 52, 187-197. | 21.4 | 108 |
| 4773 | Genome size variation in butterflies (Insecta, Lepidoptera, Papilionoidea): a thorough phylogenetic comparison. <i>Systematic Entomology</i> , 2020, 45, 571-582. | 3.9 | 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. | 12.8 | 167 |
| 4775 | Contaminations in (meta)genome data: An open issue for the scientific community. <i>IUBMB Life</i> , 2020, 72, 698-705. | 3.4 | 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. | 14.5 | 68 |
| 4778 | Deciphering the microbiota data from termite mound soil in South Africa using shotgun metagenomics. <i>Data in Brief</i> , 2020, 28, 104802. | 1.0 | 5 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4779 | Counting Kmers for Biological Sequences at Large Scale. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 99-108. | 3.6 | 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. | 3.9 | 12 |
| 4781 | A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. <i>Molecular Cell</i> , 2020, 77, 352-367.e8. | 9.7 | 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. | 2.7 | 31 |
| 4783 | Conflicting phylogenetic signals in genomic data of the coffee family (Rubiaceae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 440-460. | 3.1 | 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. | 5.7 | 33 |
| 4785 | Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020, 6, 95-106. | 9.3 | 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. | 11.2 | 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. | 8.3 | 73 |
| 4788 | Deciphering the high-quality genome sequence of coriander that causes controversial feelings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1444-1456. | 8.3 | 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. | 2.7 | 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. | 4.1 | 171 |
| 4791 | Sensitivity of the polyDetect computational pipeline for phylogenetic analyses. <i>Analytical Biochemistry</i> , 2020, 593, 113516. | 2.4 | 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. | 11.2 | 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. | 2.0 | 3 |
| 4794 | Draft Genomes of Two Artocarpus Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2020, 11, 27. | 2.4 | 30 |
| 4795 | Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus <i>Penicillium variable</i> HXQ-H-1. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 7. | 3.5 | 6 |
| 4796 | Benchmark study comparing liftover tools for genome conversion of epigenome sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa054. | 3.2 | 19 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4797 | Noninvasive 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. | 2.6 | 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. | 3.7 | 6 |
| 4799 | Control of Transcription Initiation by Biased Thermal Fluctuations on Repetitive Genomic Sequences. <i>Biomolecules</i> , 2020, 10, 1299. | 4.0 | 6 |
| 4800 | DeepAdd: Protein function prediction from k-mer embedding and additional features. <i>Computational Biology and Chemistry</i> , 2020, 89, 107379. | 2.3 | 17 |
| 4801 | Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. <i>Mitochondrion</i> , 2020, 55, 122-133. | 3.4 | 24 |
| 4802 | Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269. | 12.8 | 90 |
| 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. | 3.6 | 18 |
| 4804 | Haplotype-resolved genome analyses of a heterozygous diploid potato. <i>Nature Genetics</i> , 2020, 52, 1018-1023. | 21.4 | 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. | 0.8 | 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. | 3.0 | 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, . | 0.6 | 1 |
| 4808 | Origin and adaptation to high altitude of Tibetan semi-wild wheat. <i>Nature Communications</i> , 2020, 11, 5085. | 12.8 | 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. | 7.1 | 24 |
| 4810 | Comparative genomic analyses illuminate the distinct evolution of megabats within Chiroptera. <i>DNA Research</i> , 2020, 27, . | 3.4 | 10 |
| 4811 | Catabolic Machinery of the Human Gut Microbes Bestow Resilience Against Vanillin Antimicrobial Nature. <i>Frontiers in Microbiology</i> , 2020, 11, 588545. | 3.5 | 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. | 5.2 | 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. | 3.9 | 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, . | 3.0 | 15 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 1.8 | 22 |
| 4816 | Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584. | 27.8 | 210 |
| 4817 | DropSynth 2.0: high-fidelity multiplexed gene synthesis in emulsions. <i>Nucleic Acids Research</i> , 2020, 48, e95-e95. | 14.5 | 25 |
| 4818 | Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , 2020, 3, 371. | 4.4 | 34 |
| 4819 | IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 161-172. | 6.9 | 18 |
| 4820 | HIV-1 replication complexes accumulate in nuclear speckles and integrate into speckle-associated genomic domains. <i>Nature Communications</i> , 2020, 11, 3505. | 12.8 | 93 |
| 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. | 2.4 | 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. | 4.1 | 15 |
| 4823 | XPA deficiency affects the ubiquitin-proteasome system function. <i>DNA Repair</i> , 2020, 94, 102937. | 2.8 | 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. | 2.3 | 23 |
| 4825 | Sequence Compression Benchmark (SCB) database—A comprehensive evaluation of reference-free compressors for FASTA-formatted sequences. <i>GigaScience</i> , 2020, 9, . | 6.4 | 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. | 12.8 | 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. | 2.8 | 12 |
| 4829 | Molecular basis of resistance to organophosphate insecticides in the New World screw-worm fly. <i>Parasites and Vectors</i> , 2020, 13, 562. | 2.5 | 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. | 2.4 | 6 |
| 4831 | A High Quality Asian Genome Assembly Identifies Features of Common Missing Regions. <i>Genes</i> , 2020, 11, 1350. | 2.4 | 0 |
| 4832 | The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289. | 27.8 | 314 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4833 | Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283. | 27.8 | 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. | 2.3 | 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. | 3.3 | 17 |
| 4836 | Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. <i>Genes</i> , 2020, 11, 1345. | 2.4 | 30 |
| 4837 | Optimizing performance of GATK workflows using Apache Arrow In-Memory data framework. <i>BMC Genomics</i> , 2020, 21, 683. | 2.8 | 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 |
| 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. | 1.7 | 51 |
| 4840 | The human chd8 gene is transcribed from two distant upstream promoters. <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 190-194. | 2.1 | 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. | 6.3 | 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. | 2.3 | 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. | 7.1 | 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. | 8.8 | 23 |
| 4845 | Insertion variants missing in the human reference genome are widespread among human populations. <i>BMC Biology</i> , 2020, 18, 167. | 3.8 | 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. | 2.5 | 1 |
| 4847 | Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251. | 27.8 | 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. | 3.3 | 18 |
| 4849 | A Persisting Nontropical Focus of <i>Burkholderia pseudomallei</i> with Limited Genome Evolution over Five Decades. <i>MSystems</i> , 2020, 5, . | 3.8 | 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. | 1.8 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 4851 | Metagenomic profiling of bacterial diversity and community structure in termite mounds and surrounding soils. Archives of Microbiology, 2020, 202, 2697-2709. | 2.2 | 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). Molecular Ecology, 2020, 29, 3667-3683. | 3.9 | 20 |
| 4853 | The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. Plant Journal, 2020, 104, 662-678. | 5.7 | 52 |
| 4854 | Effects of inorganic and organic treatments on the microbial community of maize rhizosphere by a shotgun metagenomics approach. Annals of Microbiology, 2020, 70, . | 2.6 | 50 |
| 4855 | An evolutionary driver of interspersed segmental duplications in primates. Genome Biology, 2020, 21, 202. | 8.8 | 19 |
| 4856 | Multiple Anchor Staged Alignment Algorithm “ Sensitive (MASAA “ S) . , 2020, , . | | 3 |
| 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. Molecular Biology Reports, 2020, 47, 5831-5841. | 2.3 | 3 |
| 4858 | SARS-CoV-2 genomic variations associated with mortality rate of COVID-19. Journal of Human Genetics, 2020, 65, 1075-1082. | 2.3 | 316 |
| 4859 | Privately computing set-maximal matches in genomic data. BMC Medical Genomics, 2020, 13, 72. | 1.5 | 5 |
| 4860 | Ultraconserved Non-coding DNA Within Diptera and Hymenoptera. G3: Genes, Genomes, Genetics, 2020, 10, 3015-3024. | 1.8 | 3 |
| 4861 | Development of a Genome-Wide Oligonucleotide Microarray Platform for Detection of DNA Copy Number Aberrations in Feline Cancers. Veterinary Sciences, 2020, 7, 88. | 1.7 | 4 |
| 4862 | Multi-Omics Characterization of the 4T1 Murine Mammary Gland Tumor Model. Frontiers in Oncology, 2020, 10, 1195. | 2.8 | 94 |
| 4863 | Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. BMC Biology, 2020, 18, 89. | 3.8 | 24 |
| 4864 | Chromosome-level genome assembly of the coastal horseshoe crab (<i>Tachypleus gigas</i>). Molecular Ecology Resources, 2020, 20, 1748-1760. | 4.8 | 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>). Gene, 2020, 763, 144956. | 2.2 | 4 |
| 4866 | Ancestral regulatory mechanisms specify conserved midbrain circuitry in arthropods and vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19544-19555. | 7.1 | 21 |
| 4867 | Morphological divergence and the Quaternary speciation of <i>Actaea purpurea</i> (Ranunculaceae) and its relatives. Journal of Systematics and Evolution, 2022, 60, 43-54. | 3.1 | 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. Plant Journal, 2020, 104, 596-612. | 5.7 | 19 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 3.6 | 16 |
| 4870 | smsMap: mapping single molecule sequencing reads by locating the alignment starting positions. <i>BMC Bioinformatics</i> , 2020, 21, 341. | 2.6 | 7 |
| 4871 | Fusion transcript detection using spatial transcriptomics. <i>BMC Medical Genomics</i> , 2020, 13, 110. | 1.5 | 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. | 8.3 | 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. | 1.7 | 34 |
| 4875 | Mapping and Quantification of Non-Coding RNA Originating from the rDNA in Human Glioma Cells. <i>Cancers</i> , 2020, 12, 2090. | 3.7 | 7 |
| 4876 | MDACP: A Pathogen Genome and Metagenome Analysis Cloud Platform. <i>Frontiers in Genetics</i> , 2020, 11, 1007. | 2.3 | 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. | 21.4 | 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. | 3.6 | 5 |
| 4879 | Progress in quickly finding orthologs as reciprocal best hits: comparing blast, last, diamond and MMseqs2. <i>BMC Genomics</i> , 2020, 21, 741. | 2.8 | 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. | 3.5 | 18 |
| 4881 | pH-dependent transcriptional profile changes in iron-deficient <i>Arabidopsis</i> roots. <i>BMC Genomics</i> , 2020, 21, 694. | 2.8 | 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. | 3.1 | 14 |
| 4883 | Extracellular microRNA 3â€™ end modification across diverse body fluids. <i>Epigenetics</i> , 2021, 16, 1000-1015. | 2.7 | 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, . | 0.6 | 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. | 3.6 | 12 |
| 4886 | Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. <i>Scientific Data</i> , 2020, 7, 324. | 5.3 | 33 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 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, . | 3.1 | 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. | 0.9 | 4 |
| 4889 | The Phoebe genome sheds light on the evolution of magnoliids. <i>Horticulture Research</i> , 2020, 7, 146. | 6.3 | 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. | 2.3 | 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. | 5.5 | 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. | 2.8 | 15 |
| 4893 | A Novel Microduplication Spanning Exons 8â€“16 of <i>ATP2C1</i> That Was Undetectable by Standard Sanger Sequencing in a Japanese Patient With Haileyâ€“Hailey Disease. <i>Frontiers in Medicine</i> , 2020, 7, 492. | 2.6 | 3 |
| 4894 | Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295. | 2.8 | 45 |
| 4895 | Shotgun Metagenomic Survey of Maize Soil Rhizobiome. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.6 | 4 |
| 4896 | A Novel Recurrent <i>COL5A1</i> 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. | 2.4 | 30 |
| 4897 | Long-read sequencing and de novo genome assembly of marine medaka (<i>Oryzias melastigma</i>). <i>BMC Genomics</i> , 2020, 21, 640. | 2.8 | 7 |
| 4898 | Cytogenetically visible inversions are formed by multiple molecular mechanisms. <i>Human Mutation</i> , 2020, 41, 1979-1998. | 2.5 | 12 |
| 4899 | Ultrasensitive deletion detection links mitochondrial DNA replication, disease, and aging. <i>Genome Biology</i> , 2020, 21, 248. | 8.8 | 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. | 2.7 | 9 |
| 4901 | The complete chloroplast genome sequence of Red Asparagus Lettuce (<i>Lactuca sativa</i> var. asparagine L.) Tj ETQq0 0.0 rgBT /Qverlock 10 | 0.4 | 5 |
| 4902 | Positive autoregulation of <i>lag-1</i> in response to LIN-12 activation in cell fate decisions during <i>C. elegans</i> reproductive system development. <i>Development (Cambridge)</i> , 2020, 147, . | 2.5 | 8 |
| 4903 | Genomic content of chemosensory receptors in two sister blister beetles facilitates characterization of chemosensory evolution. <i>BMC Genomics</i> , 2020, 21, 589. | 2.8 | 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. | 4.4 | 29 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4905 | Sequencing and assembly of the Egyptian buffalo genome. PLoS ONE, 2020, 15, e0237087. | 2.5 | 11 |
| 4906 | New Plasmodium vivax Genomes From the China-Myanmar Border. Frontiers in Microbiology, 2020, 11, 1930. | 3.5 | 5 |
| 4907 | Identification of the SUT Gene Family in Pomegranate (Punica granatum L.) and Functional Analysis of PgL0145810.1. International Journal of Molecular Sciences, 2020, 21, 6608. | 4.1 | 9 |
| 4908 | Hedgehog signaling controls segmentation dynamics and diversity via <i>msx1</i> in a spider embryo. Science Advances, 2020, 6, . | 10.3 | 19 |
| 4909 | Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. Science Translational Medicine, 2020, 12, . | 12.4 | 17 |
| 4910 | Viral Abundance and Diversity of Production Fluids in Oil Reservoirs. Microorganisms, 2020, 8, 1429. | 3.6 | 3 |
| 4911 | The UCSC SARS-CoV-2 Genome Browser. Nature Genetics, 2020, 52, 991-998. | 21.4 | 79 |
| 4912 | Genomic characterization of malignant progression in neoplastic pancreatic cysts. Nature Communications, 2020, 11, 4085. | 12.8 | 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. Andrologia, 2020, 52, e13761. | 2.1 | 1 |
| 4914 | Organic Farming Enhances the Diversity and Community Structure of Endophytic Archaea and Fungi in Maize Plant: a Shotgun Approach. Journal of Soil Science and Plant Nutrition, 2020, 20, 2587-2599. | 3.4 | 26 |
| 4915 | Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, . | 12.6 | 105 |
| 4916 | Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. Nature Communications, 2020, 11, 6327. | 12.8 | 39 |
| 4917 | A Chromosome-Level Genome Assembly of the Anglerfish Lophius litulon. Frontiers in Genetics, 2020, 11, 581161. | 2.3 | 2 |
| 4918 | Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. International Journal of Molecular Sciences, 2020, 21, 9618. | 4.1 | 8 |
| 4919 | Hormonal regulation of microRNA expression dynamics in the gut of the yellow fever mosquito Aedes aegypti. RNA Biology, 2020, 18, 1-10. | 3.1 | 3 |
| 4920 | WY195, a New Inducible Promoter From the Rubber Powdery Mildew Pathogen, Can Be Used as an Excellent Tool for Genetic Engineering. Frontiers in Microbiology, 2020, 11, 610252. | 3.5 | 1 |
| 4921 | Use of the Illumina EPIC methylation array for epigenomic research in the crabâ€eating macaque (<i>Macaca fascicularis</i>). Neuropsychopharmacology Reports, 2020, 40, 423-426. | 2.3 | 8 |
| 4922 | An Improved Sequencing-Based Bioinformatics Pipeline to Track the Distribution and Clonal Architecture of Proviral Integration Sites. Frontiers in Microbiology, 2020, 11, 587306. | 3.5 | 5 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4923 | LSH mediates gene repression through macroH2A deposition. <i>Nature Communications</i> , 2020, 11, 5647. | 12.8 | 35 |
| 4924 | A novel method for using RNA-seq data to identify imprinted genes in social Hymenoptera with multiply mated queens. <i>Journal of Evolutionary Biology</i> , 2020, 33, 1770-1782. | 1.7 | 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, . | 3.4 | 5 |
| 4926 | Sequencing and Functional Annotation of the Whole Genome of <i>Shiraia bambusicola</i> . <i>C3: Genes, Genomes, Genetics</i> , 2020, 10, 23-35. | 1.8 | 8 |
| 4927 | A Fast and Memory-Efficient Spectral Library Search Algorithm Using Locality-Sensitive Hashing. <i>Proteomics</i> , 2020, 20, e2000002. | 2.2 | 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. | 12.8 | 29 |
| 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. | 12.8 | 224 |
| 4930 | The Evolution of Human Cancer Gene Duplications across Mammals. <i>Molecular Biology and Evolution</i> , 2020, 37, 2875-2886. | 8.9 | 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. | 3.9 | 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. | 3.7 | 15 |
| 4933 | Bioinformatic prediction of potential T cell epitopes for SARS-Cov-2. <i>Journal of Human Genetics</i> , 2020, 65, 569-575. | 2.3 | 123 |
| 4934 | Chromosome-level assembly of the horseshoe crab genome provides insights into its genome evolution. <i>Nature Communications</i> , 2020, 11, 2322. | 12.8 | 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. | 1.9 | 16 |
| 4936 | MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. <i>Plant Physiology</i> , 2020, 183, 399-413. | 4.8 | 40 |
| 4937 | TGFamFinder : a novel solution for target gene family annotation in plants. <i>New Phytologist</i> , 2020, 227, 1568-1581. | 7.3 | 23 |
| 4938 | The third generation sequencing: the advanced approach to genetic diseases. <i>Translational Pediatrics</i> , 2020, 9, 163-173. | 1.2 | 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. | 4.8 | 45 |
| 4940 | Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. <i>Cell Reports</i> , 2020, 31, 107723. | 6.4 | 62 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 4941 | Whole genome shotgun sequencing of POPs degrading bacterial community dwelling tannery effluents and petrol contaminated soil. <i>Microbiological Research</i> , 2020, 238, 126504. | 5.3 | 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. | 9.5 | 29 |
| 4943 | AnthOligo: automating the design of oligonucleotides for capture/enrichment technologies. <i>Bioinformatics</i> , 2020, 36, 4353-4356. | 4.1 | 4 |
| 4944 | Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 4518-4530. | 1.9 | 34 |
| 4945 | Genotyping by multiplexed sequencing (GMS): A customizable platform for genomic selection. <i>PLoS ONE</i> , 2020, 15, e0229207. | 2.5 | 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. | 3.3 | 30 |
| 4947 | High-quality chromosome-scale assembly of the walnut (<i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, . | 6.4 | 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. | 3.5 | 34 |
| 4949 | Synergistic CRISPRa-Regulated Chondrogenic Extracellular Matrix Deposition Without Exogenous Growth Factors. <i>Tissue Engineering - Part A</i> , 2020, 26, 1169-1179. | 3.1 | 11 |
| 4950 | First Genome Sequence of the Gunnison'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. | 2.5 | 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. | 1.8 | 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. | 3.3 | 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. | 2.5 | 13 |
| 4954 | Shotgun metagenomic sequencing data of sunflower rhizosphere microbial community in South Africa. <i>Data in Brief</i> , 2020, 31, 105831. | 1.0 | 8 |
| 4955 | Dissecting the genome of star fruit (<i>Averrhoa carambola</i> L.). <i>Horticulture Research</i> , 2020, 7, 94. | 6.3 | 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. | 4.6 | 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. | 2.7 | 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, . | 3.9 | 20 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 4959 | Cytogenetic Characterization of a Small Evolutionary Rearrangement Involving Chromosomes BTA21 and OAR18. <i>Cytogenetic and Genome Research</i> , 2020, 160, 193-198. | 1.1 | 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. | 2.3 | 6 |
| 4961 | Genome sequence and comparative analysis of reindeer (<i>Rangifer tarandus</i>) in northern Eurasia. <i>Scientific Reports</i> , 2020, 10, 8980. | 3.3 | 30 |
| 4962 | The gene-rich genome of the scallop <i>Pecten maximus</i> . <i>GigaScience</i> , 2020, 9, . | 6.4 | 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. | 2.3 | 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. | 4.1 | 6 |
| 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. | 3.5 | 9 |
| 4966 | A chromosome-level genome assembly of the parasitoid wasp <i>Pteromalus puparum</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1384-1402. | 4.8 | 35 |
| 4967 | The genetic basis of sex determination in grapes. <i>Nature Communications</i> , 2020, 11, 2902. | 12.8 | 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. | 3.5 | 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. | 12.8 | 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. | 1.9 | 5 |
| 4971 | AtXRN4 Affects the Turnover of Chosen miRNA*s in Arabidopsis. <i>Plants</i> , 2020, 9, 362. | 3.5 | 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. | 2.4 | 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. | 3.6 | 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. | 0.8 | 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. | 2.5 | 17 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 4977 | The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , 2020, 21, 60. | 8.8 | 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. | 4.7 | 12 |
| 4979 | A Partially Phase-Separated Genome Sequence Assembly of the Vitis Rootstock 'B3' (Vitis riparia L.) Tj ETQq0 0 0 rgBT /Ove Science, 2020, 11, 156. | 3.6 | 6 |
| 4980 | Small circRNAs with self-cleaving ribozymes are highly expressed in diverse metazoan transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, 5054-5064. | 14.5 | 20 |
| 4981 | Cis-regulatory analysis of <i>Onecut1</i> expression in fate-restricted retinal progenitor cells. <i>Neural Development</i> , 2020, 15, 5. | 2.4 | 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. | 4.8 | 45 |
| 4983 | Genomic characterization of human brain metastases identifies drivers of metastatic lung adenocarcinoma. <i>Nature Genetics</i> , 2020, 52, 371-377. | 21.4 | 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. | 2.5 | 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. | 1.4 | 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. | 2.5 | 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. | 5.5 | 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. | 4.9 | 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. | 2.9 | 5 |
| 4990 | A Chromosome-Scale Assembly of the Asian Honeybee <i>Apis cerana</i> Genome. <i>Frontiers in Genetics</i> , 2020, 11, 279. | 2.3 | 13 |
| 4991 | Identification of Some Errors in the Genome Assembly of Bovidae by FISH. <i>Cytogenetic and Genome Research</i> , 2020, 160, 85-93. | 1.1 | 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. | 7.1 | 17 |
| 4993 | Nuclear-mitochondrial DNA segments resemble paternally inherited mitochondrial DNA in humans. <i>Nature Communications</i> , 2020, 11, 1740. | 12.8 | 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. | 2.5 | 37 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 5.7 | 23 |
| 4996 | GSAAlign: an efficient sequence alignment tool for intra-species genomes. <i>BMC Genomics</i> , 2020, 21, 182. | 2.8 | 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. | 2.8 | 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. | 2.0 | 18 |
| 4999 | Efficient Nuclease-Directed Integration of Lentivirus Vectors into the Human Ribosomal DNA Locus. <i>Molecular Therapy</i> , 2020, 28, 1858-1875. | 8.2 | 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. | 4.8 | 28 |
| 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. | 3.8 | 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. | 4.0 | 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. | 14.5 | 7 |
| 5005 | High-density genetic map construction and identification of loci controlling flower-type traits in <i>Chrysanthemum</i> (<i>Chrysanthemum morifolium</i> Ramat.). <i>Horticulture Research</i> , 2020, 7, 108. | 6.3 | 33 |
| 5006 | Termite Societies Promote the Taxonomic and Functional Diversity of Archaeal Communities in Mound Soils. <i>Biology</i> , 2020, 9, 136. | 2.8 | 6 |
| 5007 | Stretch Profile: A pruning technique to accelerate DNA sequence search. <i>Informatics in Medicine Unlocked</i> , 2020, 19, 100323. | 3.4 | 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. | 2.9 | 15 |
| 5009 | CandiMeth: Powerful yet simple visualization and quantification of DNA methylation at candidate genes. <i>GigaScience</i> , 2020, 9, . | 6.4 | 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. | 1.8 | 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. | 10.3 | 29 |
| 5012 | Intestinal Virome in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 72, 2182-2196. | 7.3 | 74 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 2.1 | 8 |
| 5014 | Shotgun metagenomic data of root endophytic microbiome of maize (<i>Zea mays</i> L.). <i>Data in Brief</i> , 2020, 31, 105893. | 1.0 | 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. | 3.5 | 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. | 2.3 | 32 |
| 5017 | The landscape of chimeric RNAs in non-diseased tissues and cells. <i>Nucleic Acids Research</i> , 2020, 48, 1764-1778. | 14.5 | 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. | 2.3 | 6 |
| 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. | 3.1 | 31 |
| 5020 | An inferred fitness consequence map of the rice genome. <i>Nature Plants</i> , 2020, 6, 119-130. | 9.3 | 20 |
| 5021 | Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <i>Current Bioinformatics</i> , 2020, 15, 2-16. | 1.5 | 9 |
| 5022 | Evolutionary Dynamics of the POTE Gene Family in Human and Nonhuman Primates. <i>Genes</i> , 2020, 11, 213. | 2.4 | 7 |
| 5023 | New genome assembly of the barn owl (<i>Tyto alba alba</i>). <i>Ecology and Evolution</i> , 2020, 10, 2284-2298. | 1.9 | 11 |
| 5024 | Interspecific Variation in Nematode Responses to Metals. <i>Environmental Toxicology and Chemistry</i> , 2020, 39, 1006-1016. | 4.3 | 5 |
| 5025 | Complete chloroplast genome of <i>Physalis chenopodifolia</i> Lam. (Solanaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 162-163. | 0.4 | 5 |
| 5026 | The draft genome of mandrill (<i>Mandrillus sphinx</i>): An Old World monkey. <i>Scientific Reports</i> , 2020, 10, 2431. | 3.3 | 3 |
| 5027 | Exploring the computational methods for protein-ligand binding site prediction. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 417-426. | 4.1 | 112 |
| 5028 | Current Trends in Diagnostics of Viral Infections of Unknown Etiology. <i>Viruses</i> , 2020, 12, 211. | 3.3 | 49 |
| 5029 | MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. <i>Frontiers in Genetics</i> , 2019, 10, 1396. | 2.3 | 10 |
| 5030 | Enterovirus 71 Infection Shapes Host T Cell Receptor Repertoire and Presumably Expands VP1-Specific TCR β CDR3 Cluster. <i>Pathogens</i> , 2020, 9, 121. | 2.8 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 1.6 | 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. | 2.1 | 13 |
| 5033 | Evolutionary dynamics of chloroplast genomes in subfamily Aroideae (Araceae). <i>Genomics</i> , 2020, 112, 2349-2360. | 2.9 | 79 |
| 5034 | Phylogenetic informativeness analyses to clarify past diversification processes in Cucurbitaceae. <i>Scientific Reports</i> , 2020, 10, 488. | 3.3 | 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. | 3.5 | 10 |
| 5036 | Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020, 21, 47. | 2.8 | 84 |
| 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. | 1.1 | 10 |
| 5038 | Genome assembly and characterization of a complex zBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. <i>PLoS Genetics</i> , 2020, 16, e1008571. | 3.5 | 112 |
| 5039 | Investigating RNA editing in deep transcriptome datasets with REDIttools and REDItportal. <i>Nature Protocols</i> , 2020, 15, 1098-1131. | 12.0 | 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. | 2.5 | 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. | 7.5 | 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. | 3.3 | 18 |
| 5044 | O6-Methylguanine-DNA Methyltransferase (MGMT): Challenges and New Opportunities in Glioma Chemotherapy. <i>Frontiers in Oncology</i> , 2019, 9, 1547. | 2.8 | 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. | 4.1 | 7 |
| 5046 | Aging-regulated anti-apoptotic long non-coding RNA Sarrah augments recovery from acute myocardial infarction. <i>Nature Communications</i> , 2020, 11, 2039. | 12.8 | 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, . | 3.1 | 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. | 2.1 | 4 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 4.7 | 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. | 3.6 | 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. | 1.9 | 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, . | 12.6 | 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. | 3.6 | 9 |
| 5054 | Expansion and Conservation of Biosynthetic Gene Clusters in Pathogenic <i>Pyrenophora</i> spp.. <i>Toxins</i> , 2020, 12, 242. | 3.4 | 13 |
| 5055 | Phytochrome Coordinates with a hnRNP to Regulate Alternative Splicing via an Exonic Splicing Silencer. <i>Plant Physiology</i> , 2020, 182, 243-254. | 4.8 | 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. | 3.3 | 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. | 1.9 | 1 |
| 5058 | Humans Are Selectively Exposed to <i>Pneumocystis jirovecii</i> . <i>MBio</i> , 2020, 11, . | 4.1 | 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. | 2.8 | 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. | 3.6 | 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. | 1.7 | 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, . | 3.0 | 11 |
| 5063 | De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, . | 6.4 | 380 |
| 5064 | Multifaceted Hi-C benchmarking: what makes a difference in chromosome-scale genome scaffolding?. <i>GigaScience</i> , 2020, 9, . | 6.4 | 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. | 8.9 | 8 |
| 5066 | The UCSC repeat browser allows discovery and visualization of evolutionary conflict across repeat families. <i>Mobile DNA</i> , 2020, 11, 13. | 3.6 | 31 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 5067 | Deficiency in the endocytic adaptor proteins PHETA1/2 impair renal and craniofacial development. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, . | 2.4 | 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. | 1.8 | 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. | 2.3 | 7 |
| 5070 | Error, noise and bias in de novo transcriptome assemblies. <i>Molecular Ecology Resources</i> , 2021, 21, 18-29. | 4.8 | 40 |
| 5071 | Levenshtein Distance, Sequence Comparison and Biological Database Search. <i>IEEE Transactions on Information Theory</i> , 2021, 67, 3287-3294. | 2.4 | 51 |
| 5072 | FED: a web tool for foreign element detection of genome-edited organism. <i>Science China Life Sciences</i> , 2021, 64, 167-170. | 4.9 | 8 |
| 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. | 2.7 | 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. | 2.7 | 8 |
| 5075 | An Unbiased Molecular Approach Using 3â€²-UTRs Resolves the Avian Family-Level Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 108-127. | 8.9 | 99 |
| 5076 | Contributions of de novo variants to systemic lupus erythematosus. <i>European Journal of Human Genetics</i> , 2021, 29, 184-193. | 2.8 | 6 |
| 5077 | High-Throughput Sequencing to Detect DNA-RNA Changes. <i>Methods in Molecular Biology</i> , 2021, 2181, 193-212. | 0.9 | 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. | 5.6 | 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. | 2.2 | 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. | 3.7 | 9 |
| 5081 | Translation of noncoding RNAs and cancer. <i>Cancer Letters</i> , 2021, 497, 89-99. | 7.2 | 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. | 8.9 | 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. | 8.9 | 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. | 3.0 | 18 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 3.1 | 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. | 2.4 | 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. | 14.5 | 20 |
| 5088 | The celery genome sequence reveals sequential paleo- and polyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744. | 8.3 | 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. | 6.3 | 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. | 4.8 | 25 |
| 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. | 7.5 | 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. | 17.5 | 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. | 2.2 | 3 |
| 5094 | Vertebrate Chromosome Evolution. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 1-27. | 7.4 | 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. | 1.4 | 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. | 5.7 | 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. | 2.4 | 10 |
| 5098 | Neoantigen prediction in human breast cancer using RNA sequencing data. <i>Cancer Science</i> , 2021, 112, 465-475. | 3.9 | 13 |
| 5099 | Functional diversity of microbial communities in two contrasting maize rhizosphere soils. <i>Rhizosphere</i> , 2021, 17, 100282. | 3.0 | 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. | 10.0 | 10 |
| 5101 | Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology</i> 2000, 2021, 85, 12-27. | 13.4 | 16 |
| 5102 | Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021, 5, 231-242. | 7.8 | 51 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 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. | 1.6 | 4 |
| 5104 | The comparative genomic landscape of adaptive radiation in crater lake cichlid fishes. <i>Molecular Ecology</i> , 2021, 30, 955-972. | 3.9 | 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. | 3.5 | 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. | 3.8 | 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, . | 2.5 | 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. | 8.3 | 52 |
| 5109 | New methodology for repetitive sequences identification in human X and Y chromosomes. <i>Biomedical Signal Processing and Control</i> , 2021, 64, 102207. | 5.7 | 5 |
| 5110 | Molecular identification and characterisation of a novel chicken leukocyte immunoglobulin-like receptor A5. <i>British Poultry Science</i> , 2021, 62, 68-80. | 1.7 | 2 |
| 5111 | In Silico Analysis of HSP70 Gene Family in Bovine Genome. <i>Biochemical Genetics</i> , 2021, 59, 134-158. | 1.7 | 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. | 9.8 | 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. | 8.3 | 21 |
| 5114 | Challenges in gene-oriented approaches for pangenome content discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 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. | 1.6 | 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. | 3.1 | 14 |
| 5117 | Hepatitis delta virus-like circular RNAs from diverse metazoans encode conserved hammerhead ribozymes. <i>Virus Evolution</i> , 2021, 7, veab016. | 4.9 | 22 |
| 5119 | Pleiotropy and epistasis within and between signaling pathways defines the genetic architecture of fungal virulence. <i>PLoS Genetics</i> , 2021, 17, e1009313. | 3.5 | 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. | 2.1 | 9 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 5122 | Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444. | 27.8 | 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. | 1.9 | 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. | 3.6 | 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. | 2.3 | 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, . | 4.1 | 26 |
| 5128 | Improved contiguity of the threespine stickleback genome using long-read sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 1.8 | 34 |
| 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. | 1.6 | 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. | 4.8 | 20 |
| 5132 | Therapy-induced Deletion in 11q23 Leading to Fusion of <i>KMT2A</i> With <i>ARHGEF12</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. | 2.0 | 7 |
| 5133 | Shotgun metagenomics reveals the functional diversity of root-associated endophytic microbiomes in maize plant. <i>Current Plant Biology</i> , 2021, 25, 100195. | 4.7 | 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. | 0.9 | 2 |
| 5136 | Combined genomic, transcriptomic, and metabolomic analyses provide insights into chayote (<i>Sechium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 | 6.3 | 39 |
| 5137 | Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560. | 17.5 | 251 |
| 5138 | Dynamic evolution of transposable elements, demographic history, and gene content of paleognathous birds. <i>Zoological Research</i> , 2021, 42, 51-61. | 2.1 | 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, . | 0.6 | 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, . | 4.1 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 5.6 | 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. | 2.1 | 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. | 3.4 | 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. | 1.3 | 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, . | 2.5 | 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, . | 2.5 | 14 |
| 5149 | CRISPR-SE: a brute force search engine for CRISPR design. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab013. | 3.2 | 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. | 3.0 | 1 |
| 5151 | Metagenomics survey unravels diversity of biogas microbiomes with potential to enhance productivity in Kenya. <i>PLoS ONE</i> , 2021, 16, e0244755. | 2.5 | 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. | 5.5 | 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. | 0.8 | 3 |
| 5154 | Evolution of regulatory networks associated with traits under selection in cichlids. <i>Genome Biology</i> , 2021, 22, 25. | 8.8 | 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. | 2.3 | 15 |
| 5156 | Chromosome-level genome assembly of <i>Ophiorrhiza pumila</i> reveals the evolution of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 405. | 12.8 | 77 |
| 5157 | Significantly improving the quality of genome assemblies through curation. <i>GigaScience</i> , 2021, 10, . | 6.4 | 739 |
| 5158 | EUKulele: Taxonomic annotation of the unsung eukaryotic microbes. <i>Journal of Open Source Software</i> , 2021, 6, 2817. | 4.6 | 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. | 5.1 | 35 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5164 | Detecting high-scoring local alignments in pangenome graphs. <i>Bioinformatics</i> , 2021, 37, 2266-2274. | 4.1 | 6 |
| 5166 | Gene family amplification facilitates adaptation in freshwater unionid bivalve <i>Megalanaia nervosa</i> . <i>Molecular Ecology</i> , 2021, 30, 1155-1173. | 3.9 | 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, . | 1.8 | 35 |
| 5169 | Cyanobacteria in microbialites of Alchichica Crater Lake: a polyphasic characterization. <i>European Journal of Phycology</i> , 2021, 56, 428-443. | 2.0 | 8 |
| 5170 | A novel canine reference genome resolves genomic architecture and uncovers transcript complexity. <i>Communications Biology</i> , 2021, 4, 185. | 4.4 | 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. | 3.9 | 37 |
| 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, . | 3.1 | 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 β^2 Variant Transcripts and Their Distribution in Humans. <i>Journal of Nippon Medical School</i> , 2021, 88, 54-62. | 0.9 | 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. | 2.6 | 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. | 0.4 | 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. | 3.3 | 4 |
| 5178 | Simple sequence repeats drive genome plasticity and promote adaptive evolution in penaeid shrimp. <i>Communications Biology</i> , 2021, 4, 186. | 4.4 | 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. | 9.3 | 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. | 0.8 | 1 |
| 5181 | The Immense Functional Attributes of Maize Rhizosphere Microbiome: A Shotgun Sequencing Approach. <i>Agriculture (Switzerland)</i> , 2021, 11, 118. | 3.1 | 7 |
| 5182 | A comprehensive review of scaffolding methods in genome assembly. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 16 |
| 5183 | Divergence in alternative polyadenylation contributes to gene regulatory differences between humans and chimpanzees. <i>ELife</i> , 2021, 10, . | 6.0 | 11 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 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. | 2.0 | 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. | 3.3 | 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, . | 3.9 | 4 |
| 5190 | Flagellar Perturbations Activate Adhesion through Two Distinct Pathways in <i>Caulobacter crescentus</i> . <i>MBio</i> , 2021, 12, . | 4.1 | 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. | 2.5 | 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. | 3.0 | 24 |
| 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. | 0.5 | 0 |
| 5197 | BSGatlas: a unified <i>Bacillus subtilis</i> genome and transcriptome annotation atlas with enhanced information access. <i>Microbial Genomics</i> , 2021, 7, . | 2.0 | 12 |
| 5198 | Latent trait modeling of tau neuropathology in progressive supranuclear palsy. <i>Acta Neuropathologica</i> , 2021, 141, 667-680. | 7.7 | 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. | 4.8 | 17 |
| 5200 | Metagenomic Insight into the Community Structure and Functional Genes in the Sunflower Rhizosphere Microbiome. <i>Agriculture (Switzerland)</i> , 2021, 11, 167. | 3.1 | 13 |
| 5201 | Functional and Pathological Roles of AHCY. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 654344. | 3.7 | 38 |
| 5202 | Deciphering the transcriptomic regulation of heat stress responses in <i>Nothofagus pumilio</i> . <i>PLoS ONE</i> , 2021, 16, e0246615. | 2.5 | 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, . | 2.9 | 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. | 3.9 | 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. | 4.8 | 43 |
| 5207 | Searching the Dark Genome for Alzheimer's Disease Risk Variants. <i>Brain Sciences</i> , 2021, 11, 332. | 2.3 | 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. | 0.4 | 6 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 5210 | riboCIRC: a comprehensive database of translatable circRNAs. <i>Genome Biology</i> , 2021, 22, 79. | 8.8 | 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. | 4.8 | 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. | 0.4 | 1 |
| 5214 | Longitudinal study of the scalp microbiome suggests coconut oil to enrich healthy scalp commensals. <i>Scientific Reports</i> , 2021, 11, 7220. | 3.3 | 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. | 4.8 | 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, . | 1.8 | 2 |
| 5217 | Comprehensive identification of somatic nucleotide variants in human brain tissue. <i>Genome Biology</i> , 2021, 22, 92. | 8.8 | 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. | 4.4 | 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. | 0.4 | 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, . | 7.1 | 25 |
| 5221 | Comparative analysis of chloroplast genomes of kenaf cytoplasmic male sterile line and its maintainer line. <i>Scientific Reports</i> , 2021, 11, 5301. | 3.3 | 1 |
| 5222 | X chromosome-dependent disruption of placental regulatory networks in hybrid dwarf hamsters. <i>Genetics</i> , 2021, 218, . | 2.9 | 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, . | 7.1 | 30 |
| 5224 | Large-scale transcriptomics to dissect 2 years of the life of a fungal phytopathogen interacting with its host plant. <i>BMC Biology</i> , 2021, 19, 55. | 3.8 | 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. | 2.2 | 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. | 2.4 | 22 |
| 5227 | Rapid speciation via the evolution of pre-mating isolation in the Iberian Seed-eater. <i>Science</i> , 2021, 371, . | 12.6 | 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 / O | 1.8 | 3 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 5229 | The stacking strategy-based hybrid framework for identifying non-coding RNAs. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 28 |
| 5231 | Why are rare variants hard to impute? Coalescent models reveal theoretical limits in existing algorithms. Genetics, 2021, 217, . | 2.9 | 11 |
| 5232 | Whole-Genome Sequencing and Characterization of Buffalo Genetic Resources: Recent Advances and Future Challenges. Animals, 2021, 11, 904. | 2.3 | 20 |
| 5234 | The Complete Chloroplast Genome Sequence of <i>Melilotoides ruthenica</i> : Structural Comparative and Phylogenetic Analysis in Leguminosae. IOP Conference Series: Earth and Environmental Science, 2021, 697, 012014. | 0.3 | 1 |
| 5235 | Effect of thermospermine on expression profiling of different gene using massive analysis of cDNA ends (MACE) and vascular maintenance in Arabidopsis. Physiology and Molecular Biology of Plants, 2021, 27, 577-586. | 3.1 | 3 |
| 5236 | Alvis: a tool for contig and read ALignment VISualisation and chimera detection. BMC Bioinformatics, 2021, 22, 124. | 2.6 | 14 |
| 5237 | The genome of <i>Magnolia biondii</i> Pamp. provides insights into the evolution of Magnoliales and biosynthesis of terpenoids. Horticulture Research, 2021, 8, 38. | 6.3 | 32 |
| 5238 | The complete mitochondrial and plastid genomes of <i>Rhododendron simsii</i> , an important parent of widely cultivated azaleas. Mitochondrial DNA Part B: Resources, 2021, 6, 1197-1199. | 0.4 | 6 |
| 5239 | African lungfish genome sheds light on the vertebrate water-to-land transition. Cell, 2021, 184, 1362-1376.e18. | 28.9 | 99 |
| 5240 | The Pan social brain: An evolutionary history of neurochemical receptor genes and their potential impact on sociocognitive differences. Journal of Human Evolution, 2021, 152, 102949. | 2.6 | 12 |
| 5241 | Identification and Characterization of Alternatively Spliced Transcript Isoforms of IRX4 in Prostate Cancer. Genes, 2021, 12, 615. | 2.4 | 4 |
| 5243 | Fast lightweight accurate xenograft sorting. Algorithms for Molecular Biology, 2021, 16, 2. | 1.2 | 9 |
| 5244 | ACME dissociation: a versatile cell fixation-dissociation method for single-cell transcriptomics. Genome Biology, 2021, 22, 89. | 8.8 | 39 |
| 5245 | Parallel computing for genome sequence processing. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 7 |
| 5246 | Increased expression of peptides from non-coding genes in cancer proteomics datasets suggests potential tumor neoantigens. Communications Biology, 2021, 4, 496. | 4.4 | 20 |
| 5247 | Genome-Wide Analysis of Terpene Synthase Gene Family in <i>Mentha longifolia</i> and Catalytic Activity Analysis of a Single Terpene Synthase. Genes, 2021, 12, 518. | 2.4 | 22 |
| 5248 | Investigation of long interspersed elementâ€”1 retrotransposons as potential risk factors for idiopathic temporal lobe epilepsy. Epilepsia, 2021, 62, 1329-1342. | 5.1 | 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. Biomedicines, 2021, 9, 429. | 3.2 | 15 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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, . | 2.4 | 7 |
| 5252 | Single-cell transcriptome sequencing on the Nanopore platform with ScNapBar. <i>Rna</i> , 2021, 27, 763-770. | 3.5 | 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. | 3.8 | 65 |
| 5254 | Universal nomenclature for oxytocin-vasotocin ligand and receptor families. <i>Nature</i> , 2021, 592, 747-755. | 27.8 | 73 |
| 5255 | SNP detection and population structure evaluation of <i>Salix gordejewii</i> Y. L. Chang et Skv. in Hunshandake Sandland, Inner Mongolia, China. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 997-1005. | 3.1 | 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. | 3.3 | 3 |
| 5260 | Sex-Biased lncRNA Signature in Fetal Growth Restriction (FGR). <i>Cells</i> , 2021, 10, 921. | 4.1 | 5 |
| 5261 | Hapo-C, haplotype-aware polishing of genome assemblies with accurate reads. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab034. | 3.2 | 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. | 3.9 | 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. | 2.4 | 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, . | 2.0 | 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. | 3.3 | 5 |
| 5267 | The Chinese mitten crab genome provides insights into adaptive plasticity and developmental regulation. <i>Nature Communications</i> , 2021, 12, 2395. | 12.8 | 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. | 1.9 | 0 |
| 5269 | A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841. | 3.6 | 36 |
| 5270 | l ¹ Np63 is a pioneer factor that binds inaccessible chromatin and elicits chromatin remodeling. <i>Epigenetics and Chromatin</i> , 2021, 14, 20. | 3.9 | 17 |
| 5272 | Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021, 372, . | 12.6 | 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. | 3.3 | 12 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 5274 | The Meishan pig genome reveals structural variationâ€mediated gene expression and phenotypic divergence underlying Asian pig domestication. <i>Molecular Ecology Resources</i> , 2021, 21, 2077-2092. | 4.8 | 20 |
| 5275 | Chromosomal Inversion Polymorphisms in Two Sympatric Ascidian Lineages. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 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. | 1.4 | 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. | 8.2 | 43 |
| 5278 | Conserved long-range base pairings are associated with pre-mRNA processing of human genes. <i>Nature Communications</i> , 2021, 12, 2300. | 12.8 | 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, . | 3.8 | 69 |
| 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. | 8.2 | 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. | 2.3 | 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. | 7.7 | 9 |
| 5283 | Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 1.8 | 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. | 4.8 | 5 |
| 5285 | Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. <i>Genes</i> , 2021, 12, 847. | 2.4 | 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. | 12.8 | 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. | 7.0 | 73 |
| 5288 | The cytochrome P450 (CYP) superfamily in cnidarians. <i>Scientific Reports</i> , 2021, 11, 9834. | 3.3 | 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. | 12.8 | 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. | 6.3 | 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. | 4.8 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5295 | Introgressing the <i>Aegilops tauschii</i> genome into wheat as a basis for cereal improvement. <i>Nature Plants</i> , 2021, 7, 774-786. | 9.3 | 65 |
| 5296 | Hardware acceleration of genomics data analysis: challenges and opportunities. <i>Bioinformatics</i> , 2021, 37, 1785-1795. | 4.1 | 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, . | 7.1 | 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. | 3.8 | 3 |
| 5300 | Long non-coding RNAs and their targets as potential biomarkers in breast cancer. <i>IET Systems Biology</i> , 2021, 15, 137-147. | 1.5 | 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. | 5.7 | 12 |
| 5302 | Cross-Predicting Essential Genes between Two Model Eukaryotic Species Using Machine Learning. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5056. | 4.1 | 8 |
| 5303 | Long-read cDNA sequencing identifies functional pseudogenes in the human transcriptome. <i>Genome Biology</i> , 2021, 22, 146. | 8.8 | 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. | 0.7 | 9 |
| 5305 | Elephant Genomes Reveal Accelerated Evolution in Mechanisms Underlying Disease Defenses. <i>Molecular Biology and Evolution</i> , 2021, 38, 3606-3620. | 8.9 | 33 |
| 5306 | TSSFinder – fast and accurate ab initio prediction of the core promoter in eukaryotic genomes. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 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. | 4.9 | 6 |
| 5309 | Transcriptomic Analysis of Skin Color in Anole Lizards. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 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. | 2.8 | 11 |
| 5311 | Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537. | 4.4 | 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. | 3.8 | 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. | 2.3 | 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. | 4.1 | 7 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 5316 | Optimising the use of gene expression data to predict plant metabolic pathway memberships. <i>New Phytologist</i> , 2021, 231, 475-489. | 7.3 | 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. | 8.9 | 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. | 5.7 | 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, . | 7.1 | 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. | 2.2 | 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. | 5.9 | 46 |
| 5323 | Sex chromosome transformation and the origin of a male-specific X chromosome in the creeping vole. <i>Science</i> , 2021, 372, 592-600. | 12.6 | 20 |
| 5324 | Defining genome architecture at base-pair resolution. <i>Nature</i> , 2021, 595, 125-129. | 27.8 | 107 |
| 5325 | SINE jumping contributes to large-scale polymorphisms in the pig genomes. <i>Mobile DNA</i> , 2021, 12, 17. | 3.6 | 21 |
| 5327 | Tracking HIV-1-Infected Cell Clones Using Integration Site-Specific qPCR. <i>Viruses</i> , 2021, 13, 1235. | 3.3 | 10 |
| 5328 | Contiguous erosion of the inactive X in human pluripotency concludes with global DNA hypomethylation. <i>Cell Reports</i> , 2021, 35, 109215. | 6.4 | 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. | 11.1 | 30 |
| 5330 | Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, . | 10.3 | 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. | 1.4 | 1 |
| 5332 | Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. <i>Cell</i> , 2021, 184, 3542-3558.e16. | 28.9 | 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. | 2.4 | 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. | 3.8 | 14 |
| 5336 | Wolfberry genomes and the evolution of <i>Lycium</i> (Solanaceae). <i>Communications Biology</i> , 2021, 4, 671. | 4.4 | 40 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 1.8 | 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. | 4.4 | 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. | 0.4 | 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. | 2.1 | 4 |
| 5342 | Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. <i>Cancer Cell</i> , 2021, 39, 793-809.e8. | 16.8 | 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. | 2.8 | 10 |
| 5344 | Cis-regulatory evolution spotlights species differences in the adaptive potential of gene expression plasticity. <i>Nature Communications</i> , 2021, 12, 3376. | 12.8 | 25 |
| 5345 | A porcine brain-wide RNA editing landscape. <i>Communications Biology</i> , 2021, 4, 717. | 4.4 | 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. | 3.6 | 15 |
| 5347 | Comparative transcriptome analysis of <i>Salix cupularis</i> under drought stress. <i>Global Ecology and Conservation</i> , 2021, 27, e01532. | 2.1 | 3 |
| 5348 | Variant analyses of candidate genes in orofacial clefts in multi-ethnic populations. <i>Oral Diseases</i> , 2022, 28, 1921-1935. | 3.0 | 3 |
| 5349 | SaQuant: a real-time PCR assay for quantitative assessment of <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2021, 21, 174. | 3.3 | 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. | 8.3 | 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. | 8.3 | 39 |
| 5352 | The nearly complete genome of <i>Ginkgo biloba</i> illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021, 7, 748-756. | 9.3 | 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. | 3.5 | 6 |
| 5354 | LIQA: long-read isoform quantification and analysis. <i>Genome Biology</i> , 2021, 22, 182. | 8.8 | 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. | 2.2 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 5356 | Gene Expression Modification by an Autosomal Inversion Associated With Three Male Mating Morphs. <i>Frontiers in Genetics</i> , 2021, 12, 641620. | 2.3 | 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. | 0.4 | 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. | 3.6 | 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. | 8.9 | 12 |
| 5360 | Chromosome-scale genome assembly of areca palm (<i>Areca catechu</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 2504-2519. | 4.8 | 20 |
| 5361 | Draft de novo Genome Assembly of the Elusive Jaguarundi, <i>Puma yagouaroundi</i> . <i>Journal of Heredity</i> , 2021, 112, 540-548. | 2.4 | 5 |
| 5362 | Mobile element insertions and associated structural variants in longitudinal breast cancer samples. <i>Scientific Reports</i> , 2021, 11, 13020. | 3.3 | 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. | 4.1 | 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. | 3.2 | 12 |
| 5365 | Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2846-2867. | 9.4 | 83 |
| 5366 | Predicting future from past: The genomic basis of recurrent and rapid stickleback evolution. <i>Science Advances</i> , 2021, 7, . | 10.3 | 62 |
| 5367 | Echolocation in soft-furred tree mice. <i>Science</i> , 2021, 372, . | 12.6 | 28 |
| 5368 | A Curriculum for Genomic Education of Molecular Genetic Pathology Fellows. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 1218-1240. | 2.8 | 4 |
| 5372 | Dynamic partitioning of search patterns for approximate pattern matching using search schemes. <i>IScience</i> , 2021, 24, 102687. | 4.1 | 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. | 4.1 | 12 |
| 5374 | DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280. | 12.8 | 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. | 4.8 | 3 |
| 5376 | Phylogeographic analysis delimits three evolutionary significant units of least chipmunks in North America and identifies unique genetic diversity within the imperiled <i>Peñasco</i> population. <i>Ecology and Evolution</i> , 2021, 11, 12114-12128. | 1.9 | 3 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 2.9 | 12 |
| 5380 | Metagenomic and viromic data mining reveals viral threats in biologically treated domestic wastewater. <i>Environmental Science and Ecotechnology</i> , 2021, 7, 100105. | 13.5 | 23 |
| 5381 | Accurate spliced alignment of long RNA sequencing reads. <i>Bioinformatics</i> , 2021, 37, 4643-4651. | 4.1 | 28 |
| 5383 | Large palindromes on the primate X Chromosome are preserved by natural selection. <i>Genome Research</i> , 2021, 31, 1337-1352. | 5.5 | 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. | 1.6 | 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. | 4.8 | 10 |
| 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. | 2.9 | 13 |
| 5389 | Large parental differences in chromatin organization in pancreatic beta cell line explaining diabetes susceptibility effects. <i>Nature Communications</i> , 2021, 12, 4338. | 12.8 | 5 |
| 5390 | Distinct Retrotransposon Evolution Profile in the Genome of Rabbit (<i>Oryctolagus cuniculus</i>). <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 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. | 2.8 | 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. | 2.1 | 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. | 2.9 | 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, . | 6.0 | 4 |
| 5397 | Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125. | 12.8 | 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. | 3.1 | 5 |
| 5399 | Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. <i>Genome Medicine</i> , 2021, 13, 114. | 8.2 | 5 |
| 5400 | GRIDSS2: comprehensive characterisation of somatic structural variation using single breakend variants and structural variant phasing. <i>Genome Biology</i> , 2021, 22, 202. | 8.8 | 73 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 5401 | An epigenetic switch regulates the ontogeny of AXL-positive/EGFR-TKi-resistant cells by modulating miR-335 expression. <i>ELife</i> , 2021, 10, . | 6.0 | 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. | 3.9 | 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. | 3.2 | 15 |
| 5407 | Early-life social experience affects offspring DNA methylation and later life stress phenotype. <i>Nature Communications</i> , 2021, 12, 4398. | 12.8 | 11 |
| 5408 | Transcriptional Regulation of RUNX1: An Informatics Analysis. <i>Genes</i> , 2021, 12, 1175. | 2.4 | 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. | 3.6 | 17 |
| 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</i> Linn.). <i>BMC Plant Biology</i> , 2021, 21, 350. | 3.6 | 7 |
| 5412 | Sequencing and Chromosome-Scale Assembly of Plant Genomes, <i>Brassica rapa</i> as a Use Case. <i>Biology</i> , 2021, 10, 732. | 2.8 | 15 |
| 5413 | Novel function of SART1 in HNF4 α transcriptional regulation contributes to its antiviral role during HBV infection. <i>Journal of Hepatology</i> , 2021, 75, 1072-1082. | 3.7 | 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, . | 1.8 | 5 |
| 5415 | Prognostic Roles of BRAF, KIT, NRAS, IGF2R and SF3B1 Mutations in Mucosal Melanomas. <i>Cells</i> , 2021, 10, 2216. | 4.1 | 8 |
| 5417 | Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249. | 8.8 | 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. | 2.3 | 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. | 1.4 | 3 |
| 5420 | nf-LO: A Scalable, Containerized Workflow for Genome-to-Genome Lift Over. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 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. | 1.2 | 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. | 2.4 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 4.1 | 10 |
| 5426 | Evidence for and localization of proposed causative variants in cattle and pig genomes. <i>Genetics Selection Evolution</i> , 2021, 53, 67. | 3.0 | 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. | 2.7 | 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. | 3.2 | 17 |
| 5429 | Identification of three novel <scp>HLA</scp> alleles by next-generation sequencing. <i>Hla</i> , 2021, 98, 560-562. | 0.6 | 3 |
| 5430 | Highly susceptible SARS-CoV-2 model in CAG promoter-driven hACE2-transgenic mice. <i>JCI Insight</i> , 2021, 6, . | 5.0 | 21 |
| 5431 | Cancer cells are highly susceptible to accumulation of templated insertions linked to MMBIR. <i>Nucleic Acids Research</i> , 2021, 49, 8714-8731. | 14.5 | 12 |
| 5432 | Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188. | 6.3 | 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. | 3.3 | 2 |
| 5435 | Topography drives microgeographic adaptations of closely related species in two tropical tree species complexes. <i>Molecular Ecology</i> , 2021, 30, 5080-5093. | 3.9 | 16 |
| 5437 | Evidence that toxin resistance in poison birds and frogs is not rooted in sodium channel mutations and may rely on "toxin sponge" proteins. <i>Journal of General Physiology</i> , 2021, 153, . | 1.9 | 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. | 4.1 | 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. | 3.1 | 10 |
| 5441 | Molecular and functional profiling identifies therapeutically targetable vulnerabilities in plasmablastic lymphoma. <i>Nature Communications</i> , 2021, 12, 5183. | 12.8 | 26 |
| 5442 | Genome and transcriptome assemblies of the kuruma shrimp, <i>Marsupenaeus japonicus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 1.8 | 20 |
| 5443 | De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662. | 12.6 | 282 |
| 5445 | A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021, 597, 119-125. | 27.8 | 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. | 3.5 | 14 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 5447 | Planarian Anatomy Ontology: a resource to connect data within and across experimental platforms. Development (Cambridge), 2021, 148, . | 2.5 | 11 |
| 5448 | Fast and Accurate Algorithms for Mapping and Aligning Long Reads. Journal of Computational Biology, 2021, 28, 789-803. | 1.6 | 2 |
| 5449 | Nanopore sequencing of brain-derived full-length circRNAs reveals circRNA-specific exon usage, intron retention and microexons. Nature Communications, 2021, 12, 4825. | 12.8 | 54 |
| 5450 | A Genome-Wide CRISPR/Cas9 Screen Reveals the Requirement of Host Sphingomyelin Synthase 1 for Infection with Pseudorabies Virus Mutant gDΔC“Pass. Viruses, 2021, 13, 1574. | 3.3 | 9 |
| 5451 | Pan-genome of Raphanus highlights genetic variation and introgression among domesticated, wild, and weedy radishes. Molecular Plant, 2021, 14, 2032-2055. | 8.3 | 56 |
| 5452 | Gene trapping reveals a new transcriptionally active genome element: The chromosome-specific clustered trap region. Genes To Cells, 2021, 26, 874-890. | 1.2 | 0 |
| 5453 | BDV Syndrome: an Emerging Syndrome With Profound Obesity and Neurodevelopmental Delay Resembling Prader-Willi Syndrome. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 3413-3427. | 3.6 | 9 |
| 5454 | The relevance of chromosome fissions for major ribosomal DNA dispersion in hymenopteran insects. Journal of Evolutionary Biology, 2021, 34, 1466-1476. | 1.7 | 11 |
| 5455 | Lamprey lecticans link new vertebrate genes to the origin and elaboration of vertebrate tissues. Developmental Biology, 2021, 476, 282-293. | 2.0 | 5 |
| 5457 | Identification and characterization of the type II toxin-antitoxin systems in the carbapenem-resistant Acinetobacter baumannii. Microbial Pathogenesis, 2021, 158, 105052. | 2.9 | 2 |
| 5458 | Afro-alpine flagships revisited II: elucidating the evolutionary relationships and species boundaries in the giant senecios (Dendrosenecio, Asteraceae). Alpine Botany, 2022, 132, 89-105. | 2.4 | 6 |
| 5459 | Chromosome-scale assembly and evolution of the tetraploid Salvia splendens (Lamiaceae) genome. Horticulture Research, 2021, 8, 177. | 6.3 | 27 |
| 5460 | A near complete genome for goat genetic and genomic research. Genetics Selection Evolution, 2021, 53, 74. | 3.0 | 16 |
| 5461 | Transcriptomic profile of leg muscle during early growth and development in Haiyang yellow chicken. Archives Animal Breeding, 2021, 64, 405-416. | 1.4 | 6 |
| 5462 | A chromosome-level genome of <i>Antechinus flavipes</i> provides a reference for an Australian marsupial genus with male death after mating. Molecular Ecology Resources, 2022, 22, 740-754. | 4.8 | 12 |
| 5463 | Chromosome-scale assembly of the Dendrobium chrysotoxum genome enhances the understanding of orchid evolution. Horticulture Research, 2021, 8, 183. | 6.3 | 41 |
| 5464 | Genomic Epidemiology and Strain Taxonomy of <i>Corynebacterium diphtheriae</i> . Journal of Clinical Microbiology, 2021, 59, e0158121. | 3.9 | 12 |
| 5465 | The genomic basis of army ant chemosensory adaptations. Molecular Ecology, 2021, 30, 6627-6641. | 3.9 | 9 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 4.8 | 19 |
| 5467 | Linkage map and QTL mapping of red flesh locus in apple using a R1R1-RR6R6 population. <i>Horticultural Plant Journal</i> , 2021, 7, 393-400. | 5.0 | 13 |
| 5468 | Differential enrichment of yeast DNA in SARS-CoV-2 and related genomes supports synthetic origin hypothesis. <i>F1000Research</i> , 0, 10, 912. | 1.6 | 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. | 3.7 | 7 |
| 5471 | Patterns of Coevolutionary Adaptations across Time and Space in Mouse Gammaretroviruses and Three Restrictive Host Factors. <i>Viruses</i> , 2021, 13, 1864. | 3.3 | 5 |
| 5473 | RetroCHMP3 blocks budding of enveloped viruses without blocking cytokinesis. <i>Cell</i> , 2021, 184, 5419-5431.e16. | 28.9 | 8 |
| 5474 | The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399. | 5.7 | 6 |
| 5476 | Genomic anatomy of male-specific microchromosomes in a gynogenetic fish. <i>PLoS Genetics</i> , 2021, 17, e1009760. | 3.5 | 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. | 6.3 | 19 |
| 5479 | Protein-coding repeat polymorphisms strongly shape diverse human phenotypes. <i>Science</i> , 2021, 373, 1499-1505. | 12.6 | 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. | 2.3 | 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, . | 2.5 | 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. | 2.6 | 3 |
| 5483 | Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402. | 21.4 | 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. | 3.5 | 8 |
| 5485 | Tiara: deep learning-based classification system for eukaryotic sequences. <i>Bioinformatics</i> , 2022, 38, 344-350. | 4.1 | 34 |
| 5486 | MINTIA: a metagenomic INserT integrated assembly and annotation tool. <i>PeerJ</i> , 2021, 9, e11885. | 2.0 | 0 |
| 5487 | A Bayesian approach for accurate de novo transcriptome assembly. <i>Scientific Reports</i> , 2021, 11, 17663. | 3.3 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 5488 | Chemistry and Bioinformatics Considerations in Using Next-Generation Sequencing Technologies to Inferring HIV Proviral DNA Genome-Intactness. <i>Viruses</i> , 2021, 13, 1874. | 3.3 | 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. | 6.4 | 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. | 3.6 | 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. | 2.3 | 0 |
| 5494 | Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047. | 4.4 | 86 |
| 5496 | Genetic and phenotypic heterogeneity in KIAA0753 -related ciliopathies. <i>American Journal of Medical Genetics, Part A</i> , 2021, , . | 1.2 | 2 |
| 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. | 2.4 | 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. | 2.6 | 6 |
| 5499 | The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081. | 4.1 | 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. | 3.9 | 10 |
| 5501 | De Novo Genome Assembly of the Electric Fish <i>Brachyhypopomus occidentalis</i> (Hypopomidae). <i>Tj ETQq0 0,0,rgBT /Overlock 10 T</i> | 2.5 | 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. | 4.8 | 17 |
| 5503 | Characterization of the complete chloroplast genome of <i>Hordeum jubatum</i> (Poaceae: Pooideae). <i>Tj ETQq0 0,0,rgBT /Overlock 10 T</i> | 0.4 | 1 |
| 5504 | Parallel subgenome structure and divergent expression evolution of allo-tetraploid common carp and goldfish. <i>Nature Genetics</i> , 2021, 53, 1493-1503. | 21.4 | 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. | 2.8 | 5 |
| 5507 | Protocol for HSDFinder: Identifying, annotating, categorizing, and visualizing duplicated genes in eukaryotic genomes. <i>STAR Protocols</i> , 2021, 2, 100619. | 1.2 | 8 |
| 5508 | Aptamer-mediated transcriptional gene silencing of Foxp3 inhibits regulatory T cells and potentiates antitumor response. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 25, 143-151. | 5.1 | 4 |
| 5509 | Recombination Marks the Evolutionary Dynamics of a Recently Endogenized Retrovirus. <i>Molecular Biology and Evolution</i> , 2021, 38, 5423-5436. | 8.9 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 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. | 4.1 | 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. | 2.7 | 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. | 3.8 | 135 |
| 5514 | A microbial gene catalog of anaerobic digestion from full-scale biogas plants. <i>GigaScience</i> , 2021, 10, . | 6.4 | 23 |
| 5515 | Uncovering deeply conserved motif combinations in rapidly evolving noncoding sequences. <i>Genome Biology</i> , 2021, 22, 29. | 8.8 | 27 |
| 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. <i>BMC Bioinformatics</i> , 2021, 22, 9. | 2.6 | 9 |
| 5518 | The<i>Physcomitrella patens</i>chromatin adaptor PpMRG1 interacts with H3K36me3 and regulates light-responsive alternative splicing. <i>Plant Physiology</i> , 2021, 185, 1229-1241. | 4.8 | 3 |
| 5519 | Draft genome of the herbaceous bamboo <i>Raddia distichophylla</i>. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 1.8 | 6 |
| 5521 | A novel terpene synthase controls differences in anti-aphrodisiac pheromone production between closely related <i>Heliconius</i> butterflies. <i>PLoS Biology</i> , 2021, 19, e3001022. | 5.6 | 29 |
| 5522 | Identification and sequencing of 59 highly polymorphic microhaplotypes for analysis of DNA mixtures. <i>International Journal of Legal Medicine</i> , 2021, 135, 1137-1149. | 2.2 | 15 |
| 5523 | RUNX1/RUNX1T1 mediates alternative splicing and reorganises the transcriptional landscape in leukemia. <i>Nature Communications</i> , 2021, 12, 520. | 12.8 | 27 |
| 5524 | InsectORâ€”Webserver for sensitive identification of insect olfactory receptor genes from non-model genomes. <i>PLoS ONE</i> , 2021, 16, e0245324. | 2.5 | 14 |
| 5525 | Pervasive duplication of tumor suppressors in Afrotherians during the evolution of large bodies and reduced cancer risk. <i>ELife</i> , 2021, 10, . | 6.0 | 38 |
| 5526 | Curation of over 10â€”000 transcriptomic studies to enable data reuse. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, . | 3.0 | 21 |
| 5529 | Differential Gene Expression in the Auditory System. <i>Lecture Notes in Computer Science</i> , 2005, , 1-8. | 1.3 | 1 |
| 5530 | A Unifying Framework for Seed Sensitivity and Its Application to Subset Seeds. <i>Lecture Notes in Computer Science</i> , 2005, , 251-263. | 1.3 | 4 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 5531 | Microarray Probe Design Using μ -Multi-Objective Evolutionary Algorithms with Thermodynamic Criteria. Lecture Notes in Computer Science, 2006, , 184-195. | 1.3 | 7 |
| 5532 | Using Semantic Web Tools to Integrate Experimental Measurement Data on Our Own Terms. Lecture Notes in Computer Science, 2006, , 679-688. | 1.3 | 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. | 0.9 | 2 |
| 5537 | Genome resources for the DT40 community. Sub-Cellular Biochemistry, 2006, 40, 25-37. | 2.4 | 2 |
| 5538 | Transcriptome Analyses to Investigate the Pathogenesis of RNA Splicing Factor Retinitis Pigmentosa. Advances in Experimental Medicine and Biology, 2012, 723, 519-525. | 1.6 | 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. Methods in Molecular Biology, 2014, 1164, 23-32. | 0.9 | 1 |
| 5542 | GENCODE Pseudogenes. Methods in Molecular Biology, 2014, 1167, 129-155. | 0.9 | 29 |
| 5543 | High-Throughput Genomic Mapping of Vector Integration Sites in Gene Therapy Studies. Methods in Molecular Biology, 2014, 1185, 321-344. | 0.9 | 33 |
| 5544 | Case Study: Systematic Detection and Prioritization of Gene Fusions in Cancer by RNA-Seq: A DIY Toolkit. Methods in Molecular Biology, 2020, 2079, 69-79. | 0.9 | 3 |
| 5545 | Comparative Genomics. Methods in Molecular Biology, 2007, 366, 229-251. | 0.9 | 4 |
| 5546 | Identification of mRNA Polyadenylation Sites in Genomes Using cDNA Sequences, Expressed Sequence Tags, and Trace. Methods in Molecular Biology, 2008, 419, 23-37. | 0.9 | 14 |
| 5547 | Computational Gene Annotation in New Genome Assemblies Using GeneID. Methods in Molecular Biology, 2009, 537, 243-261. | 0.9 | 28 |
| 5548 | Analysis of Genomic DNA with the UCSC Genome Browser. Methods in Molecular Biology, 2009, 537, 277-301. | 0.9 | 8 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5549 | Gene Targeting in Mouse Embryonic Stem Cells. Methods in Molecular Biology, 2009, 530, 141-164. | 0.9 | 14 |
| 5550 | An Introduction to the Lagan Alignment Toolkit. Methods in Molecular Biology, 2007, 395, 205-219. | 0.9 | 9 |
| 5551 | Comparative Genomic Analysis Using the UCSC Genome Browser. Methods in Molecular Biology, 2007, 395, 17-33. | 0.9 | 23 |
| 5552 | Visualization of Syntenic Relationships With SynBrowse. Methods in Molecular Biology, 2007, 396, 153-163. | 0.9 | 9 |
| 5553 | Fast Masking of Repeated Primer Binding Sites in Eukaryotic Genomes. Methods in Molecular Biology, 2007, 402, 201-217. | 0.9 | 3 |
| 5554 | Microarray Probe Mapping and Annotation in Cross-Species Comparative Toxicogenomics. Methods in Molecular Biology, 2008, 460, 159-183. | 0.9 | 2 |
| 5555 | An Introduction to Mitochondrial Informatics. Methods in Molecular Biology, 2010, 628, 259-274. | 0.9 | 1 |
| 5556 | Gramene Database: A Hub for Comparative Plant Genomics. Methods in Molecular Biology, 2011, 678, 247-275. | 0.9 | 42 |
| 5557 | An Overview of the Computational Analyses and Discovery of Transcription Factor Binding Sites. Methods in Molecular Biology, 2010, 674, 1-22. | 0.9 | 11 |
| 5558 | Identification of Transcription Factor Binding Sites Derived from Transposable Element Sequences Using ChIP-seq. Methods in Molecular Biology, 2010, 674, 225-240. | 0.9 | 5 |
| 5559 | Annotating the Regulatory Genome. Methods in Molecular Biology, 2010, 674, 313-349. | 0.9 | 2 |
| 5560 | Computational Identification of miRNAs Involved in Cancer. Methods in Molecular Biology, 2011, 676, 23-41. | 0.9 | 5 |
| 5561 | Discovery of RNA Motifs Using a Computational Pipeline that Allows Insertions in Paired Regions and Filtering of Candidate Sequences. Methods in Molecular Biology, 2012, 848, 145-158. | 0.9 | 4 |
| 5562 | HORDE: Comprehensive Resource for Olfactory Receptor Genomics. Methods in Molecular Biology, 2013, 1003, 23-38. | 0.9 | 49 |
| 5563 | Heuristic Alignment Methods. Methods in Molecular Biology, 2014, 1079, 29-43. | 0.9 | 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. Springer Theses, 2014, , 69-80. | 0.1 | 7 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5567 | The Kiwifruit Genome. Compendium of Plant Genomes, 2016, , 101-114. | 0.5 | 1 |
| 5568 | Performing Local Similarity Searches with Variable Length Seeds. Lecture Notes in Computer Science, 2004, , 373-387. | 1.3 | 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. Lecture Notes in Computer Science, 2008, , 318-329. | 1.3 | 5 |
| 5573 | Using Bloom Filters for Large Scale Gene Sequence Analysis in Haskell. Lecture Notes in Computer Science, 2008, , 183-194. | 1.3 | 5 |
| 5574 | Mining of cis-Regulatory Motifs Associated with Tissue-Specific Alternative Splicing. Lecture Notes in Computer Science, 2009, , 260-271. | 1.3 | 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. | 1.3 | 11 |
| 5577 | Designing Workflows on the Fly Using e-BioFlow. Lecture Notes in Computer Science, 2009, , 470-484. | 1.3 | 6 |
| 5578 | A Randomized Numerical Aligner (rNA). Lecture Notes in Computer Science, 2010, , 512-523. | 1.3 | 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. | 1.3 | 1 |
| 5581 | K-mulus: Strategies for BLAST in the Cloud. Lecture Notes in Computer Science, 2014, , 237-246. | 1.3 | 2 |
| 5582 | Efficient Indexed Alignment of Contigs to Optical Maps. Lecture Notes in Computer Science, 2014, , 68-81. | 1.3 | 16 |
| 5583 | Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96. | 1.3 | 2 |
| 5584 | Crop Genome Annotation: A Case Study for the Brassica rapa Genome. Compendium of Plant Genomes, 2015, , 53-64. | 0.5 | 1 |
| 5585 | Genomics and Transcriptomics Advance in Plant Sciences. Energy, Environment, and Sustainability, 2019, , 419-448. | 1.0 | 5 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 5586 | Hybrid sequencing resolves two germline ultra-complex chromosomal rearrangements consisting of 137 breakpoint junctions in a single carrier. <i>Human Genetics</i> , 2021, 140, 775-790. | 3.8 | 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. <i>Aquaculture</i> , 2017, 479, 200-207. | 3.5 | 1 |
| 5590 | Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020, 30, 2040-2054.e5. | 6.4 | 45 |
| 5591 | Rapid Detection of Wheat Blast Pathogen <i>Magnaporthe oryzae</i> Triticum Pathotype Using Genome-Specific Primers and Cas12a-mediated Technology. <i>Engineering</i> , 2021, 7, 1326-1335. | 6.7 | 26 |
| 5592 | Comparative analysis of genome sequences of the conifer tree pathogen, <i>Heterobasidion annosum</i> s.s .. <i>Genomics Data</i> , 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. | 5.9 | 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.) <i>Tj</i> ETQq1 1 0.784314 rgBT /Overl | 6.3 | 51 |
| 5598 | Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159. | 17.5 | 123 |
| 5599 | Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020, 52, 342-352. | 21.4 | 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. | 5.3 | 53 |
| 5601 | Draft genomic and transcriptome resources for marine chelicerate <i>Tachypleus tridentatus</i> . <i>Scientific Data</i> , 2019, 6, 190029. | 5.3 | 15 |
| 5602 | The sequence and de novo assembly of <i>Oxygymnocypris stewartii</i> genome. <i>Scientific Data</i> , 2019, 6, 190009. | 5.3 | 29 |
| 5603 | Flatworms have lost the right open reading frame kinase 3 gene during evolution. <i>Scientific Reports</i> , 2015, 5, 9417. | 3.3 | 7 |
| 5604 | Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011, 2, 118-141. | 4.4 | 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, . | 3.4 | 13 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 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. | 2.5 | 17 |
| 5607 | A New Dinoflagellate Genome Illuminates a Conserved Gene Cluster Involved in Sunscreen Biosynthesis. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 31 |
| 5608 | Evaluating human autosomal loci for sexually antagonistic viability selection in two large biobanks. <i>Genetics</i> , 2021, 217, 1-10. | 2.9 | 19 |
| 5609 | Long-read assembly of the <i>Brassica napus</i> reference genome Darmor-bzh. <i>GigaScience</i> , 2020, 9, . | 6.4 | 64 |
| 5610 | Genotyping of herpes simplex virus type 1 by whole-genome sequencing. <i>Journal of General Virology</i> , 2016, 97, 2732-2741. | 2.9 | 27 |
| 5611 | Detection, infection dynamics and small RNA response against Culex Y virus in mosquito-derived cells. <i>Journal of General Virology</i> , 2018, 99, 1739-1745. | 2.9 | 23 |
| 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. | 2.0 | 9 |
| 5613 | The diversity of ice algal communities on the Greenland Ice Sheet as revealed by oligotyping. <i>Microbial Genomics</i> , 2018, 4, . | 2.0 | 39 |
| 5614 | SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, . | 2.0 | 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, . | 2.0 | 7 |
| 5616 | Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. <i>Microbial Genomics</i> , 2020, 6, . | 2.0 | 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. | 2.9 | 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. | 2.2 | 12 |
| 5789 | The pseudogenes of barley. <i>Plant Journal</i> , 2018, 93, 502-514. | 5.7 | 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 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 5793 | Large scale genomic sequence SVM classifiers. , 2005, , . | | 27 |
| 5794 | Darwin. ACM SIGPLAN Notices, 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. International Journal of Genomics, 2020, 2020, 1-16. | 1.6 | 4 |
| 5799 | Intact HIV-1 proviruses accumulate at distinct chromosomal positions during prolonged antiretroviral therapy. Journal of Clinical Investigation, 2019, 129, 988-998. | 8.2 | 209 |
| 5800 | HIV-1 viremia not suppressible by antiretroviral therapy can originate from large T cell clones producing infectious virus. Journal of Clinical Investigation, 2020, 130, 5847-5857. | 8.2 | 85 |
| 5801 | Comparative genomic tools and databases: providing insights into the human genome. Journal of Clinical Investigation, 2003, 111, 1099-1106. | 8.2 | 60 |
| 5802 | In vivo selection of hematopoietic progenitor cells and temozolomide dose intensification in rhesus macaques through lentiviral transduction with a drug resistance gene. Journal of Clinical Investigation, 2009, 119, 1952-63. | 8.2 | 53 |
| 5803 | Vector design influences hepatic genotoxicity after adeno-associated virus gene therapy. Journal of Clinical Investigation, 2015, 125, 870-880. | 8.2 | 287 |
| 5804 | Gapless assembly of maize chromosomes using long-read technologies. Genome Biology, 2020, 21, 121. | 8.8 | 101 |
| 5805 | Personalized and graph genomes reveal missing signal in epigenomic data. Genome Biology, 2020, 21, 124. | 8.8 | 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. Mobile DNA, 2020, 11, 6. | 3.6 | 12 |
| 5808 | From zebrafish heart jogging genes to mouse and human orthologs: using Gene Ontology to investigate mammalian heart development.. F1000Research, 2013, 2, 242. | 1.6 | 7 |
| 5809 | From zebrafish heart jogging genes to mouse and human orthologs: using Gene Ontology to investigate mammalian heart development.. F1000Research, 2013, 2, 242. | 1.6 | 6 |
| 5810 | Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. F1000Research, 2013, 2, 244. | 1.6 | 13 |
| 5811 | Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. F1000Research, 2013, 2, 244. | 1.6 | 9 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5812 | G-Links: a gene-centric link acquisition service. F1000Research, 2014, 3, 285. | 1.6 | 3 |
| 5813 | A reanalysis of mouse ENCODE comparative gene expression data. F1000Research, 2015, 4, 121. | 1.6 | 91 |
| 5814 | Characterization of an APC Promoter 1B deletion in a Patient Diagnosed with Familial Adenomatous Polyposis via Whole Genome Shotgun Sequencing. F1000Research, 2015, 4, 170. | 1.6 | 5 |
| 5815 | Accelerated Evolution of the ASPM Gene Controlling Brain Size Begins Prior to Human Brain Expansion. PLoS Biology, 2004, 2, e126. | 5.6 | 176 |
| 5816 | Epigenomic Consequences of Immortalized Plant Cell Suspension Culture. PLoS Biology, 2008, 6, e302. | 5.6 | 179 |
| 5817 | Most “Dark Matter” Transcripts Are Associated With Known Genes. PLoS Biology, 2010, 8, e1000371. | 5.6 | 377 |
| 5818 | Evolutionary Conservation and Diversification of Puf RNA Binding Proteins and Their mRNA Targets. PLoS Biology, 2015, 13, e1002307. | 5.6 | 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> . PLoS Biology, 2016, 14, e1002391. | 5.6 | 78 |
| 5820 | Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. PLoS Biology, 2016, 14, e1002394. | 5.6 | 127 |
| 5821 | Spliced integrated retrotransposed element (SpIRE) formation in the human genome. PLoS Biology, 2018, 16, e2003067. | 5.6 | 11 |
| 5822 | Integration and Fixation Preferences of Human and Mouse Endogenous Retroviruses Uncovered with Functional Data Analysis. PLoS Computational Biology, 2016, 12, e1004956. | 3.2 | 41 |
| 5823 | MUMmer4: A fast and versatile genome alignment system. PLoS Computational Biology, 2018, 14, e1005944. | 3.2 | 1,412 |
| 5824 | Long- and Short-Term Selective Forces on Malaria Parasite Genomes. PLoS Genetics, 2010, 6, e1001099. | 3.5 | 30 |
| 5825 | Analysis of 62 hybrid assembled human Y chromosomes exposes rapid structural changes and high rates of gene conversion. PLoS Genetics, 2017, 13, e1006834. | 3.5 | 42 |
| 5826 | A new domestic cat genome assembly based on long sequence reads empowers feline genomic medicine and identifies a novel gene for dwarfism. PLoS Genetics, 2020, 16, e1008926. | 3.5 | 79 |
| 5827 | Tentative Mapping of Transcription-Induced Interchromosomal Interaction using Chimeric EST and mRNA Data. PLoS ONE, 2007, 2, e254. | 2.5 | 20 |
| 5828 | Demographic Histories of ERV-K in Humans, Chimpanzees and Rhesus Monkeys. PLoS ONE, 2007, 2, e1026. | 2.5 | 15 |
| 5829 | Canine Population Structure: Assessment and Impact of Intra-Breed Stratification on SNP-Based Association Studies. PLoS ONE, 2007, 2, e1324. | 2.5 | 66 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5830 | Genome-Wide Analysis of Abnormal H3K9 Acetylation in Cloned Mice. PLoS ONE, 2008, 3, e1905. | 2.5 | 22 |
| 5831 | Horizontal Gene Transfers Link a Human MRSA Pathogen to Contagious Bovine Mastitis Bacteria. PLoS ONE, 2008, 3, e3074. | 2.5 | 36 |
| 5832 | Identification of Nuclear and Cytoplasmic mRNA Targets for the Shuttling Protein SF2/ASF. PLoS ONE, 2008, 3, e3369. | 2.5 | 98 |
| 5833 | Complete Genome Sequence of the Aerobic CO-Oxidizing Thermophile Thermomicrobium roseum. PLoS ONE, 2009, 4, e4207. | 2.5 | 113 |
| 5834 | Transcription Factor Binding Sites Are Genetic Determinants of Retroviral Integration in the Human Genome. PLoS ONE, 2009, 4, e4571. | 2.5 | 87 |
| 5835 | A Novel Endo-Hydrogenase Activity Recycles Hydrogen Produced by Nitrogen Fixation. PLoS ONE, 2009, 4, e4695. | 2.5 | 7 |
| 5836 | Molecular Identification and Expression Analysis of Filaggrin-2, a Member of the S100 Fused-Type Protein Family. PLoS ONE, 2009, 4, e5227. | 2.5 | 103 |
| 5837 | Genetic Structures of Copy Number Variants Revealed by Genotyping Single Sperm. PLoS ONE, 2009, 4, e5236. | 2.5 | 3 |
| 5838 | Mapping Accuracy of Short Reads from Massively Parallel Sequencing and the Implications for Quantitative Expression Profiling. PLoS ONE, 2009, 4, e6323. | 2.5 | 19 |
| 5839 | Repertoire of Bovine miRNA and miRNA-Like Small Regulatory RNAs Expressed upon Viral Infection. PLoS ONE, 2009, 4, e6349. | 2.5 | 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. | 2.5 | 719 |
| 5841 | Polyploidy Did Not Predate the Evolution of Nodulation in All Legumes. PLoS ONE, 2010, 5, e11630. | 2.5 | 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. | 2.5 | 23 |
| 5843 | SAW: A Method to Identify Splicing Events from RNA-Seq Data Based on Splicing Fingerprints. PLoS ONE, 2010, 5, e12047. | 2.5 | 7 |
| 5844 | Genome Rearrangements Detected by SNP Microarrays in Individuals with Intellectual Disability Referred with Possible Williams Syndrome. PLoS ONE, 2010, 5, e12349. | 2.5 | 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. | 2.5 | 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. | 2.5 | 45 |
| 5847 | Abundant Human DNA Contamination Identified in Non-Primate Genome Databases. PLoS ONE, 2011, 6, e16410. | 2.5 | 100 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 5848 | Metatranscriptomic Approach to Analyze the Functional Human Gut Microbiota. PLoS ONE, 2011, 6, e17447. | 2.5 | 302 |
| 5849 | Chromosome Conformation Capture Uncovers Potential Genome-Wide Interactions between Human Conserved Non-Coding Sequences. PLoS ONE, 2011, 6, e17634. | 2.5 | 19 |
| 5850 | Evaluating the Fidelity of De Novo Short Read Metagenomic Assembly Using Simulated Data. PLoS ONE, 2011, 6, e19984. | 2.5 | 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. | 2.5 | 112 |
| 5852 | Transcriptional Profiling of Human Liver Identifies Sex-Biased Genes Associated with Polygenic Dyslipidemia and Coronary Artery Disease. PLoS ONE, 2011, 6, e23506. | 2.5 | 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. | 2.5 | 7 |
| 5854 | Common Promoter Elements in Odorant and Vomeronasal Receptor Genes. PLoS ONE, 2011, 6, e29065. | 2.5 | 32 |
| 5855 | Whole Genome Resequencing Reveals Natural Target Site Preferences of Transposable Elements in <i>Drosophila melanogaster</i> . PLoS ONE, 2012, 7, e30008. | 2.5 | 114 |
| 5856 | Exploring the Switchgrass Transcriptome Using Second-Generation Sequencing Technology. PLoS ONE, 2012, 7, e34225. | 2.5 | 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. | 2.5 | 156 |
| 5858 | Rapid Transcriptional Pulsing Dynamics of High Expressing Retroviral Transgenes in Embryonic Stem Cells. PLoS ONE, 2012, 7, e37130. | 2.5 | 5 |
| 5859 | High Accuracy Mutation Detection in Leukemia on a Selected Panel of Cancer Genes. PLoS ONE, 2012, 7, e38463. | 2.5 | 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. | 2.5 | 5 |
| 5861 | Bovine Polledness â€“ An Autosomal Dominant Trait with Allelic Heterogeneity. PLoS ONE, 2012, 7, e39477. | 2.5 | 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. | 2.5 | 16 |
| 5863 | FAST-SeqS: A Simple and Efficient Method for the Detection of Aneuploidy by Massively Parallel Sequencing. PLoS ONE, 2012, 7, e41162. | 2.5 | 65 |
| 5864 | Eco-Geographical Diversification of Bitter Taste Receptor Genes (TAS2Rs) among Subspecies of Chimpanzees (<i>Pan troglodytes</i>). PLoS ONE, 2012, 7, e43277. | 2.5 | 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. | 2.5 | 3 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 5866 | An Alu-Based Phylogeny of Lemurs (Infraorder: Lemuriformes). PLoS ONE, 2012, 7, e44035. | 2.5 | 21 |
| 5867 | Discovery and Characterization of Human Exonic Transcriptional Regulatory Elements. PLoS ONE, 2012, 7, e46098. | 2.5 | 14 |
| 5868 | A Statistical Framework for Accurate Taxonomic Assignment of Metagenomic Sequencing Reads. PLoS ONE, 2012, 7, e46450. | 2.5 | 23 |
| 5869 | Selective Constraint on Copy Number Variation in Human Piwi-Interacting RNA Loci. PLoS ONE, 2012, 7, e46611. | 2.5 | 5 |
| 5870 | Comparative Genomics of Neuroglobin Reveals Its Early Origins. PLoS ONE, 2012, 7, e47972. | 2.5 | 27 |
| 5871 | Reanalysis of RNA-Sequencing Data Reveals Several Additional Fusion Genes with Multiple Isoforms. PLoS ONE, 2012, 7, e48745. | 2.5 | 72 |
| 5872 | Deep Sequencing Reveals Differences in the Transcriptional Landscapes of Fibers from Two Cultivated Species of Cotton. PLoS ONE, 2012, 7, e48855. | 2.5 | 37 |
| 5873 | A Structural-Based Strategy for Recognition of Transcription Factor Binding Sites. PLoS ONE, 2013, 8, e52460. | 2.5 | 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. | 2.5 | 150 |
| 5875 | Genome-Wide Characterization and Linkage Mapping of Simple Sequence Repeats in Mei (<i>Prunus mume</i>) Tj ETQq1.1.0.784314 rgBT (Ov | 2.5 | 41 |
| 5876 | Widespread Divergence of the CEACAM/PSG Genes in Vertebrates and Humans Suggests Sensitivity to Selection. PLoS ONE, 2013, 8, e61701. | 2.5 | 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. | 2.5 | 117 |
| 5878 | Optimizing Information in Next-Generation-Sequencing (NGS) Reads for Improving De Novo Genome Assembly. PLoS ONE, 2013, 8, e69503. | 2.5 | 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. | 2.5 | 52 |
| 5880 | Genome Sequencing and Analysis of BCG Vaccine Strains. PLoS ONE, 2013, 8, e71243. | 2.5 | 84 |
| 5881 | Breakpoint Features of Genomic Rearrangements in Neuroblastoma with Unbalanced Translocations and Chromothripsis. PLoS ONE, 2013, 8, e72182. | 2.5 | 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. | 2.5 | 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. | 2.5 | 30 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5884 | Revealing of Mycobacterium marinum Transcriptome by RNA-seq. PLoS ONE, 2013, 8, e75828. | 2.5 | 21 |
| 5885 | Global Transcriptome Analysis of Lactococcus garvieae Strains in Response to Temperature. PLoS ONE, 2013, 8, e79692. | 2.5 | 30 |
| 5886 | A New Family of Predicted KrÄppel-Like Factor Genes and Pseudogenes in Placental Mammals. PLoS ONE, 2013, 8, e81109. | 2.5 | 42 |
| 5887 | Evaluation of Assembly Strategies Using RNA-Seq Data Associated with Grain Development of Wheat (Triticum aestivum L.). PLoS ONE, 2013, 8, e83530. | 2.5 | 33 |
| 5888 | Rapid Diversification of FoxP2 in Teleosts through Gene Duplication in the Teleost-Specific Whole Genome Duplication Event. PLoS ONE, 2013, 8, e83858. | 2.5 | 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. | 2.5 | 16 |
| 5890 | Detection of Chromosomal Breakpoints in Patients with Developmental Delay and Speech Disorders. PLoS ONE, 2014, 9, e90852. | 2.5 | 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. | 2.5 | 65 |
| 5892 | The Draft Genome Sequence of European Pear (Pyrus communis L. â€Bartlettâ€™). PLoS ONE, 2014, 9, e92644. | 2.5 | 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. | 2.5 | 10 |
| 5894 | Characterization of Natural Antisense Transcript, Sclerotia Development and Secondary Metabolism by Strand-Specific RNA Sequencing of Aspergillus flavus. PLoS ONE, 2014, 9, e97814. | 2.5 | 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. | 2.5 | 72 |
| 5896 | Systematic Identification and Characterization of RNA Editing in Prostate Tumors. PLoS ONE, 2014, 9, e101431. | 2.5 | 15 |
| 5897 | NCI-60 Whole Exome Sequencing and Pharmacological CellMiner Analyses. PLoS ONE, 2014, 9, e101670. | 2.5 | 38 |
| 5898 | Quickly Finding Orthologs as Reciprocal Best Hits with BLAT, LAST, and UBLAST: How Much Do We Miss?. PLoS ONE, 2014, 9, e101850. | 2.5 | 133 |
| 5899 | GHOSTX: An Improved Sequence Homology Search Algorithm Using a Query Suffix Array and a Database Suffix Array. PLoS ONE, 2014, 9, e103833. | 2.5 | 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. | 2.5 | 35 |
| 5901 | Long Distance Linkage Disequilibrium and Limited Hybridization Suggest Cryptic Speciation in Atlantic Cod. PLoS ONE, 2014, 9, e106380. | 2.5 | 37 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5902 | Evolution of an Expanded Mannose Receptor Gene Family. PLoS ONE, 2014, 9, e110330. | 2.5 | 48 |
| 5903 | Divergence of Gene Body DNA Methylation and Evolution of Plant Duplicate Genes. PLoS ONE, 2014, 9, e110357. | 2.5 | 48 |
| 5904 | Transcriptome of the Invasive Brown Marmorated Stink Bug, <i>Halyomorpha halys</i> (Stål) (Heteroptera: Pentatomidae). PLoS ONE, 2014, 9, e110367. | 2.5 | 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. | 2.5 | 32 |
| 5906 | A Transcriptome Derived Female-Specific Marker from the Invasive Western Mosquitofish (<i>Gambusia holbrooki</i>) (Pisces: Cyprinodontiformes). PLoS ONE, 2015, 10, e0117645. | 2.5 | 26 |
| 5907 | Flexible, Fast and Accurate Sequence Alignment Profiling on GPGPU with PaSWAS. PLoS ONE, 2015, 10, e0122524. | 2.5 | 13 |
| 5908 | Comparative Whole-Genome Analysis of Clinical Isolates Reveals Characteristic Architecture of <i>Mycobacterium tuberculosis</i> Pangenome. PLoS ONE, 2015, 10, e0122979. | 2.5 | 49 |
| 5909 | Differential Gene Expression Profiling of Dystrophic Dog Muscle after MuStem Cell Transplantation. PLoS ONE, 2015, 10, e0123336. | 2.5 | 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. | 2.5 | 48 |
| 5911 | Identification of Pathogen Signatures in Prostate Cancer Using RNA-seq. PLoS ONE, 2015, 10, e0128955. | 2.5 | 34 |
| 5912 | Comprehensive Analysis of Disease-Related Genes in Chronic Lymphocytic Leukemia by Multiplex PCR-Based Next Generation Sequencing. PLoS ONE, 2015, 10, e0129544. | 2.5 | 23 |
| 5913 | Quantitative Trait Loci Associated with the Tocochromanol (Vitamin E) Pathway in Barley. PLoS ONE, 2015, 10, e0133767. | 2.5 | 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. | 2.5 | 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. | 2.5 | 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. | 2.5 | 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. | 2.5 | 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. | 2.5 | 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. | 2.5 | 32 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 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. | 2.5 | 26 |
| 5921 | Placenta-Enriched lincRNAs MIR503HG and LINC00629 Decrease Migration and Invasion Potential of JEG-3 Cell Line. PLoS ONE, 2016, 11, e0151560. | 2.5 | 36 |
| 5922 | Using a Candidate Gene-Based Genetic Linkage Map to Identify QTL for Winter Survival in Perennial Ryegrass. PLoS ONE, 2016, 11, e0152004. | 2.5 | 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. | 2.5 | 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. | 2.5 | 33 |
| 5925 | Genomic Aberrations in Crizotinib Resistant Lung Adenocarcinoma Samples Identified by Transcriptome Sequencing. PLoS ONE, 2016, 11, e0153065. | 2.5 | 18 |
| 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. | 2.5 | 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. | 2.5 | 5 |
| 5928 | Comorbid Analysis of Genes Associated with Autism Spectrum Disorders Reveals Differential Evolutionary Constraints. PLoS ONE, 2016, 11, e0157937. | 2.5 | 24 |
| 5929 | Identification and Validation of SNP Markers Linked to Dwarf Traits Using SLAF-Seq Technology in Lagerstroemia. PLoS ONE, 2016, 11, e0158970. | 2.5 | 23 |
| 5930 | A De Novo Genome Sequence Assembly of the <i>Arabidopsis thaliana</i> Accession Niederzenz-1 Displays Presence/Absence Variation and Strong Synteny. PLoS ONE, 2016, 11, e0164321. | 2.5 | 63 |
| 5931 | Comparative Analysis of Vertebrate Diurnal/Circadian Transcriptomes. PLoS ONE, 2017, 12, e0169923. | 2.5 | 29 |
| 5932 | Accurate Breakpoint Mapping in Apparently Balanced Translocation Families with Discordant Phenotypes Using Whole Genome Mate-Pair Sequencing. PLoS ONE, 2017, 12, e0169935. | 2.5 | 31 |
| 5933 | The first complete chloroplast genome sequences of <i>Ulmus</i> species by de novo sequencing: Genome comparative and taxonomic position analysis. PLoS ONE, 2017, 12, e0171264. | 2.5 | 80 |
| 5934 | A new GTF2I-BRAF fusion mediating MAPK pathway activation in pilocytic astrocytoma. PLoS ONE, 2017, 12, e0175638. | 2.5 | 27 |
| 5935 | TRE5-A retrotransposon profiling reveals putative RNA polymerase III transcription complex binding sites on the <i>Dictyostelium</i> extrachromosomal rDNA element. PLoS ONE, 2017, 12, e0175729. | 2.5 | 2 |
| 5936 | Population genetic structure of Guiana dolphin (<i>Sotalia guianensis</i>) from the southwestern Atlantic coast of Brazil. PLoS ONE, 2017, 12, e0183645. | 2.5 | 9 |
| 5937 | Candidate genes for first flower node identified in pepper using combined SLAF-seq and BSA. PLoS ONE, 2018, 13, e0194071. | 2.5 | 23 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5938 | Mitochondrial D-loop sequence variation and maternal lineage in the endangered Cleveland Bay horse. PLoS ONE, 2020, 15, e0243247. | 2.5 | 4 |
| 5939 | The full transcription map of mouse papillomavirus type 1 (MmuPV1) in mouse wart tissues. PLoS Pathogens, 2017, 13, e1006715. | 4.7 | 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. | 4.7 | 22 |
| 5942 | Concentration-Dependent Recruitment of Mammalian Odorant Receptors. ENeuro, 2020, 7, ENEURO.0103-19.2019. | 1.9 | 12 |
| 5943 | Screening for mutations in selected miRNA genes in hypogonadotropic hypogonadism patients. Endocrine Connections, 2019, 8, 506-509. | 1.9 | 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. | 1.8 | 18 |
| 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?. Aging, 2016, 8, 260-271. | 3.1 | 16 |
| 5947 | The evolution of CpG density and lifespan in conserved primate and mammalian promoters. Aging, 2018, 10, 561-572. | 3.1 | 23 |
| 5948 | Next generation mapping reveals novel large genomic rearrangements in prostate cancer. Oncotarget, 2017, 8, 23588-23602. | 1.8 | 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. Oncotarget, 2019, 10, 3641-3653. | 1.8 | 1 |
| 5950 | A novel retroviral mutagenesis screen identifies prognostic genes in RUNX1 mediated myeloid leukemogenesis. Oncotarget, 2015, 6, 30664-30674. | 1.8 | 5 |
| 5951 | Genome and transcriptome delineation of two major oncogenic pathways governing invasive ductal breast cancer development. Oncotarget, 2015, 6, 36652-36674. | 1.8 | 24 |
| 5952 | A novel gammaretroviral shuttle vector insertional mutagenesis screen identifies <i>SHARPIN</i> as a breast cancer metastasis gene and prognostic biomarker. Oncotarget, 2015, 6, 39507-39520. | 1.8 | 25 |
| 5953 | Bioinformatics tools for analysing viral genomic data. OIE Revue Scientifique Et Technique, 2016, 35, 271-285. | 1.2 | 16 |
| 5954 | Computational Approaches in Detecting Non- Coding RNA. Current Genomics, 2013, 14, 371-377. | 1.6 | 41 |
| 5955 | Defind: Detecting Genomic Deletions by Integrating Read Depth, GC Content, Mapping Quality and Paired-end Mapping Signatures of Next Generation Sequencing Data. Current Bioinformatics, 2019, 14, 130-138. | 1.5 | 3 |
| 5956 | Single-molecule Real-time (SMRT) Isoform Sequencing (Iso-Seq) in Plants: The Status of the Bioinformatics Tools to Unravel the Transcriptome Complexity. Current Bioinformatics, 2019, 14, 566-573. | 1.5 | 13 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 5957 | Target Site Preferences of Subgroup C Rous Sarcoma Virus Integration into the Chicken DNA. The Open Genomics Journal, 2008, 1, 6-12. | 0.5 | 2 |
| 5958 | Using Metagenomics to Connect Microbial Community Biodiversity and Functions. Current Issues in Molecular Biology, 2017, 24, 103-118. | 2.4 | 47 |
| 5959 | Analysis of MBOAT family reveals the diversity of MBOAT1 amplification in Solanaceae. Archives of Biological Sciences, 2015, 67, 1349-1356. | 0.5 | 1 |
| 5960 | Identification of common carp innate immune genes with whole-genome sequencing and RNA-Seq data. Journal of Integrative Bioinformatics, 2011, 8, 169. | 1.5 | 12 |
| 5961 | Improving the performance of Transposable Elements detection tools. Journal of Integrative Bioinformatics, 2013, 10, 231. | 1.5 | 10 |
| 5962 | COMPARATIVE METAGENOMICS ANALYSIS OF PALM OIL MILL EFFLUENT (POME) USING THREE DIFFERENT BIOINFORMATICS PIPELINES. IIUM Engineering Journal, 2019, 20, 1-11. | 0.8 | 3 |
| 5963 | Population Structure and Antimicrobial Resistance of Invasive Serotype IV Group <i>Streptococcus</i> , Toronto, Ontario, Canada. Emerging Infectious Diseases, 2015, 21, 585-591. | 4.3 | 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. Acta Naturae, 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. Agronomy, 2020, 10, 114. | 3.0 | 11 |
| 5966 | Characterization of ESTâ€™SSR markers in bread wheat EST related to drought tolerance and functional analysis of SSRâ€™containing unigenes. , 0, , 1-12. | | 3 |
| 5968 | LINE-1 family member GCRG123 gene is up-regulated in human gastric signet-ring cell carcinoma. World Journal of Gastroenterology, 2008, 14, 758. | 3.3 | 2 |
| 5969 | Microarray evaluation of bovine hepatic gene response to fescue toxicosis. World Mycotoxin Journal, 2013, 6, 419-426. | 1.4 | 2 |
| 5970 | An improved understanding of cancer genomics through massively parallel sequencing. Translational Cancer Research, 2014, 3, 243-259. | 1.0 | 10 |
| 5971 | LAS. Advances in Medical Diagnosis, Treatment, and Care, 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 | Handbook of Research on Systems Biology Applications in Medicine. , 2009, , . | | 8 |
| 5974 | Computational Sequence Design Techniques for DNA Microarray Technologies. Advances in Bioinformatics and Biomedical Engineering Book Series, 0, , 57-91. | 0.4 | 1 |
| 5975 | mBLAST: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. Journal of Data Mining in Genomics & Proteomics, 2013, 04, . | 0.5 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 5976 | Towards a Comprehensive Search of Putative Chitinases Sequences in Environmental Metagenomic Databases. Natural Science, 2014, 06, 323-337. | 0.4 | 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. Fottea, 2019, 19, 115-131. | 0.9 | 19 |
| 5979 | Deep Sequencing Data Analysis: Challenges and Solutions. , 0, , . | | 4 |
| 5980 | Bioinformatics as a Tool for the Structural and Evolutionary Analysis of Proteins. , 0, , . | | 7 |
| 5981 | FusionScan: accurate prediction of fusion genes from RNA-Seq data. Genomics and Informatics, 2019, 17, e26. | 0.8 | 10 |
| 5982 | Accelerating next generation sequencing data analysis: an evaluation of optimized best practices for Genome Analysis Toolkit algorithms. Genomics and Informatics, 2020, 18, e10. | 0.8 | 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. Bioinformation, 2008, 2, 469-470. | 0.5 | 33 |
| 5984 | Computational Epigenetics: the new scientific paradigm. Bioinformation, 2010, 4, 331-337. | 0.5 | 36 |
| 5985 | Integrative genomic analysis of the human immune response to influenza vaccination. ELife, 2013, 2, e00299. | 6.0 | 126 |
| 5986 | APOBEC3A deaminates transiently exposed single-strand DNA during LINE-1 retrotransposition. ELife, 2014, 3, e02008. | 6.0 | 113 |
| 5987 | Metagenomic chromosome conformation capture (meta3C) unveils the diversity of chromosome organization in microorganisms. ELife, 2014, 3, e03318. | 6.0 | 154 |
| 5988 | Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of Albugo candida, a generalist parasite. ELife, 2015, 4, . | 6.0 | 71 |
| 5989 | Genomic variations of the mevalonate pathway in porokeratosis. ELife, 2015, 4, e06322. | 6.0 | 71 |
| 5990 | Viruses are a dominant driver of protein adaptation in mammals. ELife, 2016, 5, . | 6.0 | 267 |
| 5991 | Resolving rates of mutation in the brain using single-neuron genomics. ELife, 2016, 5, . | 6.0 | 139 |
| 5992 | Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. ELife, 2016, 5, . | 6.0 | 48 |
| 5993 | Evolution of gene dosage on the Z-chromosome of schistosome parasites. ELife, 2018, 7, . | 6.0 | 31 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 5994 | The Aquilegia genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , 2018, 7, . | 6.0 | 120 |
| 5995 | Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, . | 6.0 | 26 |
| 5996 | The genetic factors of bilaterian evolution. <i>ELife</i> , 2020, 9, . | 6.0 | 44 |
| 5997 | A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. <i>ELife</i> , 2019, 8, . | 6.0 | 41 |
| 5998 | Cardiac mitochondrial function depends on BUD23 mediated ribosome programming. <i>ELife</i> , 2020, 9, . | 6.0 | 10 |
| 5999 | Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, . | 6.0 | 33 |
| 6000 | Clusters of polymorphic transmembrane genes control resistance to schistosomes in snail vectors. <i>ELife</i> , 2020, 9, . | 6.0 | 18 |
| 6001 | Multiple comparative metagenomics using multiset k-mer counting. <i>PeerJ Computer Science</i> , 0, 2, e94. | 4.5 | 88 |
| 6002 | BiSCoT: improving large eukaryotic genome assemblies with optical maps. <i>PeerJ</i> , 2020, 8, e10150. | 2.0 | 13 |
| 6003 | GenomePeek€”an online tool for prokaryotic genome and metagenome analysis. <i>PeerJ</i> , 2015, 3, e1025. | 2.0 | 12 |
| 6004 | Improving transcriptome assembly through error correction of high-throughput sequence reads. <i>PeerJ</i> , 2013, 1, e113. | 2.0 | 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. | 2.0 | 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. | 2.0 | 7 |
| 6007 | RelocaTE2: a high resolution transposable element insertion site mapping tool for population resequencing. <i>PeerJ</i> , 2017, 5, e2942. | 2.0 | 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. | 2.0 | 265 |
| 6009 | Divide and Conquer (DC) BLAST: fast and easy BLAST execution within HPC environments. <i>PeerJ</i> , 2017, 5, e3486. | 2.0 | 10 |
| 6010 | Comparative analysis of whole flower transcriptomes in the Zingiberales. <i>PeerJ</i> , 2018, 6, e5490. | 2.0 | 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. | 2.0 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 6012 | imGLAD: accurate detection and quantification of target organisms in metagenomes. PeerJ, 2018, 6, e5882. | 2.0 | 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. PeerJ, 2019, 7, e7649. | 2.0 | 19 |
| 6014 | Comparative genomics and phylogenetic discordance of cultivated tomato and close wild relatives. PeerJ, 2015, 3, e793. | 2.0 | 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>). PeerJ, 2020, 8, e9552. | 2.0 | 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. PeerJ, 2020, 8, e9755. | 2.0 | 13 |
| 6017 | Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. Molecular Biology and Evolution, 2022, 39, . | 8.9 | 10 |
| 6018 | AnnoLnc: A One-Stop Portal to Systematically Annotate Novel Human Long Noncoding RNAs. Methods in Molecular Biology, 2021, 2254, 111-131. | 0.9 | 1 |
| 6020 | High-quality genome assembly of an important biodiesel plant, <i>Euphorbia lathyris</i> L. DNA Research, 2021, 28, . | 3.4 | 11 |
| 6022 | RGD v2.0: a major update of the ruminant functional and evolutionary genomics database. Nucleic Acids Research, 2022, 50, D1091-D1099. | 14.5 | 24 |
| 6023 | Phylogenomics of <i>Salvia</i> L. subgenus <i>Calospatha</i> (Lamiaceae). Frontiers in Plant Science, 2021, 12, 725900. | 3.6 | 7 |
| 6025 | Deep RNA Sequencing Revealed Fusion Junctional Heterogeneity May Predict Crizotinib Treatment Efficacy in ALK-Rearranged NSCLC. Journal of Thoracic Oncology, 2022, 17, 264-276. | 1.1 | 15 |
| 6026 | Chromosomal-Level Genome Assembly of a True Bug, <i>Aspongopus chinensis</i> Dallas, 1851 (Hemiptera: Dinidoridae). Genome Biology and Evolution, 2021, 13, . | 2.5 | 3 |
| 6027 | Differential enrichment of yeast DNA in SARS-CoV-2 and related genomes supports synthetic origin hypothesis. F1000Research, 0, 10, 912. | 1.6 | 0 |
| 6029 | Phylogeny of <i>Crataegus</i> (Rosaceae) based on 257 nuclear loci and chloroplast genomes: evaluating the impact of hybridization. PeerJ, 2021, 9, e12418. | 2.0 | 6 |
| 6030 | MINTIE: identifying novel structural and splice variants in transcriptomes using RNA-seq data. Genome Biology, 2021, 22, 296. | 8.8 | 16 |
| 6031 | SeekFusion - A Clinically Validated Fusion Transcript Detection Pipeline for PCR-Based Next-Generation Sequencing of RNA. Frontiers in Genetics, 2021, 12, 739054. | 2.3 | 9 |
| 6032 | An <i>Emiliania huxleyi</i> pan-transcriptome reveals basal strain specificity in gene expression patterns. Scientific Reports, 2021, 11, 20795. | 3.3 | 7 |
| 6036 | MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. Journal of Computational Biology, 2021, 28, 1063-1074. | 1.6 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 6037 | The long non-coding RNA ET-20 mediates EMT by impairing desmosomes in breast cancer cells. Journal of Cell Science, 2021, 134, . | 2.0 | 9 |
| 6038 | RBPmap: A Tool for Mapping and Predicting the Binding Sites of RNA-Binding Proteins Considering the Motif Environment. Methods in Molecular Biology, 2022, 2404, 53-65. | 0.9 | 11 |
| 6039 | A novel exome probe set captures phototransduction genes across birds (Aves) enabling efficient analysis of vision evolution. Molecular Ecology Resources, 2022, 22, 587-601. | 4.8 | 3 |
| 6040 | Evaluation of accessible regions of Escherichia coli fimH mRNA through computational prediction and experimental investigation. Iranian Journal of Microbiology, 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. Current Protocols in Human Genetics, 2004, 41, Unit 1.10. | 3.5 | 0 |
| 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. | 1.5 | 2 |
| 6050 | Data Structures for Genome Annotation, Alternative Splicing, and Validation. Lecture Notes in Computer Science, 2006, , 114-123. | 1.3 | 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. | 2.7 | 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. | 0.3 | 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. | 0.4 | 0 |
| 6061 | A Dynamic Neighboring Extension Search Algorithm for Genome Coordinate Conversion in the Presence of Short Sequence Duplications. Gene Expression To Genetical Genomics, 0, 2, 29-36. | 1.0 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 6062 | Analysis of Cis-Regulatory Motifs in Cassette Exons by Incorporating Exon Skipping Rates. Lecture Notes in Computer Science, 2009, , 272-283. | 1.3 | 1 |
| 6063 | A Reconfigurable Bloom Filter Architecture for BLASTN. Lecture Notes in Computer Science, 2009, , 40-49. | 1.3 | 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 |
| 6068 | BatchGenAna: a batch platform for large-scale genomic analysis of mammalian small RNAs. Bioinformatics, 2009, 3, 336-348. | 0.5 | 0 |
| 6069 | COCAW: A Genome-wide Pattern Search System for Designing Microbial Probes. Genomics and Informatics, 2009, 7, 178-180. | 0.8 | 0 |
| 6070 | A CNV detection algorithm based on statistical analysis of the aligned reads. The KIPS Transactions PartD, 2009, 16D, 661-672. | 0.2 | 0 |
| 6071 | Bioinformatics Tools for Crop Research and Breeding. , 2010, , 97-116. | | 0 |
| 6072 | Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378. | | 0 |
| 6073 | Mapping Affymetrix Microarray Probes to the Rat Genome via a Persistent Index. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 48-65. | 0.8 | 0 |
| 6074 | Comparative Gene Finding. Computational Biology, 2010, , 157-180. | 0.2 | 3 |
| 6075 | Spaced Seeds for Cross-species CDNA-to-genome Sequence Alignment. Communications in Information and Systems, 2010, 10, 115-136. | 0.5 | 1 |
| 6076 | e-BioFlow: Improving Practical Use of Workflow Systems in Bioinformatics. Lecture Notes in Computer Science, 2010, , 1-15. | 1.3 | 1 |
| 6077 | The Draft Soybean Genome Sequence. , 2010, , 223-244. | | 0 |
| 6078 | An Integrated Genomic Resource Based on Korean Cattle (Hanwoo) Transcripts. Asian-Australasian Journal of Animal Sciences, 2010, 23, 1399-1404. | 2.4 | 1 |
| 6079 | Bioinformatics of High-Throughput Insertional Mutagenesis. , 2011, , 167-188. | | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 6080 | Analysis of Mutations that Influence Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2011, 703, 137-160. | 0.9 | 0 |
| 6081 | Bioinformatics Resources for the Brassica Species. , 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. | 0.6 | 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. | 0.5 | 0 |
| 6084 | Identification of Hematopoietic Stem Cell Engraftment Genes in Gene Therapy Studies. <i>Journal of Stem Cell Research & 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. | 1.3 | 3 |
| 6087 | Taxonomic Assignment in Metagenomics with TANGO. <i>EMBNET Journal</i> , 2011, 17, 16. | 0.6 | 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. | 0.8 | 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 & Hall/CRC Mathematical and Computational Biology Series</i> , 2012, , . | 0.1 | 0 |
| 6095 | Dynamic Annotation Systems. <i>Chapman & Hall/CRC Mathematical and Computational Biology Series</i> , 2012, , . | 0.1 | 0 |
| 6096 | Sequence Homology Handling. <i>Computational Biology</i> , 2013, , 301-334. | 0.2 | 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. | 0.6 | 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 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 6100 | GHOSTM. , 2013, , 1-4. | | 0 |
| 6102 | MetaBioME. , 2013, , 1-12. | | 0 |
| 6103 | Identification of segmental duplications in the human genome. Sri Lanka Journal of Biomedical Information, 2013, 3, 12. | 0.1 | 1 |
| 6104 | Parallel Two Master Method to Improve BLAST Algorithm's Performance. International Journal of Computer Applications, 2013, 63, 8-14. | 0.2 | 14 |
| 6105 | Staircase Method: A Novel Method for Parallelizing S-W Algorithm. International Journal of Computer Applications, 2013, 63, 1-7. | 0.2 | 0 |
| 6106 | Primer Design for Large-Scale Multiplex PCR and Arrayed Primer Extension. , 2013, , 199-208. | | 0 |
| 6110 | An Efficient Algorithm for Microarray Probes Re-annotation. Lecture Notes in Computer Science, 2014, , 201-218. | 1.3 | 0 |
| 6112 | High Performance Genomic Sequencing: A Filtered Approach. Advances in Intelligent Systems and Computing, 2014, , 129-136. | 0.6 | 0 |
| 6114 | Identification and Analysis of Genomic Homing Endonuclease Target Sites. Methods in Molecular Biology, 2014, 1123, 245-264. | 0.9 | 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. | 0.8 | 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. | 0.2 | 0 |
| 6121 | Fast Masking of Repeated Primer Binding Sites in Eukaryotic Genomes. Methods in Molecular Biology, 2015, 1275, 1-16. | 0.9 | 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. | 0.5 | 0 |
| 6124 | Large-scale detection and application of expressed sequence tag single nucleotide polymorphisms in Nicotiana. Genetics and Molecular Research, 2015, 14, 7793-7800. | 0.2 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 6131 | BlastXtract2: Improving early exploration of (meta) genomes. <i>Bioinformation</i> , 2015, 11, 173-175. | 0.5 | 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. <i>F1000Research</i> , 2014, 3, 285. | 1.6 | 2 |
| 6140 | Decrypting the Treasures of Regulatory Non-coding RNAs in Hightthroughput Era. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2016, 07, . | 0.5 | 0 |
| 6142 | Genetic Technologies and Causal Variant Discovery. <i>Translational Bioinformatics</i> , 2016, , 277-293. | 0.0 | 0 |
| 6149 | An Efficient Bulk Synchronous Parallelized Scheduler for Bioinformatics Application on Public Cloud. <i>International Journal of Computer Applications</i> , 2016, 145, 22-30. | 0.2 | 0 |
| 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>. <i>PeerJ</i> , 2017, 5, e3165. | 2.0 | 1 |
| 6179 | AP4 Transcription Factor Binding Site is a Repressor Element in ek2 Promoter of Human Liver Carcinoma Cell Line, HepG2. <i>Sains Malaysiana</i> , 2017, 46, 1887-1893. | 0.5 | 0 |
| 6193 | Prospects for the use of third generation sequencers for quantitative profiling of transcriptome. <i>Biomedical Chemistry Research and Methods</i> , 2018, 1, e00086. | 0.4 | 2 |
| 6194 | Nup153 Unlocks the Nuclear Pore Complex for HIV-1 Nuclear Import in Non-Dividing Cells. <i>SSRN Electronic Journal</i> , 0, , . | 0.4 | 0 |
| 6197 | A BLAST-Based Algorithm to Find Evenly Distributed Unique Subsequences. <i>Lecture Notes in Computer Science</i> , 2018, , 265-269. | 1.3 | 0 |
| 6241 | Neem Genome Annotation. <i>Compendium of Plant Genomes</i> , 2019, , 73-92. | 0.5 | 0 |
| 6242 | The Genome of <i>Prunus mume</i> . <i>Compendium of Plant Genomes</i> , 2019, , 31-52. | 0.5 | 0 |
| 6244 | GMeta: A Novel Algorithm to Utilize Highly Connected Components for Metagenomic Binning. <i>Lecture Notes in Computer Science</i> , 2019, , 545-559. | 1.3 | 0 |
| 6246 | Transcriptional Signatures of Progressive Neuropathology in Transgenic Models of Tau and Amyloid Pathology. <i>SSRN Electronic Journal</i> , 0, , . | 0.4 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 0.7 | 1 |
| 6272 | Bioinformatic pipelines for whole transcriptome sequencing data exploitation in leukemia patients with complex structural variants. PeerJ, 2019, 7, e7071. | 2.0 | 1 |
| 6295 | From EST to structure models for functional inference of APP, BACE1, PSEN1, PSEN2 genes. Bioinformation, 2019, 15, 760-771. | 0.5 | 0 |
| 6299 | Biological Sequence Analysis. , 0, , 55-69. | | 2 |
| 6308 | Identification and Characterization of Cis-Regulatory Elements for Photoreceptor-Type-Specific Transcription in ZebraFish. Methods in Molecular Biology, 2020, 2092, 123-145. | 0.9 | 2 |
| 6336 | A Rapid Evolving microRNA Cluster Rewires Its Target Regulatory Networks in Drosophila. Frontiers in Genetics, 2021, 12, 760530. | 2.3 | 1 |
| 6337 | Nanopore sequencing of SARS-CoV-2: Comparison of short and long PCR-tiling amplicon protocols. PLoS ONE, 2021, 16, e0259277. | 2.5 | 16 |
| 6338 | Plastome sequencing reveals phylogenetic relationships among <i>Comastoma</i> and related taxa (Gentianaceae) from the Qinghai-Tibetan Plateau. Ecology and Evolution, 2021, 11, 16034-16046. | 1.9 | 6 |
| 6339 | Unique <i>k</i> -mer sequences for validating cancer-related substitution, insertion and deletion mutations. NAR Cancer, 2020, 2, zcaa034. | 3.1 | 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. Microbiology Resource Announcements, 2020, 9, . | 0.6 | 1 |
| 6346 | Whole genome sequencing of an edible and medicinal mushroom, <i>Russula griseocarnosa</i> , and its association with mycorrhizal characteristics. Gene, 2022, 808, 145996. | 2.2 | 4 |
| 6348 | Updates on Legume Genome Sequencing. Methods in Molecular Biology, 2020, 2107, 1-18. | 0.9 | 6 |
| 6349 | Computational prediction and characterisation of miRNAs and their pathway genes in human schistosomiasis caused by <i>Schistosoma haematobium</i> . Memorias Do Instituto Oswaldo Cruz, 2020, 115, e190378. | 1.6 | 4 |
| 6350 | Methods for Target Enrichment Sequencing via Probe Capture in Legumes. Methods in Molecular Biology, 2020, 2107, 199-231. | 0.9 | 2 |
| 6357 | InsectBase 2.0: a comprehensive gene resource for insects. Nucleic Acids Research, 2022, 50, D1040-D1045. | 14.5 | 74 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 6363 | Genome-Wide Identification of Tomato Xylem Sap Fitness Factors for Three Plant-Pathogenic <i>Ralstonia</i> Species. <i>MSystems</i> , 2021, 6, e0122921. | 3.8 | 7 |
| 6364 | CSC software corrects off-target mediated gRNA depletion in CRISPR-Cas9 essentiality screens. <i>Nature Communications</i> , 2021, 12, 6461. | 12.8 | 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. | 3.1 | 4 |
| 6366 | Benchmarking pipelines for subclonal deconvolution of bulk tumour sequencing data. <i>Nature Communications</i> , 2021, 12, 6396. | 12.8 | 10 |
| 6368 | Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. <i>Nature Genetics</i> , 2021, 53, 1606-1615. | 21.4 | 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. | 9.5 | 20 |
| 6370 | Transposable elements that have recently been mobile in the human genome. <i>BMC Genomics</i> , 2021, 22, 789. | 2.8 | 12 |
| 6371 | Comprehensive analysis of complete mitochondrial genome of <i>Sapindus mukorossi</i> Gaertn.: an important industrial oil tree species in China. <i>Industrial Crops and Products</i> , 2021, 174, 114210. | 5.2 | 16 |
| 6375 | First Report of Citrus Viroid V and Citrus Viroid VI in Australia Infecting Citrus. <i>Plant Disease</i> , 2020, 104, 2037. | 1.4 | 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. <i>Journal of Clinical Investigation</i> , 2003, 111, 1099-1106. | 8.2 | 20 |
| 6381 | Genomic Data Visualization: The Bluejay System. , 2009, , 395-409. | | 0 |
| 6382 | Exhaustive Peptide Searching Using Relations. <i>Lecture Notes in Computer Science</i> , 2007, , 13-24. | 1.3 | 2 |
| 6389 | Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena (<i>Hyaena</i>) Tj ETQq1 1,0,784314,rgBT /Ove 1,9 | | |
| 6390 | The complete mitochondrial genome of an endangered tree: <i>Malaria oleifera</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3829-3830. | 0.4 | 2 |
| 6394 | Fusion Transcript Detection from RNA-Seq using Jaccard Distance. , 2020, , . | | 3 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 6395 | Dedicated transcriptomics combined with power analysis lead to functional understanding of genes with weak phenotypic changes in knockout lines. <i>PLoS Computational Biology</i> , 2020, 16, e1008354. | 3.2 | 6 |
| 6396 | NEIBank: genomics and bioinformatics resources for vision research. <i>Molecular Vision</i> , 2008, 14, 1327-37. | 1.1 | 30 |
| 6398 | Expressed sequence tag analysis of guinea pig (<i>Cavia porcellus</i>) eye tissues for NEIBank. <i>Molecular Vision</i> , 2008, 14, 2413-27. | 1.1 | 17 |
| 6399 | MapToGenome: a comparative genomic tool that aligns transcript maps to sequenced genomes. <i>Evolutionary Bioinformatics</i> , 2007, 3, 15-25. | 1.2 | 3 |
| 6400 | MLGA: a cost-effective approach to the diagnosis of gene deletions in eye development anomalies. <i>Molecular Vision</i> , 2009, 15, 1445-8. | 1.1 | 3 |
| 6401 | PositionMatcher: A Fast Custom-Annotation Tool for Short DNA Sequences. <i>Summit on Translational Bioinformatics</i> , 2010, 2010, 25-9. | 0.7 | 1 |
| 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, . | 0.4 | 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. | 3.2 | 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. | 1.7 | 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. | 2.3 | 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. | 4.8 | 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. | 4.8 | 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. | 3.5 | 2 |
| 6419 | The U1 snRNP component RBP45d regulates temperature-responsive flowering in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2022, 34, 834-851. | 6.6 | 18 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 6420 | Chloranthus genome provides insights into the early diversification of angiosperms. Nature Communications, 2021, 12, 6930. | 12.8 | 44 |
| 6421 | PCR Primer Design for the Rapidly Evolving SARS-CoV-2 Genome. Methods in Molecular Biology, 2022, 2392, 185-197. | 0.9 | 2 |
| 6422 | Epigenetic Dysregulation of KCNK9 Imprinting and Triple-Negative Breast Cancer. Cancers, 2021, 13, 6031. | 3.7 | 1 |
| 6423 | Resolving the Microalgal Gene Landscape at the Strain Level: a Novel Hybrid Transcriptome of <i>Emiliana huxleyi</i> CCMP3266. Applied and Environmental Microbiology, 2022, 88, AEM0141821. | 3.1 | 6 |
| 6425 | Genome-wide survey and characterization of transcription factors in the silk gland of the silkworm, Bombyx mori. PLoS ONE, 2021, 16, e0259870. | 2.5 | 3 |
| 6427 | Molecular evolution of chloroplast genomes in subfamily Zingiberoideae (Zingiberaceae). BMC Plant Biology, 2021, 21, 558. | 3.6 | 26 |
| 6428 | ASER: Animal Sex Reversal Database. Genomics, Proteomics and Bioinformatics, 2021, 19, 873-881. | 6.9 | 5 |
| 6429 | Origins and Function of VL30 lncRNA Packaging in Small Extracellular Vesicles: Implications for Cellular Physiology and Pathology. Biomedicines, 2021, 9, 1742. | 3.2 | 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. | 2.4 | 17 |
| 6431 | Baiting out a full length sequence from unmapped RNA-seq data. BMC Genomics, 2021, 22, 857. | 2.8 | 3 |
| 6432 | Vertical Inheritance Facilitates Interspecies Diversification in Biosynthetic Gene Clusters and Specialized Metabolites. MBio, 2021, 12, e0270021. | 4.1 | 23 |
| 6433 | scpMammaPrint and scpBluePrint comprehensively capture the cancer hallmarks in early-stage breast cancer patients. Genes Chromosomes and Cancer, 2022, 61, 148-160. | 2.8 | 11 |
| 6434 | Systematic Identification of Endogenous Retroviral Protein-Coding Genes Expressed in Canine Oral Malignant Melanoma. Frontiers in Virology, 2021, 1, . | 1.4 | 0 |
| 6435 | Genetic and functional evidence links a missense variant in <i>B4GALT1</i> to lower LDL and fibrinogen. Science, 2021, 374, 1221-1227. | 12.6 | 14 |
| 6436 | Error-prone, stress-induced 3' flap-based Okazaki fragment maturation supports cell survival. Science, 2021, 374, 1252-1258. | 12.6 | 9 |
| 6437 | Rare and potentially pathogenic variants in hydroxycarboxylic acid receptor genes identified in breast cancer cases. BMC Medical Genomics, 2021, 14, 284. | 1.5 | 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, , . | 1.3 | 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. | 3.6 | 8 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 6440 | Whence Came These Plants Most Foul? Phylogenomics and Biogeography of Lowiaceae (Zingiberales). <i>Frontiers in Ecology and Evolution</i> , 2022, 9, . | 2.2 | 1 |
| 6441 | Chromosome-Level Genome Assembly of a Human Fungal Pathogen Reveals Synteny among Geographically Distinct Species. <i>MBio</i> , 2022, 13, e0257421. | 4.1 | 7 |
| 6442 | CLUSTER guide RNAs enable precise and efficient RNA editing with endogenous ADAR enzymes in vivo. <i>Nature Biotechnology</i> , 2022, 40, 759-768. | 17.5 | 49 |
| 6443 | Whole Genome Assembly of Human Papillomavirus by Nanopore Long-Read Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 798608. | 2.3 | 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. <i>Molecular Ecology Resources</i> , 2022, 22, 1919-1938. | 4.8 | 11 |
| 6445 | Next-generation sequencing markup language (NCSML): a medium for the representation and exchange of NCS data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, PP, 1-1. | 3.0 | 2 |
| 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. | 3.3 | 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. | 8.8 | 38 |
| 6448 | Partitioning RNAs by length improves transcriptome reconstruction from short-read RNA-seq data. <i>Nature Biotechnology</i> , 2022, 40, 741-750. | 17.5 | 7 |
| 6449 | Genomically Hardwired Regulation of Gene Activity Orchestrates Cellular Iron Homeostasis in <i>Arabidopsis</i> . <i>RNA Biology</i> , 2022, 19, 143-161. | 3.1 | 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. | 2.3 | 2 |
| 6451 | De novo mutations identified by whole-genome sequencing implicate chromatin modifications in obsessive-compulsive disorder. <i>Science Advances</i> , 2022, 8, eabi6180. | 10.3 | 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. | 1.6 | 0 |
| 6453 | A Chromosome-Level Genome Assembly of Yellowtail Kingfish (<i>Seriola lalandi</i>). <i>Frontiers in Genetics</i> , 2021, 12, 825742. | 2.3 | 1 |
| 6454 | Dysgu: efficient structural variant calling using short or long reads. <i>Nucleic Acids Research</i> , 2022, 50, e53-e53. | 14.5 | 13 |
| 6455 | Somatic and Germline Genomic Alterations in Very Young Women with Breast Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2339-2348. | 7.0 | 20 |
| 6456 | A Superior Contiguous Whole Genome Assembly for Shrimp (<i>Penaeus indicus</i>). <i>Frontiers in Marine Science</i> , 2022, 8, . | 2.5 | 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 | 2.8 | 6 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 6458 | Mitochondrial DNA variation across 56,434 individuals in gnomAD. <i>Genome Research</i> , 2022, 32, 569-582. | 5.5 | 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. | 3.0 | 0 |
| 6460 | Metatranscriptome Profiling of a Specialized Microbial Consortium during the Degradation of Nixtamalized Maize Pericarp. <i>Microbiology Spectrum</i> , 2022, 10, e0231821. | 3.0 | 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. | 2.4 | 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. | 2.3 | 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, . | 7.1 | 13 |
| 6464 | Differential enrichment of yeast DNA in SARS-CoV-2 and related genomes supports synthetic origin hypothesis. <i>F1000Research</i> , 0, 10, 912. | 1.6 | 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. | 2.4 | 2 |
| 6466 | Evolution of DNA Methylation Across Ecdysozoa. <i>Journal of Molecular Evolution</i> , 2022, 90, 56-72. | 1.8 | 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. | 3.0 | 5 |
| 6468 | Trade-off between sex and growth in diatoms: Molecular mechanisms and demographic implications. <i>Science Advances</i> , 2022, 8, eabj9466. | 10.3 | 10 |
| 6470 | The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159. | 0.9 | 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. | 1.0 | 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. | 3.9 | 2 |
| 6473 | Characterizing mobile element insertions in 5675 genomes. <i>Nucleic Acids Research</i> , 2022, 50, 2493-2508. | 14.5 | 16 |
| 6474 | High Stability of the Epigenome in <i>Drosophila</i> Interspecific Hybrids. <i>Genome Biology and Evolution</i> , 2022, 14, . | 2.5 | 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. | 2.8 | 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. | 3.5 | 18 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 6477 | Capture-C: a modular and flexible approach for high-resolution chromosome conformation capture. <i>Nature Protocols</i> , 2022, 17, 445-475. | 12.0 | 24 |
| 6478 | WormBase in 2022—data, processes, and tools for analyzing <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2022, 220, . | 2.9 | 128 |
| 6479 | Novel patterns of expression and recruitment of new genes on the <i>Y</i> -haplotype, a mouse selfish chromosome. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20211985. | 2.6 | 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. | 2.3 | 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. | 12.8 | 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. | 3.0 | 3 |
| 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. | 4.8 | 9 |
| 6484 | HSDFinder: A BLAST-Based Strategy for Identifying Highly Similar Duplicated Genes in Eukaryotic Genomes. <i>Frontiers in Bioinformatics</i> , 2021, 1, . | 2.1 | 5 |
| 6485 | The evolution study on by whole-genome sequencing. <i>Journal of Genetics</i> , 2019, 98, . | 0.7 | 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, . | 6.4 | 10 |
| 6487 | Amplicon-based and metagenomic approaches provide insights into toxigenic potential in understudied Atlantic Canadian lakes. <i>Facets</i> , 2022, 7, 194-214. | 2.4 | 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, . | 6.4 | 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. | 6.5 | 13 |
| 6492 | Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. <i>Genome Biology</i> , 2022, 23, 46. | 8.8 | 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. | 3.4 | 5 |
| 6494 | Background splicing as a predictor of aberrant splicing in genetic disease. <i>RNA Biology</i> , 2022, 19, 256-265. | 3.1 | 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, . | 6.3 | 16 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 6497 | Chromosome-level genome assembly of a xerophytic plant, <i>Haloxylon ammodendron</i> . DNA Research, 2022, 29, . | 3.4 | 15 |
| 6498 | Conservation of chromatin conformation in carnivores. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 11 |
| 6499 | Genome-Wide Methylation Profiling in the Thalamus of Scrapie Sheep. Frontiers in Veterinary Science, 2022, 9, 824677. | 2.2 | 2 |
| 6500 | Comparative Genome Analysis Reveals Cis-Regulatory Elements on Gene-Sized Chromosomes of Ciliated Protists. Frontiers in Microbiology, 2022, 13, 775646. | 3.5 | 5 |
| 6501 | Microbial Community Structure and Functional Potential of Deep-Sea Sediments on Low Activity Hydrothermal Area in the Central Indian Ridge. Frontiers in Marine Science, 2022, 9, . | 2.5 | 6 |
| 6503 | Gene losses may contribute to subterranean adaptations in naked mole-rat and blind mole-rat. BMC Biology, 2022, 20, 44. | 3.8 | 10 |
| 6504 | Chromosome-level genome assembly of the diploid blueberry <i>Vaccinium darrowii</i> provides insights into its subtropical adaptation and cuticle synthesis. Plant Communications, 2022, 3, 100307. | 7.7 | 10 |
| 6505 | NRD: Nicotiana Resistance Database, a Comprehensive Platform of Stress Tolerance in Nicotiana. Agronomy, 2022, 12, 508. | 3.0 | 0 |
| 6506 | Reference genome of lumpfish <i>Cyclopterus lumpus</i> Linnaeus provides evidence of male heterogametic sex determination through the AMH pathway. Molecular Ecology Resources, 2022, 22, 1427-1439. | 4.8 | 16 |
| 6507 | Comparison of Immune Checkpoint Molecules PD-1 and PD-L1 in Paired Primary and Recurrent Glioma: Increasing Trend When Recurrence. Brain Sciences, 2022, 12, 266. | 2.3 | 0 |
| 6508 | Transcriptomic Analysis Suggests Auxin Regulation in Dorsal-Ventral Petal Asymmetry of Wild Progenitor <i>Sinningia speciosa</i> . International Journal of Molecular Sciences, 2022, 23, 2073. | 4.1 | 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. Frontiers in Genetics, 2022, 13, 821026. | 2.3 | 2 |
| 6510 | Comprehensive RNA dataset of tissue and plasma from patients with esophageal cancer or precursor lesions. Scientific Data, 2022, 9, 86. | 5.3 | 1 |
| 6511 | Recently Integrated Alu Elements in Capuchin Monkeys: A Resource for Cebus/Sapajus Genomics. Genes, 2022, 13, 572. | 2.4 | 4 |
| 6512 | Targeted Sanger sequencing to recover key mutations in SARS-CoV-2 variant genome assemblies produced by next-generation sequencing. Microbial Genomics, 2022, 8, . | 2.0 | 7 |
| 6513 | Linking genomic and epidemiologic information to advance the study of COVID-19. Scientific Data, 2022, 9, 121. | 5.3 | 3 |
| 6514 | Landscape of adenosine-to-inosine RNA recoding across human tissues. Nature Communications, 2022, 13, 1184. | 12.8 | 46 |
| 6515 | Original Leaf Colonisers Shape Fungal Decomposer Communities of <i>Phragmites australis</i> in Intermittent Habitats. Journal of Fungi (Basel, Switzerland), 2022, 8, 284. | 3.5 | 6 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 6516 | Ethylene Response Factor109 Attunes Immunity, Photosynthesis, and Iron Homeostasis in Arabidopsis Leaves. <i>Frontiers in Plant Science</i> , 2022, 13, 841366. | 3.6 | 7 |
| 6517 | ADARs act as potent regulators of circular transcriptome in cancer. <i>Nature Communications</i> , 2022, 13, 1508. | 12.8 | 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. | 6.4 | 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. | 3.5 | 1 |
| 6520 | A point mutation in HIV-1 integrase redirects proviral integration into centromeric repeats. <i>Nature Communications</i> , 2022, 13, 1474. | 12.8 | 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. | 2.8 | 18 |
| 6522 | Exome sequencing identifies variants in infants with sacral agenesis. <i>Birth Defects Research</i> , 2022, 114, 215-227. | 1.5 | 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. | 3.0 | 1 |
| 6524 | PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2. <i>Npj Genomic Medicine</i> , 2022, 7, 19. | 3.8 | 2 |
| 6525 | The evolution, evolvability and engineering of gene regulatory DNA. <i>Nature</i> , 2022, 603, 455-463. | 27.8 | 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. | 14.5 | 12 |
| 6527 | Clonal lineage tracing reveals shared origin of conventional and plasmacytoid dendritic cells. <i>Immunity</i> , 2022, 55, 405-422.e11. | 14.3 | 37 |
| 6528 | ExceS-A: an exon-centric split aligner. <i>Journal of Integrative Bioinformatics</i> , 2022, 19, . | 1.5 | 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. | 7.7 | 3 |
| 6530 | Extensive sequence divergence between the reference genomes of two zebrafish strains, Tuebingen and AB. <i>Molecular Ecology Resources</i> , 2022, , . | 4.8 | 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. | 1.9 | 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. | 3.9 | 13 |
| 6533 | Evidence for yeast artificial synthesis in SARS-CoV-2 and SARS-CoV-1 genomic sequences. <i>F1000Research</i> , 0, 10, 912. | 1.6 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 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. | 8.3 | 21 |
| 6535 | The <i>Gastrodia menghaiensis</i> (Orchidaceae) genome provides new insights of orchid mycorrhizal interactions. <i>BMC Plant Biology</i> , 2022, 22, 179. | 3.6 | 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. | 7.1 | 5 |
| 6537 | A Chromosome-Level Reference Genome of Chinese Balloon Flower (<i>Platycodon grandiflorus</i>). <i>Frontiers in Genetics</i> , 2022, 13, 869784. | 2.3 | 7 |
| 6538 | Accurate detection of tumor-specific gene fusions reveals strongly immunogenic personal neo-antigens. <i>Nature Biotechnology</i> , 2022, 40, 1276-1284. | 17.5 | 25 |
| 6539 | Precise in vivo functional analysis of DNA variants with base editing using ACEofBASEs target prediction. <i>ELife</i> , 2022, 11, . | 6.0 | 12 |
| 6540 | Putting small and big pieces together: a genome assembly approach reveals the largest Lamiid plastome in a woody vine. <i>PeerJ</i> , 2022, 10, e13207. | 2.0 | 3 |
| 6541 | Relationship between nitrifying microorganisms and other microorganisms residing in the maize rhizosphere. <i>Archives of Microbiology</i> , 2022, 204, 246. | 2.2 | 3 |
| 6542 | De novo genome assembly of <i>Bradysia cellarum</i> (Diptera: Sciaridae), a notorious pest in traditional special vegetables in China. <i>Insect Molecular Biology</i> , 2022, 31, 508-518. | 2.0 | 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 H^2 cells. <i>Nature Communications</i> , 2022, 13, 1815. | 12.8 | 6 |
| 6544 | Dosage sensitivity and exon shuffling shape the landscape of polymorphic duplicates in <i>Drosophila</i> and humans. <i>Nature Ecology and Evolution</i> , 2022, 6, 273-287. | 7.8 | 12 |
| 6545 | Identification of Novel Regulatory Regions Induced by Intrauterine Growth Restriction in Rat Islets. <i>Endocrinology</i> , 2022, 163, . | 2.8 | 3 |
| 6547 | Medium levels of transcription and replication related chromosomal instability are associated with poor clinical outcome. <i>Scientific Reports</i> , 2021, 11, 23429. | 3.3 | 1 |
| 6548 | Long-read assemblies reveal structural diversity in genomes of organelles – an example with <i>Acacia pycnantha</i> . <i>GigaByte</i> , 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. <i>PeerJ</i> , 2021, 9, e12474. | 2.0 | 3 |
| 6550 | Genomic analysis of <i>Elsinoë arachidis</i> reveals its potential pathogenic mechanism and the biosynthesis pathway of elsinochrome toxin. <i>PLoS ONE</i> , 2021, 16, e0261487. | 2.5 | 3 |
| 6551 | Generation and mutational analysis of a transgenic mouse model of human <i>SRY</i> . <i>Human Mutation</i> , 2022, 43, 362-379. | 2.5 | 3 |
| 6552 | Identification of starch candidate genes using SLAF-seq and BSA strategies and development of related SNP-CAPS markers in tetraploid potato. <i>PLoS ONE</i> , 2021, 16, e0261403. | 2.5 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 6553 | Species-specific partial gene duplication in <i>Arabidopsis thaliana</i> evolved novel phenotypic effects on morphological traits under strong positive selection. <i>Plant Cell</i> , 2022, 34, 802-817. | 6.6 | 15 |
| 6554 | Genetic and Molecular Characterization of a Self-Compatible <i>Brassica rapa</i> Line Possessing a New Class II S Haplotype. <i>Plants</i> , 2021, 10, 2815. | 3.5 | 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. <i>Zoological Research</i> , 2022, 43, 423-441. | 2.1 | 5 |
| 6556 | OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2022, , . | 14.5 | 3 |
| 6557 | Intraspecific <i>de novo</i> gene birth revealed by presence-absence variant genes in <i>Caenorhabditis elegans</i> . <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac031. | 3.2 | 7 |
| 6558 | Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in <i>Drosophila</i> . <i>Nature Communications</i> , 2022, 13, 1948. | 12.8 | 53 |
| 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, , . | 1.8 | 0 |
| 6560 | Open reading frame dominance indicates protein-coding potential of RNAs. <i>EMBO Reports</i> , 2022, 23, e54321. | 4.5 | 7 |
| 6561 | A draft genome of Drung cattle reveals clues to its chromosomal fusion and environmental adaptation. <i>Communications Biology</i> , 2022, 5, 353. | 4.4 | 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. | 12.8 | 48 |
| 6826 | Global mapping of RNA homodimers in living cells. <i>Genome Research</i> , 2022, , . | 5.5 | 3 |
| 6827 | Using surveys of Affymetrix GeneChips to study antisense expression. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, . | 1.5 | 1 |
| 6828 | Automatic knowledge extraction in sequencing analysis with multiagent system and grid computing. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 206. | 1.5 | 2 |
| 6829 | ANI analysis of poxvirus genomes reveals its potential application to viral species rank demarcation. <i>Virus Evolution</i> , 2022, 8, . | 4.9 | 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, . | 6.4 | 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. | 3.6 | 13 |
| 6833 | EBV genome variations enhance clinicopathological features of nasopharyngeal carcinoma in a non-endemic region. <i>Cancer Science</i> , 2022, , . | 3.9 | 7 |
| 6834 | Evolution of coastal forests based on a full set of mangrove genomes. <i>Nature Ecology and Evolution</i> , 2022, 6, 738-749. | 7.8 | 41 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 6835 | Comprehensive 16S rRNA and metagenomic data from the gut microbiome of aging and rejuvenation mouse models. <i>Scientific Data</i> , 2022, 9, 197. | 5.3 | 1 |
| 6837 | Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123. | 6.5 | 70 |
| 6838 | Rampant nuclearâ€“mitochondrialâ€“plastid phylogenomic discordance in globally distributed calcifying microalgae. <i>New Phytologist</i> , 2022, 235, 1394-1408. | 7.3 | 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. | 7.1 | 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, . | 3.9 | 7 |
| 6841 | CircMiMi: a stand-alone software for constructing circular RNA-microRNA-mRNA interactions across species. <i>BMC Bioinformatics</i> , 2022, 23, 164. | 2.6 | 8 |
| 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. | 1.3 | 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. | 2.8 | 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, , . | 2.9 | 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. | 2.4 | 4 |
| 6846 | Phyloepigenetics. <i>Biology</i> , 2022, 11, 754. | 2.8 | 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. | 2.2 | 0 |
| 6849 | First Chromosome-Scale Assembly and Deep Floral-Bud Transcriptome of a Male Kiwifruit. <i>Frontiers in Genetics</i> , 2022, 13, . | 2.3 | 9 |
| 6850 | The assembled and annotated genome of the masked palm civet (<i>Paguma larvata</i>). <i>GigaScience</i> , 2022, 11, . | 6.4 | 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. | 2.1 | 3 |
| 6858 | Triobinned 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. | 4.8 | 13 |
| 6860 | Semi-subterranean environment and soil metagenomic datasets of the Gyeongju Seokbinggo (stone ice) Tj ETQq0 0.0 rgBT /Qverlock 10 | 1.0 | 0 |
| 6861 | <i>mebipred</i> : identifying metal-binding potential in protein sequence. <i>Bioinformatics</i> , 2022, 38, 3532-3540. | 4.1 | 15 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 6862 | Repetitive Elements, Sequence Turnover and Cyto-Nuclear Gene Transfer in Gymnosperm Mitogenomes. <i>Frontiers in Genetics</i> , 0, 13, . | 2.3 | 2 |
| 6864 | Chromosome-scale genome assembly of an important medicinal plant honeysuckle. <i>Scientific Data</i> , 2022, 9, . | 5.3 | 7 |
| 6866 | Intron losses and gains in the nematodes. <i>Biology Direct</i> , 2022, 17, . | 4.6 | 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. | 4.1 | 6 |
| 6868 | Genome-wide specificity of plant genome editing by both CRISPRâ€‘Cas9 and TALEN. <i>Scientific Reports</i> , 2022, 12, . | 3.3 | 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, . | 2.2 | 1 |
| 6871 | Full-length transcripts facilitates <i>Portunus trituberculatus</i> genome structure annotation. <i>Journal of Oceanology and Limnology</i> , 2022, 40, 2042-2051. | 1.3 | 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. | 2.0 | 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, . | 6.4 | 9 |
| 6874 | Computationally designed hyperactive Cas9 enzymes. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 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, . | 7.1 | 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. | 1.7 | 5 |
| 6877 | Blood-derived lncRNAs as biomarkers for cancer diagnosis: the Good, the Bad and the Beauty. <i>Npj Precision Oncology</i> , 2022, 6, . | 5.4 | 50 |
| 6878 | Cytogenetic Characterization and Molecular Marker Development for a Wheat-<i>T. boeoticum</i>4A^b (4B) Disomic Substitution Line with Stripe Rust Resistance. <i>Plant Disease</i> , 2023, 107, 125-130. | 1.4 | 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, . | 2.6 | 3 |
| 6880 | Human Follicular Mites: Ectoparasites Becoming Symbionts. <i>Molecular Biology and Evolution</i> , 2022, 39, . | 8.9 | 6 |
| 6881 | Genome sequence of <i>Gossypium anomalum</i> facilitates interspecific introgression breeding. <i>Plant Communications</i> , 2022, 3, 100350. | 7.7 | 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 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 6883 | Complex Feline Disease Mapping Using a Dense Genotyping Array. <i>Frontiers in Veterinary Science</i> , 0, 9, . | 2.2 | 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. | 4.1 | 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. | 1.9 | 1 |
| 6886 | Introduction to the principles and methods underlying the recovery of metagenome-assembled genomes from metagenomic data. <i>MicrobiologyOpen</i> , 2022, 11, . | 3.0 | 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. | 4.8 | 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 |
| 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. | 5.2 | 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, . | 1.8 | 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. | 4.8 | 10 |
| 6892 | Turnover in Life-Strategies Recapitulates Marine Microbial Succession Colonizing Model Particles. <i>Frontiers in Microbiology</i> , 0, 13, . | 3.5 | 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, , . | 5.7 | 0 |
| 6895 | Chromosome-level genome assembly and annotation of the native Chinese wild blueberry <i>Vaccinium bracteatumFruit Research, 2022, 2, 1-14. | 2.0 | 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. | 0.9 | 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, . | 6.4 | 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, . | 3.6 | 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. | 4.1 | 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. | 4.1 | 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, , . | 1.8 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 6902 | Along the <i>Bos taurus</i> genome, uncover candidate imprinting control regions. <i>BMC Genomics</i> , 2022, 23, . | 2.8 | 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. | 3.1 | 7 |
| 6904 | Comprehensive identification and characterization of the HERV-K (HML-9) group in the human genome. <i>Retrovirology</i> , 2022, 19, . | 2.0 | 8 |
| 6906 | Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050. | 21.4 | 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, . | 3.0 | 11 |
| 6908 | Efficient compression of SARS-CoV-2 genome data using Nucleotide Archival Format (NAF). <i>Patterns</i> , 2022, , 100562. | 5.9 | 1 |
| 6909 | Evidence for yeast artificial synthesis in SARS-CoV-2 and SARS-CoV-1 genomic sequences. <i>F1000Research</i> , 0, 10, 912. | 1.6 | 1 |
| 6910 | Deep Sequencing Analysis of Individual HIV-1 Proviruses Reveals Frequent Asymmetric Long Terminal Repeats. <i>Journal of Virology</i> , 2022, 96, . | 3.4 | 8 |
| 6911 | Screening of Genes Related to Sex Determination and Differentiation in Mandarin Fish (<i>Siniperca</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 4.1 | 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, . | 2.8 | 9 |
| 6914 | REDfly: An Integrated Knowledgebase for Insect Regulatory Genomics. <i>Insects</i> , 2022, 13, 618. | 2.2 | 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. | 2.8 | 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. | 4.8 | 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, . | 8.9 | 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. | 1.3 | 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, . | 2.5 | 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, . | 2.6 | 13 |
| 6924 | Identification of fusions with potential clinical significance in melanoma. <i>Modern Pathology</i> , 2022, 35, 1837-1847. | 5.5 | 8 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 6925 | Comparative repeatome analysis reveals new evidence on genome evolution in wild diploid <i>Arachis</i> (Fabaceae) species. <i>Planta</i> , 2022, 256, . | 3.2 | 4 |
| 6927 | Addressing nontarget amplification in DNA metabarcoding studies of arthropod-feeding rodents. <i>Mammal Research</i> , 0, , . | 1.3 | 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, . | 3.3 | 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, . | 5.3 | 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, . | 3.4 | 3 |
| 6933 | ZW sex-chromosome evolution and contagious parthenogenesis in <i>Artemia</i> brine shrimp. <i>Genetics</i> , 2022, 222, . | 2.9 | 5 |
| 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. | 4.1 | 5 |
| 6936 | A diversified and segregated mRNA spliced-leader system in the parasitic Perkinsozoa. <i>Open Biology</i> , 2022, 12, . | 3.6 | 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, . | 3.8 | 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. | 5.7 | 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, . | 3.0 | 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. | 4.1 | 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, . | 11.1 | 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. | 3.5 | 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. | 6.5 | 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, . | 1.5 | 3 |
| 6947 | Twinkle twinkle brittle star: the draft genome of <i>Ophioderma brevispinum</i> (Echinodermata: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 T | 2.8 | 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. | 3.5 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|-----|-----------|
| 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. | 2.0 | 3 |
| 6952 | Fusion of High Mobility Group AT-hook 2 Gene (<i>HMGA2</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. | 2.0 | 5 |
| 6953 | Interpreting alignment-free sequence comparison: what makes a score a good score?. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, . | 3.2 | 2 |
| 6954 | Monotreme-specific conserved putative proteins derived from retroviral reverse transcriptase. <i>Virus Evolution</i> , 2022, 8, . | 4.9 | 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. | 3.1 | 6 |
| 6957 | Multiple genome alignment in the telomere-to-telomere assembly era. <i>Genome Biology</i> , 2022, 23, . | 8.8 | 17 |
| 6959 | HPV genotyping by L1 amplicon sequencing of archived invasive cervical cancer samples: a pilot study. <i>Infectious Agents and Cancer</i> , 2022, 17, . | 2.6 | 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, . | 3.6 | 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, . | 4.4 | 6 |
| 6963 | A survey of current methods to detect and genotype inversions. <i>Human Mutation</i> , 2022, 43, 1576-1589. | 2.5 | 11 |
| 6964 | Comparative genome analysis unravels pathogenicity of <i>Xanthomonas albilineans</i> causing sugarcane leaf scald disease. <i>BMC Genomics</i> , 2022, 23, . | 2.8 | 2 |
| 6965 | Multi-omics provides new insights into the domestication and improvement of dark jute (<i>T. ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T</i>) | 5.7 | 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. | 1.6 | 1 |
| 6967 | Evaluation and characterization of expression quantitative trait analysis methods in the Hybrid Rat Diversity Panel. <i>Frontiers in Genetics</i> , 0, 13, . | 2.3 | 2 |
| 6968 | Regulation of Nodal signaling propagation by receptor interactions and positive feedback. <i>ELife</i> , 0, 11, . | 6.0 | 5 |
| 6969 | False gene and chromosome losses in genome assemblies caused by GC content variation and repeats. <i>Genome Biology</i> , 2022, 23, . | 8.8 | 21 |
| 6970 | Characterization of the Urinary Metagenome and Virome in Healthy Children. <i>Biomedicines</i> , 2022, 10, 2412. | 3.2 | 2 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 6971 | Unique Evolution of Antiviral Tetherin in Bats. <i>Journal of Virology</i> , 2022, 96, . | 3.4 | 14 |
| 6972 | Dynamic genome evolution in a model fern. <i>Nature Plants</i> , 2022, 8, 1038-1051. | 9.3 | 56 |
| 6974 | Comprehensive survey of transposon mPing insertion sites and transcriptome analysis for identifying candidate genes controlling high protein content of rice. <i>Frontiers in Plant Science</i> , 0, 13, . | 3.6 | 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, . | 7.1 | 19 |
| 6976 | Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics. <i>Nature Genetics</i> , 2022, 54, 1553-1563. | 21.4 | 46 |
| 6977 | Tail Wags Dogâ€™s SINE: Retropositional Mechanisms of Can SINE Depend on Its A-Tail Structure. <i>Biology</i> , 2022, 11, 1403. | 2.8 | 3 |
| 6978 | Comparative mitogenome analysis reveals mitochondrial genome characteristics in eight strains of <i>Beauveria</i> . <i>PeerJ</i> , 0, 10, e14067. | 2.0 | 2 |
| 6980 | Broad genomic workup including optical genome mapping uncovers a DDX3X: MLLT10 gene fusion in acute myeloid leukemia. <i>Frontiers in Oncology</i> , 0, 12, . | 2.8 | 4 |
| 6981 | Nuclear-embedded mitochondrial DNA sequences in 66,083 human genomes. <i>Nature</i> , 2022, 611, 105-114. | 27.8 | 69 |
| 6982 | Lineage-specific, fast-evolving GATA-like gene regulates zygotic gene activation to promote endoderm specification and pattern formation in the Theridiidae spider. <i>BMC Biology</i> , 2022, 20, . | 3.8 | 5 |
| 6983 | Efficacy and safety of universal (TCRKO) ARI-0001 CAR-T cells for the treatment of B-cell lymphoma. <i>Frontiers in Immunology</i> , 0, 13, . | 4.8 | 4 |
| 6984 | Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and within-host species divergence. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3468-3484. | 3.0 | 4 |
| 6986 | A highly contiguous, scaffold-level nuclear genome assembly for the fever tree (<i>Cinchona pubescens</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf 0,0 1 | 8.0 | 1 |
| 6987 | Genomic characterization of <i>Francisella tularensis</i> and other diverse <i>Francisella</i> species from complex samples. <i>PLoS ONE</i> , 2022, 17, e0273273. | 2.5 | 4 |
| 6989 | Mitochondrial Control Region Variants Related to Breast Cancer. <i>Genes</i> , 2022, 13, 1962. | 2.4 | 0 |
| 6990 | Miniature Inverted-repeat Transposable Elements Drive Rapid MicroRNA Diversification in Angiosperms. <i>Molecular Biology and Evolution</i> , 2022, 39, . | 8.9 | 10 |
| 6991 | Stable Transgenic Mouse Strain with Enhanced Photoactivatable Cre Recombinase for Spatiotemporal Genome Manipulation. <i>Advanced Science</i> , 2022, 9, . | 11.2 | 5 |
| 6992 | Spatiotemporal variations in retrovirus-host interactions among Darwinâ€™s finches. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 4 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 6993 | A cryptic transcription factor regulates <i>Caulobacter</i> adhesin development. <i>PLoS Genetics</i> , 2022, 18, e1010481. | 3.5 | 6 |
| 6994 | Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. <i>Nature Ecology and Evolution</i> , 2022, 6, 1891-1906. | 7.8 | 23 |
| 6997 | COX7A2L genetic variants determine cardiorespiratory fitness in mice and human. <i>Nature Metabolism</i> , 2022, 4, 1336-1351. | 11.9 | 10 |
| 6998 | Cebidae Alu Element Alignments and a Complex Non-Human Primate Radiation. <i>Life</i> , 2022, 12, 1655. | 2.4 | 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. <i>Frontiers in Microbiology</i> , 0, 13, . | 3.5 | 1 |
| 7000 | Gapless genome assembly of azalea and multi-omics investigation into divergence between two species with distinct flower color. <i>Horticulture Research</i> , 2023, 10, . | 6.3 | 11 |
| 7002 | An overview of online resources for intra-species detection of gene duplications. <i>Frontiers in Genetics</i> , 0, 13, . | 2.3 | 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. | 1.2 | 0 |
| 7005 | Thirteen Dipteroocarpoideae genomes provide insights into their evolution and borneol biosynthesis. <i>Plant Communications</i> , 2022, 3, 100464. | 7.7 | 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, . | 2.8 | 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. | 2.0 | 5 |
| 7008 | A method of large DNA fragment enrichment for nanopore sequencing in region 22q11.2. <i>Frontiers in Genetics</i> , 0, 13, . | 2.3 | 0 |
| 7009 | De novo assembly and characterization of the draft genome of the cashew (<i>Anacardium occidentale</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf 9.3 4 | 9.3 | 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. | 19.0 | 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, . | 8.9 | 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. | 2.6 | 6 |
| 7013 | Comprehensive analysis and accurate quantification of unintended large gene modifications induced by CRISPR-Cas9 gene editing. <i>Science Advances</i> , 2022, 8, . | 10.3 | 25 |
| 7014 | Target-enriched long-read sequencing (TELSeq) contextualizes antimicrobial resistance genes in metagenomes. <i>Microbiome</i> , 2022, 10, . | 11.1 | 8 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 7016 | Computational Genomic Signatures. Synthesis Lectures on Biomedical Engineering, 2011, , . | 0.1 | 0 |
| 7017 | Multigenic regulation in the ethylene biosynthesis pathway during coffee flowering. Physiology and Molecular Biology of Plants, 2022, 28, 1657-1669. | 3.1 | 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. Human Genetics and Genomics Advances, 2023, 4, 100159. | 1.7 | 2 |
| 7020 | Deeper genomic insights into tomato CLE genes repertoire identify new active peptides. BMC Genomics, 2022, 23, . | 2.8 | 10 |
| 7021 | Maize rhizosphere modulates the microbiome diversity and community structure to enhance plant health. Saudi Journal of Biological Sciences, 2023, 30, 103499. | 3.8 | 7 |
| 7022 | Identification of the Telomere elongation Mutation in Drosophila. Cells, 2022, 11, 3484. | 4.1 | 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. Animal Bioscience, 0, , . | 2.0 | 0 |
| 7025 | Owl Monkey Alu Insertion Polymorphisms and Aotus Phylogenetics. Genes, 2022, 13, 2069. | 2.4 | 2 |
| 7026 | Complete mitochondrial genome of <i>Pseudoechthistatus hei</i> (Coleoptera: Cerambycidae): Tj ETQq1 1 0.784314 rgBT /Overlock 100.0 | 0.4 | 1 |
| 7027 | Structure and evolution of the squamate major histocompatibility complex as revealed by two Anolis lizard genomes. Frontiers in Genetics, 0, 13, . | 2.3 | 5 |
| 7030 | Identification of iron and zinc responsive genes in pearl millet using genome-wide RNA-sequencing approach. Frontiers in Nutrition, 0, 9, . | 3.7 | 0 |
| 7032 | No phylogenomic support for a Cenozoic origin of the “living fossil” <i>Isoetes</i> . American Journal of Botany, 2023, 110, . | 1.7 | 2 |
| 7033 | Temporal progress of gene expression analysis with RNA-Seq data: A review on the relationship between computational methods. Computational and Structural Biotechnology Journal, 2023, 21, 86-98. | 4.1 | 8 |
| 7034 | Neoplasia-associated Chromosome Translocations Resulting in Gene Truncation. Cancer Genomics and Proteomics, 2022, 19, 647-672. | 2.0 | 3 |
| 7035 | Improved microbial genomes and gene catalog of the chicken gut from metagenomic sequencing of high-fidelity long reads. GigaScience, 2022, 11, . | 6.4 | 12 |
| 7036 | Effect of an anti-methanogenic supplement on enteric methane emission, fermentation, and whole rumen metagenome in sheep. Frontiers in Microbiology, 0, 13, . | 3.5 | 5 |
| 7037 | The UCSC Genome Browser database: 2023 update. Nucleic Acids Research, 2023, 51, D1188-D1195. | 14.5 | 144 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 7038 | Complete Mitogenome and Phylogenetic Analyses of <i>Galerita orientalis</i> Schmidt-Goebel, 1846 (Insecta: Tj ETQq0 0.0 rgBT /Qverlock 10 | 2.4 | 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, . | 2.8 | 3 |
| 7042 | Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. <i>Cell</i> , 2022, 185, 4587-4603.e23. | 28.9 | 29 |
| 7043 | Comparative genomics reveals insight into the evolutionary origin of massively scrambled genomes. <i>ELife</i> , 0, 11, . | 6.0 | 5 |
| 7044 | Enhancing diagnosis of T-cell lymphoma using non-recombined T-cell receptor sequences. <i>Frontiers in Oncology</i> , 0, 12, . | 2.8 | 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. | 4.1 | 5 |
| 7049 | Complete mitochondrial genome and phylogenetic analysis of <i>Mastax latefasciata</i> Liebke 1931 (Insecta: Coleoptera: Carabidae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 2040-2043. | 0.4 | 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. | 16.3 | 6 |
| 7052 | Whole-Exome Sequencing Among Chinese Patients With Hereditary Diffuse Gastric Cancer. <i>JAMA Network Open</i> , 2022, 5, e2245836. | 5.9 | 3 |
| 7053 | Genetics of tibia bone properties of crossbred commercial laying hens in different housing systems. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, . | 1.8 | 1 |
| 7058 | How to survive in the worldâ€™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, . | 3.6 | 2 |
| 7059 | Parallel evolution of reduced cancer risk and tumor suppressor duplications in <i>Xenarthra</i> . <i>ELife</i> , 0, 11, . | 6.0 | 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, . | 3.4 | 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, , . | 4.8 | 1 |
| 7063 | Chromosome Translocation t(10;19)(q26;q13) in a CIC-sarcoma. <i>In Vivo</i> , 2023, 37, 57-69. | 1.3 | 1 |
| 7064 | Efficient querying of genomic reference databases with <i>gget</i> . <i>Bioinformatics</i> , 2023, 39, . | 4.1 | 11 |
| 7065 | The hitchhikersâ€™ guide to RNA sequencing and functional analysis. <i>Briefings in Bioinformatics</i> , 2023, 24, . | 6.5 | 8 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 7066 | Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. <i>Functional and Integrative Genomics</i> , 2023, 23, . | 3.5 | 39 |
| 7067 | Identification of extremely GC-rich micro RNAs for RT-qPCR data normalization in human plasma. <i>Frontiers in Genetics</i> , 0, 13, . | 2.3 | 0 |
| 7068 | Pulmonary artery embolism: comprehensive transcriptomic analysis in understanding the pathogenic mechanisms of the disease. <i>BMC Genomics</i> , 2023, 24, . | 2.8 | 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, . | 3.4 | 2 |
| 7070 | Complete chloroplast genomes and comparative analysis of <i>Ligustrum</i> species. <i>Scientific Reports</i> , 2023, 13, . | 3.3 | 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, . | 2.3 | 5 |
| 7072 | A draft <i>Diabrotica virgifera virgifera</i> genome: insights into control and host plant adaption by a major maize pest insect. <i>BMC Genomics</i> , 2023, 24, . | 2.8 | 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. | 3.0 | 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, , . | 1.5 | 1 |
| 7076 | Anomalies in dye-terminator DNA sequencing caused by a natural G-quadruplex. <i>PLoS ONE</i> , 2022, 17, e0279423. | 2.5 | 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. | 2.0 | 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, . | 3.2 | 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, . | 4.8 | 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, Callithrichidae, and Aotidae. <i>Genes</i> , 2023, 14, 249. | 2.4 | 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. | 3.5 | 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. | 2.3 | 1 |
| 7084 | Persistent mutation burden drives sustained anti-tumor immune responses. <i>Nature Medicine</i> , 2023, 29, 440-449. | 30.7 | 35 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 7085 | Molecular classification and therapeutics in diffuse large B-cell lymphoma. <i>Frontiers in Molecular Biosciences</i> , 0, 10, . | 3.5 | 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, . | 2.6 | 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, . | 12.4 | 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. | 2.0 | 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. | 1.0 | 0 |
| 7094 | The Michigan Genomics Initiative: A biobank linking genotypes and electronic clinical records in Michigan Medicine patients. <i>Cell Genomics</i> , 2023, 3, 100257. | 6.5 | 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, . | 3.6 | 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. | 9.3 | 18 |
| 7098 | <i>Renal-pancreatic</i> dysplasia type 2: Perinatal lethal condition or a multisystemic disorder with variable expressivity. <i>Molecular Genetics & Genomic Medicine</i> , 2023, 11, . | 1.2 | 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. | 3.1 | 14 |
| 7100 | Dissecting the genetic basis of heterosis in elite super-hybrid rice. <i>Plant Physiology</i> , 2023, 192, 307-325. | 4.8 | 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, . | 2.8 | 4 |
| 7103 | Specific-Locus Amplified Fragment Sequencing (SLAF-Seq). <i>Methods in Molecular Biology</i> , 2023, , 165-171. | 0.9 | 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. | 3.3 | 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. | 0.4 | 1 |
| 7106 | Precipitation is the main axis of tropical plant phylogenetic turnover across space and time. <i>Science Advances</i> , 2023, 9, . | 10.3 | 12 |
| 7107 | Metabolic Background, Not Photosynthetic Physiology, Determines Drought and Drought Recovery Responses in C3 and C2 Moringas. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4094. | 4.1 | 1 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 7108 | FixItFelix: improving genomic analysis by fixing reference errors. <i>Genome Biology</i> , 2023, 24, . | 8.8 | 7 |
| 7109 | Roadmap to the study of gene and protein phylogeny and evolutionâ€”A practical guide. <i>PLoS ONE</i> , 2023, 18, e0279597. | 2.5 | 4 |
| 7111 | The diatom <i>Fragilariopsis cylindrus</i> : A model alga to understand cold-adapted life. <i>Journal of Phycology</i> , 2023, 59, 301-306. | 2.3 | 4 |
| 7112 | A cytosine-patch sequence motif identified in the conserved region of lincRNA-p21 interacts with the KH3 domain of hnRNP. <i>Current Research in Structural Biology</i> , 2023, 5, 100099. | 2.2 | 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. | 3.2 | 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, . | 2.1 | 2 |
| 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, . | 3.6 | 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. | 2.5 | 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, . | 2.0 | 0 |
| 7118 | Plastid Genome Assembly Using Long-read data. <i>Molecular Ecology Resources</i> , 2023, 23, 1442-1457. | 4.8 | 4 |
| 7119 | Regulatory and coding sequences of TRNP1 co-evolve with brain size and cortical folding in mammals. <i>ELife</i> , 0, 12, . | 6.0 | 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, . | 1.8 | 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, . | 2.9 | 2 |
| 7123 | Improved chromosomal-level genome assembly and re-annotation of leopard coral grouper. <i>Scientific Data</i> , 2023, 10, . | 5.3 | 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, . | 2.6 | 1 |
| 7126 | Pan-cancer analysis identifies tumor-specific antigens derived from transposable elements. <i>Nature Genetics</i> , 2023, 55, 631-639. | 21.4 | 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. | 3.7 | 5 |
| 7128 | Determining chromatin architecture with Micro Capture-C. <i>Nature Protocols</i> , 2023, 18, 1687-1711. | 12.0 | 7 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 7129 | Crystal Structure of an iâ€Motif from the <i>HRAS</i> Oncogene Promoter. Angewandte Chemie - International Edition, 2023, 62, . | 13.8 | 5 |
| 7130 | Crystal Structure of an iâ€Motif from the <i>HRAS</i> Oncogene Promoter. Angewandte Chemie, 2023, 135, . | 2.0 | 0 |
| 7131 | CRISPR/Cas9-Mediated Genome Editing in Zebrafish. Methods in Molecular Biology, 2023, , 371-380. | 0.9 | 0 |
| 7132 | Targetâ€capture probes for phylogenomics of the Caenogastropoda. Molecular Ecology Resources, 0, , . | 4.8 | 1 |
| 7134 | Shine: A novel strategy to extract specific, sensitive and well-conserved biomarkers from massive microbial genomic datasets. BMC Bioinformatics, 2023, 24, . | 2.6 | 0 |
| 7135 | Identification and validation of new MADS-box homologous genes in 3010 rice pan-genome. Plant Cell Reports, 0, , . | 5.6 | 1 |
| 7137 | Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species. Nature Genetics, 2023, 55, 852-860. | 21.4 | 43 |
| 7138 | Genomic and transcriptomic analysis of checkpoint blockade response in advanced non-small cell lung cancer. Nature Genetics, 2023, 55, 807-819. | 21.4 | 18 |
| 7139 | Expanding known viral diversity in the healthy infant gut. Nature Microbiology, 2023, 8, 986-998. | 13.3 | 31 |
| 7141 | Definition of the transcriptional units of inherited retinal disease genes by meta-analysis of human retinal transcriptome data. BMC Genomics, 2023, 24, . | 2.8 | 0 |
| 7142 | The Complete Chloroplast Genomes of Gynostemma Reveal the Phylogenetic Relationships of Species within the Genus. Genes, 2023, 14, 929. | 2.4 | 2 |
| 7144 | A complex structural variant near SOX3 causes X-linked split-hand/foot malformation. Human Genetics and Genomics Advances, 2023, 4, 100200. | 1.7 | 0 |
| 7145 | Mouse B2 SINE elements function as IFN-inducible enhancers. ELife, 0, 12, . | 6.0 | 7 |
| 7146 | Identification of novel microRNAs in the embryonic mouse brain using deep sequencing. Molecular and Cellular Biochemistry, 2024, 479, 297-311. | 3.1 | 0 |
| 7147 | Tracking the emergence of antigenic variants in influenza A virus epidemics in Brazil. Virus Evolution, 2023, 9, . | 4.9 | 2 |
| 7149 | Reduction of <i>Paraoxonase</i> Expression Followed by Inactivation across Independent Semiaquatic Mammals Suggests Stepwise Path to Pseudogenization. Molecular Biology and Evolution, 2023, 40, . | 8.9 | 1 |
| 7150 | ADAR1-mediated RNA editing of SCD1 drives drug resistance and self-renewal in gastric cancer. Nature Communications, 2023, 14, . | 12.8 | 7 |
| 7164 | A new Merluccius polli reference genome to investigate the effects of global change in West African waters. Frontiers in Marine Science, 0, 10, . | 2.5 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|------|-----------|
| 7165 | Validation of phylogenetic informative Y-InDels in Y-chromosomal haplogroup O-M175. <i>Frontiers in Genetics</i> , 0, 14, . | 2.3 | 0 |
| 7166 | Fine mapping of a QTL and identification of candidate genes associated with cold tolerance during germination in peanut (<i>Arachis hypogaea</i> L.) on chromosome B09 using whole genome re-sequencing. <i>Frontiers in Plant Science</i> , 0, 14, . | 3.6 | 3 |
| 7167 | Comparison of tumor-informed and tumor-naïve sequencing assays for ctDNA detection in breast cancer. <i>EMBO Molecular Medicine</i> , 2023, 15, . | 6.9 | 2 |
| 7168 | <i>Gossypium mustelinum</i> genome and an introgression population enrich interspecific genetics and breeding in cotton. <i>Theoretical and Applied Genetics</i> , 2023, 136, . | 3.6 | 1 |
| 7169 | Epigenetic targets in B- and T-cell lymphomas: latest developments. <i>Therapeutic Advances in Hematology</i> , 2023, 14, 204062072311734. | 2.5 | 0 |
| 7170 | Evaluation of Afidopyropen Toxicity at Environmentally Relevant Doses to the Asian Honeybee (<i>Apis</i> Tj ETQq1 1 0.784314 rgBT /Ove Chemistry, 2023, 71, 8834-8845. | 5.2 | 1 |
| 7171 | Unraveling the functional genes present in rhizosphere microbiomes of <i>Solanum lycopersicum</i> . <i>PeerJ</i> , 0, 11, e15432. | 2.0 | 1 |
| 7172 | Molekulare Klassifizierung und Therapien des diffusen großzelligen B-Zell-Lymphoms. <i>Karger Kompass Onkologie</i> , 2023, 10, 59-76. | 0.0 | 0 |
| 7174 | Clonal reproduction of <i>Moniliophthora roreri</i> and the emergence of unique lineages with distinct genomes during range expansion. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, . | 1.8 | 0 |
| 7175 | A local-scale One Health genomic surveillance of <i>Clostridioides difficile</i> demonstrates highly related strains from humans, canines, and the environment. <i>Microbial Genomics</i> , 2023, 9, . | 2.0 | 1 |
| 7176 | An initial molecular resolution of the mantellid frogs of the <i>Guibemantis liber</i> complex reveals three new species from northern Madagascar. <i>Vertebrate Zoology</i> , 0, 73, 397-432. | 2.0 | 0 |
| 7177 | Multiplatform molecular profiling uncovers two subgroups of malignant peripheral nerve sheath tumors with distinct therapeutic vulnerabilities. <i>Nature Communications</i> , 2023, 14, . | 12.8 | 4 |
| 7178 | RDA coupled with deep sequencing detects somatic SVA-retrotranspositions and mosaicism in the human brain. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, . | 3.7 | 1 |
| 7179 | Alkalinity modulates a unique suite of genes to recalibrate growth and pH homeostasis. <i>Frontiers in Plant Science</i> , 0, 14, . | 3.6 | 2 |
| 7180 | Metagenomics Reveals the Microbiome Multifunctionalities of Environmental Importance From Termite Mound Soils. <i>Bioinformatics and Biology Insights</i> , 2023, 17, . | 2.0 | 1 |
| 7181 | Characteristics of Human and Microbiome RNA Profiles in Saliva. <i>RNA Biology</i> , 2023, 20, 398-408. | 3.1 | 3 |
| 7182 | Microbiota present in combined endodontic-periodontal diseases and its risks for endocarditis. <i>Clinical Oral Investigations</i> , 2023, 27, 4757-4771. | 3.0 | 0 |
| 7183 | Long-read sequencing reveals the complex structure of extra dic(21;21) chromosome and its biological effects. <i>Human Genetics</i> , 2023, 142, 1375-1384. | 3.8 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|--|-----|-----------|
| 7184 | The chromosome-scale reference genome and transcriptome analysis of <i>Solanum torvum</i> provides insights into resistance to root-knot nematodes. <i>Frontiers in Plant Science</i> , 0, 14, . | 3.6 | 1 |
| 7185 | Complete chloroplast genomes of three wild perennial <i>Hordeum</i> species from Central Asia: genome structure, mutation hotspot, phylogenetic relationships, and comparative analysis. <i>Frontiers in Plant Science</i> , 0, 14, . | 3.6 | 0 |
| 7186 | Genomic insights into the genetic basis of eagleâ€¢beak jaw, large head, and long tail in the bigâ€¢headed turtle. <i>Ecology and Evolution</i> , 2023, 13, . | 1.9 | 0 |
| 7187 | A <i>GFP</i> splicing reporter in a <i>coilin</i> mutant background reveals links between alternative splicing, siRNAs, and coilin function in <i>Arabidopsis thaliana</i>. <i>G3: Genes, Genomes, Genetics</i> , 0, , . | 1.8 | 0 |
| 7188 | Tackling Tissue Macrophage Heterogeneity by SplitCre Transgenesis. <i>Methods in Molecular Biology</i> , 2024, , 481-503. | 0.9 | 0 |
| 7189 | Phylogenomic analysis provides diagnostic tools for the identification of <i>Anastrepha fraterculus</i> (Diptera: Tephritidae) species complex. <i>Evolutionary Applications</i> , 2023, 16, 1598-1618. | 3.1 | 2 |
| 7190 | Trade-off between local replication and long-distance dissemination during experimental evolution of a satellite RNA. <i>Frontiers in Microbiology</i> , 0, 14, . | 3.5 | 0 |
| 7191 | Identification and functional analysis of novel protein-encoding sequences related to stress-resistance. <i>Frontiers in Microbiology</i> , 0, 14, . | 3.5 | 0 |
| 7192 | Identification of novel genetic risk factors of dilated cardiomyopathy: from canine to human. <i>Genome Medicine</i> , 2023, 15, . | 8.2 | 1 |
| 7193 | A first draft genome of holm oak (<i>Quercus ilex</i> subsp. <i>ballota</i>), the most representative species of the Mediterranean forest and the Spanish agrosylvopastoral ecosystem â€œdehesaâ€¢. <i>Frontiers in Molecular Biosciences</i> , 0, 10, . | 3.5 | 2 |
| 7194 | High-volume hybridoma sequencing on the NeuroMabSeq platform enables efficient generation of recombinant monoclonal antibodies and scFvs for neuroscience research. <i>Scientific Reports</i> , 2023, 13, . | 3.3 | 0 |
| 7195 | An efficient qPCR assay for the quantification of human cells in preclinical animal models by targeting human specific DNA in the intron of BRCA1. <i>Molecular Biology Reports</i> , 0, , . | 2.3 | 0 |
| 7198 | Chloroplast genome assembly of <i>Serjania erecta</i> Raldk: comparative analysis reveals gene number variation and selection in protein-coding plastid genes of Sapindaceae. <i>Frontiers in Plant Science</i> , 0, 14, . | 3.6 | 0 |
| 7199 | Hybridization led to a rewired pluripotency network in the allotetraploid <i>Xenopus laevis</i> . <i>ELife</i> , 0, 12, . | 6.0 | 0 |
| 7200 | Genetic screening for anticancer genes highlights FBLN5 as a synthetic lethal partner of MYC. <i>Cell Communication and Signaling</i> , 2023, 21, . | 6.5 | 0 |
| 7201 | Genome evolution and initial breeding of the Triticeae grass <i>Leymus chinensis</i> dominating the Eurasian Steppe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, . | 7.1 | 4 |
| 7202 | Local and Environmental Reservoirs of <i>Salmonella enterica</i> After Hurricane Florence Flooding. <i>GeoHealth</i> , 2023, 7, . | 4.0 | 0 |
| 7203 | Resequencing of the TMF-1 (TATA Element Modulatory Factor) regulated protein (TRNP1) gene in domestic and wild canids. <i>Canine Medicine and Genetics</i> , 2023, 10, . | 4.0 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 7204 | Metagenomic binning of PacBio HiFi data prior to assembly reveals a complete genome of <i>Cosmopolites sordidus</i> (Germar) (Coleoptera: Curculionidae, Dryophthorinae) the most damaging arthropod pest of bananas and plantains. PeerJ, 0, 11, e16276. | 2.0 | 0 |
| 7205 | Introduction and benchmarking of pyMLST: open-source software for assessing bacterial clonality using core genome MLST. Microbial Genomics, 2023, 9, . | 2.0 | 0 |
| 7207 | De novo assembly and comparative analysis of the mitochondrial genome of <i>Reynoutria japonica</i> . Frontiers in Genetics, 0, 14, . | 2.3 | 0 |
| 7208 | Microsatellite imputation using <i>scp>SNP</scp></i> data for parentage verification in four Italian sheep breeds. Journal of Animal Breeding and Genetics, 0, , . | 2.0 | 0 |
| 7209 | The reference genome and abiotic stress responses of the model perennial grass <i>Brachypodium sylvaticum</i> . G3: Genes, Genomes, Genetics, 2023, 14, . | 1.8 | 0 |
| 7210 | Generation of somatic de novo structural variation as a hallmark of cellular senescence in human lung fibroblasts. Frontiers in Cell and Developmental Biology, 0, 11, . | 3.7 | 0 |
| 7211 | Proteinortho6: pseudo-reciprocal best alignment heuristic for graph-based detection of (co-)orthologs. Frontiers in Bioinformatics, 0, 3, . | 2.1 | 0 |
| 7212 | Chromosome-level genome assembly of hadal snailfish reveals mechanisms of deep-sea adaptation in vertebrates. ELife, 0, 12, . | 6.0 | 1 |
| 7213 | DNA Quadruplex Structure with a Unique Cation Dependency. Angewandte Chemie - International Edition, 2024, 63, . | 13.8 | 0 |
| 7214 | DNA Quadruplex Structure with a Unique Cation Dependency. Angewandte Chemie, 2024, 136, . | 2.0 | 0 |
| 7215 | Genome assembly and population genomic data of a pulmonate snail <i>Ellobium chinense</i> . Scientific Data, 2024, 11, . | 5.3 | 0 |
| 7216 | Genomic insights into the evolution and adaptation of secondary metabolite gene clusters in fungicolous species <i>Cladobotryum mycophilum</i> ATHUM6906. G3: Genes, Genomes, Genetics, 2024, 14, . | 1.8 | 0 |
| 7217 | Hepatic transcriptome analyses of juvenile white bass (<i>Morone chrysops</i>) when fed diets where fish meal is partially or totally replaced by alternative protein sources. Frontiers in Physiology, 0, 14, . | 2.8 | 0 |
| 7218 | Swine influenza A virus isolates containing the pandemic H1N1 origin matrix gene elicit greater disease in the murine model. Microbiology Spectrum, 2024, 12, . | 3.0 | 0 |
| 7219 | Chromosome-level genome assembly and annotation of eel goby (<i>Odontamblyopus rebecca</i>). Scientific Data, 2024, 11, . | 5.3 | 0 |
| 7220 | Comparative genomic analysis of symbiotic and free-living <i>Fluviibacter phosphoraccumulans</i> strains provides insights into the evolutionary origins of obligate <i>Euplotes</i> “bacterial endosymbioses. Applied and Environmental Microbiology, 0, , . | 3.1 | 0 |
| 7221 | Genomic analysis of <i>Nypa fruticans</i> elucidates its intertidal adaptations and early palm evolution. Journal of Integrative Plant Biology, 2024, 66, 824-843. | 8.5 | 0 |
| 7222 | Comprehensive characterization of ERV-K (HML-8) in the chimpanzee genome revealed less genomic activity than humans. Frontiers in Cellular and Infection Microbiology, 0, 14, . | 3.9 | 0 |

| # | ARTICLE | IF | CITATIONS |
|------|---|------|-----------|
| 7223 | Accurate Detection of Fusion Genes in Long-Read Transcriptome Datasets from Multiple Cancer Cell Lines. , 2024, , . | | 0 |
| 7224 | The macroevolutionary singularity of snakes. Science, 2024, 383, 918-923. | 12.6 | 0 |
| 7225 | Patterns of recombination in snakes reveal a tug-of-war between PRDM9 and promoter-like features. Science, 2024, 383, . | 12.6 | 0 |
| 7227 | In Silico Models on Algal Cultivation and Processing. , 2023, , 989-1016. | | 0 |