

# Base-Calling of Automated Sequencer Traces Using *E*

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Citation Report

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | Mutation Scanning for the Clinical Laboratory: Automated Fluorescent Sequencing. , 2004, 92, 81-114.  |     | 1         |
| 3  | Book Reviews : The Combustion of Organic Polymers. C. F. Cullis and M. M. Hirschler. Clarendon Press, Oxford. 1981. 419 pages. \$59.00. Textile Reseach Journal, 1982, 52, 543-543. | 1.1 | 0         |
| 4  | DNA sequence diversity in a 9.7-kb region of the human lipoprotein lipase gene. Nature Genetics, 1998, 19, 233-240.   | 9.4 | 483       |
| 5  | Using BODIPY dye-primer chemistry in large-scale sequencing. IEEE Engineering in Medicine and Biology Magazine, 1998, 17, 88-93.  | 1.1 | 3         |
| 6  | Sequence Assembly withâ€™CAFTOOLS. Genome Research, 1998, 8, 260-267.   | 2.4 | 16        |
| 7  | SeqHelp: A Program to Analyze Molecular Sequences Utilizing Common Computationalâ€™Resources. Genome Research, 1998, 8, 306-312.  | 2.4 | 26        |
| 8  | Base-Calling of Automated Sequencer Traces Using<i>Phred.</i>â€™f. Accuracyâ€™Assessment. Genome Research, 1998, 8, 175-185.  | 2.4 | 5,939     |
| 9  | Estimation of Errors in â€™Rawâ€™DNA Sequences: A Validationâ€™Study. Genome Research, 1998, 8, 251-259.  | 2.4 | 104       |
| 10 | Analysis of the Quality and Utility of Random Shotgun Sequencing at Low Redundancies. Genome Research, 1998, 8, 1074-1084.  | 2.4 | 59        |
| 11 | Snapshot of a Large Dynamic Replicon in a Halophilic Archaeon: Megaplasmid or Minichromosome?. Genome Research, 1998, 8, 1131-1141.   | 2.4 | 113       |
| 12 | Automated Sequence Preprocessing in a Large-Scale Sequencing Environment. Genome Research, 1998, 8, 975-984.  | 2.4 | 26        |
| 13 | Toward a Complete Human Genome Sequence. Genome Research, 1998, 8, 1097-1108.   | 2.4 | 64        |
| 15 | Cloning and assembly strategies in microbial genome projects. Microbiology (United Kingdom), 1999, 145, 2625-2634.  | 0.7 | 56        |
| 16 | Neural network input representations that produce accurate consensus sequences from DNA fragment assemblies. Bioinformatics, 1999, 15, 723-728.                                     | 1.8 | 16        |
| 17 | Identification of Candidate Coding Region Single Nucleotide Polymorphisms in 165 Human Genes Using Assembled Expressed Sequence Tags. Genome Research, 1999, 9, 1087-1092.          | 2.4 | 100       |
| 18 | Using Quality Measures to Facilitate Allele Calling in High-Throughput Genotyping. Genome Research, 1999, 9, 1002-1012.   | 2.4 | 37        |
| 19 | Toward Real-World Sequencing by Microdevice Electrophoresis. Genome Research, 1999, 9, 853-858.   | 2.4 | 61        |
| 20 | Sequence Analysis of a Total of Three Megabases of DNA in Two Regions of Chromosome 8p. DNA Research, 1999, 6, 387-399.   | 1.5 | 0         |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 21 | High throughput direct end sequencing of BAC clones. <i>Nucleic Acids Research</i> , 1999, 27, 1539-1546.  | 6.5  | 67        |
| 22 | A 356-Kb Sequence of the Subtelomeric Part of the MHC Class I Region. <i>DNA Sequence</i> , 1999, 10, 263-299.   | 0.7  | 25        |
| 23 | Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 9739-9744.                                      | 3.3  | 66        |
| 24 | Molecular cloning and characterization of prostase, an androgen-regulated serine protease with prostate-restricted expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 3114-3119. | 3.3  | 202       |
| 25 | High-throughput plasmid DNA purification for 3 cents per sample. <i>Nucleic Acids Research</i> , 1999, 27, 37e-37.   | 6.5  | 43        |
| 26 | CAP3: A DNA Sequence Assembly Program. <i>Genome Research</i> , 1999, 9, 868-877.  | 2.4  | 4,533     |
| 27 | The mahogany protein is a receptor involved in suppression of obesity. <i>Nature</i> , 1999, 398, 148-152.   | 13.7 | 181       |
| 28 | The mouse mahogany locus encodes a transmembrane form of human attractin. <i>Nature</i> , 1999, 398, 152-156.  | 13.7 | 194       |
| 29 | Toward an evolutionary genomics of the avian Mhc. <i>Immunological Reviews</i> , 1999, 167, 119-132.   | 2.8  | 52        |
| 30 | Gene expression informatics â€”it's all in your mine. <i>Nature Genetics</i> , 1999, 21, 51-55.  | 9.4  | 375       |
| 31 | An encyclopedia of mouse genes. <i>Nature Genetics</i> , 1999, 21, 191-194.  | 9.4  | 114       |
| 32 | Reliable identification of large numbers of candidate SNPs from public EST data. <i>Nature Genetics</i> , 1999, 21, 323-325.   | 9.4  | 250       |
| 33 | A general approach to single-nucleotide polymorphism discovery. <i>Nature Genetics</i> , 1999, 23, 452-456.  | 9.4  | 550       |
| 34 | ABI Sequencing Analysis: Manipulation of Sequence Data from the ABI DNA Sequencer. <i>Molecular Biotechnology</i> , 1999, 13, 137-152.   | 1.3  | 2         |
| 35 | High-Throughput DNA Sequencing: A Genomic Data Manufacturing Process. <i>DNA Sequence</i> , 1999, 10, 149-153.   | 0.7  | 11        |
| 36 | Genome Duplications and Other Features in 12 Mb of DNA Sequence from Human Chromosome 16p and 16q. <i>Genomics</i> , 1999, 60, 295-308.  | 1.3  | 140       |
| 37 | The FSHD Region on Human Chromosome 4q35 Contains Potential Coding Regions among Pseudogenes and a High Density of Repeat Elements. <i>Genomics</i> , 1999, 61, 55-65.   | 1.3  | 47        |
| 38 | Characterization of the Human and Mouse Unconventional Myosin XV Genes Responsible for Hereditary Deafness DFNB3 and Shaker 2. <i>Genomics</i> , 1999, 61, 243-258.  | 1.3  | 153       |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 39 | DNA Sequencing: Current Tactics. , 0, , 325-360.   |      | 0         |
| 40 | Individual variation in protein-coding sequences of human genome. <i>Advances in Protein Chemistry</i> , 2000, 54, 409-437.  | 4.4  | 11        |
| 41 | Automated analysis of electrophoretic gels by image digitalization and processing. <i>Imaging Science Journal</i> , 2000, 48, 177-183.   | 0.2  | 3         |
| 42 | Cross-talk filtering in four dye fluorescence-based DNA sequencing. <i>Electrophoresis</i> , 2000, 21, 2983-2989.  | 1.3  | 3         |
| 43 | Quality control in databanks for molecular biology. <i>BioEssays</i> , 2000, 22, 1024-1034.  | 1.2  | 16        |
| 44 | Sub-microliter DNA sequencing for capillary array electrophoresis. <i>Journal of Chromatography A</i> , 2000, 894, 191-201.  | 1.8  | 14        |
| 45 | The mitochondrial genome of the Mediterranean fruit fly, <i>Ceratitis capitata</i> . <i>Insect Molecular Biology</i> , 2000, 9, 139-144.   | 1.0  | 118       |
| 46 | The virulence plasmid pWR100 and the repertoire of proteins secreted by the type III secretion apparatus of <i>Shigella flexneri</i> . <i>Molecular Microbiology</i> , 2000, 38, 760-771.                          | 1.2  | 357       |
| 47 | Mutation of a gene encoding a putative chaperonin causes McKusick-Kaufman syndrome. <i>Nature Genetics</i> , 2000, 25, 79-82.  | 9.4  | 195       |
| 48 | Analysis of expressed sequence tags indicates 35,000 human genes. <i>Nature Genetics</i> , 2000, 25, 232-234.  | 9.4  | 336       |
| 49 | Sampling SNPs. <i>Nature Genetics</i> , 2000, 26, 13-14.   | 9.4  | 56        |
| 50 | Genome-wide analysis of single-nucleotide polymorphisms in human expressed sequences. <i>Nature Genetics</i> , 2000, 26, 233-236.  | 9.4  | 147       |
| 51 | A transcription map of the minimally deleted region from 13q14 in B-cell chronic lymphocytic leukemia as defined by large scale sequencing of the 650â€‰kb critical region. <i>Oncogene</i> , 2000, 19, 5772-5780. | 2.6  | 15        |
| 52 | An SNP map of the human genome generated by reduced representation shotgun sequencing. <i>Nature</i> , 2000, 407, 513-516.   | 13.7 | 658       |
| 53 | An SNP map of human chromosome 22. <i>Nature</i> , 2000, 407, 516-520.   | 13.7 | 145       |
| 54 | Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.   | 13.7 | 234       |
| 55 | The biosynthetic gene cluster for the microtubule-stabilizing agents epothilones A and B from <i>Sorangium cellulosum</i> So ce90. <i>Chemistry and Biology</i> , 2000, 7, 97-109.                                 | 6.2  | 280       |
| 56 | A maximum-likelihood base caller for DNA sequencing. <i>IEEE Transactions on Biomedical Engineering</i> , 2000, 47, 1271-1280.   | 2.5  | 15        |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 57 | Modification of a commercially available DNA sequencer to increase sample throughput. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2000, 19, 101-106.  | 1.1 | 2         |
| 58 | EST analysis online: WWW tools for detection of SNPs and alternative splice forms. <i>Trends in Genetics</i> , 2000, 16, 416-418.  | 2.9 | 16        |
| 59 | Genomics – the new rock and roll?. <i>Trends in Genetics</i> , 2000, 16, 456-461.  | 2.9 | 9         |
| 60 | Preliminary profile of the <i>Cryptosporidium parvum</i> genome: an expressed sequence tag and genome survey sequence analysis. <i>Molecular and Biochemical Parasitology</i> , 2000, 107, 1-32.   | 0.5 | 81        |
| 61 | Complete Genomic Sequence of the <i>Amsacta moorei</i> Entomopoxvirus: Analysis and Comparison with Other Poxviruses. <i>Virology</i> , 2000, 274, 120-139.  | 1.1 | 124       |
| 62 | A 500-kb region on chromosome 16p13.1 contains the pseudoxanthoma elasticum locus: high-resolution mapping and genomic structure. <i>Journal of Molecular Medicine</i> , 2000, 78, 36-46.  | 1.7 | 63        |
| 63 | Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 123-132.   | 1.0 | 15        |
| 64 | An integrated web interface for large-scale characterization of sequence data. <i>Functional and Integrative Genomics</i> , 2000, 1, 70-75.  | 1.4 | 2         |
| 65 | Genes active in developing wheat endosperm. <i>Functional and Integrative Genomics</i> , 2000, 1, 44-55.   | 1.4 | 36        |
| 66 | Magnetic, Microplate-Format Plasmid Isolation Protocol for High-Yield, Sequencing-Grade DNA. <i>BioTechniques</i> , 2000, 29, 786-792.   | 0.8 | 19        |
| 67 | The Mosaic Structure of Human Pericentromeric DNA: A Strategy for Characterizing Complex Regions of the Human Genome. <i>Genome Research</i> , 2000, 10, 839-852.  | 2.4 | 105       |
| 68 | Comparative genomic sequence analysis of the human and mouse cystic fibrosis transmembrane conductance regulator genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 1172-1177.                                | 3.3 | 64        |
| 69 | Genome sequence of <i>Halobacterium</i> species NRC-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 12176-12181.   | 3.3 | 672       |
| 70 | Expression-based Genetic/Physical Maps of Single-Nucleotide Polymorphisms Identified by the Cancer Genome Anatomy Project. <i>Genome Research</i> , 2000, 10, 1259-1265.   | 2.4 | 37        |
| 71 | Sequencing of the <i>Francisella tularensis</i> Strain Schu 4 Genome Reveals the Shikimate and Purine Metabolic Pathways, Targets for the Construction of a Rationally Attenuated Auxotrophic Vaccine. <i>Microbial &amp; Comparative Genomics</i> , 2000, 5, 25-39. | 0.6 | 48        |
| 72 | Decoding the human genome sequence. <i>Human Molecular Genetics</i> , 2000, 9, 2353-2358.  | 1.4 | 20        |
| 73 | Complete Genomic Sequence of 195 Kb of Human DNA Containing the Gene GABRG2. <i>DNA Sequence</i> , 2000, 11, 373-382.  | 0.7 | 1         |
| 74 | A 39-kb Sequence Around a Blackbird Mhc Class II Gene: Ghost of Selection Past and Songbird Genome Architecture. <i>Molecular Biology and Evolution</i> , 2000, 17, 1384-1395.   | 3.5 | 43        |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 75 | Rapid gene discovery in plant parasitic nematodes via Expressed Sequence Tags. <i>Nematology</i> , 2000, 2, 719-731.   | 0.2 | 34        |
| 76 | Filtering technique for fluorescence-based DNA sequencing data. , 0, , .   |     | 1         |
| 77 | A Case for Evolutionary Genomics and the Comprehensive Examination of Sequence Biodiversity. <i>Molecular Biology and Evolution</i> , 2000, 17, 1776-1788.   | 3.5 | 63        |
| 78 | Hd1, a Major Photoperiod Sensitivity Quantitative Trait Locus in Rice, Is Closely Related to the Arabidopsis Flowering Time Gene CONSTANS. <i>Plant Cell</i> , 2000, 12, 2473.   | 3.1 | 32        |
| 79 | Characterization of transposon Tn1549, conferring VanB-type resistance in <i>Enterococcus</i> spp. The GenBank accession number for the 33803Åbp sequence of Tn1549 is AJ192329.. <i>Microbiology (United Tj ETQq0 00rgBT /Overlock 10</i> |     |           |
| 80 | Hd1, a Major Photoperiod Sensitivity Quantitative Trait Locus in Rice, Is Closely Related to the Arabidopsis Flowering Time Gene CONSTANS. <i>Plant Cell</i> , 2000, 12, 2473-2483.  | 3.1 | 1,417     |
| 81 | Sequence Diversity and Large-Scale Typing of SNPs in the Human Apolipoprotein E Gene. <i>Genome Research</i> , 2000, 10, 1532-1545.  | 2.4 | 156       |
| 82 | The Genomic Region Encompassing the Nephropathic Cystinosis Gene (CTNS): Complete Sequencing of a 200-kb Segment and Discovery of a Novel Gene within the Common Cystinosis-Causing Deletion. <i>Genome Research</i> , 2000, 10, 165-173.  | 2.4 | 118       |
| 83 | The Genome of Fowlpox Virus. <i>Journal of Virology</i> , 2000, 74, 3815-3831.   | 1.5 | 290       |
| 84 | A sea urchin genome project: Sequence scan, virtual map, and additional resources. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 9514-9518.   | 3.3 | 107       |
| 85 | Isolation and Expression of PASK, a Serine/Threonine Kinase, During Rat Embryonic Development, with Special Emphasis on the Pancreas. <i>Journal of Histochemistry and Cytochemistry</i> , 2000, 48, 1391-1400.                            | 1.3 | 19        |
| 86 | Genomic Sequence Analysis of Fugu rubripes CFTR and Flanking Genes in a 60 kb Region Conserving Synteny with 800 kb of Human Chromosome 7. <i>Genome Research</i> , 2000, 10, 1194-1203.   | 2.4 | 26        |
| 87 | Octamer-primed sequencing technology: development of primer identification software. <i>Nucleic Acids Research</i> , 2000, 28, 22e-22.   | 6.5 | 1         |
| 88 | Molecular structure and evolution of an alpha satellite/non-alpha satellite junction at 16p11. <i>Human Molecular Genetics</i> , 2000, 9, 113-123.   | 1.4 | 85        |
| 89 | Disruption of two novel genes by a translocation co-segregating with schizophrenia. <i>Human Molecular Genetics</i> , 2000, 9, 1415-1423.  | 1.4 | 1,135     |
| 90 | An optimized protocol for analysis of EST sequences. <i>Nucleic Acids Research</i> , 2000, 28, 3657-3665.  | 6.5 | 121       |
| 91 | MHC Class II Pseudogene and Genomic Signature of a 32-kb Cosmid in the House Finch ( <i>Carpodacus</i> ) Tj ETQq0 0 0rgBT /Overlock 10 Tf  | 2.4 | 68        |
| 92 | Complete genomic sequence of the human ABCA1 gene: Analysis of the human and mouse ATP-binding cassette A promoter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 7987-7992.          | 3.3 | 196       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 93  | Characterization and Repeat Analysis of the Compact Genome of the Freshwater Pufferfish <i>Tetraodon nigroviridis</i> . <i>Genome Research</i> , 2000, 10, 939-949.   | 2.4 | 121       |
| 94  | Rice Transposable Elements: A Survey of 73,000 Sequence-Tagged-Connectors. <i>Genome Research</i> , 2000, 10, 982-990.  | 2.4 | 187       |
| 95  | Gene Survey of the Pathogenic Protozoan <i>Trypanosoma cruzi</i> . <i>Genome Research</i> , 2000, 10, 1103-1107.  | 2.4 | 41        |
| 96  | A BAC-Based Physical Map of the Major Autosomes of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2271-2274.  | 6.0 | 142       |
| 97  | Comparative Sequence Analysis of 634 kb of the Mouse Chromosome 16 Region of Conserved Synteny with the Human Velocardiofacial Syndrome Region on Chromosome 22q11.2. <i>Genomics</i> , 2000, 63, 374-383.  | 1.3 | 45        |
| 98  | Characterization, Chromosomal Localization, and the Complete 30-kb DNA Sequence of the Human Jagged2 (JAG2) Gene. <i>Genomics</i> , 2000, 63, 133-138.  | 1.3 | 18        |
| 99  | Human BAC Ends Quality Assessment and Sequence Analyses. <i>Genomics</i> , 2000, 63, 321-332.   | 1.3 | 45        |
| 100 | Chromosomal Location and Genomic Structure of the Human Translin-Associated Factor X Gene (TRAX; TSNAX) Revealed by Intergenic Splicing to DISC1, a Gene Disrupted by a Translocation Segregating with Schizophrenia. <i>Genomics</i> , 2000, 67, 69-77.  | 1.3 | 106       |
| 101 | Construction of a High-Resolution Physical Map of the Chromosome 10q22-q23 Dilated Cardiomyopathy Locus and Analysis of Candidate Genes. <i>Genomics</i> , 2000, 67, 109-127.   | 1.3 | 34        |
| 102 | Molecular Characterization of the Mouse p47-phox (Ncf1) Gene and Comparative Analysis of the Mouse p47-phox (Ncf1) Gene to the Human NCF1 Gene. <i>Molecular Cell Biology Research Communications: MCBRC: Part B of Biochemical and Biophysical Research Communications</i> , 2000, 3, 224-230. | 1.7 | 4         |
| 103 | DNA Pooling in Mutation Detection with Reference to Sequence Analysis. <i>American Journal of Human Genetics</i> , 2000, 66, 1689-1692.   | 2.6 | 48        |
| 104 | Genomic Exploration of the Hemiascomycetous Yeasts: 2. Data generation and processing. <i>FEBS Letters</i> , 2000, 487, 13-16.  | 1.3 | 29        |
| 105 | Genomic Exploration of the Hemiascomycetous Yeasts: 3. Methods and strategies used for sequence analysis and annotation. <i>FEBS Letters</i> , 2000, 487, 17-30.  | 1.3 | 37        |
| 106 | Genomic Exploration of the Hemiascomycetous Yeasts: 9. <i>Saccharomyces kluyveri</i> . <i>FEBS Letters</i> , 2000, 487, 56-60.  | 1.3 | 18        |
| 107 | Genomic Exploration of the Hemiascomycetous Yeasts: 17. <i>Yarrowia lipolytica</i> . <i>FEBS Letters</i> , 2000, 487, 95-100.   | 1.3 | 88        |
| 108 | An Automated System for Genome Analysis to Support Microbial Whole-genome Shotgun Sequencing. <i>Bioscience, Biotechnology and Biochemistry</i> , 2000, 64, 670-673.  | 0.6 | 38        |
| 109 | Automation for Genomics, Part Two: Sequencers, Microarrays, and Future Trends. <i>Genome Research</i> , 2000, 10, 1288-1303.  | 2.4 | 114       |
| 110 | A data-analysis pipeline for large-scale gene expression analysis. , 2000, , .  |     | 1         |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 111 | The Genome of a Very Virulent Marek's Disease Virus. <i>Journal of Virology</i> , 2000, 74, 7980-7988.  | 1.5  | 238       |
| 112 | Genomic engineering: moving beyond DNA sequence to function. <i>Proceedings of the IEEE</i> , 2000, 88, 1949-1971.  | 16.4 | 41        |
| 113 | A Mutation in PRKAG3 Associated with Excess Glycogen Content in Pig Skeletal Muscle. <i>Science</i> , 2000, 288, 1248-1251.   | 6.0  | 647       |
| 114 | Sequence analysis of genes and genomes. <i>Journal of Biotechnology</i> , 2000, 76, 1-31.   | 1.9  | 46        |
| 115 | Comparative architectural aspects of regions of conserved synteny on human chromosome 11p15.3 and mouse chromosome 7 (including genes WEE1 and LMO1). <i>Cytogenetic and Genome Research</i> , 2001, 93, 277-283.       | 0.6  | 3         |
| 116 | A high-throughput distributed DNA sequence analysis and database system. <i>IBM Systems Journal</i> , 2001, 40, 464-486.  | 3.1  | 4         |
| 117 | Comprehensive analysis of a large genomic sequence at the putative B-cell chronic lymphocytic leukaemia (B-CLL) tumour suppresser gene locus. <i>Mutation Research - Mutation Research Genomics</i> , 2001, 458, 55-70. | 1.2  | 20        |
| 118 | Goodbye to 'one by one' genetics. <i>Genome Biology</i> , 2001, 2, comment2004.1.   | 13.9 | 5         |
| 119 | Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.   | 13.7 | 653       |
| 120 | New DNA Sequencing Methods. <i>Annual Review of Biomedical Engineering</i> , 2001, 3, 195-223.  | 5.7  | 104       |
| 121 | Regions of Microsynteny in <i>Magnaporthe grisea</i> and <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2001, 33, 137-143.   | 0.9  | 33        |
| 122 | Identification of Mesoderm Development (mesd) Candidate Genes by Comparative Mapping and Genome Sequence Analysis. <i>Genomics</i> , 2001, 72, 88-98.   | 1.3  | 17        |
| 123 | Human and Mouse ABCA1 Comparative Sequencing and Transgenesis Studies Revealing Novel Regulatory Sequences. <i>Genomics</i> , 2001, 73, 66-76.  | 1.3  | 31        |
| 124 | Molecular and Functional Analyses of the Human and Mouse Genes Encoding AFG3L1, a Mitochondrial Metalloprotease Homologous to the Human Spastic Paraplegia Protein. <i>Genomics</i> , 2001, 76, 58-65.                  | 1.3  | 43        |
| 125 | Genetic and Physical Delineation of the Region Overlapping the Progressive Motor Neuropathy (pmn) Locus on Mouse Chromosome 13. <i>Genomics</i> , 2001, 75, 9-16.   | 1.3  | 3         |
| 126 | Songbird Genomics: Analysis of 45 kb Upstream of a Polymorphic Mhc Class II Gene in Red-Winged Blackbirds ( <i>Agelaius phoeniceus</i> ). <i>Genomics</i> , 2001, 75, 26-34.  | 1.3  | 46        |
| 127 | Complex High-Resolution Linkage Disequilibrium and Haplotype Patterns of Single-Nucleotide Polymorphisms in 2.5 Mb of Sequence on Human Chromosome 21. <i>Genomics</i> , 2001, 78, 64-72.                               | 1.3  | 18        |
| 128 | Mouse BAC Ends Quality Assessment and Sequence Analyses. <i>Genome Research</i> , 2001, 11, 1736-1745.  | 2.4  | 48        |



| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 129 | Mutations of the Protocadherin Gene PCDH15 Cause Usher Syndrome Type 1F. American Journal of Human Genetics, 2001, 69, 25-34.   | 2.6  | 379       |
| 130 | Genomic sequence and expression analyses of human chromatin assembly factor 1 p150 gene. Gene, 2001, 264, 187-196.  | 1.0  | 11        |
| 131 | Characterization of the genomic structure and tissue-specific promoter of the human nuclear receptor NR5A2 (hB1F) gene. Gene, 2001, 273, 239-249.   | 1.0  | 41        |
| 132 | Mutations in the Gene Encoding Tight Junction Claudin-14 Cause Autosomal Recessive Deafness DFNB29. Cell, 2001, 104, 165-172.   | 13.5 | 430       |
| 133 | The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9889-9894.                     | 3.3  | 282       |
| 134 | Genomic analysis of orthologous mouse and human olfactory receptor loci. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 7390-7395.  | 3.3  | 94        |
| 137 | An XML application for genomic data interoperation. , 2001, , .   |      | 1         |
| 138 | An Apolipoprotein Influencing Triglycerides in Humans and Mice Revealed by Comparative Sequencing. Science, 2001, 294, 169-173.   | 6.0  | 842       |
| 139 | Mechanisms of Evolution in Rickettsia conorii and R. prowazekii. Science, 2001, 293, 2093-2098.   | 6.0  | 408       |
| 141 | Sequence, Regulation, and Evolution of the Maize 22-kD $\hat{\pm}$ Zein Gene Family. Genome Research, 2001, 11, 1817-1825.  | 2.4  | 118       |
| 142 | PCR Template Preparation for Capillary DNA Sequencing. BioTechniques, 2001, 30, 537-542.  | 0.8  | 34        |
| 143 | Amino acid translation program for full-length cDNA sequences with frameshift errors. Physiological Genomics, 2001, 5, 81-87.   | 1.0  | 36        |
| 144 | Software Scripts for Quality Checking of High-Throughput Nucleic Acid Sequencers. BioTechniques, 2001, 30, 1300-1305.   | 0.8  | 17        |
| 145 | Genetic variation in mRNA coding sequences of highly conserved genes. Physiological Genomics, 2001, 5, 113-118.   | 1.0  | 14        |
| 146 | A Fully Automated Process Using a Magnetic Particle Based Kit for Removal of Dye Terminators from Sequencing Reactions. Journal of the Association for Laboratory Automation, 2001, 6, 63-66.   | 2.8  | 1         |
| 147 | Identification of polymorphisms within Disrupted in Schizophrenia 1 and Disrupted in Schizophrenia 2, and an investigation of their association with schizophrenia and bipolar affective disorder. Psychiatric Genetics, 2001, 11, 71-78. | 0.6  | 116       |
| 148 | Single nucleotide polymorphism identification in candidate gene systems of obesity. Pharmacogenomics Journal, 2001, 1, 193-203.   | 0.9  | 13        |
| 149 | Human and Mouse alpha -Synuclein Genes: Comparative Genomic Sequence Analysis and Identification of a Novel Gene Regulatory Element. Genome Research, 2001, 11, 78-86.  | 2.4  | 109       |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 150 | Nucleotide sequence, transcription map, and mutation analysis of the 13q14 chromosomal region deleted in B-cell chronic lymphocytic leukemia. <i>Blood</i> , 2001, 97, 2098-2104.  | 0.6 | 181       |
| 151 | The frequent classes of expressed genes in wheat endosperm tissue as possible sources of genetic markers. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1181.   | 1.5 | 6         |
| 154 | High-Throughput Variation Detection and Genotyping Using Microarrays. <i>Genome Research</i> , 2001, 11, 1913-1925.  | 2.4 | 258       |
| 155 | Single Nucleotide Polymorphism Markers for Genetic Mapping in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2001, 11, 1100-1113.   | 2.4 | 87        |
| 156 | Analysis of a 1-Mb BAC contig overlapping the mouse <i>Nkrp1</i> cluster of genes: cloning of three new <i>Nkrp1</i> members, <i>Nkrp1d</i> , <i>Nkrp1e</i> , and <i>Nkrp1f</i> . <i>Immunogenetics</i> , 2001, 53, 592-598.                     | 1.2 | 44        |
| 157 | High-throughput sequence identification of gene coding variants within alcohol-related QTLs. <i>Mammalian Genome</i> , 2001, 12, 657-663.  | 1.0 | 34        |
| 158 | Lipopolysaccharide biosynthesis in <i>Xanthomonas campestris</i> pv. <i>campestris</i> : a cluster of 15 genes is involved in the biosynthesis of the LPS O-antigen and the LPS core. <i>Molecular Genetics and Genomics</i> , 2001, 266, 79-95. | 1.0 | 67        |
| 159 | Genes expressed during early stages of rice infection with the rice blast fungus <i>Magnaporthe grisea</i> . <i>Molecular Plant Pathology</i> , 2001, 2, 347-354.  | 2.0 | 78        |
| 160 | Molecular characterization of ribosomal DNA polymorphisms discriminating among chromosomal forms of <i>Anopheles gambiae</i> s.s.. <i>Insect Molecular Biology</i> , 2001, 10, 19-23.  | 1.0 | 243       |
| 161 | Preliminary analysis and annotation of the partial genome sequence of <i>Francisella tularensis</i> strain Schu 4. <i>Journal of Applied Microbiology</i> , 2001, 91, 614-620.   | 1.4 | 46        |
| 162 | SNPping in the human genome. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 78-85.  | 2.8 | 56        |
| 163 | A genomics approach towards salt stress tolerance. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 295-311.   | 2.8 | 176       |
| 164 | A semi-automated system for analysis and storage of SNPs. <i>Human Mutation</i> , 2001, 17, 243-254.   | 1.1 | 4         |
| 165 | High-performance genetic analysis using microfabricated capillary array electrophoresis microplates. <i>Electrophoresis</i> , 2001, 22, 3845-3856.   | 1.3 | 90        |
| 166 | The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.   | 6.0 | 12,623    |
| 167 | The White Spot Syndrome Virus DNA Genome Sequence. <i>Virology</i> , 2001, 286, 7-22.  | 1.1 | 513       |
| 168 | Functional genomics and cell wall biosynthesis in loblolly pine. <i>Plant Molecular Biology</i> , 2001, 47, 275-291.   | 2.0 | 110       |
| 169 | Title is missing!. <i>Molecular Breeding</i> , 2001, 7, 151-161.   | 1.0 | 109       |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 170 | Title is missing!. Molecular Breeding, 2001, 8, 255-261.   | 1.0  | 45        |
| 171 | Genomic characterization of human SEC14L1 splice variants within a 17q25 candidate tumor suppressor gene region and identification of an unrelated embedded expressed sequence tag. Mammalian Genome, 2001, 12, 925-929. | 1.0  | 19        |
| 172 | Interleukin-8 haplotype structure from nucleotide sequence variation in commercial populations of U.S. beef cattle. Mammalian Genome, 2001, 12, 219-226.   | 1.0  | 38        |
| 173 | The DNA sequence and comparative analysis of human chromosome 20. Nature, 2001, 414, 865-871.  | 13.7 | 287       |
| 174 | Creation of genome-wide protein expression libraries using random activation of gene expression. Nature Biotechnology, 2001, 19, 440-445.  | 9.4  | 66        |
| 175 | Rapid gene mapping in Caenorhabditis elegans using a high density polymorphism map. Nature Genetics, 2001, 28, 160-164.  | 9.4  | 584       |
| 176 | Genetic mapping with SNP markers in Drosophila. Nature Genetics, 2001, 29, 475-481.  | 9.4  | 150       |
| 177 | NEDD4L on human chromosome 18q21 has multiple forms of transcripts and is a homologue of the mouse Nedd4-2 gene. European Journal of Human Genetics, 2001, 9, 922-930.   | 1.4  | 52        |
| 178 | The genomic organisation of the metabotropic glutamate receptor subtype 5 gene, and its association with schizophrenia. Molecular Psychiatry, 2001, 6, 311-314.  | 4.1  | 87        |
| 179 | Identification of sequence variants and analysis of the role of the glycogen synthase kinase 3 $\beta$ gene and promoter in late onset Alzheimer's disease. Molecular Psychiatry, 2001, 6, 320-324.                      | 4.1  | 61        |
| 180 | A novel member of the WD-repeat gene family, WDR11, maps to the 10q26 region and is disrupted by a chromosome translocation in human glioblastoma cells. Oncogene, 2001, 20, 5378-5392.                                  | 2.6  | 47        |
| 181 | Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.   | 13.7 | 21,074    |
| 182 | The sharing of cDNA microarray data. Nature Reviews Neuroscience, 2001, 2, 438-440.  | 4.9  | 36        |
| 186 | Strategies for the systematic sequencing of complex genomes. Nature Reviews Genetics, 2001, 2, 573-583.  | 7.7  | 158       |
| 188 | Comparison of Global Brain Gene Expression Profiles Between Inbred Long-Sleep and Inbred Short-Sleep Mice by High-Density Gene Array Hybridization. Alcoholism: Clinical and Experimental Research, 2001, 25, 810-818.   | 1.4  | 42        |
| 189 | Paramecium genome survey: a pilot project. Trends in Genetics, 2001, 17, 306-308.  | 2.9  | 65        |
| 190 | Analysis of cellular adhesion by microarray expression profiling. Journal of Immunological Methods, 2001, 250, 15-28.  | 0.6  | 9         |
| 191 | Automated processing of raw DNA sequence data. IEEE Engineering in Medicine and Biology Magazine, 2001, 20, 41-48.   | 1.1  | 2         |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 192 | Convergence of distinct pathways to heart patterning revealed by the small molecule concentramide and the mutation heart-and-soul. <i>Current Biology</i> , 2001, 11, 1481-1491.   | 1.8 | 139       |
| 193 | High-Throughput Plasmid Purification for Capillary Sequencing. <i>Genome Research</i> , 2001, 11, 1269-1274.   | 2.4 | 47        |
| 194 | Surveying <i>Saccharomyces</i> Genomes to Identify Functional Elements by Comparative DNA Sequence Analysis. <i>Genome Research</i> , 2001, 11, 1175-1186.   | 2.4 | 218       |
| 195 | A Comparative Molecular Analysis of Developing Mouse Forelimbs and Hindlimbs Using Serial Analysis of Gene Expression (SAGE). <i>Genome Research</i> , 2001, 11, 1686-1698.  | 2.4 | 67        |
| 196 | Sequence and Analysis of the Tomato JOINTLESS Locus. <i>Plant Physiology</i> , 2001, 126, 1331-1340.   | 2.3 | 36        |
| 197 | Gene discovery and gene function assignment in filamentous fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5110-5115.  | 3.3 | 111       |
| 198 | The Y chromosome in the liverwort <i>Marchantia polymorpha</i> has accumulated unique repeat sequences harboring a male-specific gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9454-9459. | 3.3 | 95        |
| 199 | The interplay of biology and technology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 10051-10054.   | 3.3 | 23        |
| 200 | Complete Genome Sequence of an Aerobic Thermoacidophilic Crenarchaeon, <i>Sulfolobus tokodaii</i> strain 7. <i>DNA Research</i> , 2001, 8, 123-140.  | 1.5 | 286       |
| 201 | Gene expression in the developing mouse retina by EST sequencing and microarray analysis. <i>Nucleic Acids Research</i> , 2001, 29, 4983-4993.   | 6.5 | 68        |
| 202 | Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36 000 bovine ESTs. <i>Nucleic Acids Research</i> , 2001, 29, 108e-108.  | 6.5 | 24        |
| 203 | Genes That Are Uniquely Stress Regulated in Salt Overly Sensitive (sos) Mutants. <i>Plant Physiology</i> , 2001, 126, 363-375.   | 2.3 | 160       |
| 204 | Single pass cDNA sequencing - a powerful tool to analyse gene expression in preparasitic juveniles of the southern root-knot nematode <i>Meloidogyne incognita</i> . <i>Nematology</i> , 2001, 3, 129-139.   | 0.2 | 47        |
| 205 | Identification of SNPs in human gamma aminobutyric acid A receptor $\hat{\gamma}2$ gene. <i>International Journal of Molecular Medicine</i> , 2001, 8, 205.  | 1.8 | 1         |
| 206 | Genomic evidence for a complete sexual cycle in <i>Candida albicans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 3249-3253.  | 3.3 | 182       |
| 207 | From First Base: The Sequence of the Tip of the X Chromosome of <i>Drosophila melanogaster</i> , a Comparison of Two Sequencing Strategies. <i>Genome Research</i> , 2001, 11, 710-730.  | 2.4 | 24        |
| 208 | Sequence Analysis of a 101-Kilobase Plasmid Required for Agar Degradation by a <i>Microscilla</i> Isolate. <i>Applied and Environmental Microbiology</i> , 2001, 67, 5771-5779.  | 1.4 | 52        |
| 209 | Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16. <i>Human Molecular Genetics</i> , 2001, 10, 339-352.   | 1.4 | 81        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 210 | Chapter 20. Bioinformatics in the drug discovery process. Annual Reports in Medicinal Chemistry, 2001, 36, 201-210.  | 0.5 | 1         |
| 211 | The sequence of the <i>Helicoverpa armigera</i> single nucleocapsid nucleopolyhedrovirus genome. Journal of General Virology, 2001, 82, 241-257.   | 1.3 | 200       |
| 212 | Basecalling with LifeTrace. Genome Research, 2001, 11, 875-888.  | 2.4 | 19        |
| 213 | Identification of Nucleotide Sequences for the Specific and Rapid Detection of <i>Yersinia pestis</i> . Applied and Environmental Microbiology, 2001, 67, 3759-3762.   | 1.4 | 51        |
| 214 | A Marker-Dense Physical Map of the <i>Bradyrhizobium japonicum</i> Genome. Genome Research, 2001, 11, 1434-1440.   | 2.4 | 11        |
| 215 | Cloning of a Genetically Unstable Cytochrome P-450 Gene Cluster Involved in Degradation of the Pollutant Ethyl tert -Butyl Ether by <i>Rhodococcus ruber</i> . Journal of Bacteriology, 2001, 183, 6551-6557.    | 1.0 | 91        |
| 216 | Sequence and Analysis of Chromosome I of the Amitochondriate Intracellular Parasite <i>Encephalitozoon cuniculi</i> (Microspora). Genome Research, 2001, 11, 198-207.  | 2.4 | 30        |
| 217 | A Fully Automated Process Using a Magnetic Particle Based Kit for Removal of Dye Terminators from Sequencing Reactions. Journal of the Association for Laboratory Automation, 2001, 6, 63-66.                    | 2.8 | 2         |
| 218 | Genome Sequence of a Baculovirus Pathogenic for <i>Culex nigripalpus</i> . Journal of Virology, 2001, 75, 11157-11165.   | 1.5 | 155       |
| 219 | The Genome of Turkey Herpesvirus. Journal of Virology, 2001, 75, 971-978.  | 1.5 | 119       |
| 220 | The <i>Drosophila</i> U2 snRNP protein U2A' has an essential function that is SNF/U2B'' independent. Nucleic Acids Research, 2001, 29, 3841-3847.  | 6.5 | 16        |
| 221 | GenMapDB: a database of mapped human BAC clones. Nucleic Acids Research, 2001, 29, 144-147.  | 6.5 | 10        |
| 222 | Nucleotide sequence and predicted functions of the entire <i>Sinorhizobium meliloti</i> pSymA megaplasmid. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9883-9888. | 3.3 | 278       |
| 223 | Tamoxifen and Breast Cancer Incidence Among Women With Inherited Mutations in BRCA1 and BRCA2. JAMA - Journal of the American Medical Association, 2001, 286, 2251.  | 3.8 | 673       |
| 224 | African Swine Fever Virus Multigene Family 360 and 530 Genes Are Novel Macrophage Host Range Determinants. Journal of Virology, 2001, 75, 3066-3076.   | 1.5 | 101       |
| 225 | Plant Cell Walls. , 2001, , .  |     | 8         |
| 226 | DNA sequence quality trimming and vector removal. Bioinformatics, 2001, 17, 1093-1104.   | 1.8 | 450       |
| 227 | Comparative Sequence Analysis of Colinear Barley and Rice Bacterial Artificial Chromosomes. Plant Physiology, 2001, 125, 1342-1353.  | 2.3 | 204       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 228 | Automated Finishing with Autofinish. <i>Genome Research</i> , 2001, 11, 614-625.  | 2.4 | 336       |
| 229 | The Universal Primers and the Shotgun DNA. , 2001, 167, 013-031.  |     | 3         |
| 230 | Sequence-Based Detection of Single Nucleotide Polymorphisms. , 2001, 175, 029-035.  |     | 14        |
| 231 | Sequencing Bacterial Artificial Chromosomes. , 2001, 175, 217-234.  |     | 3         |
| 232 | Human-Ovine Comparative Sequencing of a 250-kb Imprinted Domain Encompassing the Callipyge (clpg) Locus and Identification of Six Imprinted Transcripts: DLK1, DAT, GTL2, PEG11, antiPEG11, and MEG8. <i>Genome Research</i> , 2001, 11, 850-862.   | 2.4 | 183       |
| 233 | The Human Ribosomal Protein Genes: Sequencing and Comparative Analysis of 73 Genes. <i>Genome Research</i> , 2002, 12, 379-390.   | 2.4 | 160       |
| 234 | Comparative Genome Sequencing for Discovery of Novel Polymorphisms in <i>Bacillus anthracis</i> . <i>Science</i> , 2002, 296, 2028-2033.  | 6.0 | 413       |
| 235 | Single Nucleotide Polymorphism Mapping Using Genome-Wide Unique Sequences. <i>Genome Research</i> , 2002, 12, 1106-1111.  | 2.4 | 12        |
| 236 | The Genomes of Sheeppox and Goatpox Viruses. <i>Journal of Virology</i> , 2002, 76, 6054-6061.  | 1.5 | 285       |
| 237 | Automated identification of single nucleotide polymorphisms from sequencing data. , 0, ,  |     | 7         |
| 238 | Mating-Type Locus of <i>Cryptococcus neoformans</i> : a Step in the Evolution of Sex Chromosomes. <i>Eukaryotic Cell</i> , 2002, 1, 704-718.  | 3.4 | 258       |
| 239 | RePS: A Sequence Assembler That Masks Exact Repeats Identified from the Shotgun Data. <i>Genome Research</i> , 2002, 12, 824-831.   | 2.4 | 62        |
| 240 | Association of a lysine-232/alanine polymorphism in a bovine gene encoding acyl-CoA:diacylglycerol acyltransferase (DGAT1) with variation at a quantitative trait locus for milk fat content. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9300-9305. | 3.3 | 307       |
| 241 | Identifying novel transcripts and novel genes in the human genome by using novel SAGE tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12257-12262.   | 3.3 | 143       |
| 242 | Acyclic and dideoxy terminator preferences denote divergent sugar recognition by archaeon and Taq DNA polymerases. <i>Nucleic Acids Research</i> , 2002, 30, 605-613.   | 6.5 | 79        |
| 243 | High-throughput genotyping of single nucleotide polymorphisms using new biplex invader technology. <i>Nucleic Acids Research</i> , 2002, 30, 53e-53.  | 6.5 | 73        |
| 244 | Exploring root symbiotic programs in the model legume <i>Medicago truncatula</i> using EST analysis. <i>Nucleic Acids Research</i> , 2002, 30, 5579-5592.   | 6.5 | 193       |
| 245 | ZTR: a new format for DNA sequence trace data. <i>Bioinformatics</i> , 2002, 18, 3-10.  | 1.8 | 26        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 246 | Separation of nearly identical repeats in shotgun assemblies using defined nucleotide positions, DNPs. <i>Bioinformatics</i> , 2002, 18, 379-388.  | 1.8 | 24        |
| 247 | Ordered catenation of sequence-tagged sites and multiplexed SNP genotyping by sequencing. <i>Nucleic Acids Research</i> , 2002, 30, 11e-11.  | 6.5 | 6         |
| 248 | Methylation-Spanning Linker Libraries Link Gene-Rich Regions and Identify Epigenetic Boundaries in <i>Zea mays</i> . <i>Genome Research</i> , 2002, 12, 1345-1349.   | 2.4 | 40        |
| 249 | A Complete Sequence of the <i>T. tengcongensis</i> Genome. <i>Genome Research</i> , 2002, 12, 689-700.   | 2.4 | 209       |
| 250 | Physical Maps for Genome Analysis of Serotype A and D Strains of the Fungal Pathogen <i>Cryptococcus neoformans</i> . <i>Genome Research</i> , 2002, 12, 1445-1453.  | 2.4 | 38        |
| 251 | Expressed Sequence Tag-Based Gene Expression Analysis under Aluminum Stress in Rye,. <i>Plant Physiology</i> , 2002, 130, 1706-1716.   | 2.3 | 105       |
| 252 | Genomic database resources for <i>Dictyostelium discoideum</i> . <i>Nucleic Acids Research</i> , 2002, 30, 84-86.  | 6.5 | 13        |
| 253 | The complete genome of hyperthermophile <i>Methanopyrus kandleri</i> AV19 and monophyly of archaeal methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4644-4649. | 3.3 | 283       |
| 254 | The <i>Drosophila</i> Gene Collection: Identification of Putative Full-Length cDNAs for 70% of <i>D. melanogaster</i> Genes. <i>Genome Research</i> , 2002, 12, 1294-1300.   | 2.4 | 180       |
| 255 | Mutation of a transcription factor, <i>TFCP2L3</i> , causes progressive autosomal dominant hearing loss, <i>DFNA28</i> . <i>Human Molecular Genetics</i> , 2002, 11, 2877-2885.  | 1.4 | 91        |
| 256 | Systematic sequencing of cDNA clones using the transposon <i>Tn5</i> . <i>Nucleic Acids Research</i> , 2002, 30, 2469-2477.  | 6.5 | 55        |
| 257 | Merging classical and modern genetic tools in the identification of disease genes. <i>Upsala Journal of Medical Sciences</i> , 2002, 107, 1-8.   | 0.4 | 0         |
| 258 | Computational SNP Discovery in DNA Sequence Data. , 2003, 212, 085-110.  |     | 5         |
| 259 | An efficient strategy for large-scale high-throughput transposon-mediated sequencing of cDNA clones. <i>Nucleic Acids Research</i> , 2002, 30, 2460-2468.  | 6.5 | 29        |
| 260 | Comparison of RNA Expression Profiles Based on Maize Expressed Sequence Tag Frequency Analysis and Micro-Array Hybridization. <i>Plant Physiology</i> , 2002, 128, 896-910.  | 2.3 | 96        |
| 261 | Identification of mixups among DNA sequencing plates. <i>Bioinformatics</i> , 2002, 18, 1418-1426.   | 1.8 | 6         |
| 262 | Site-Specific Recombination with the Chromosomal <i>tRNA Leu</i> Gene by the Large Conjugative <i>Haemophilus</i> Resistance Plasmid. <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 1602-1603.                      | 1.4 | 38        |
| 263 | RIDOM: Ribosomal Differentiation of Medical Micro-organisms Database. <i>Nucleic Acids Research</i> , 2002, 30, 416-417.   | 6.5 | 103       |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 264 | The human (PEDB) and mouse (mPEDB) Prostate Expression Databases. <i>Nucleic Acids Research</i> , 2002, 30, 218-220.   | 6.5 | 27        |
| 265 | Generation and Comparative Analysis of 3.3 Mb of Mouse Genomic Sequence Orthologous to the Region of Human Chromosome 7q11.23 Implicated in Williams Syndrome. <i>Genome Research</i> , 2002, 12, 3-15.  | 2.4 | 72        |
| 266 | High throughput DNA sequencing with a microfabricated 96-lane capillary array electrophoresis bioprocessor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 574-579.  | 3.3 | 251       |
| 267 | Quantitative Trait Loci Affecting Initial Sensitivity and Acute Functional Tolerance to Ethanol-Induced Ataxia and Brain cAMP Signaling in BXD Recombinant Inbred Mice. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2002, 302, 1238-1245.                                       | 1.3 | 56        |
| 268 | Sequence analysis of mouse vomeronasal receptor gene clusters reveals common promoter motifs and a history of recent expansion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 291-296.  | 3.3 | 67        |
| 269 | A 384-Well, Fully-Automatable, Superparamagnetic-Particle Based Dye Terminator Removal Kit. <i>Journal of the Association for Laboratory Automation</i> , 2002, 7, 50-57.  | 2.8 | 0         |
| 270 | 16S rDNA sequence analysis of environmental <i>Bdellovibrio</i> -and-like organisms (BALO) reveals extensive diversity. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 2089-2094.  | 0.8 | 48        |
| 271 | Progress of <i>Aspergillus oryzae</i> Genomics. <i>Advances in Applied Microbiology</i> , 2002, 51, 81-107e.   | 1.3 | 81        |
| 272 | Random Sequencing of <i>Paramecium</i> Somatic DNA. <i>Eukaryotic Cell</i> , 2002, 1, 341-352.   | 3.4 | 39        |
| 273 | Multilocus Sequence Typing for Characterization of Clinical and Environmental <i>Salmonella</i> Strains. <i>Journal of Clinical Microbiology</i> , 2002, 40, 1626-1635.  | 1.8 | 160       |
| 274 | Genome Dynamics and Evolution of the <i>Mla</i> (Powdery Mildew) Resistance Locus in Barley[W]. <i>Plant Cell</i> , 2002, 14, 1903-1917.   | 3.1 | 229       |
| 275 | Automated High Throughput Purification of BigDye <sup>®</sup> , <sup>®</sup> Terminator Fluorescent DNA Sequencing Reactions Using WizardA <sup>®</sup> MagneSil <sup>®</sup> , <sup>®</sup> Paramagnetic Particles. <i>Journal of the Association for Laboratory Automation</i> , 2002, 7, 75-79. | 2.8 | 2         |
| 276 | Elucidation of the Metabolic Fate of Glucose in the Filamentous Fungus <i>Trichoderma reesei</i> Using Expressed Sequence Tag (EST) Analysis and cDNA Microarrays. <i>Journal of Biological Chemistry</i> , 2002, 277, 13983-13988.  | 1.6 | 128       |
| 277 | Bacteriophage HP2 of <i>Haemophilus influenzae</i> . <i>Journal of Bacteriology</i> , 2002, 184, 6893-6905.  | 1.0 | 32        |
| 278 | Analysis of the Complete Genome Sequence of the Hz-1 Virus Suggests that It Is Related to Members of the Baculoviridae. <i>Journal of Virology</i> , 2002, 76, 9024-9034.  | 1.5 | 74        |
| 279 | Contiguous Genomic DNA Sequence Comprising the 19-kD Zein Gene Family from Maize. <i>Plant Physiology</i> , 2002, 130, 1626-1635.  | 2.3 | 61        |
| 280 | Positional Candidate Cloning of a QTL in Dairy Cattle: Identification of a Missense Mutation in the Bovine DGAT1 Gene with Major Effect on Milk Yield and Composition. <i>Genome Research</i> , 2002, 12, 222-231.   | 2.4 | 803       |
| 281 | Temperature-Regulated Transcription in the Pathogenic Fungus <i>Cryptococcus neoformans</i> . <i>Genome Research</i> , 2002, 12, 1386-1400.  | 2.4 | 84        |



| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 282 | Automated High Throughput Purification of BigDye <sup>®</sup> , <sup>®</sup> Terminator Fluorescent DNA Sequencing Reactions Using Wizard <sup>®</sup> , <sup>®</sup> MagneSil <sup>®</sup> , <sup>®</sup> Paramagnetic Particles. <i>Journal of the Association for Laboratory Automation</i> , 2002, 7, 75-79. | 2.8  | 0         |
| 283 | Sequence variation and phylogenetic history of the mouse <i>Ahr</i> gene. <i>Pharmacogenetics and Genomics</i> , 2002, 12, 151-163.  | 5.7  | 54        |
| 284 | <i>Yli</i> , a Non <sup>®</sup> LTR Retrotransposon L1 Family in the Dimorphic Yeast <i>Yarrowia lipolytica</i> . <i>Molecular Biology and Evolution</i> , 2002, 19, 664-677.  | 3.5  | 33        |
| 285 | Sequence Assembly and Finishing Methods. <i>Methods of Biochemical Analysis</i> , 2002, 43, 303-322.   | 0.2  | 48        |
| 286 | Heterozygote Detection Using Automated Fluorescence <sup>®</sup> -Based Sequencing. <i>Current Protocols in Human Genetics</i> , 2002, 35, 7.9.1.  | 3.5  | 0         |
| 287 | Identification of genomic organisation, sequence variants and analysis of the role of the human <i>dishevelled 1</i> gene in late onset Alzheimer's disease. <i>Molecular Psychiatry</i> , 2002, 7, 104-109.   | 4.1  | 8         |
| 288 | GAI Homologues in the Hawaiian Silversword Alliance (Asteraceae-Madiinae): Molecular Evolution of Growth Regulators in a Rapidly Diversifying Plant Lineage. <i>Molecular Biology and Evolution</i> , 2002, 19, 1563-1574.   | 3.5  | 31        |
| 289 | Identification of the Single Base Change Causing the Callipyge Muscle Hypertrophy Phenotype, the Only Known Example of Polar Overdominance in Mammals. <i>Genome Research</i> , 2002, 12, 1496-1506.   | 2.4  | 195       |
| 290 | Conservation of the T-Cell Receptor $\alpha/\beta$ Linkage in the Teleost Fish <i>Tetraodon nigroviridis</i> . <i>Genomics</i> , 2002, 79, 241-248.  | 1.3  | 78        |
| 291 | Identification of a Psoriasis Susceptibility Candidate Gene by Linkage Disequilibrium Mapping with a Localized Single Nucleotide Polymorphism Map. <i>Genomics</i> , 2002, 79, 305-314.  | 1.3  | 99        |
| 292 | Isothermal Strand-Displacement Amplification Applications for High-Throughput Genomics. <i>Genomics</i> , 2002, 80, 691-698.   | 1.3  | 89        |
| 293 | Empirical Statistical Model To Estimate the Accuracy of Peptide Identifications Made by MS/MS and Database Search. <i>Analytical Chemistry</i> , 2002, 74, 5383-5392.  | 3.2  | 4,503     |
| 294 | Functional and Comparative Bioinformatic Analysis of Expressed Genes from Wheat Spikes Infected with <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 445-455.  | 1.4  | 93        |
| 295 | A <i>Drosophila</i> full-length cDNA resource. <i>Genome Biology</i> , 2002, 3, research0080.1.  | 13.9 | 163       |
| 297 | High-Density Microarray of Small-Subunit Ribosomal DNA Probes. <i>Applied and Environmental Microbiology</i> , 2002, 68, 2535-2541.  | 1.4  | 277       |
| 298 | A Draft Sequence of the Rice Genome ( <i>Oryza sativa</i> L. ssp. <i>indica</i> ). <i>Science</i> , 2002, 296, 79-92.  | 6.0  | 3,146     |
| 299 | A probabilistic approach for long read-length DNA sequence analysis. , 0, , .  |      | 4         |
| 300 | Expressed sequence tags for the chicken genome from a normalized 10-day-old white leghorn whole-embryo cDNA library. 3. DNA sequence analysis of genetic variation in commercial chicken populations. <i>Genome</i> , 2002, 45, 261-267.   | 0.9  | 19        |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 302 | Analysis of 106 kb of contiguous DNA sequence from the D genome of wheat reveals high gene density and a complex arrangement of genes related to disease resistance. <i>Genome</i> , 2002, 45, 963-972. | 0.9 | 48        |
| 303 | Putative cytochrome P450 genes in rice genome ( <i>Oryza sativa</i> L. ssp. indica) and their EST evidence. <i>Science in China Series C: Life Sciences</i> , 2002, 45, 512.                            | 1.3 | 11        |
| 304 | A Cascade of Complex Subtelomeric Duplications during the Evolution of the Hominoid and Old World Monkey Genomes. <i>American Journal of Human Genetics</i> , 2002, 70, 269-278.                        | 2.6 | 27        |
| 305 | The use of direct cDNA selection to rapidly and effectively identify genes in the fungus <i>Aspergillus fumigatus</i> . <i>Fungal Genetics and Biology</i> , 2002, 36, 59-70.                           | 0.9 | 14        |
| 306 | Probing carotenoid biosynthesis in developing seed coats of <i>Bixa orellana</i> (Bixaceae) through expressed sequence tag analysis. <i>Plant Science</i> , 2002, 163, 141-145.                         | 1.7 | 32        |
| 307 | Genomic organization, transcript variants and comparative analysis of the human nucleoporin 155 (NUP155) gene. <i>Gene</i> , 2002, 288, 9-18.   | 1.0 | 9         |
| 308 | Identification of candidate tumor suppressor genes from critical deletions of long arm of chromosome 6 in hematopoietic neoplasm. <i>International Congress Series</i> , 2002, 1246, 251-260.           | 0.2 | 0         |
| 309 | Polymorphisms of chromogranin B gene associated with schizophrenia in Chinese Han population. <i>Neuroscience Letters</i> , 2002, 323, 229-233.   | 1.0 | 23        |
| 310 | Target-Selected Inactivation of the Zebrafish rag1 Gene. <i>Science</i> , 2002, 297, 99-102.  | 6.0 | 397       |
| 311 | A Sequence-Based Map of the Nine Genes of the Human Interleukin-1 Cluster. <i>Genomics</i> , 2002, 79, 718-725.   | 1.3 | 185       |
| 312 | Automatic Assembly and Editing of Genomic Data. , 2002, , 51-65.  |     | 2         |
| 313 | Novel genes are enriched in normalized cDNA libraries from drought-stressed seedlings of rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Ove  | 0.9 | 75        |
| 314 | Synthetic Peptides Identified from Phage-displayed Combinatorial Libraries as Immunodiagnostic Assay Surrogate Quality-Control Targets. <i>Clinical Chemistry</i> , 2002, 48, 410-420.                  | 1.5 | 38        |
| 316 | SNPCEQer: Detecting SNPs in Sequences Generated by the Beckman CEQ<sup>TM</sup>2000 DNA Analysis System. <i>BioTechniques</i> , 2002, 33, 814-822.  | 0.8 | 2         |
| 317 | Loader Lite: A New Software Tool for the ABI PRISM<sup>®</sup> 3700 DNA Sequencer. <i>BioTechniques</i> , 2002, 32, 1366-1371.  | 0.8 | 0         |
| 318 | Evaluation of single-nucleotide polymorphisms in CAPN1 for association with meat tenderness in cattle <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2002, 80, 3077-3085.                          | 0.2 | 203       |
| 319 | High-Speed Plasmid Isolation Using 96-Well, Size-Exclusion Filter Plates. <i>BioTechniques</i> , 2002, 32, 626-631.   | 0.8 | 5         |
| 321 | Cross-Hybridization of Closely Related Genes on High-Density Macroarrays. <i>BioTechniques</i> , 2002, 32, 620-625.   | 0.8 | 32        |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 322 | Resuspension of DNA Sequencing Reaction Products in Agarose Increases Sequence Quality on an Automated Sequencer. <i>BioTechniques</i> , 2002, 33, 532-538.                           | 0.8 | 7         |
| 323 | A review on SNP and other types of molecular markers and their use in animal genetics. <i>Genetics Selection Evolution</i> , 2002, 34, 275-305.                                       | 1.2 | 676       |
| 324 | A Comprehensive Collection of Chicken cDNAs. <i>Current Biology</i> , 2002, 12, 1965-1969.  | 1.8 | 305       |
| 325 | A family of novel DNA sequencing instruments based on single-photon detection. <i>Electrophoresis</i> , 2002, 23, 2804-2817.  | 1.3 | 35        |
| 326 | DNA Technologies: Sequencing Technology. , 0, , 165-208.  |     | 0         |
| 327 | Lack of association between HoxA1 and HoxB1 gene variants and autism in 110 multiplex families. <i>American Journal of Medical Genetics Part A</i> , 2002, 114, 24-30.                | 2.4 | 39        |
| 328 | Identification of novel protein-coding genes from human fetal hippocampus ESTs database. <i>Neuroscience Research Communications</i> , 2002, 31, 93-99.                               | 0.2 | 1         |
| 329 | Microarrays and genetic epidemiology: A multipurpose tool for a multifaceted field. <i>Genetic Epidemiology</i> , 2002, 23, 4-20.   | 0.6 | 19        |
| 330 | Genes involved in the anaerobic degradation of ethylbenzene in a denitrifying bacterium, strain EbN1. <i>Archives of Microbiology</i> , 2002, 178, 506-516.                           | 1.0 | 118       |
| 331 | Selection and use of SNP markers for animal identification and paternity analysis in U.S. beef cattle. <i>Mammalian Genome</i> , 2002, 13, 272-281.                                   | 1.0 | 199       |
| 332 | Genetic mapping of an insertional hydrocephalus-inducing mutation allelic to hy3. <i>Mammalian Genome</i> , 2002, 13, 625-632.  | 1.0 | 25        |
| 333 | Association of bovine neonatal Fc receptor a-chain gene (FCGRT) haplotypes with serum IgG concentration in newborn calves. <i>Mammalian Genome</i> , 2002, 13, 704-710.               | 1.0 | 42        |
| 334 | A framework for integrating the songbird brain. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2002, 188, 961-980.           | 0.7 | 31        |
| 335 | Gene expression profiles in young adult <i>Ciona intestinalis</i> . <i>Development Genes and Evolution</i> , 2002, 212, 173-185.  | 0.4 | 99        |
| 336 | Sequence polymorphism at the human apolipoprotein AII gene (APOA2): unexpected deficit of variation in an African-American sample. <i>Human Genetics</i> , 2002, 111, 75-87.          | 1.8 | 28        |
| 337 | Transposable elements, genes and recombination in a 215-kb contig from wheat chromosome 5Am. <i>Functional and Integrative Genomics</i> , 2002, 2, 70-80.                             | 1.4 | 153       |
| 338 | W44C mutation in the connexin 26 gene associated with dominant non-syndromic deafness. <i>Clinical Genetics</i> , 2002, 59, 269-273.  | 1.0 | 19        |
| 339 | A novel frameshift founder mutation in the cytochrome P450 1B1 (CYP1B1) gene is associated with primary congenital glaucoma in Morocco. <i>Clinical Genetics</i> , 2002, 62, 334-339. | 1.0 | 56        |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 340 | Definitive high resolution typing of HLA-E allelic polymorphisms: Identifying potential errors in existing allele data. <i>Tissue Antigens</i> , 2002, 60, 206-212.   | 1.0  | 78        |
| 341 | Genetics of the immune response: identifying immune variation within the MHC and throughout the genome. <i>Immunological Reviews</i> , 2002, 190, 69-85.  | 2.8  | 49        |
| 342 | Organization of six functional mouse alcohol dehydrogenase genes on two overlapping bacterial artificial chromosomes. <i>FEBS Journal</i> , 2002, 269, 224-232.   | 0.2  | 31        |
| 343 | Molecular barcodes for soil nematode identification. <i>Molecular Ecology</i> , 2002, 11, 839-850.  | 2.0  | 650       |
| 344 | Genome sequence of <i>Streptococcus agalactiae</i> , a pathogen causing invasive neonatal disease. <i>Molecular Microbiology</i> , 2002, 45, 1499-1513.   | 1.2  | 439       |
| 345 | Development of a high-volume aerosol collection system for the identification of air-borne micro-organisms. <i>Letters in Applied Microbiology</i> , 2002, 34, 162-167.   | 1.0  | 99        |
| 346 | A Novel Connexin 26 Mutation in a Patient Diagnosed with Keratitisâ€“Ichthyosisâ€“Deafness Syndrome. <i>Journal of Investigative Dermatology</i> , 2002, 118, 724-727.  | 0.3  | 146       |
| 347 | Single-nucleotide polymorphism characterization in species with limited available sequence information: high nucleotide diversity revealed in the avian genome. <i>Molecular Ecology</i> , 2002, 11, 603-612.             | 2.0  | 299       |
| 348 | Single nucleotide polymorphism (SNP) discovery in porcine expressed genes. <i>Animal Genetics</i> , 2002, 33, 186-195.  | 0.6  | 62        |
| 349 | An integrated comparative map of the porcine X chromosome. <i>Animal Genetics</i> , 2002, 33, 178-185.  | 0.6  | 26        |
| 350 | New syndrome of hypotrichosis, striate palmoplantar keratoderma, acro-osteolysis and periodontitis not due to mutations in cathepsin C. <i>British Journal of Dermatology</i> , 2002, 147, 575-581.                       | 1.4  | 25        |
| 351 | HID and KID syndromes are associated with the same connexin 26 mutation. <i>British Journal of Dermatology</i> , 2002, 146, 938-942.  | 1.4  | 130       |
| 352 | Construction of a <i>unigene</i> <sup>TM</sup> cDNA clone set by oligonucleotide fingerprinting allows access to 25â€“f000 potential sugar beet genes. <i>Plant Journal</i> , 2002, 32, 845-857.                          | 2.8  | 41        |
| 353 | The <i>Brugia malayi</i> genome project: expressed sequence tags and gene discovery. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2002, 96, 7-17.  | 0.7  | 67        |
| 354 | F-MuLV acceleration of myelomonocytic tumorigenesis in SV40 large T antigen transgenic mice is accompanied by retroviral insertion at <i>Fli1</i> and a novel locus, <i>Fim4</i> . <i>Leukemia</i> , 2002, 16, 1827-1834. | 3.3  | 5         |
| 355 | Sequence of <i>Plasmodium falciparum</i> chromosome 12. <i>Nature</i> , 2002, 419, 534-537.   | 13.7 | 58        |
| 356 | Sequence and analysis of rice chromosome 4. <i>Nature</i> , 2002, 420, 316-320.   | 13.7 | 471       |
| 357 | The mosaic structure of variation in the laboratory mouse genome. <i>Nature</i> , 2002, 420, 574-578.   | 13.7 | 448       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 358 | A genome sequence survey of the mollicute corn stunt spiroplasma <i>Spiroplasma kunkelii</i> . <i>FEMS Microbiology Letters</i> , 2002, 210, 7-17.  | 0.7 | 40        |
| 359 | Gene Coding Variant in Cas1 Between the C57BL/6J and DBA/2J Inbred Mouse Strains: Linkage to a QTL for Ethanol-Induced Locomotor Activation. <i>Alcoholism: Clinical and Experimental Research</i> , 2002, 26, 1-7.   | 1.4 | 17        |
| 360 | Fine Mapping of Polymorphic Alcohol-Related Quantitative Trait Loci Candidate Genes Using Interval-Specific Congenic Recombinant Mice. <i>Alcoholism: Clinical and Experimental Research</i> , 2002, 26, 1603-1608.   | 1.4 | 10        |
| 361 | The Genome of Camelpox Virus. <i>Virology</i> , 2002, 295, 1-9.   | 1.1 | 84        |
| 362 | A high-density cytogenetic map of the <i>Aegilops tauschii</i> genome incorporating retrotransposons and defense-related genes: insights into cereal chromosome structure and function. <i>Plant Molecular Biology</i> , 2002, 48, 767-789.                   | 2.0 | 95        |
| 363 | Insertion-deletion polymorphisms in 3' regions of maize genes occur frequently and can be used as highly informative genetic markers. <i>Plant Molecular Biology</i> , 2002, 48, 539-547.   | 2.0 | 140       |
| 364 | An F-box gene linked to the self-incompatibility (S) locus of <i>Antirrhinum</i> is expressed specifically in pollen and tapetum. <i>Plant Molecular Biology</i> , 2002, 50, 29-41.   | 2.0 | 318       |
| 365 | Genomic structure of metabotropic glutamate receptor 7 and comparison of genomic structures of extracellular domains of mGluR family. <i>Science Bulletin</i> , 2002, 47, 1330.   | 1.7 | 1         |
| 366 | EST Sequencing, Annotation and Macroarray Transcriptome Analysis Identify Preferentially Root-Expressed Genes in Sugar Beet. <i>Plant Biology</i> , 2002, 4, 700-710.   | 1.8 | 23        |
| 367 | Temporal progression of gene expression responses to salt shock in maize roots. <i>Plant Molecular Biology</i> , 2003, 52, 873-891.   | 2.0 | 102       |
| 368 | Investigation of DUSP8 and CALCA in alcohol dependence. <i>Addiction Biology</i> , 2003, 8, 305-312.  | 1.4 | 5         |
| 369 | Characterization of Microbial Communities from Coastal Waters using Microarrays. <i>Environmental Monitoring and Assessment</i> , 2003, 81, 327-336.  | 1.3 | 25        |
| 370 | IntelliGEN: A Distributed Workflow System for Discovering Protein-Protein Interactions. <i>Distributed and Parallel Databases</i> , 2003, 13, 43-72.  | 1.0 | 67        |
| 371 | The complete genome sequence of the avian pathogen <i>Mycoplasma gallisepticum</i> strain Rlow. <i>Microbiology (United Kingdom)</i> , 2003, 149, 2307-2316.  | 0.7 | 204       |
| 372 | <i>Lactarius sanguifluus</i> versus <i>Lactarius vinosus</i> – Molecular and morphological analyses. <i>Mycological Progress</i> , 2003, 2, 227-234.  | 0.5 | 31        |
| 373 | Case-control association studies of the UBAP1 gene and nasopharyngeal carcinoma in southern Chinese. <i>Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association</i> , Beijing Institute for Cancer Research, 2003, 15, 157-160. | 0.7 | 0         |
| 374 | ESTs as a source for sequence polymorphism discovery in sugarcane: example of the Adh genes. <i>Theoretical and Applied Genetics</i> , 2003, 106, 190-197.  | 1.8 | 63        |
| 375 | High resolution genetic mapping and candidate gene identification at the xa5 locus for bacterial blight resistance in rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2003, 107, 62-73.   | 1.8 | 72        |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 376 | Construction and utility of 10-kb libraries for efficient clone-gap closure for rice genome sequencing. <i>Theoretical and Applied Genetics</i> , 2003, 107, 652-660.   | 1.8 | 18        |
| 377 | Deep Origin of Plastid/Parasite ATP/ADP Translocases. <i>Journal of Molecular Evolution</i> , 2003, 56, 137-150.  | 0.8 | 55        |
| 378 | EST-based gene discovery in pig: virtual expression patterns and comparative mapping to human. <i>Mammalian Genome</i> , 2003, 14, 565-579.   | 1.0 | 54        |
| 379 | Prion gene sequence variation within diverse groups of U.S. sheep, beef cattle, and deer. <i>Mammalian Genome</i> , 2003, 14, 765-777.  | 1.0 | 104       |
| 380 | Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito <i>Anopheles gambiae</i> . <i>Molecular Genetics and Genomics</i> , 2003, 268, 720-728.            | 1.0 | 26        |
| 381 | Gene content and organization of an 85-kb DNA segment from the genome of the phytopathogenic mollicute <i>Spiroplasma kunkelii</i> . <i>Molecular Genetics and Genomics</i> , 2003, 269, 592-602.   | 1.0 | 18        |
| 382 | Snipping polymorphisms from large EST collections in barley ( <i>Hordeum vulgare</i> L.). <i>Molecular Genetics and Genomics</i> , 2003, 270, 24-33.  | 1.0 | 116       |
| 383 | Analysis of the transcriptional response to Rice Yellow Mottle Virus infection in <i>Oryza sativa indica</i> and japonica cultivars. <i>Molecular Genetics and Genomics</i> , 2003, 270, 253-262.   | 1.0 | 17        |
| 384 | Evolution and microsynteny of the apyrase gene family in three legume genomes. <i>Molecular Genetics and Genomics</i> , 2003, 270, 347-361.   | 1.0 | 50        |
| 385 | The chloroplast genome of the 'basal' angiosperm <i>Calycanthus fertilis</i> ? structural and phylogenetic analyses. <i>Plant Systematics and Evolution</i> , 2003, 242, 119-135.   | 0.3 | 66        |
| 386 | Nontranslated polyadenylated RNAs from <i>Entamoeba histolytica</i> . <i>Trends in Parasitology</i> , 2003, 19, 286-289.  | 1.5 | 8         |
| 387 | 400,000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , 2003, 19, 283-286.  | 1.5 | 61        |
| 388 | Computational biology: biological insight from 1s and 0s. <i>Biosilico</i> , 2003, 1, 27-35.  | 0.5 | 0         |
| 389 | Reading the fine print of the human genome. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2003, 22, 105-108.   | 1.1 | 0         |
| 390 | heart of glass Regulates the Concentric Growth of the Heart in Zebrafish. <i>Current Biology</i> , 2003, 13, 2138-2147.   | 1.8 | 224       |
| 391 | The complete sequence of marine bacteriophage VpV262 infecting <i>vibrio parahaemolyticus</i> indicates that an ancestral component of a T7 viral supergroup is widespread in the marine environment. <i>Virology</i> , 2003, 310, 359-371. | 1.1 | 68        |
| 392 | trap: Tandem Repeat Assembly Program produces improved shotgun assemblies of repetitive sequences. <i>Computer Methods and Programs in Biomedicine</i> , 2003, 70, 47-59.   | 2.6 | 11        |
| 393 | Single-cell immunohistochemical mutation load assay (SCIMLA) using human paraffin-embedded tissues. <i>Environmental and Molecular Mutagenesis</i> , 2003, 42, 206-215.   | 0.9 | 1         |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 394 | Variants of $\mu$ -opioid receptor gene and mRNA in alcohol-preferring and alcohol-avoiding mice. <i>Alcohol</i> , 2003, 29, 39-49.   | 0.8 | 27        |
| 395 | Complete nucleotide sequence and molecular characterization of two lytic <i>Staphylococcus aureus</i> phages: 44AHJD and P68. <i>FEMS Microbiology Letters</i> , 2003, 219, 275-283.                                      | 0.7 | 60        |
| 396 | Genes that determine flower color: the role of regulatory changes in the evolution of phenotypic adaptations. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 507-518.   | 1.2 | 73        |
| 397 | Microfluidic devices for DNA sequencing: sample preparation and electrophoretic analysis. <i>Current Opinion in Biotechnology</i> , 2003, 14, 42-50.  | 3.3 | 181       |
| 398 | The first nonsense mutation in <i>alsin</i> results in a homogeneous phenotype of infantile-onset ascending spastic paralysis with bulbar involvement in two siblings. <i>Clinical Genetics</i> , 2003, 64, 210-215.      | 1.0 | 83        |
| 399 | Development of a single nucleotide polymorphism map of porcine chromosome 2. <i>Animal Genetics</i> , 2003, 34, 429-437.  | 0.6 | 19        |
| 400 | High-Cot sequence analysis of the maize genome. <i>Plant Journal</i> , 2003, 34, 249-255.   | 2.8 | 120       |
| 401 | An ancient R gene from the wild potato species <i>Solanum bulbocastanum</i> confers broad-spectrum resistance to <i>Phytophthora infestans</i> in cultivated potato and tomato. <i>Plant Journal</i> , 2003, 36, 867-882. | 2.8 | 406       |
| 402 | RIDOM: Comprehensive and public sequence database for identification of <i>Mycobacterium</i> species. <i>BMC Infectious Diseases</i> , 2003, 3, 26.   | 1.3 | 141       |
| 403 | Genomic structure around joining segments and constant regions of swine T-cell receptor alpha/delta (TRA/TRD) locus. <i>Immunology</i> , 2003, 109, 515-526.  | 2.0 | 34        |
| 404 | An integrated analysis of the genome of the hyperthermophilic archaeon <i>Pyrococcus abyssi</i> . <i>Molecular Microbiology</i> , 2003, 47, 1495-1512.  | 1.2 | 165       |
| 405 | A set of polymorphic SSR loci for subarctic willow ( <i>Salix lanata</i> , <i>S. lapponum</i> and <i>S. herbacea</i> ). <i>Molecular Ecology Notes</i> , 2003, 3, 280-282.  | 1.7 | 31        |
| 406 | COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF <i>PORPHYRA YEZOENSIS</i> (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS. <i>Journal of Phycology</i> , 2003, 39, 923-930.         | 1.0 | 99        |
| 407 | Intraspecific comparative genomics to identify avirulence genes from <i>Phytophthora</i> . <i>New Phytologist</i> , 2003, 159, 63-72.   | 3.5 | 50        |
| 408 | A double-screening method to identify reliable candidate non-synonymous SNPs from chicken EST data. <i>Animal Genetics</i> , 2003, 34, 249-254.   | 0.6 | 34        |
| 409 | Characterization of three single nucleotide polymorphisms in the porcine BMP15 gene. <i>Animal Genetics</i> , 2003, 34, 305-306.  | 0.6 | 2         |
| 410 | BMPR1B maps to chromosome 8 in swine. <i>Animal Genetics</i> , 2003, 34, 306-306.   | 0.6 | 1         |
| 411 | Radiation hybrid mapping of three skeletal muscle genes (CKM, ECH1 and TNNT1) to porcine chromosome 6. <i>Animal Genetics</i> , 2003, 34, 302-303.  | 0.6 | 7         |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 412 | Radiation hybrid mapping and genomic organization of canine TBX2 and TBX4. <i>Animal Genetics</i> , 2003, 34, 307-309.  | 0.6  | 3         |
| 413 | Identification of a novel lysine-171 allele in the ovine prion protein (PRNP) gene. <i>Animal Genetics</i> , 2003, 34, 303-305.   | 0.6  | 20        |
| 414 | Mutations in the limbin gene previously associated with dwarfism in Japanese brown cattle are not responsible for dwarfism in the American Angus breed. <i>Animal Genetics</i> , 2003, 34, 311-312. | 0.6  | 7         |
| 415 | Linkage mapping of IGF2 on cattle chromosome 29. <i>Animal Genetics</i> , 2003, 34, 313-313.  | 0.6  | 22        |
| 416 | Linkage mapping of a SNP in the porcine MADH1 gene to a region of chromosome 8 that contains QTL for uterine capacity. <i>Animal Genetics</i> , 2003, 34, 310-311.                                  | 0.6  | 4         |
| 417 | Linkage mapping of the bovine bone morphogenetic protein receptor-1B (BMPRII) to chromosome 6. <i>Animal Genetics</i> , 2003, 34, 311-311.  | 0.6  | 4         |
| 418 | Linkage and radiation hybrid mapping of the porcine PIK3R1 gene to chromosome 16. <i>Animal Genetics</i> , 2003, 34, 313-315.   | 0.6  | 0         |
| 419 | FISH and RH mapping of the bovine alpha (2)/delta calcium channel subunit gene (CACNA2D1). <i>Animal Genetics</i> , 2003, 34, 309-310.  | 0.6  | 11        |
| 420 | Thirty-one polymorphic microsatellite markers for genetic mapping in rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Journal of Heredity</i> , 2003, 94, 10-15.                                    | 0.6  | 5         |
| 421 | Linkage mapping of the porcine hairless gene (HR) to chromosome 14. <i>Animal Genetics</i> , 2003, 34, 317-318.   | 0.6  | 5         |
| 422 | Transcriptome characterization of the dimorphic and pathogenic fungus <i>Paracoccidioides brasiliensis</i> by EST analysis. <i>Yeast</i> , 2003, 20, 263-271.                                       | 0.8  | 74        |
| 423 | Verification of a new gene on <i>Saccharomyces cerevisiae</i> chromosome III. <i>Yeast</i> , 2003, 20, 731-738.   | 0.8  | 5         |
| 424 | Analysis of <i>Chlamydomonas reinhardtii</i> Genome Structure Using Large-Scale Sequencing of Regions on Linkage Groups I and III. <i>Journal of Eukaryotic Microbiology</i> , 2003, 50, 145-155.   | 0.8  | 24        |
| 425 | Unique physiological and pathogenic features of <i>Leptospira interrogans</i> revealed by whole-genome sequencing. <i>Nature</i> , 2003, 422, 888-893.  | 13.7 | 513       |
| 426 | Novel potential ALL low-risk markers revealed by gene expression profiling with new high-throughput SSH-PCR. <i>Leukemia</i> , 2003, 17, 1891-1900.   | 3.3  | 12        |
| 427 | High prevalence of rare dopamine receptor D4 alleles in children diagnosed with attention-deficit hyperactivity disorder. <i>Molecular Psychiatry</i> , 2003, 8, 536-545.                           | 4.1  | 171       |
| 428 | Proteomics: the first decade and beyond. <i>Nature Genetics</i> , 2003, 33, 311-323.  | 9.4  | 660       |
| 429 | Massive parallelism, randomness and genomic advances. <i>Nature Genetics</i> , 2003, 33, 219-227.   | 9.4  | 68        |



| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 430 | Sequence Characterization of Teleost Fish Melanocortin Receptors. <i>Annals of the New York Academy of Sciences</i> , 2003, 994, 319-330.   | 1.8  | 30        |
| 431 | Fungal Genomics: An Overview. <i>Applied Mycology and Biotechnology</i> , 2003, 3, 1-13.  | 0.3  | 2         |
| 432 | Viewing and Editing Assembled Sequences Using Consed. <i>Current Protocols in Bioinformatics</i> , 2003, 2, Unit11.2.   | 25.8 | 160       |
| 433 | Diversity Among Strains of <i>Xanthomonas campestris</i> pv. <i>vitians</i> from Lettuce. <i>Phytopathology</i> , 2003, 93, 64-70.  | 1.1  | 33        |
| 434 | Identification of residues critical for catalysis in a class C $\beta$ -lactamase by combinatorial scanning mutagenesis. <i>Protein Science</i> , 2003, 12, 1633-1645.  | 3.1  | 31        |
| 435 | Distinct geographic patterns of genetic diversity are maintained in wild barley ( <i>Hordeum vulgare</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Ovele of America, 2003, 100, 10812-10817.  | 3.3  | 94        |
| 436 | The Remarkable Flexibility of the Human Antibody Repertoire; Isolation of Over One Thousand Different Antibodies to a Single Protein, BLYS. <i>Journal of Molecular Biology</i> , 2003, 334, 103-118.   | 2.0  | 97        |
| 437 | Transcriptional profiling of <i>Medicago truncatula</i> roots after infection with <i>Aphanomyces euteiches</i> (oomycota) identifies novel genes upregulated during this pathogenic interaction. <i>Physiological and Molecular Plant Pathology</i> , 2003, 63, 17-26. | 1.3  | 50        |
| 438 | Trypanothione synthetase locus in <i>Trypanosoma cruzi</i> CL Brener strain shows an extensive allelic divergence. <i>Acta Tropica</i> , 2003, 87, 269-278.   | 0.9  | 7         |
| 439 | Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : Implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8007-8012.  | 3.3  | 341       |
| 440 | LNCIB human full-length cDNAs collection: towards a better comprehension of the human transcriptome. <i>Comptes Rendus - Biologies</i> , 2003, 326, 967-970.  | 0.1  | 2         |
| 441 | Quantification of single nucleotide polymorphisms by automated DNA sequencing. <i>Biochemical and Biophysical Research Communications</i> , 2003, 309, 331-338.   | 1.0  | 22        |
| 442 | Complete Genome Sequence of the Ammonia-Oxidizing Bacterium and Obligate Chemolithoautotroph <i>Nitrosomonas europaea</i> . <i>Journal of Bacteriology</i> , 2003, 185, 2759-2773.  | 1.0  | 510       |
| 443 | The complete mitochondrial genome sequence of the pathogenic yeast <i>Candida (Torulopsis) glabrata</i> . <i>FEBS Letters</i> , 2003, 534, 39-48.   | 1.3  | 68        |
| 444 | The mitochondrial genome of the thermal dimorphic fungus <i>Penicillium marneffeii</i> is more closely related to those of molds than yeasts. <i>FEBS Letters</i> , 2003, 555, 469-477.   | 1.3  | 56        |
| 445 | Human malaria parasites display a receptor for activated C kinase ortholog. <i>Biochemical and Biophysical Research Communications</i> , 2003, 306, 995-1001.   | 1.0  | 29        |
| 446 | Temporal and molecular separation of the kit receptor tyrosine kinase's roles in zebrafish melanocyte migration and survival. <i>Developmental Biology</i> , 2003, 262, 152-161.  | 0.9  | 66        |
| 447 | Whole genome shotgun sequencing guided by bioinformatics pipelines is an optimized approach for an established technique. <i>Journal of Biotechnology</i> , 2003, 106, 121-133.   | 1.9  | 25        |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 448 | Comparison of two <i>Xanthomonas campestris</i> pathovar <i>campestris</i> genomes revealed differences in their gene composition. <i>Journal of Biotechnology</i> , 2003, 106, 193-202.                              | 1.9  | 26        |
| 449 | The gene encoding GABBR1 is not associated with childhood absence epilepsy in the Chinese Han population. <i>Neuroscience Letters</i> , 2003, 343, 151-154.   | 1.0  | 10        |
| 450 | Extensive Linkage Disequilibrium, a Common 16.7-Kilobase Deletion, and Evidence of Balancing Selection in the Human Protocadherin $\hat{\pm}$ Cluster. <i>American Journal of Human Genetics</i> , 2003, 72, 621-635. | 2.6  | 51        |
| 451 | Rapid Direct Sequence Analysis of the Dystrophin Gene. <i>American Journal of Human Genetics</i> , 2003, 72, 931-939.   | 2.6  | 178       |
| 452 | Complete genome sequence of the marine planctomycete <i>Pirellulasp.</i> strain 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8298-8303.                     | 3.3  | 460       |
| 453 | Expressed sequences from the basidiomycetous tree pathogen <i>Heterobasidion annosum</i> during early infection of scots pine. <i>Fungal Genetics and Biology</i> , 2003, 39, 51-59.                                  | 0.9  | 51        |
| 454 | Identification of genes differentially expressed during aflatoxin biosynthesis in <i>Aspergillus flavus</i> and <i>Aspergillus parasiticus</i> . <i>Fungal Genetics and Biology</i> , 2003, 39, 118-127.              | 0.9  | 79        |
| 455 | Characterization of the genomic organization of the region bordering the centromere of chromosome V of <i>Podospora anserina</i> by direct sequencing. <i>Fungal Genetics and Biology</i> , 2003, 39, 250-263.        | 0.9  | 25        |
| 456 | Functional and genetic characterization of calmodulin from the dimorphic and pathogenic fungus <i>Paracoccidioides brasiliensis</i> . <i>Fungal Genetics and Biology</i> , 2003, 39, 204-210.                         | 0.9  | 27        |
| 457 | The structure and evolution of the melanocortin and MCH receptors in fish and mammals. <i>Genomics</i> , 2003, 81, 184-191.   | 1.3  | 139       |
| 458 | Nucleotide variation, haplotype structure, and association with end-stage renal disease of the human interleukin-1 gene cluster. <i>Genomics</i> , 2003, 82, 194-217.   | 1.3  | 42        |
| 459 | Structural and functional genomics and evolutionary relationships in the cluster of genes encoding murine 2â€²,5â€²-oligoadenylate synthetases. <i>Genomics</i> , 2003, 82, 537-552.                                  | 1.3  | 63        |
| 460 | Expressed sequence tags: alternative or complement to whole genome sequences?. <i>Trends in Plant Science</i> , 2003, 8, 321-329.   | 4.3  | 263       |
| 461 | Recombinant Environmental Libraries Provide Access to Microbial Diversity for Drug Discovery from Natural Products. <i>Applied and Environmental Microbiology</i> , 2003, 69, 49-55.                                  | 1.4  | 305       |
| 462 | Mutational analysis of the MYOCILIN gene in patients with primary open-angle glaucoma in Morocco. <i>Ophthalmic Genetics</i> , 2003, 24, 153-160.   | 0.5  | 30        |
| 463 | 2,5-Dialkylresorcinol Biosynthesis in <i>Pseudomonas aurantiaca</i> : Novel Head-to-Head Condensation of Two Fatty Acid-Derived Precursors. <i>Journal of Bacteriology</i> , 2003, 185, 860-869.                      | 1.0  | 52        |
| 464 | Pilot survey of expressed sequence tags (ESTs) from the asexual blood stages of <i>Plasmodium vivax</i> in human patients. <i>Malaria Journal</i> , 2003, 2, 21.  | 0.8  | 7         |
| 465 | Comparison of the canine and human olfactory receptor gene repertoires. <i>Genome Biology</i> , 2003, 4, R80.   | 13.9 | 90        |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 466 | Expressed sequence tag analysis in <i>Cycas</i> , the most primitive living seed plant. <i>Genome Biology</i> , 2003, 4, R78.   | 13.9 | 74        |
| 467 | Reinvestigation of the <i>Saccharomyces cerevisiae</i> genome annotation by comparison to the genome of a related fungus: <i>Ashbya gossypii</i> . <i>Genome Biology</i> , 2003, 4, R45.                                  | 13.9 | 96        |
| 468 | The mosaic structure of the symbiotic plasmid of <i>Rhizobium etli</i> CFN42 and its relation to other symbiotic genome compartments. <i>Genome Biology</i> , 2003, 4, R36.   | 13.9 | 167       |
| 469 | Analysis and functional classification of transcripts from the nematode <i>Meloidogyne incognita</i> . <i>Genome Biology</i> , 2003, 4, R26.  | 13.9 | 133       |
| 470 | Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast <i>Candida glabrata</i> . <i>Genome Biology</i> , 2003, 4, R10.  | 13.9 | 97        |
| 472 | BioNotes: a system for biosequence annotation. , 0, , .   |      | 1         |
| 473 | The DNA Sequence Quality Machine at IFOM: A Simple Web-based Tool for Quantitative Assessment of Sequencing Reactions. <i>DNA Sequence</i> , 2003, 14, 327-330.   | 0.7  | 1         |
| 474 | Complete Sequence and Characterization of the Channel Catfish Mitochondrial Genome. <i>DNA Sequence</i> , 2003, 14, 265-277.  | 0.7  | 48        |
| 475 | Fugu ESTs: New Resources for Transcription Analysis and Genome Annotation. <i>Genome Research</i> , 2003, 13, 2747-2753.  | 2.4  | 41        |
| 476 | Genomic Sequence of C 1 , the First Streptococcal Phage. <i>Journal of Bacteriology</i> , 2003, 185, 3325-3332.   | 1.0  | 51        |
| 477 | Complete sequence of the mitochondrial genome of <i>Tetrahymena thermophila</i> and comparative methods for identifying highly divergent genes. <i>Nucleic Acids Research</i> , 2003, 31, 1673-1682.                      | 6.5  | 64        |
| 478 | Multilocus Sequence Typing Reveals a Lack of Diversity among <i>Escherichia coli</i> O157:H7 Isolates That Are Distinct by Pulsed-Field Gel Electrophoresis. <i>Journal of Clinical Microbiology</i> , 2003, 41, 675-679. | 1.8  | 159       |
| 479 | ESTAP—an automated system for the analysis of EST data. <i>Bioinformatics</i> , 2003, 19, 1720-1722.  | 1.8  | 46        |
| 480 | Species-Specific Class I Gene Expansions Formed the Telomeric 1 Mb of the Mouse Major Histocompatibility Complex. <i>Genome Research</i> , 2003, 13, 589-600.   | 2.4  | 24        |
| 481 | Limited microsynteny between the genomes of <i>Pristionchus pacificus</i> and <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2003, 31, 2553-2560.  | 6.5  | 25        |
| 482 | Single nucleotide polymorphisms (SNPs) that map to gaps in the human SNP map. <i>Nucleic Acids Research</i> , 2003, 31, 4910-4916.  | 6.5  | 21        |
| 483 | Comparative Genome Organization of Human, Murine, and Feline MHC Class II Region. <i>Genome Research</i> , 2003, 13, 1169-1179.   | 2.4  | 101       |
| 484 | Microbial Diversity of Biofilms in Dental Unit Water Systems. <i>Applied and Environmental Microbiology</i> , 2003, 69, 3412-3420.  | 1.4  | 84        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 485 | Comparative Genome Analysis of <i>Vibrio vulnificus</i> , a Marine Pathogen. <i>Genome Research</i> , 2003, 13, 2577-2587.   | 2.4 | 350       |
| 486 | Genetic markers and their application in poultry breeding. <i>Poultry Science</i> , 2003, 82, 952-957.   | 1.5 | 41        |
| 487 | Molecular Characterization and Expression of Porcine Bone Morphogenetic Protein Receptor-IB in the Uterus of Cyclic and Pregnant Gilts1. <i>Biology of Reproduction</i> , 2003, 68, 735-743.   | 1.2 | 25        |
| 488 | Correcting errors in shotgun sequences. <i>Nucleic Acids Research</i> , 2003, 31, 4663-4672.   | 6.5 | 38        |
| 489 | A Survey of Canine Expressed Sequence Tags and a Display of Their Annotations Through a Flexible Web-Based Interface. , 2003, 94, 15-22.   |     | 4         |
| 490 | Whole-Genome Sequence Variation among Multiple Isolates of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2003, 185, 1316-1325.  | 1.0 | 195       |
| 491 | Multilocus Variable-Number Tandem Repeat Analysis Distinguishes Outbreak and Sporadic <i>Escherichia coli</i> O157:H7 Isolates. <i>Journal of Clinical Microbiology</i> , 2003, 41, 5389-5397. | 1.8 | 174       |
| 492 | Complete genome sequence and analysis of <i>Wolinella succinogenes</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11690-11695.      | 3.3 | 199       |
| 493 | Genomic organization of the DGAT2/MOGAT gene family in cattle ( <i>Bos taurus</i> ) and other mammals. <i>Cytogenetic and Genome Research</i> , 2003, 102, 42-47.                              | 0.6 | 26        |
| 494 | Systematic screening of sheep skin cDNA libraries for microsatellite sequences. <i>Cytogenetic and Genome Research</i> , 2003, 102, 79-84.   | 0.6 | 3         |
| 495 | The human cytomegalovirus genome revisited: comparison with the chimpanzee cytomegalovirus genome FN1. <i>Journal of General Virology</i> , 2003, 84, 17-28.                                   | 1.3 | 361       |
| 496 | The Phusion Assembler. <i>Genome Research</i> , 2003, 13, 81-90.   | 2.4 | 181       |
| 497 | Pericentromeric Duplications in the Laboratory Mouse. <i>Genome Research</i> , 2003, 13, 55-63.  | 2.4 | 36        |
| 498 | Molecular Evidence for Novel Planctomycete Diversity in a Municipal Wastewater Treatment Plant. <i>Applied and Environmental Microbiology</i> , 2003, 69, 7354-7363.                           | 1.4 | 138       |
| 499 | <i>Cryptococcus neoformans</i> Gene Expression during Experimental Cryptococcal Meningitis. <i>Eukaryotic Cell</i> , 2003, 2, 1336-1349.   | 3.4 | 129       |
| 500 | BayGenomics: a resource of insertional mutations in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2003, 31, 278-281.   | 6.5 | 220       |
| 501 | A novel algorithm for computational identification of contaminated EST libraries. <i>Nucleic Acids Research</i> , 2003, 31, 1067-1074.   | 6.5 | 75        |
| 502 | Design of oligonucleotides for microarrays and perspectives for design of multi-transcriptome arrays. <i>Nucleic Acids Research</i> , 2003, 31, 3491-3496.                                     | 6.5 | 100       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 503 | Generating consensus sequences from partial order multiple sequence alignment graphs. <i>Bioinformatics</i> , 2003, 19, 999-1008.   | 1.8 | 81        |
| 504 | Coding potential of laboratory and clinical strains of human cytomegalovirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14976-14981.                            | 3.3 | 450       |
| 505 | Open Bioinformatics. <i>Bioinformatics</i> , 2003, 19, 679-680.   | 1.8 | 11        |
| 506 | Comparative Analyses of Potato Expressed Sequence Tag Libraries. <i>Plant Physiology</i> , 2003, 131, 419-429.  | 2.3 | 174       |
| 507 | Allelic variants of ovine prion protein gene (PRNP) in Oklahoma sheep. <i>Cytogenetic and Genome Research</i> , 2003, 102, 89-94.   | 0.6 | 43        |
| 508 | TRAIT (TRANscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003, 19, 661-662.   | 1.8 | 4         |
| 509 | The Parasitome of the Phytonematode <i>Heterodera glycines</i> . <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 720-726.   | 1.4 | 257       |
| 510 | Characterization of a Spontaneous Nonmagnetic Mutant of <i>Magnetospirillum gryphiswaldense</i> Reveals a Large Deletion Comprising a Putative Magnetosome Island. <i>Journal of Bacteriology</i> , 2003, 185, 5779-5790. | 1.0 | 200       |
| 511 | An Eulerian Path Approach to Global Multiple Alignment for DNA Sequences. <i>Journal of Computational Biology</i> , 2003, 10, 803-819.  | 0.8 | 29        |
| 512 | An Evolutionary Analysis of Orphan Genes in <i>Drosophila</i> . <i>Genome Research</i> , 2003, 13, 2213-2219.   | 2.4 | 223       |
| 513 | A mutation in the canine BHD gene is associated with hereditary multifocal renal cystadenocarcinoma and nodular dermatofibrosis in the German Shepherd dog. <i>Human Molecular Genetics</i> , 2003, 12, 3043-3053.        | 1.4 | 157       |
| 514 | The Genome Sequence of <i>Yersinia pestis</i> Bacteriophage $\phi$ A1122 Reveals an Intimate History with the Coliphage T3 and T7 Genomes. <i>Journal of Bacteriology</i> , 2003, 185, 5248-5262.                         | 1.0 | 95        |
| 515 | Co-duplication of olfactory receptor and MHC class I genes in the mouse major histocompatibility complex. <i>Human Molecular Genetics</i> , 2003, 12, 3025-3040.  | 1.4 | 34        |
| 516 | Complete Sequence and Genomic Analysis of Rhesus Cytomegalovirus. <i>Journal of Virology</i> , 2003, 77, 6620-6636.   | 1.5 | 161       |
| 517 | Expressed sequence tag analysis of <i>Sarcoptes scabiei</i> . <i>Parasitology</i> , 2003, 127, 139-145.   | 0.7 | 24        |
| 518 | Two novel spliced genes in human cytomegalovirus. <i>Journal of General Virology</i> , 2003, 84, 1117-1122.   | 1.3 | 126       |
| 519 | Gene Expression Profile of the Human Trabecular Meshwork: NEIBank Sequence Tag Analysis. , 2003, 44, 2588.  |     | 158       |
| 520 | Genome Sequence of an M3 Strain of <i>Streptococcus pyogenes</i> Reveals a Large-Scale Genomic Rearrangement in Invasive Strains and New Insights into Phage Evolution. <i>Genome Research</i> , 2003, 13, 1042-1055.     | 2.4 | 248       |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 521 | Automated Identification of Single Nucleotide Polymorphisms from Sequencing Data. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 253-265.  | 0.3 | 73        |
| 522 | The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13418-13423.           | 3.3 | 105       |
| 523 | Genome of Bovine Herpesvirus 5. <i>Journal of Virology</i> , 2003, 77, 10339-10347.  | 1.5 | 136       |
| 524 | The expression and function of the achaete-scute genes in <i>Tribolium castaneum</i> reveals conservation and variation in neural pattern formation and cell fate specification. <i>Development (Cambridge)</i> , 2003, 130, 4373-4381.                    | 1.2 | 65        |
| 525 | A 1-Mb resolution radiation hybrid map of the canine genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5296-5301.  | 3.3 | 219       |
| 526 | Development of an integrated laboratory information management system for the maize mapping project. <i>Bioinformatics</i> , 2003, 19, 2022-2030.  | 1.8 | 31        |
| 527 | Mapping multiple co-sequenced T-DNA integration sites within the <i>Arabidopsis</i> genome. <i>Bioinformatics</i> , 2003, 19, 579-586.   | 1.8 | 3         |
| 528 | Apparent homology of expressed genes from wood-forming tissues of loblolly pine ( <i>Pinus taeda</i> L.) with <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7383-7388. | 3.3 | 174       |
| 529 | MtDB: a database for personalized data mining of the model legume <i>Medicago truncatula</i> transcriptome. <i>Nucleic Acids Research</i> , 2003, 31, 196-201.   | 6.5 | 61        |
| 530 | The Genome Sequence of <i>Caenorhabditis briggsae</i> : A Platform for Comparative Genomics. <i>PLoS Biology</i> , 2003, 1, e45.   | 2.6 | 812       |
| 531 | Sequence analysis of three mitochondrial DNA molecules reveals interesting differences among <i>Saccharomyces</i> yeasts. <i>Nucleic Acids Research</i> , 2003, 31, 3081-3091.   | 6.5 | 30        |
| 532 | Genomic Colinearity as a Tool for Plant Gene Isolation. , 2003, 236, 109-122.  |     | 8         |
| 533 | Combined ESTs from Plant-Microbe Interactions: Using GC Counting to Determine the Species of Origin. , 2003, 236, 79-84.   |     | 7         |
| 534 | Mutational Profiling in the Human Genome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 23-30.  | 2.0 | 7         |
| 535 | Gene Identification and Expression Analysis of 86,136 Expressed Sequence Tags (EST) from the Rice Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 26-42.   | 3.0 | 18        |
| 536 | A Genome Sequence of Novel SARS-CoV Isolates: the Genotype, GD-Ins29, Leads to a Hypothesis of Viral Transmission in South China. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 101-107.   | 3.0 | 17        |
| 537 | EST Pipeline System: Detailed and Automated EST Data Processing and Mining. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 236-242.   | 3.0 | 12        |
| 538 | Functional Genomics of Wood Quality and Properties. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 263-278.   | 3.0 | 3         |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 539 | SNP Discovery and PCR-Based Assay Design: From In Silico Data to the Laboratory Experiment. , 0, , 203-215.  |     | 1         |
| 540 | A Profile of Putative Parasitism Genes Expressed in the Esophageal Gland Cells of the Root-knot Nematode <i>Meloidogyne incognita</i> . <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 376-381.           | 1.4 | 211       |
| 541 | Gene Expression Informatics and Analysis. , 0, , 317-344.  |     | 0         |
| 544 | beta-thalassemia intermedia in a Brazilian patient with - 101(C > T) and codon 39 (C > T) mutations. <i>Sao Paulo Medical Journal</i> , 2003, 121, 28-30.  | 0.4 | 0         |
| 545 | Molecular Epidemiology of O139 <i>Vibrio cholerae</i> : Mutation, Lateral Gene Transfer, and Founder Flush. <i>Emerging Infectious Diseases</i> , 2003, 9, 810-814.  | 2.0 | 74        |
| 546 | Rapid development of gene-tagged microsatellite markers from bacterial artificial chromosome clones using anchored TAA repeat primers. <i>BioTechniques</i> , 2003, 35, 976-979.                                   | 0.8 | 56        |
| 547 | Single-Stranded Conformational Polymorphism Analysis Using Automated Capillary Array Electrophoresis Apparatuses. <i>BioTechniques</i> , 2003, 34, 746-750.  | 0.8 | 27        |
| 549 | A comprehensive nonredundant expressed sequence tag collection for the developing <i>Rattus norvegicus</i> heart. <i>Physiological Genomics</i> , 2004, 17, 245-252.   | 1.0 | 7         |
| 551 | SSHSuite: an integrated software package for analysis of large-scale suppression subtractive hybridization data. <i>BioTechniques</i> , 2004, 36, 1043-1045.   | 0.8 | 7         |
| 552 | Functional allelic heterogeneity and pleiotropy of a repeat polymorphism in tyrosine hydroxylase: prediction of catecholamines and response to stress in twins. <i>Physiological Genomics</i> , 2004, 19, 277-291. | 1.0 | 80        |
| 553 | Expressed sequence tags from callus of <i>Euphorbia tirucalli</i> : A resource for genes involved in triterpenoid and sterol biosynthesis. <i>Plant Biotechnology</i> , 2004, 21, 349-353.                         | 0.5 | 11        |
| 554 | Using the TIGR Assembler in Shotgun Sequencing Projects. , 2004, 255, 279-294.   |     | 17        |
| 555 | Assembly of DNA Sequencing Data. , 2004, 255, 319-332.   |     | 0         |
| 556 | BAC Finishing Strategies. , 2004, 255, 255-278.  |     | 4         |
| 557 | Genome Sequencing and Annotation. , 2004, 266, 29-45.  |     | 4         |
| 558 | Development of rationally designed nucleic acid signatures for microbial pathogens. <i>Expert Review of Molecular Diagnostics</i> , 2004, 4, 303-315.  | 1.5 | 9         |
| 559 | Comparative Analysis of <i>Twoslc11</i> ( <i>Nramp</i> ) Loci in <i>Takifugu rubripes</i> . <i>DNA and Cell Biology</i> , 2004, 23, 45-58.   | 0.9 | 14        |
| 560 | Analyses of cDNAs from growth and slug stages of <i>Dictyostelium discoideum</i> . <i>Nucleic Acids Research</i> , 2004, 32, 1647-1653.  | 6.5 | 41        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 561 | Comparative analysis of a Brassica BAC clone containing several major aliphatic glucosinolate genes with its corresponding Arabidopsis sequence. <i>Genome</i> , 2004, 47, 666-679.                    | 0.9 | 61        |
| 562 | Complete Genome Sequence of the Genetically Tractable Hydrogenotrophic Methanogen <i>Methanococcus maripaludis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 6956-6969.                            | 1.0 | 208       |
| 563 | A Comparison of Rice Chloroplast Genomes. <i>Plant Physiology</i> , 2004, 135, 412-420.  | 2.3 | 142       |
| 564 | Pattern of diversity in the genomic region near the maize domestication gene <i>tb1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 700-707. | 3.3 | 294       |
| 565 | Natural Genetic Variation Caused by Transposable Elements in Humans. <i>Genetics</i> , 2004, 168, 933-951.   | 1.2 | 138       |
| 566 | The mouse homeobox gene <i>Not</i> is required for caudal notochord development and affected by the truncate mutation. <i>Genes and Development</i> , 2004, 18, 1725-1736.                             | 2.7 | 84        |
| 567 | Automated correction of genome sequence errors. <i>Nucleic Acids Research</i> , 2004, 32, 562-569.   | 6.5 | 42        |
| 568 | Single nucleotide polymorphisms in protein tyrosine phosphatase 1A (PTPN1) are associated with essential hypertension and obesity. <i>Human Molecular Genetics</i> , 2004, 13, 1885-1892.              | 1.4 | 48        |
| 569 | Complete Genome Sequence of <i>Yersinia pestis</i> Strain 91001, an Isolate Avirulent to Humans. <i>DNA Research</i> , 2004, 11, 179-197.  | 1.5 | 241       |
| 570 | Development and Application of a Salmonid EST Database and cDNA Microarray: Data Mining and Interspecific Hybridization Characteristics. <i>Genome Research</i> , 2004, 14, 478-490.                   | 2.4 | 279       |
| 571 | Genetic content of wild-type human cytomegalovirus. <i>Journal of General Virology</i> , 2004, 85, 1301-1312.  | 1.3 | 500       |
| 572 | An intermediate grade of finished genomic sequence suitable for comparative analyses. <i>Genome Research</i> , 2004, 14, 2235-2244.  | 2.4 | 72        |
| 573 | Germline E-cadherin mutations in hereditary diffuse gastric cancer: assessment of 42 new families and review of genetic screening criteria. <i>Journal of Medical Genetics</i> , 2004, 41, 508-517.    | 1.5 | 327       |
| 574 | The Human MitoChip: A High-Throughput Sequencing Microarray for Mitochondrial Mutation Detection. <i>Genome Research</i> , 2004, 14, 812-819.  | 2.4 | 218       |
| 575 | Complete Genome Sequence of <i>Rickettsia typhi</i> and Comparison with Sequences of Other Rickettsiae. <i>Journal of Bacteriology</i> , 2004, 186, 5842-5855.   | 1.0 | 223       |
| 576 | Fosmid-Based Physical Mapping of the <i>Histoplasma capsulatum</i> Genome. <i>Genome Research</i> , 2004, 14, 1603-1609.   | 2.4 | 23        |
| 577 | Comparative Mapping in the Pinaceae. <i>Genetics</i> , 2004, 168, 447-461.   | 1.2 | 117       |
| 578 | Biography of Phil Green. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13991-13993.  | 3.3 | 2         |



| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 579 | Molecular Population Genetics of Male Accessory Gland Proteins in the <i>Drosophila simulans</i> Complex. <i>Genetics</i> , 2004, 167, 725-735.   | 1.2 | 56        |
| 580 | Construction of an <i>Enterococcus faecalis</i> Tn917-Mediated-Gene-Disruption Library Offers Insight into Tn917 Insertion Patterns. <i>Journal of Bacteriology</i> , 2004, 186, 7280-7289. | 1.0 | 54        |
| 581 | Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. <i>Genome Research</i> , 2004, 14, 1176-1187.  | 2.4 | 260       |
| 582 | Functional Characterization of a Catabolic Plasmid from Polychlorinated- Biphenyl-Degrading <i>Rhodococcus</i> sp. Strain RHA1. <i>Journal of Bacteriology</i> , 2004, 186, 7783-7795.      | 1.0 | 65        |
| 583 | Statistical modeling of sequencing errors in SAGE libraries. <i>Bioinformatics</i> , 2004, 20, i31-i39.   | 1.8 | 93        |
| 584 | PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries. <i>Nucleic Acids Research</i> , 2004, 32, 484D-488.                      | 6.5 | 80        |
| 585 | EICO (Expression-based Imprint Candidate Organizer): finding disease-related imprinted genes. <i>Nucleic Acids Research</i> , 2004, 32, 548D-551.   | 6.5 | 17        |
| 587 | ESSENTIAL EUKARYOTIC CORE. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 441.  | 1.1 | 0         |
| 588 | Construction and Evaluation of cDNA Libraries for Large-Scale Expressed Sequence Tag Sequencing in Wheat ( <i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 595-608.              | 1.2 | 57        |
| 589 | Genotype-phenotype correlations in Peutz-Jeghers syndrome. <i>Journal of Medical Genetics</i> , 2004, 41, 327-333.  | 1.5 | 157       |
| 590 | The <i>Pseudomonas aeruginosa</i> PAO1 Gene Collection. <i>Genome Research</i> , 2004, 14, 2190-2200.   | 2.4 | 78        |
| 591 | The Genomic Sequence and Comparative Analysis of the Rat Major Histocompatibility Complex. <i>Genome Research</i> , 2004, 14, 631-639.  | 2.4 | 108       |
| 592 | Haplotypes in the APOA1-C3-A4-A5 gene cluster affect plasma lipids in both humans and baboons. <i>Human Molecular Genetics</i> , 2004, 13, 1049-1056.                                       | 1.4 | 25        |
| 593 | The Genome of Canarypox Virus. <i>Journal of Virology</i> , 2004, 78, 353-366.  | 1.5 | 167       |
| 594 | Heterogeneity detector: finding heterogeneous positions in Phred/Phrap assemblies. <i>Bioinformatics</i> , 2004, 20, 2863-2864.   | 1.8 | 19        |
| 595 | Excess of Amino Acid Substitutions Relative to Polymorphism Between X-Linked Duplications in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2004, 22, 273-284.   | 3.5 | 46        |
| 596 | Sequence and Comparative Analysis of the Maize NB Mitochondrial Genome. <i>Plant Physiology</i> , 2004, 136, 3486-3503.   | 2.3 | 279       |
| 597 | Partial Analysis of the Genomes of Two Nontypeable <i>Haemophilus influenzae</i> Otitis Media Isolates. <i>Infection and Immunity</i> , 2004, 72, 3002-3010.                                | 1.0 | 37        |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 598 | Transferable Antibiotic Resistance Elements in <i>Haemophilus influenzae</i> Share a Common Evolutionary Origin with a Diverse Family of Syntenic Genomic Islands. <i>Journal of Bacteriology</i> , 2004, 186, 8114-8122.                                       | 1.0 | 111       |
| 599 | Discrepancies in dbSNP confirmation rates and allele frequency distributions from varying genotyping error rates and patterns. <i>Bioinformatics</i> , 2004, 20, 1022-1032.   | 1.8 | 52        |
| 600 | Analysis for free: Comparing programs for sequence analysis. <i>Briefings in Bioinformatics</i> , 2004, 5, 82-87.   | 3.2 | 170       |
| 601 | EST-PAGE—managing and analyzing EST data. <i>Bioinformatics</i> , 2004, 20, 286-288.  | 1.8 | 26        |
| 602 | Correction of sequence-based artifacts in serial analysis of gene expression. <i>Bioinformatics</i> , 2004, 20, 1254-1263.  | 1.8 | 41        |
| 603 | Estimating and comparing the rates of gene discovery and expressed sequence tag (EST) frequencies in EST surveys. <i>Bioinformatics</i> , 2004, 20, 2279-2287.  | 1.8 | 31        |
| 604 | Algorithms for sequence analysis via mutagenesis. <i>Bioinformatics</i> , 2004, 20, 2401-2410.  | 1.8 | 13        |
| 605 | The Minimal Eukaryotic Ribosomal DNA Units in the Primitive Red Alga <i>Cyanidioschyzon merolae</i> . <i>DNA Research</i> , 2004, 11, 83-91.  | 1.5 | 26        |
| 606 | Comparative Analysis of Multilocus Sequence Typing and Pulsed-Field Gel Electrophoresis for Characterizing <i>Listeria monocytogenes</i> Strains Isolated from Environmental and Clinical Sources. <i>Journal of Clinical Microbiology</i> , 2004, 42, 276-285. | 1.8 | 87        |
| 607 | Detection and Selection of Microsatellites in the Genome of <i>Paracoccidioides brasiliensis</i> as Molecular Markers for Clinical and Epidemiological Studies. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5007-5014.                                  | 1.8 | 29        |
| 608 | Assessment of Evolution of Pandemic <i>Vibrio parahaemolyticus</i> by Multilocus Sequence Typing. <i>Journal of Clinical Microbiology</i> , 2004, 42, 1280-1282.  | 1.8 | 96        |
| 609 | Analysis of the first complete genome sequence of an Old World monkey adenovirus reveals a lineage distinct from the six human adenovirus species. <i>Journal of General Virology</i> , 2004, 85, 2799-2807.  | 1.3 | 34        |
| 610 | A Transcript Finishing Initiative for Closing Gaps in the Human Transcriptome. <i>Genome Research</i> , 2004, 14, 1413-1423.  | 2.4 | 22        |
| 611 | Contribution of Asian mouse subspecies <i>Mus musculus molossinus</i> to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis. <i>Genome Research</i> , 2004, 14, 2439-2447.  | 2.4 | 90        |
| 612 | Composition and Structure of the Centromeric Region of Rice Chromosome 8[W]. <i>Plant Cell</i> , 2004, 16, 967-976.   | 3.1 | 122       |
| 613 | Characterization of Full-length Enriched Expressed Sequence Tags of Stress-treated Poplar Leaves. <i>Plant and Cell Physiology</i> , 2004, 45, 1738-1748.   | 1.5 | 82        |
| 614 | Genome coverage and sequence fidelity of $\Phi$ 29 polymerase-based multiple strand displacement whole genome amplification. <i>Nucleic Acids Research</i> , 2004, 32, e71-e71.   | 6.5 | 266       |
| 615 | Mutation Rate and Predicted Phenotypic Target Sizes in Ethylnitrosourea-Treated Mice. <i>Genetics</i> , 2004, 168, 953-959.   | 1.2 | 82        |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 616 | Characterization of <i>Lactarius tesquorum</i> Ectomycorrhizae on <i>Cistus</i> sp. and Molecular Phylogeny of Related European <i>Lactarius</i> Taxa. <i>Mycologia</i> , 2004, 96, 272.  | 0.8 | 10        |
| 617 | BGI-RIS: an integrated information resource and comparative analysis workbench for rice genomics. <i>Nucleic Acids Research</i> , 2004, 32, 377D-382.   | 6.5 | 108       |
| 618 | ChickVD: a sequence variation database for the chicken genome. <i>Nucleic Acids Research</i> , 2004, 33, D438-D441.   | 6.5 | 33        |
| 619 | CR-EST: a resource for crop ESTs. <i>Nucleic Acids Research</i> , 2004, 33, D619-D621.  | 6.5 | 38        |
| 620 | Phylogenetic Footprint Analysis of IGF2 in Extant Mammals. <i>Genome Research</i> , 2004, 14, 1726-1732.  | 2.4 | 41        |
| 621 | A fuzzy confidence value for DNA bases. , 0, , .  |     | 2         |
| 622 | The genome sequence of the probiotic intestinal bacterium <i>Lactobacillus johnsonii</i> NCC 533. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2512-2517.                      | 3.3 | 476       |
| 623 | Systematic Recovery and Analysis of Full-ORF Human cDNA Clones. <i>Genome Research</i> , 2004, 14, 2083-2092.   | 2.4 | 28        |
| 624 | Genome sequence of <i>Haloarcula marismortui</i> : A halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004, 14, 2221-2234.   | 2.4 | 268       |
| 625 | Shotgun Sequence Assembly. <i>Advances in Computers</i> , 2004, 60, 193-248.  | 1.2 | 20        |
| 626 | Genomic analysis of <i>Bacteroides fragilis</i> reveals extensive DNA inversions regulating cell surface adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14919-14924. | 3.3 | 241       |
| 627 | Molecular analysis of high-copy insertion sites in maize. <i>Nucleic Acids Research</i> , 2004, 32, e54-e54.  | 6.5 | 82        |
| 628 | The Atlas Genome Assembly System. <i>Genome Research</i> , 2004, 14, 721-732.   | 2.4 | 139       |
| 629 | Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.   | 2.4 | 80        |
| 630 | Structural features of the rice chromosome 4 centromere. <i>Nucleic Acids Research</i> , 2004, 32, 2023-2030.   | 6.5 | 95        |
| 631 | The organization and evolution of the Dipteran and Hymenopteran Down syndrome cell adhesion molecule ( <i>Dscam</i> ) genes. <i>Rna</i> , 2004, 10, 1499-1506.  | 1.6 | 87        |
| 632 | PartiGene--constructing partial genomes. <i>Bioinformatics</i> , 2004, 20, 1398-1404.   | 1.8 | 129       |
| 633 | Genetic Divergence of the Rhesus Macaque Major Histocompatibility Complex. <i>Genome Research</i> , 2004, 14, 1501-1515.  | 2.4 | 195       |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 634 | Characterization of synthetic DNA bar codes in <i>Saccharomyces cerevisiae</i> gene-deletion strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11046-11051. | 3.3 | 69        |
| 635 | Genomes of the Parapoxviruses Orf Virus and Bovine Papular Stomatitis Virus. <i>Journal of Virology</i> , 2004, 78, 168-177.   | 1.5 | 247       |
| 636 | Haplotype Reconstruction from SNP Alignment. <i>Journal of Computational Biology</i> , 2004, 11, 505-516.  | 0.8 | 35        |
| 638 | Unique features revealed by the genome sequence of <i>Acinetobacter</i> sp. ADP1, a versatile and naturally transformation competent bacterium. <i>Nucleic Acids Research</i> , 2004, 32, 5766-5779.                   | 6.5 | 308       |
| 639 | Identification and Management of <i>Colletotrichum acutatum</i> on Immature Bell Peppers. <i>Plant Disease</i> , 2004, 88, 1198-1204.  | 0.7 | 77        |
| 640 | Shotgun Library Construction for DNA Sequencing. , 2004, 255, 171-188.   |     | 25        |
| 641 | A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.  | 2.3 | 287       |
| 642 | Comparative Sequence Analysis of the Region Harboring the Hardness Locus in Barley and Its Colinear Region in Rice. <i>Plant Physiology</i> , 2004, 136, 3177-3190.  | 2.3 | 68        |
| 643 | The Genome Sequence of <i>Mycoplasma hyopneumoniae</i> Strain 232, the Agent of Swine Mycoplasmosis. <i>Journal of Bacteriology</i> , 2004, 186, 7123-7133.  | 1.0 | 233       |
| 644 | Convergent Evolution of Chromosomal Sex-Determining Regions in the Animal and Fungal Kingdoms. <i>PLoS Biology</i> , 2004, 2, e384.  | 2.6 | 218       |
| 645 | ReDiT: Repeat Discrepancy Tagger—a shotgun assembly finishing aid. <i>Bioinformatics</i> , 2004, 20, 803-804.  | 1.8 | 4         |
| 646 | Fragment assembly with short reads. <i>Bioinformatics</i> , 2004, 20, 2067-2074.   | 1.8 | 166       |
| 647 | Large-scale analysis of non-synonymous coding region single nucleotide polymorphisms. <i>Bioinformatics</i> , 2004, 20, 1006-1014.   | 1.8 | 70        |
| 648 | The Centre for Modeling Human Disease Gene Trap resource. <i>Nucleic Acids Research</i> , 2004, 32, 557D-559.  | 6.5 | 28        |
| 649 | Differential expression of a novel ankyrin containing E3 ubiquitin-protein ligase, Hace1, in sporadic Wilms' tumor versus normal kidney. <i>Human Molecular Genetics</i> , 2004, 13, 2061-2074.                        | 1.4 | 100       |
| 650 | Unlocking hidden genomic sequence. <i>Nucleic Acids Research</i> , 2004, 32, 35e-35.   | 6.5 | 21        |
| 651 | Feline Polycystic Kidney Disease Mutation Identified in PKD1. <i>Journal of the American Society of Nephrology: JASN</i> , 2004, 15, 2548-2555.  | 3.0 | 120       |
| 652 | Adjust quality scores from alignment and improve sequencing accuracy. <i>Nucleic Acids Research</i> , 2004, 32, 5183-5191.   | 6.5 | 33        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 653 | Assign 2.0: software for the analysis of Phred quality values for quality control of HLA sequencing-based typing. <i>Tissue Antigens</i> , 2004, 64, 556-565.  | 1.0  | 16        |
| 654 | Strain-specific genomic regions of <i>Ruminococcus flavefaciens</i> FD-1 as revealed by combinatorial random-phase genome sequencing and suppressive subtractive hybridization. <i>Environmental Microbiology</i> , 2004, 6, 335-346.                                    | 1.8  | 21        |
| 655 | The genome of <i>Desulfotalea psychrophila</i> , a sulfate-reducing bacterium from permanently cold Arctic sediments. <i>Environmental Microbiology</i> , 2004, 6, 887-902.  | 1.8  | 204       |
| 656 | Assessment of the rind microbial diversity in a farmhouse-produced vs a pasteurized industrially produced soft red-smear cheese using both cultivation and rDNA-based methods. <i>Journal of Applied Microbiology</i> , 2004, 97, 546-556.                               | 1.4  | 94        |
| 657 | Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.   | 2.8  | 137       |
| 658 | Sequence composition, organization, and evolution of the core Triticeae genome. <i>Plant Journal</i> , 2004, 40, 500-511.  | 2.8  | 204       |
| 659 | Male-specific SRY and ZFY haplotypes in US beef cattle. <i>Animal Genetics</i> , 2004, 35, 246-249.  | 0.6  | 1         |
| 660 | Assignment of 10 canine genes to the canine linkage and comparative maps. <i>Animal Genetics</i> , 2004, 35, 249-251.  | 0.6  | 3         |
| 661 | Iron-regulated transcription and capsule formation in the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Molecular Microbiology</i> , 2004, 55, 1452-1472.  | 1.2  | 90        |
| 662 | Characterization of SCAR markers of <i>Eimeria</i> spp. of domestic fowl and construction of a public relational database (The <i>Eimeria</i> SCARdb). <i>FEMS Microbiology Letters</i> , 2004, 238, 183-188.  | 0.7  | 19        |
| 663 | ESSENTIAL EUKARYOTIC CORE. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 441-446.   | 1.1  | 8         |
| 664 | Complete genome sequence of the metabolically versatile photosynthetic bacterium <i>Rhodospseudomonas palustris</i> . <i>Nature Biotechnology</i> , 2004, 22, 55-61.   | 9.4  | 675       |
| 665 | Quality assessment of the human genome sequence. <i>Nature</i> , 2004, 429, 365-368.   | 13.7 | 172       |
| 666 | A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.  | 13.7 | 391       |
| 667 | A survey of <i>Leishmania braziliensis</i> genome by shotgun sequencing. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 81-86.   | 0.5  | 20        |
| 668 | mRNA sequences for <i>Haemonchus contortus</i> intestinal cathepsin B-like cysteine proteases display an extreme in abundance and diversity compared with other adult mammalian parasitic nematodes. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 297-305. | 0.5  | 51        |
| 669 | Analysis, statistical validation and dissemination of large-scale proteomics datasets generated by tandem MS. <i>Drug Discovery Today</i> , 2004, 9, 173-181.  | 3.2  | 168       |
| 670 | Accumulation of Maize chlorotic dwarf virus proteins in its plant host and leafhopper vector. <i>Virology</i> , 2004, 325, 379-388.  | 1.1  | 13        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 671 | A highly pathogenic porcine reproductive and respiratory syndrome virus generated from an infectious cDNA clone retains the in vivo virulence and transmissibility properties of the parental virus. <i>Virology</i> , 2004, 325, 308-319. | 1.1 | 105       |
| 672 | ESTIMA, a tool for EST management in a multi-project environment. <i>BMC Bioinformatics</i> , 2004, 5, 176.  | 1.2 | 35        |
| 673 | prot4EST: translating expressed sequence tags from neglected genomes. <i>BMC Bioinformatics</i> , 2004, 5, 187.  | 1.2 | 118       |
| 674 | FRAGS: estimation of coding sequence substitution rates from fragmentary data. <i>BMC Bioinformatics</i> , 2004, 5, 8.   | 1.2 | 3         |
| 675 | Section-level relationships of North American Agalinis (Orobanchaceae) based on DNA sequence analysis of three chloroplast gene regions. <i>BMC Evolutionary Biology</i> , 2004, 4, 15.  | 3.2 | 16        |
| 676 | An enigmatic fourth runt domain gene in the fugu genome: ancestral gene loss versus accelerated evolution. <i>BMC Evolutionary Biology</i> , 2004, 4, 43.  | 3.2 | 15        |
| 677 | From biomedicine to natural history research: EST resources for ambystomatid salamanders. <i>BMC Genomics</i> , 2004, 5, 54.   | 1.2 | 79        |
| 678 | POSA: Perl Objects for DNA Sequencing Data Analysis. <i>BMC Genomics</i> , 2004, 5, 60.  | 1.2 | 5         |
| 679 | Microarrays for global expression constructed with a low redundancy set of 27,500 sequenced cDNAs representing an array of developmental stages and physiological conditions of the soybean plant. <i>BMC Genomics</i> , 2004, 5, 73.      | 1.2 | 91        |
| 680 | High Coding Density on the Largest Paramecium tetraurelia Somatic Chromosome. <i>Current Biology</i> , 2004, 14, 1397-1404.  | 1.8 | 52        |
| 681 | The Master Sex-Determination Locus in Threespine Sticklebacks Is on a Nascent Y Chromosome. <i>Current Biology</i> , 2004, 14, 1416-1424.  | 1.8 | 367       |
| 682 | Development of an Expressed Sequence Tag (EST) Resource for Wheat ( <i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 585-593.  | 1.2 | 87        |
| 683 | Identification and analysis of single nucleotide polymorphisms (SNPs) in citrus. <i>Euphytica</i> , 2004, 138, 227-237.  | 0.6 | 32        |
| 684 | Characteristics of the Lotus Japonicus Gene Repertoire Deduced from Large-Scale Expressed Sequence Tag (EST) Analysis. <i>Plant Molecular Biology</i> , 2004, 54, 405-414.   | 2.0 | 63        |
| 685 | Automated SNP Detection in Expressed Sequence Tags: Statistical Considerations and Application to Maritime Pine Sequences. <i>Plant Molecular Biology</i> , 2004, 54, 461-470.   | 2.0 | 65        |
| 686 | Isolation and characterization of genomic and transcribed retrotransposon sequences from sorghum. <i>Molecular Genetics and Genomics</i> , 2004, 271, 308-316.   | 1.0 | 20        |
| 687 | Predicted ATP-binding cassette systems in the phytopathogenic mollicute <i>Spiroplasma kunkelii</i> . <i>Molecular Genetics and Genomics</i> , 2004, 271, 325-338.   | 1.0 | 12        |
| 688 | Sequencing of the <i>Triticum monococcum</i> Hardness locus reveals good microcolinearity with rice. <i>Molecular Genetics and Genomics</i> , 2004, 271, 377-386.  | 1.0 | 85        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 689 | Construction of a BAC library of Korean ginseng and initial analysis of BAC-end sequences. <i>Molecular Genetics and Genomics</i> , 2004, 271, 709-716.  | 1.0 | 56        |
| 690 | Molecular characterization of the B-2 DNA puff gene of <i>Rhynchosciara americana</i> . <i>Chromosoma</i> , 2004, 113, 167-76.   | 1.0 | 21        |
| 691 | Satellite repeats in the functional centromere and pericentromeric heterochromatin of <i>Medicago truncatula</i> . <i>Chromosoma</i> , 2004, 113, 276-283.   | 1.0 | 58        |
| 692 | EST and microarray analyses of pathogen-responsive genes in hot pepper ( <i>Capsicum annuum</i> L.) non-host resistance against soybean pustule pathogen ( <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> ). <i>Functional and Integrative Genomics</i> , 2004, 4, 196-205. | 1.4 | 56        |
| 693 | Structural and functional analysis of rice genome. <i>Journal of Genetics</i> , 2004, 83, 79-99.   | 0.4 | 53        |
| 694 | The EDNAP mitochondrial DNA population database (EMPOP) collaborative exercises: organisation, results and perspectives. <i>Forensic Science International</i> , 2004, 139, 215-226.   | 1.3 | 105       |
| 695 | EST-analysis of the thermo-acidophilic red microalga <i>Galdieriasulphuraria</i> reveals potential for lipid A biosynthesis and unveils the pathway of carbon export from rhodoplasts. <i>Plant Molecular Biology</i> , 2004, 55, 17-32.                                       | 2.0 | 91        |
| 696 | Bacterial artificial chromosome (BAC) library resource for positional cloning of pest and disease resistance genes in cassava ( <i>Manihot esculenta</i> Crantz). <i>Plant Molecular Biology</i> , 2004, 56, 555-561.  | 2.0 | 19        |
| 697 | Large-scale computational analysis of poplar ESTs reveals the repertoire and unique features of expressed genes in the poplar genome. <i>Molecular Breeding</i> , 2004, 14, 429-440.   | 1.0 | 13        |
| 698 | Comparative genomics of the keratin-associated protein (KAP) gene clusters in human, chimpanzee, and baboon. <i>Mammalian Genome</i> , 2004, 15, 179-192.  | 1.0 | 8         |
| 699 | Beta-2-microglobulin haplotypes in U.S. beef cattle and association with failure of passive transfer in newborn calves. <i>Mammalian Genome</i> , 2004, 15, 227-236.   | 1.0 | 33        |
| 700 | Characterization of soybean genomic features by analysis of its expressed sequence tags. <i>Theoretical and Applied Genetics</i> , 2004, 108, 903-913.   | 1.8 | 83        |
| 701 | An EST survey of the sugarcane transcriptome. <i>Theoretical and Applied Genetics</i> , 2004, 108, 851-863.  | 1.8 | 67        |
| 702 | Annotation of a 95-kb <i>Populus deltoides</i> genomic sequence reveals a disease resistance gene cluster and novel class I and class II transposable elements. <i>Theoretical and Applied Genetics</i> , 2004, 109, 10-22.  | 1.8 | 37        |
| 703 | The anthracnose resistance locus Co-4 of common bean is located on chromosome 3 and contains putative disease resistance-related genes. <i>Theoretical and Applied Genetics</i> , 2004, 109, 690-699.  | 1.8 | 50        |
| 704 | Robust simple sequence repeat markers for spruce ( <i>Picea</i> spp.) from expressed sequence tags. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1283-1294.  | 1.8 | 181       |
| 705 | An expression profile of human pancreatic islet mRNAs by Serial Analysis of Gene Expression (SAGE). <i>Diabetologia</i> , 2004, 47, 284-299.   | 2.9 | 41        |
| 706 | Analysis of the contribution to type 2 diabetes susceptibility of sequence variation in the gene encoding stearoyl-CoA desaturase, a key regulator of lipid and carbohydrate metabolism. <i>Diabetologia</i> , 2004, 47, 2168-2175.  | 2.9 | 27        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 707 | Discrepancies in Bacterial Recovery from Dental Unit Water Samples on R2A Medium and a Commercial Sampling Device. <i>Current Microbiology</i> , 2004, 48, 243-246.  | 1.0 | 5         |
| 708 | Predation Pattern and Phylogenetic Analysis of Bdellovibrionaceae from the Great Salt Lake, Utah. <i>Current Microbiology</i> , 2004, 48, 113-117.   | 1.0 | 51        |
| 709 | Structural features and transcript-editing analysis of sugarcane ( <i>Saccharum officinarum</i> L.) chloroplast genome. <i>Current Genetics</i> , 2004, 46, 366-373.   | 0.8 | 76        |
| 710 | Genes involved in the anaerobic degradation of toluene in a denitrifying bacterium, strain EbN1. <i>Archives of Microbiology</i> , 2004, 181, 182-194.   | 1.0 | 90        |
| 711 | Mutation Exposed: A Neutral Explanation for Extreme Base Composition of an Endosymbiont Genome. <i>Journal of Molecular Evolution</i> , 2004, 59, 849-858.   | 0.8 | 30        |
| 712 | Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003. <i>BMC Infectious Diseases</i> , 2004, 4, 32.  | 1.3 | 58        |
| 713 | CLC-2 single nucleotide polymorphisms (SNPs) as potential modifiers of cystic fibrosis disease severity. <i>BMC Medical Genetics</i> , 2004, 5, 26.  | 2.1 | 13        |
| 714 | Detection and characterization of SNPs useful for identity control and parentage testing in major European dairy breeds. <i>Animal Genetics</i> , 2004, 35, 44-49.   | 0.6 | 94        |
| 715 | Mutations in PITX2 may contribute to cases of omphalocele and VATER-like syndromes. <i>American Journal of Medical Genetics Part A</i> , 2004, 130A, 277-283.  | 2.4 | 21        |
| 716 | Lack of evidence for an association between WNT2 and RELN polymorphisms and autism. <i>American Journal of Medical Genetics Part A</i> , 2004, 126B, 51-57.  | 2.4 | 88        |
| 717 | Effect of TERT and ATM on gene expression profiles in human fibroblasts. <i>Genes Chromosomes and Cancer</i> , 2004, 39, 298-310.  | 1.5 | 11        |
| 718 | GEISHA, a whole-mount in situ hybridization gene expression screen in chicken embryos. <i>Developmental Dynamics</i> , 2004, 229, 677-687.   | 0.8 | 88        |
| 719 | MAGIC Database and Interfaces: An Integrated Package for Gene Discovery and Expression. <i>Comparative and Functional Genomics</i> , 2004, 5, 268-275.   | 2.0 | 16        |
| 720 | Basecalling using hidden Markov models. <i>Journal of the Franklin Institute</i> , 2004, 341, 23-36.   | 1.9 | 16        |
| 721 | Protein expression clone repositories for functional proteomics. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 98-102.   | 2.8 | 13        |
| 722 | Functional Proteomics Mapping of a Human Signaling Pathway. <i>Genome Research</i> , 2004, 14, 1324-1332.  | 2.4 | 278       |
| 723 | Analysis of a 108-kb Region of the <i>Saccharopolyspora spinosa</i> Genome Covering the Obscurin Polyketide Synthase Locus. <i>DNA Sequence</i> , 2004, 15, 123-134.   | 0.7 | 11        |
| 724 | Changes in gene expression during meristem activation processes in <i>Solanum tuberosum</i> with a focus on the regulation of an auxin response factor gene*. <i>Journal of Experimental Botany</i> , 2004, 55, 613-622. | 2.4 | 78        |



| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 725 | Genomics, Proteomics, and Clinical Bacteriology. , 2004, , .   |      | 4         |
| 727 | Gene Conversion and the Evolution of Protocadherin Gene Cluster Diversity. <i>Genome Research</i> , 2004, 14, 354-366.   | 2.4  | 100       |
| 728 | Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004, 32, 2386-2395.            | 6.5  | 460       |
| 729 | Extensive and breed-specific linkage disequilibrium in <i>Canis familiaris</i> . <i>Genome Research</i> , 2004, 14, 2388-2396.   | 2.4  | 273       |
| 730 | Expression Islands Clustered on the Symbiosis Island of the <i>Mesorhizobium loti</i> Genome. <i>Journal of Bacteriology</i> , 2004, 186, 2439-2448.   | 1.0  | 205       |
| 731 | Gene Expression Profile of the Rat Eye Iridocorneal Angle: NEIBank Expressed Sequence Tag Analysis. , 2004, 45, 3081.  |      | 18        |
| 732 | Selecting a Maximally Informative Set of Single-Nucleotide Polymorphisms for Association Analyses Using Linkage Disequilibrium. <i>American Journal of Human Genetics</i> , 2004, 74, 106-120.   | 2.6  | 1,469     |
| 733 | The Genome Sequence of Silkworm, <i>Bombyx mori</i> . <i>DNA Research</i> , 2004, 11, 27-35.   | 1.5  | 594       |
| 734 | The promise of a DNA taxonomy. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004, 359, 669-679.   | 1.8  | 422       |
| 735 | Localization and Characterization of Two Novel Genes Encoding Stereospecific Dioxygenases Catalyzing 2(2,4-Dichlorophenoxy)propionate Cleavage in <i>Delftia acidovorans</i> MC1. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5357-5365. | 1.4  | 46        |
| 736 | The BDGP Gene Disruption Project. <i>Genetics</i> , 2004, 167, 761-781.  | 1.2  | 774       |
| 737 | Microarray-based resequencing of multiple <i>Bacillus anthracis</i> isolates. <i>Genome Biology</i> , 2004, 6, R10.  | 13.9 | 64        |
| 738 | Defining the CREB Regulon. <i>Cell</i> , 2004, 119, 1041-1054.   | 13.5 | 506       |
| 739 | Complete nucleotide sequence and organization of the naphthalene catabolic plasmid pND6-1 from <i>Pseudomonas</i> sp. strain ND6. <i>Gene</i> , 2004, 336, 231-240.  | 1.0  | 102       |
| 740 | Identification and characterization of a novel gene family YPEL in a wide spectrum of eukaryotic species. <i>Gene</i> , 2004, 340, 31-43.  | 1.0  | 55        |
| 741 | Transcript profiling of salinity stress responses by large-scale expressed sequence tag analysis in <i>Mesembryanthemum crystallinum</i> . <i>Gene</i> , 2004, 341, 83-92.   | 1.0  | 105       |
| 742 | Characterization of SCAR markers of spp. of domestic fowl and construction of a public relational database (The SCARdb). <i>FEMS Microbiology Letters</i> , 2004, 238, 183-188.  | 0.7  | 17        |
| 743 | Association of apolipoprotein A5 variants with LDL particle size and triglyceride in Japanese Americans. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2004, 1688, 1-9.  | 1.8  | 54        |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 744 | Inversion, duplication, and changes in gene context are associated with human chromosome 18 evolution. <i>Genomics</i> , 2004, 83, 493-501.   | 1.3 | 55        |
| 745 | TAFAs: a novel secreted family with conserved cysteine residues and restricted expression in the brain. <i>Genomics</i> , 2004, 83, 727-734.  | 1.3 | 97        |
| 746 | The immunoglobulin $\lambda$ variable light-chain region in primates has been shaped by multiple, independent, small-scale and large-scale insertion/deletion events. <i>Genomics</i> , 2004, 84, 678-685.                            | 1.3 | 1         |
| 747 | Mining single nucleotide polymorphisms from EST data of silkworm, <i>Bombyx mori</i> , inbred strain Dazao. <i>Insect Biochemistry and Molecular Biology</i> , 2004, 34, 523-530.   | 1.2 | 51        |
| 748 | Annotated expressed sequence tags for studies of the regulation of reproductive modes in aphids. <i>Insect Biochemistry and Molecular Biology</i> , 2004, 34, 809-822.  | 1.2 | 21        |
| 749 | Genome analyses of <i>Streptomyces peucetius</i> ATCC 27952 for the identification and comparison of cytochrome P450 complement with other <i>Streptomyces</i> . <i>Archives of Biochemistry and Biophysics</i> , 2004, 425, 233-241. | 1.4 | 51        |
| 750 | Evaluation and validation of quality assessment of mitochondrial control region sequence data by Phred. <i>International Congress Series</i> , 2004, 1261, 94-96.   | 0.2 | 2         |
| 751 | Assessment of the gene content of the chromosomal regions flanking bovine DGAT1. <i>Genomics</i> , 2004, 83, 172-180.   | 1.3 | 18        |
| 752 | New Genomic Tools for Molecular Studies of Evolutionary Change in Threespine Sticklebacks. <i>Behaviour</i> , 2004, 141, 1331-1344.   | 0.4 | 64        |
| 753 | Sequencing Strategies for Parasite Genomes. , 2004, 270, 001-016.   |     | 1         |
| 754 | Expressed Sequence Tags: Medium-Throughput Protocols<I>. , 2004, 270, 075-092.  |     | 63        |
| 755 | Expressed Sequence Tags: Analysis and Annotation<I>. , 2004, 270, 093-126.  |     | 11        |
| 756 | Does Smearing Inoculum Reflect the Bacterial Composition of the Smear at the End of the Ripening of a French Soft, Red-Smear Cheese?. <i>Journal of Dairy Science</i> , 2004, 87, 3189-3197.  | 1.4 | 89        |
| 757 | Both Rare and Common Polymorphisms Contribute Functional Variation at CHGA, a Regulator of Catecholamine Physiology. <i>American Journal of Human Genetics</i> , 2004, 74, 197-207.   | 2.6 | 104       |
| 758 | Sequence-Based Linkage Analysis. <i>American Journal of Human Genetics</i> , 2004, 75, 647-653.   | 2.6 | 4         |
| 759 | Establishment of publicly available cDNA material and information resource of <i>Chlamydomonas reinhardtii</i> (Chlorophyta) to facilitate gene function analysis. <i>Phycologia</i> , 2004, 43, 722-726.                             | 0.6 | 24        |
| 760 | Finishing "Working Draft" BAC Projects by Directed Sequencing With ThermoFidelase and Fimers. , 2004, 255, 295-308.   |     | 8         |
| 761 | Gene Discovery and Gene Expression in the Rice Blast Fungus, <i>Magnaporthe grisea</i> : Analysis of Expressed Sequence Tags. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1337-1347.                                      | 1.4 | 83        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 763 | Identification and Expression Analysis of EST-based Genes in the Bud of <i>Lycoris longituba</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2004, 2, 43-46.  | 3.0 | 5         |
| 764 | Target-Selected Gene Inactivation in Zebrafish. <i>Methods in Cell Biology</i> , 2004, 77, 69-90.  | 0.5 | 48        |
| 765 | Characterisation of SNP haplotype structure in chemokine and chemokine receptor genes using CEPH pedigrees and statistical estimation. <i>Human Genomics</i> , 2004, 1, 195-207.   | 1.4 | 3         |
| 766 | Combination of Suppression Subtractive Hybridization and Microarray Technologies to Enumerate Biomass-Induced Genes in the Cellulolytic Fungus <i>Trichoderma reesei</i> . <i>Applied Mycology and Biotechnology</i> , 2005, , 275-299.    | 0.3 | 2         |
| 767 | The genome sequence of <i>Salmonella enterica</i> serovar Choleraesuis, a highly invasive and resistant zoonotic pathogen. <i>Nucleic Acids Research</i> , 2005, 33, 1690-1698.  | 6.5 | 193       |
| 768 | Biological workflow with BlastQuest. <i>Data and Knowledge Engineering</i> , 2005, 53, 75-97.  | 2.1 | 10        |
| 770 | A Mitochondrial Genome Sequence of the Tibetan Antelope ( <i>Pantholops hodgsonii</i> ). <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 5-17.   | 3.0 | 60        |
| 771 | Neighboring-Nucleotide Effects on the Mutation Patterns of the Rice Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 158-168.   | 3.0 | 3         |
| 772 | Genome sequence of <i>Blochmannia pennsylvanicus</i> indicates parallel evolutionary trends among bacterial mutualists of insects. <i>Genome Research</i> , 2005, 15, 1023-1033.   | 2.4 | 169       |
| 774 | Large-Scale DNA Sequencing. , 2005, , 337-351.   |     | 2         |
| 775 | Combined Transcriptome Profiling Reveals a Novel Family of Arbuscular Mycorrhizal-Specific <i>Medicago truncatula</i> Lectin Genes. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 771-782.                                       | 1.4 | 63        |
| 776 | Base composition analysis of human mitochondrial DNA using electrospray ionization mass spectrometry: A novel tool for the identification and differentiation of humans. <i>Analytical Biochemistry</i> , 2005, 344, 53-69.                | 1.1 | 45        |
| 777 | Intraspecific gene expression variability in the yeast revealed by micro-array analysis. <i>FEMS Yeast Research</i> , 2005, 5, 595-604.  | 1.1 | 10        |
| 778 | Human response to $\alpha$ -adrenergic agonist stimulation studied in an isolated vascular bed in vivo: Biphasic influence of dose, age, gender, and receptor genotype. <i>Clinical Pharmacology and Therapeutics</i> , 2005, 77, 388-403. | 2.3 | 25        |
| 779 | Pharmacogenomics of responsiveness to interferon IFN- $\gamma$ treatment in multiple sclerosis: A genetic screen of 100 type I interferon-inducible genes. <i>Clinical Pharmacology and Therapeutics</i> , 2005, 78, 635-635.              | 2.3 | 71        |
| 780 | Isolation and annotation of 10828 putative full length cDNAs from indica rice. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 445.  | 1.3 | 17        |
| 781 | â€œBeijing Regionâ€ (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         |
| 782 | Representation and Highâ€Quality Annotation of the <i>Physcomitrella patens</i> Transcriptome Demonstrates a High Proportion of Proteins Involved in Metabolism in Mosses. <i>Plant Biology</i> , 2005, 7, 238-250.                        | 1.8 | 96        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 783 | HarvEST. , 2005, 406, 161-177.   |      | 33        |
| 784 | Association of CommonCRP Gene Variants with CRP Levels and Cardiovascular Events. <i>Annals of Human Genetics</i> , 2005, 69, 623-638.   | 0.3  | 199       |
| 785 | Analyses of coding region polymorphisms in apical and basolateral human organic anion transporter (OAT) genes [OAT1 (NKT), OAT2, OAT3, OAT4, URAT (RST)] Rapid Communication. <i>Kidney International</i> , 2005, 68, 1491-1499. | 2.6  | 85        |
| 786 | Differentially expressed genes during seed development in soybean. <i>Physiologia Plantarum</i> , 2005, 123, 321-330.  | 2.6  | 2         |
| 787 | Biotechnological improvement of cotton fibre maturity.. <i>Physiologia Plantarum</i> , 2005, 124, 285-294.   | 2.6  | 94        |
| 788 | Genomic tools and cDNA derived markers for butterflies. <i>Molecular Ecology</i> , 2005, 14, 2883-2897.  | 2.0  | 37        |
| 789 | Use of sequence data from rainbow trout and Atlantic salmon for SNP detection in Pacific salmon. <i>Molecular Ecology</i> , 2005, 14, 4193-4203.   | 2.0  | 165       |
| 790 | A set of testis-specific novel genes collected from a collection of Korean Native Chicken ESTs. <i>Animal Genetics</i> , 2005, 36, 346-348.  | 0.6  | 16        |
| 791 | Genome sequence of the chlorinated compoundâ€œrespiring bacterium <i>Dehalococcoides</i> species strain CBDB1. <i>Nature Biotechnology</i> , 2005, 23, 1269-1273.  | 9.4  | 277       |
| 792 | The complete genome sequence of <i>Francisella tularensis</i> , the causative agent of tularemia. <i>Nature Genetics</i> , 2005, 37, 153-159.  | 9.4  | 436       |
| 793 | Technology: A genome sequencing center in every lab. <i>European Journal of Human Genetics</i> , 2005, 13, 1167-1168.  | 1.4  | 11        |
| 794 | Norepinephrine Transporter: A Candidate Gene for Initial Ethanol Sensitivity in Inbred Long-Sleep and Short-Sleep Mice. <i>Alcoholism: Clinical and Experimental Research</i> , 2005, 29, 1759-1768.                             | 1.4  | 20        |
| 795 | Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005, 437, 1162-1166.  | 13.7 | 419       |
| 796 | Identification and Validation of Single Nucleotide Polymorphisms in Poplar Using Publicly Expressed Sequence Tags. <i>Journal of Integrative Plant Biology</i> , 2005, 47, 1493-1499.  | 4.1  | 28        |
| 797 | Molecular serotyping of <i>Salmonella</i> : identification of the phase 1 H antigen based on partial sequencing of the <i>fliC</i> gene. <i>Apmis</i> , 2005, 113, 340-348.  | 0.9  | 10        |
| 798 | Identification of a DNA fragment that increases mitotic stability of episomal linear DNAs in <i>Leishmania major</i> . <i>International Journal for Parasitology</i> , 2005, 35, 973-980.  | 1.3  | 3         |
| 799 | Molecular characterization of the insulin-like growth factor-I (IGF-I) gene in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005, 1731, 139-148.            | 2.4  | 23        |
| 800 | Genetic markers in blue crabs ( <i>Callinectes sapidus</i> ). <i>Journal of Experimental Marine Biology and Ecology</i> , 2005, 319, 15-27.  | 0.7  | 44        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 801 | Comparative analysis of selected genes from Diachasmimorpha longicaudata entomopoxvirus and other poxviruses. <i>Journal of Insect Physiology</i> , 2005, 51, 207-220.   | 0.9 | 16        |
| 802 | Expressed sequence tags from the plant trypanosomatid <i>Phytomonas serpens</i> . <i>Molecular and Biochemical Parasitology</i> , 2005, 142, 149-157.  | 0.5 | 18        |
| 803 | Differentially expressed sequences from a cestode parasite reveals conserved developmental genes in platyhelminthes. <i>Molecular and Biochemical Parasitology</i> , 2005, 144, 114-118.   | 0.5 | 14        |
| 804 | Advances in sequencing technology. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2005, 573, 13-40.  | 0.4 | 124       |
| 805 | Plasmid pB8 is closely related to the prototype IncP-1 $\hat{2}$ plasmid R751 but transfers poorly to <i>Escherichia coli</i> and carries a new transposon encoding a small multidrug resistance efflux protein. <i>Plasmid</i> , 2005, 54, 135-148. | 0.4 | 56        |
| 806 | Development of comprehensive functional genomic screens to identify novel mediators of osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2005, 13, 508-518.  | 0.6 | 43        |
| 807 | A method for finding single-nucleotide polymorphisms with allele frequencies in sequences of deep coverage. <i>BMC Bioinformatics</i> , 2005, 6, 220.  | 1.2 | 10        |
| 808 | XenDB: Full length cDNA prediction and cross species mapping in <i>Xenopus laevis</i> . <i>BMC Genomics</i> , 2005, 6, 123.  | 1.2 | 5         |
| 809 | EST analysis in <i>Ginkgo biloba</i> : an assessment of conserved developmental regulators and gymnosperm specific genes. <i>BMC Genomics</i> , 2005, 6, 143.  | 1.2 | 34        |
| 810 | Expression and genomic organization of zonadhesin-like genes in three species of fish give insight into the evolutionary history of a mosaic protein. <i>BMC Genomics</i> , 2005, 6, 165.  | 1.2 | 9         |
| 811 | An EST-based approach for identifying genes expressed in the intestine and gills of pre-smolt Atlantic salmon ( <i>Salmo salar</i> ). <i>BMC Genomics</i> , 2005, 6, 171.  | 1.2 | 22        |
| 812 | High-throughput sequencing: a failure mode analysis. <i>BMC Genomics</i> , 2005, 6, 2.   | 1.2 | 10        |
| 813 | Marine Genomics: A clearing-house for genomic and transcriptomic data of marine organisms. <i>BMC Genomics</i> , 2005, 6, 34.  | 1.2 | 34        |
| 814 | Floral gene resources from basal angiosperms for comparative genomics research. <i>BMC Plant Biology</i> , 2005, 5, 5.   | 1.6 | 100       |
| 815 | Development of real-time diagnostic assays specific for <i>Mycoplasma mycoides</i> subspecies <i>mycoides</i> Small Colony. <i>Veterinary Microbiology</i> , 2005, 111, 51-58.   | 0.8 | 19        |
| 816 | Complete genome sequence of bacteriophage T5. <i>Virology</i> , 2005, 332, 45-65.  | 1.1 | 106       |
| 817 | Sequence analysis of the complete genome of <i>Trichoplusia ni</i> single nucleopolyhedrovirus and the identification of a baculoviral photolyase gene. <i>Virology</i> , 2005, 338, 209-226.  | 1.1 | 71        |
| 818 | Virulence differences between monkeypox virus isolates from West Africa and the Congo basin. <i>Virology</i> , 2005, 340, 46-63.   | 1.1 | 342       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 819 | Matrix conditioning for lengthened capillary DNA sequencing. <i>Electrophoresis</i> , 2005, 26, 102-111.  | 1.3 | 5         |
| 820 | Contaminant-induced current decline in capillary array electrophoresis. <i>Electrophoresis</i> , 2005, 26, 2128-2137.   | 1.3 | 0         |
| 821 | Temperature-dependence of preconditioning for lengthened capillary DNA sequencing. <i>Electrophoresis</i> , 2005, 26, 4440-4448.  | 1.3 | 0         |
| 822 | EST sequencing for gene discovery in Chinese hamster ovary cells. <i>Biotechnology and Bioengineering</i> , 2005, 91, 592-606.  | 1.7 | 70        |
| 823 | DNA methylation in the CTCF-binding site I and the expression pattern of the H19 gene: Does positive expression predict poor prognosis in early stage head and neck carcinomas?. <i>Molecular Carcinogenesis</i> , 2005, 44, 102-110.                   | 1.3 | 24        |
| 824 | Hantaviruses in Central South America: Phylogenetic analysis of the S segment from HPS cases in Paran ıj, Brazil. <i>Journal of Medical Virology</i> , 2005, 76, 553-562.   | 2.5 | 36        |
| 825 | Investigation of the Mechanism of Resistance to Third-Generation Cephalosporins by Class C $\beta$ -Lactamases by Using Chemical Complementation. <i>ChemBioChem</i> , 2005, 6, 2055-2067.  | 1.3 | 8         |
| 826 | The Korea Brassica Genome Project: a Glimpse of the Brassica Genome Based on Comparative Genome Analysis With Arabidopsis. <i>Comparative and Functional Genomics</i> , 2005, 6, 138-146.   | 2.0 | 69        |
| 827 | PAQR Proteins: A Novel Membrane Receptor Family Defined by an Ancient 7-Transmembrane Pass Motif. <i>Journal of Molecular Evolution</i> , 2005, 61, 372-380.  | 0.8 | 304       |
| 828 | BEGAIN: A novel imprinted gene that generates paternally expressed transcripts in a tissue- and promoter-specific manner in sheep. <i>Mammalian Genome</i> , 2005, 16, 801-814.   | 1.0 | 19        |
| 829 | Analysis of expressed sequence tags and the identification of associated short tandem repeats in switchgrass. <i>Theoretical and Applied Genetics</i> , 2005, 111, 956-964.   | 1.8 | 50        |
| 830 | Random sheared fosmid library as a new genomic tool to accelerate complete finishing of rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overl...<br>euchromatic portions of the genome. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1596-1607. | 1.8 | 36        |
| 831 | Characteristics of the tomato nuclear genome as determined by sequencing undermethylated EcoRI digested fragments. <i>Theoretical and Applied Genetics</i> , 2005, 112, 72-84.  | 1.8 | 19        |
| 832 | Association analysis of candidate genes for maysin and chlorogenic acid accumulation in maize silks. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1324-1333.  | 1.8 | 124       |
| 833 | Fertility restorer locus Rf1 of sorghum ( <i>Sorghum bicolor</i> L.) encodes a pentatricopeptide repeat protein not present in the colinear region of rice chromosome 12. <i>Theoretical and Applied Genetics</i> , 2005, 111, 994-1012.                | 1.8 | 179       |
| 834 | Toward closing rice telomere gaps: mapping and sequence characterization of rice subtelomere regions. <i>Theoretical and Applied Genetics</i> , 2005, 111, 467-478.   | 1.8 | 21        |
| 835 | The genome sequence of an anaerobic aromatic-degrading denitrifying bacterium, strain EbN1. <i>Archives of Microbiology</i> , 2005, 183, 27-36.   | 1.0 | 266       |
| 836 | Applications of fuzzy logic in genomics. <i>Fuzzy Sets and Systems</i> , 2005, 152, 125-138.  | 1.6 | 14        |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 837 | In-depth sequence analysis of the tomato chromosome 12 centromeric region: identification of a large CAA block and characterization of pericentromere retrotransposons. <i>Chromosoma</i> , 2005, 114, 103-117.            | 1.0 | 52        |
| 838 | Comparative analysis of expressed sequence tags from cold-acclimated and non-acclimated leaves of <i>Rhododendron catawbiense</i> Michx. <i>Planta</i> , 2005, 221, 406-416.   | 1.6 | 81        |
| 839 | Isogene specific oligo arrays reveal multifaceted changes in gene expression during grape berry ( <i>Vitis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf   | 1.8 | 246       |
| 840 | Cycloheximide treatment of cotton ovules alters the abundance of specific classes of mRNAs and generates novel ESTs for microarray expression profiling. <i>Molecular Genetics and Genomics</i> , 2005, 274, 477-493.      | 1.0 | 21        |
| 841 | BRCA1 variants in a family study of African-American and Latina women. <i>Human Genetics</i> , 2005, 116, 497-506.   | 1.8 | 24        |
| 842 | Complex HTR2C linkage disequilibrium and promoter associations with body mass index and serum leptin. <i>Human Genetics</i> , 2005, 117, 545-557.  | 1.8 | 32        |
| 843 | <i>Agrobacterium</i> T-DNA integration in <i>Arabidopsis</i> is correlated with DNA sequence compositions that occur frequently in gene promoter regions. <i>Functional and Integrative Genomics</i> , 2005, 5, 240-253.   | 1.4 | 43        |
| 844 | Cloning, expression, and characterization of a highly thermostable family 18 chitinase from <i>Rhodothermus marinus</i> . <i>Extremophiles</i> , 2005, 9, 53-64.   | 0.9 | 48        |
| 845 | Applications of the double-barreled data in whole-genome shotgun sequence assembly and analysis. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 300-306.  | 1.3 | 0         |
| 846 | Identification and chromosomal localization of repeat sequences through BAC end sequence analysis in Korean cattle. <i>Journal of Genetics</i> , 2005, 84, 329-335.  | 0.4 | 4         |
| 847 | The effect of replicate number and image analysis method on sweetpotato [ <i>Ipomoea batatas</i> (L.) Lam.] cDNA microarray results. <i>Plant Molecular Biology Reporter</i> , 2005, 23, 367-381.                          | 1.0 | 1         |
| 848 | Large-scale computational analysis of poplar ESTs reveals the repertoire and unique features of expressed genes in the poplar genome. <i>Molecular Breeding</i> , 2005, 14, 429-440.                                       | 1.0 | 2         |
| 849 | Conservation genetics and Pacific fisheries bycatch: Mitochondrial differentiation and population assignment in black-footed albatrosses ( <i>Phoebastria nigripes</i> ). <i>Conservation Genetics</i> , 2005, 6, 289-295. | 0.8 | 25        |
| 850 | Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies. <i>Plant Molecular Biology</i> , 2005, 57, 375-391.   | 2.0 | 104       |
| 851 | Potato Expressed Sequence Tag Generation and Analysis using Standard and Unique cDNA Libraries. <i>Plant Molecular Biology</i> , 2005, 59, 407-433.  | 2.0 | 51        |
| 852 | Expressed sequence tags from the Yukon ecotype of <i>Thellungiella</i> reveal that gene expression in response to cold, drought and salinity shows little overlap. <i>Plant Molecular Biology</i> , 2005, 58, 561-574.     | 2.0 | 125       |
| 853 | Complete Chloroplast Genome Sequence of <i>Glycine max</i> and Comparative Analyses with other Legume Genomes. <i>Plant Molecular Biology</i> , 2005, 59, 309-322.   | 2.0 | 255       |
| 854 | Proteome analysis of early somatic embryogenesis in <i>Picea glauca</i> . <i>Proteomics</i> , 2005, 5, 461-473.  | 1.3 | 166       |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 856 | Single Nucleotide Polymorphism discovery and genotyping within the chicken Tapasin gene. Italian Journal of Animal Science, 2005, 4, 103-105.   | 0.8  | 0         |
| 857 | Genome organization and structural aspects of the SARS-related virus. , 2005, , 101-128.  |      | 4         |
| 860 | Errors in sequence assembly and corrections. , 2005, , .  |      | 0         |
| 862 | The Wolbachia Genome of <i>Brugia malayi</i> : Endosymbiont Evolution within a Human Pathogenic Nematode. PLoS Biology, 2005, 3, e121.  | 2.6  | 529       |
| 863 | Simple, robust methods for high-throughput nanoliter-scale DNA sequencing. Genome Research, 2005, 15, 1447-1450.  | 2.4  | 13        |
| 864 | SNPdetector: A Software Tool for Sensitive and Accurate SNP Detection. PLoS Computational Biology, 2005, 1, e53.  | 1.5  | 109       |
| 865 | RNA Viral Community in Human Feces: Prevalence of Plant Pathogenic Viruses. PLoS Biology, 2005, 4, e3.  | 2.6  | 589       |
| 866 | Olfactory Receptor Sequence Polymorphism Within and Between Breeds of Dogs. Journal of Heredity, 2005, 96, 812-816.   | 1.0  | 58        |
| 867 | novoSNP, a novel computational tool for sequence variation discovery. Genome Research, 2005, 15, 436-442.   | 2.4  | 254       |
| 868 | SAFA: Semi-automated footprinting analysis software for high-throughput quantification of nucleic acid footprinting experiments. Rna, 2005, 11, 344-354.  | 1.6  | 299       |
| 869 | Dogs really are man's best friend--Canine genomics has applications in veterinary and human medicine!. Briefings in Functional Genomics & Proteomics, 2005, 4, 112-128.   | 3.8  | 106       |
| 870 | An Attenuated LC16m8 Smallpox Vaccine: Analysis of Full-Genome Sequence and Induction of Immune Protection. Journal of Virology, 2005, 79, 11873-11891.   | 1.5  | 78        |
| 871 | Complete genome sequencing of <i>Anaplasma marginale</i> reveals that the surface is skewed to two superfamilies of outer membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 844-849. | 3.3  | 238       |
| 872 | Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of <i>Phytophthora infestans</i> . Molecular Biology and Evolution, 2005, 22, 659-672.  | 3.5  | 140       |
| 873 | Type II Collagen Gene Variants and Inherited Osteonecrosis of the Femoral Head. New England Journal of Medicine, 2005, 352, 2294-2301.  | 13.9 | 166       |
| 874 | Patterns of Polymorphism and Divergence from Noncoding Sequences of <i>Drosophila melanogaster</i> and <i>D. simulans</i> : Evidence for Nonequilibrium Processes. Molecular Biology and Evolution, 2005, 22, 51-62.                              | 3.5  | 42        |
| 875 | Complete Nucleotide Sequence of the LE1 Prophage from the Spirochete <i>Leptospira biflexa</i> and Characterization of Its Replication and Partition Functions. Journal of Bacteriology, 2005, 187, 3931-3940.                                    | 1.0  | 34        |
| 876 | Molecular Basis of Evolutionary Events That Shaped the Hardness Locus in Diploid and Polyploid Wheat Species ( <i>Triticum</i> and <i>Aegilops</i> ). Plant Cell, 2005, 17, 1033-1045.  | 3.1  | 360       |



| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 877 | Countrywide Survey Shows Very High Prevalence of Plasmodium falciparum Multilocus Resistance Genotypes in Cambodia. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 3147-3152.                                      | 1.4 | 52        |
| 878 | Analysis of long-lived <i>C. elegans</i> <i>daf-2</i> mutants using serial analysis of gene expression. <i>Genome Research</i> , 2005, 15, 603-615.  | 2.4 | 180       |
| 879 | DNA Rearrangement in Orthologous Orp Regions of the Maize, Rice and Sorghum Genomes. <i>Genetics</i> , 2005, 170, 1209-1220.   | 1.2 | 62        |
| 880 | Genome of Deerpox Virus. <i>Journal of Virology</i> , 2005, 79, 966-977.   | 1.5 | 55        |
| 881 | Evidence for Domesticated and Wild Populations of <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2005, 1, e5.  | 1.5 | 416       |
| 882 | The bovine PPARGC1A gene: molecular characterization and association of an SNP with variation of milk fat synthesis. <i>Physiological Genomics</i> , 2005, 21, 1-13.   | 1.0 | 127       |
| 883 | Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. <i>Genome Research</i> , 2005, 15, 174-183.  | 2.4 | 79        |
| 884 | Genomics of the thermo-acidophilic red alga <i>Galdieria sulphuraria</i> . , 2005, , .   |     | 2         |
| 885 | Automated genomic sequence analysis of the three collagen VI genes: applications to Ullrich congenital muscular dystrophy and Bethlem myopathy. <i>Journal of Medical Genetics</i> , 2005, 42, 108-120.                      | 1.5 | 119       |
| 886 | Identifying the Basal Angiosperm Node in Chloroplast Genome Phylogenies: Sampling One's Way Out of the Felsenstein Zone. <i>Molecular Biology and Evolution</i> , 2005, 22, 1948-1963.                                       | 3.5 | 242       |
| 887 | Mutator -Like Element in the Yeast <i>Yarrowia lipolytica</i> Displays Multiple Alternative Splicings. <i>Eukaryotic Cell</i> , 2005, 4, 615-624.  | 3.4 | 41        |
| 888 | Sorghum Expressed Sequence Tags Identify Signature Genes for Drought, Pathogenesis, and Skotomorphogenesis from a Milestone Set of 16,801 Unique Transcripts. <i>Plant Physiology</i> , 2005, 139, 869-884.                  | 2.3 | 66        |
| 889 | Serial Analysis of Gene Expression Reveals Conserved Links between Protein Kinase A, Ribosome Biogenesis, and Phosphate Metabolism in <i>Ustilago maydis</i> . <i>Eukaryotic Cell</i> , 2005, 4, 2029-2043.                  | 3.4 | 25        |
| 890 | Isolation and Characterization of a Native Composite Transposon, Tn 14751 , Carrying 17.4 Kilobases of <i>Corynebacterium glutamicum</i> Chromosomal DNA. <i>Applied and Environmental Microbiology</i> , 2005, 71, 407-416. | 1.4 | 19        |
| 891 | Rapid and efficient cDNA library screening by self-ligation of inverse PCR products (SLIP). <i>Nucleic Acids Research</i> , 2005, 33, e185-e185.   | 6.5 | 21        |
| 892 | Finding Fibrosis Genes. , 2005, 117, 293-313.  |     | 2         |
| 893 | ESTIMATION OF THE EXTENT OF LINKAGE DISEQUILIBRIUM IN SEVEN REGIONS OF THE PORCINE GENOME. <i>Animal Biotechnology</i> , 2005, 16, 41-54.  | 0.7 | 17        |
| 894 | Bioinformatic Tools for Gene and Protein Sequence Analysis. , 2005, , 387-407.   |     | 1         |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 895 | High Throughput Identification of Potential Arabidopsis Mitogen-activated Protein Kinases Substrates. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1558-1568.  | 2.5 | 223       |
| 896 | Discovery of a unique Ig heavy-chain isotype (IgT) in rainbow trout: Implications for a distinctive B cell developmental pathway in teleost fish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6919-6924.    | 3.3 | 437       |
| 897 | Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : Chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005, 15, 1-18.   | 2.4 | 453       |
| 898 | High-Diversity Genes in the Arabidopsis Genome Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. DQ132063, DQ132370.. <i>Genetics</i> , 2005, 170, 1897-1911.   | 1.2 | 35        |
| 899 | A mouse atlas of gene expression: Large-scale digital gene-expression profiles from precisely defined developing C57BL/6J mouse tissues and cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18485-18490. | 3.3 | 112       |
| 900 | An evolutionary constraint: Strongly disfavored class of change in DNA sequence during divergence of cis-regulatory modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11769-11774.                       | 3.3 | 35        |
| 901 | Genomic characterization of non-O1, non-O139 <i>Vibrio cholerae</i> reveals genes for a type III secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3465-3470.                                   | 3.3 | 217       |
| 902 | Genes "Waiting" for Recruitment by the Adaptive Immune System: The Insights from <i>Amphioxus</i> . <i>Journal of Immunology</i> , 2005, 174, 3493-3500.  | 0.4 | 58        |
| 903 | The $\alpha$ - and $\beta$ -subunits of the Human UDP-N-acetylglucosamine:Lysosomal Enzyme Phosphotransferase Are Encoded by a Single cDNA. <i>Journal of Biological Chemistry</i> , 2005, 280, 36141-36149.  | 1.6 | 108       |
| 904 | Genomic Sequence of an Otitis Media Isolate of Nontypeable <i>Haemophilus influenzae</i> : Comparative Study with <i>H. influenzae</i> Serotype d, Strain KW20. <i>Journal of Bacteriology</i> , 2005, 187, 4627-4636.  | 1.0 | 195       |
| 905 | Genetic Variation at the Human $\beta$ 2-Adrenergic Receptor Locus. <i>Hypertension</i> , 2005, 45, 1207-1213.  | 1.3 | 27        |
| 906 | Gene Discovery and Expression Profile Analysis through Sequencing of Expressed Sequence Tags from Different Developmental Stages of the Chytridiomycete <i>Blastocladiella emersonii</i> . <i>Eukaryotic Cell</i> , 2005, 4, 455-464.                               | 3.4 | 21        |
| 907 | Novel Major Bacterial Candidate Division within a Municipal Anaerobic Sludge Digester. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2145-2153.   | 1.4 | 107       |
| 908 | A tale of two clades: monkeypox viruses. <i>Journal of General Virology</i> , 2005, 86, 2661-2672.  | 1.3 | 548       |
| 909 | Analysis and mapping of randomly chosen bacterial artificial chromosome clones from hexaploid bread wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 19243-19248.   | 3.3 | 86        |
| 910 | A genome-wide survey of structural variation between human and chimpanzee. <i>Genome Research</i> , 2005, 15, 1344-1356.  | 2.4 | 153       |
| 911 | Conservation of regulatory sequences and gene expression patterns in the disintegrating <i>Drosophila</i> Hox gene complex. <i>Genome Research</i> , 2005, 15, 692-700.   | 2.4 | 48        |
| 912 | Transcriptome analysis of the aphid bacteriocyte, the symbiotic host cell that harbors an endocellular mutualistic bacterium, <i>Buchnera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5477-5482.      | 3.3 | 212       |

| #   | ARTICLE  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 913 | The <i>Chlamydomonas reinhardtii</i> genome sequence reveals an array of variable proteins that contribute to interspecies variation. <i>Genome Research</i> , 2005, 15, 629-640.  | 2.4 | 158       |
| 914 | The Lacrimal Gland Transcriptome Is an Unusually Rich Source of Rare and Poorly Characterized Gene Transcripts. , 2005, 46, 1572.  |     | 45        |
| 915 | The Growth Hormone Receptor Gene is Associated with Mandibular Height in a Chinese Population. <i>Journal of Dental Research</i> , 2005, 84, 1052-1056.  | 2.5 | 60        |
| 916 | Multilocus Sequence Typing versus Pulsed-Field Gel Electrophoresis for Characterization of Extended-Spectrum Beta-Lactamase-Producing <i>Escherichia coli</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2005, 43, 1776-1781.                 | 1.8 | 67        |
| 917 | Composition and Structure of Microbial Communities from Stromatolites of Hamelin Pool in Shark Bay, Western Australia. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4822-4832.  | 1.4 | 203       |
| 918 | Cloning and Characterization of MicroRNAs from Rice. <i>Plant Cell</i> , 2005, 17, 1397-1411.  | 3.1 | 462       |
| 919 | Exploring the Genome of <i>Trypanosoma vivax</i> through GSS and In Silico Comparative Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 116-128.   | 1.0 | 4         |
| 920 | A Comprehensive Survey of the Genes Involved in Maturation and Development of the Rainbow Trout Ovary1. <i>Biology of Reproduction</i> , 2005, 72, 687-699.  | 1.2 | 95        |
| 921 | Ancient haplotypes resulting from extensive molecular rearrangements in the wheat A genome have been maintained in species of three different ploidy levels. <i>Genome Research</i> , 2005, 15, 526-536.   | 2.4 | 68        |
| 922 | Nucleotide sequence comparison of a chromosome rearrangement on human chromosome 12 and the corresponding ape chromosomes. <i>Cytogenetic and Genome Research</i> , 2005, 108, 83-90.  | 0.6 | 19        |
| 923 | Sequencing and mapping hemoglobin gene clusters in the Australian model marsupial <i>Sminthopsis macroura</i> . <i>Cytogenetic and Genome Research</i> , 2005, 108, 333-341.   | 0.6 | 16        |
| 924 | Large-Scale Analysis of Adeno-Associated Virus Vector Integration Sites in Normal Human Cells. <i>Journal of Virology</i> , 2005, 79, 11434-11442.   | 1.5 | 148       |
| 925 | Characterization of the flexible genome complement of the commensal <i>Escherichia coli</i> strain AO 34/86 (O83â€¦â€¦K24â€¦â€¦H31). <i>Microbiology (United Kingdom)</i> , 2005, 151, 385-398.  | 0.7 | 45        |
| 926 | Hypervariable Noncoding Sequences in <i>Saccharomyces cerevisiae</i> Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY942206, AY942556.. <i>Genetics</i> , 2005, 170, 1575-1587.        | 1.2 | 30        |
| 927 | The <i>Oryza</i> bacterial artificial chromosome library resource: Construction and analysis of 12 deep-coverage large-insert BAC libraries that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Research</i> , 2005, 16, 140-147. | 2.4 | 197       |
| 928 | A missense mutation in the type II hair keratin hHb3 is associated with monilethrix. <i>Journal of Medical Genetics</i> , 2005, 42, e19-e19.   | 1.5 | 70        |
| 929 | Functional Analysis of All Nonribosomal Peptide Synthetases in <i>Cochliobolus heterostrophus</i> Reveals a Factor, NPS6, Involved in Virulence and Resistance to Oxidative Stress. <i>Eukaryotic Cell</i> , 2005, 4, 545-555.                         | 3.4 | 144       |
| 930 | Method for discovering novel DNA viruses in blood using viral particle selection and shotgun sequencing. <i>BioTechniques</i> , 2005, 39, 729-736.   | 0.8 | 150       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 931 | Microbes on the human vaginal epithelium. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7952-7957.  | 3.3 | 281       |
| 932 | Genomic Comparison of Plant Pathogenic and Nonpathogenic <i>Serratia marcescens</i> Strains by Suppressive Subtractive Hybridization. Applied and Environmental Microbiology, 2005, 71, 7716-7723.              | 1.4 | 32        |
| 933 | Complete Sequences of Four Plasmids of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> SK11 Reveal Extensive Adaptation to the Dairy Environment. Applied and Environmental Microbiology, 2005, 71, 8371-8382. | 1.4 | 150       |
| 934 | The IncP-6 Plasmid Rms149 Consists of a Small Mobilizable Backbone with Multiple Large Insertions. Journal of Bacteriology, 2005, 187, 4728-4738.   | 1.0 | 78        |
| 935 | A Large-Scale Screen for Artificial Selection in Maize Identifies Candidate Agronomic Loci for Domestication and Crop Improvement. Plant Cell, 2005, 17, 2859-2872.   | 3.1 | 234       |
| 936 | Identification and characterization of endogenous small interfering RNAs from rice. Nucleic Acids Research, 2005, 33, 4443-4454.  | 6.5 | 92        |
| 937 | Mutation analysis of the MCHR1 gene in human obesity. European Journal of Endocrinology, 2005, 152, 851-862.  | 1.9 | 34        |
| 938 | Single-Nucleotide Polymorphisms and Haplotype LD Analysis of the 29-kb IGF2 Region on Chromosome 11p15.5 in the Korean Population. Human Heredity, 2005, 60, 73-80.   | 0.4 | 4         |
| 939 | GenColors: accelerated comparative analysis and annotation of prokaryotic genomes at various stages of completeness. Bioinformatics, 2005, 21, 3669-3671.   | 1.8 | 16        |
| 940 | TargetIdentifier: a webserver for identifying full-length cDNAs from EST sequences. Nucleic Acids Research, 2005, 33, W669-W672.  | 6.5 | 44        |
| 941 | Mapping of transcription start sites in <i>Saccharomyces cerevisiae</i> using 5' SAGE. Nucleic Acids Research, 2005, 33, 2838-2851.   | 6.5 | 180       |
| 942 | EST Data Mining and Applications in Fungal Genomics. Applied Mycology and Biotechnology, 2005, 5, 33-70.  | 0.3 | 0         |
| 943 | Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. Methods in Enzymology, 2005, 395, 348-384.  | 0.4 | 410       |
| 944 | Mutations in ABCA12 Underlie the Severe Congenital Skin Disease Harlequin Ichthyosis. American Journal of Human Genetics, 2005, 76, 794-803.  | 2.6 | 302       |
| 945 | Mutations in TCF8 Cause Posterior Polymorphous Corneal Dystrophy and Ectopic Expression of COL4A3 by Corneal Endothelial Cells. American Journal of Human Genetics, 2005, 77, 694-708.                          | 2.6 | 177       |
| 946 | Phylogenetics of modern birds in the era of genomics. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 979-992.  | 1.2 | 83        |
| 947 | The <i>C. elegans</i> Interactome: Its Generation and Visualization. , 2005, , 113-133.   |     | 0         |
| 948 | Medical Biomethods Handbook. , 2005, , .  |     | 3         |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 949 | Xylella and Xanthomonas Mobil'omics. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 146-159.  | 1.0 | 46        |
| 950 | Isolation and Enrichment of Abundant Microsatellites from a Channel Catfish ( <i>Ictalurus punctatus</i> ) Brain cDNA Library. <i>Animal Biotechnology</i> , 2005, 16, 103-116.   | 0.7 | 17        |
| 951 | A Genomic Region Evolving Toward Different GC Contents in Humans and Chimpanzees Indicates a Recent and Regionally Limited Shift in the Mutation Pattern. <i>Molecular Biology and Evolution</i> , 2005, 22, 1240-1245.       | 3.5 | 10        |
| 952 | Nucleotide Diversity and Linkage Disequilibrium in Cold-Hardiness- and Wood Quality-Related Candidate Genes in Douglas Fir. <i>Genetics</i> , 2005, 171, 2029-2041.   | 1.2 | 167       |
| 953 | Defining operational taxonomic units using DNA barcode data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1935-1943.  | 1.8 | 729       |
| 954 | The human genome project: software challenges and future directions. , 0, , .   |     | 0         |
| 955 | A comparative survey, by expressed sequence tag analysis, of genes expressed in peach leaves infected with <i>Plum pox virus</i> (PPV) and free from PPV. <i>Canadian Journal of Plant Pathology</i> , 2005, 27, 410-419.     | 0.8 | 12        |
| 956 | Emerging technologies in DNA sequencing. <i>Genome Research</i> , 2005, 15, 1767-1776.  | 2.4 | 384       |
| 957 | Characterization of 8p21.3 chromosomal deletions in B-cell lymphoma: TRAIL-R1 and TRAIL-R2 as candidate dosage-dependent tumor suppressor genes. <i>Blood</i> , 2005, 106, 3214-3222.   | 0.6 | 137       |
| 958 | Expression analysis and physical mapping of low-molecular-weight glutenin loci in hexaploid wheat ( <i>Triticum aestivum</i> L.). <i>Genome</i> , 2005, 48, 401-410.  | 0.9 | 16        |
| 959 | A novel class of herpesvirus with bivalve hosts. <i>Journal of General Virology</i> , 2005, 86, 41-53.  | 1.3 | 260       |
| 961 | The Development of a High-Density Canine Microarray. <i>Journal of Heredity</i> , 2005, 96, 817-820.  | 1.0 | 12        |
| 962 | Interaction of Heterochromatin Protein 2 with HP1 Defines a Novel HP1-Binding Domain. <i>Biochemistry</i> , 2005, 44, 13394-13403.  | 1.2 | 22        |
| 963 | Complete Nucleotide Sequence of the Chloroplast Genome from the Tasmanian Blue Gum, <i>Eucalyptus globulus</i> (Myrtaceae). <i>DNA Research</i> , 2005, 12, 215-220.  | 1.5 | 104       |
| 964 | The cathepsin L-like proteinases from the midgut of <i>Tenebrio molitor</i> larvae: Sequence, properties, immunocytochemical localization and function. <i>Insect Biochemistry and Molecular Biology</i> , 2005, 35, 883-901. | 1.2 | 83        |
| 965 | Promoter-2-derived expression in bovine granulosa cells coincides with gene-specific DNA hypo-methylation. <i>Molecular and Cellular Endocrinology</i> , 2005, 233, 57-64.  | 1.6 | 54        |
| 966 | Synaptopodin and 4 novel genes identified in primary sensory neurons. <i>Molecular and Cellular Neurosciences</i> , 2005, 30, 316-325.  | 1.0 | 3         |
| 967 | The first complete chloroplast genome sequence of a lycophyte, <i>Huperzia lucidula</i> (Lycopodiaceae). <i>Gene</i> , 2005, 350, 117-128.  | 1.0 | 101       |

| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 968 | Development of a spot reliability evaluation score for DNA microarrays. <i>Gene</i> , 2005, 350, 149-160.   | 1.0 | 1         |
| 969 | Genetic linkage map of medaka with polymerase chain reaction length polymorphisms. <i>Gene</i> , 2005, 363, 24-31.  | 1.0 | 31        |
| 970 | Activation of TLR3 and TLR5 in channel catfish exposed to virulent. <i>Developmental and Comparative Immunology</i> , 2005, 29, 713-721.  | 1.0 | 127       |
| 971 | Pre- and post-introduction patterns in neutral genetic diversity in the leafy spurge gall midge, <i>Spurgia capitigena</i> (Bremi) (Diptera: Cecidomyiidae). <i>Biological Control</i> , 2005, 33, 153-164. | 1.4 | 20        |
| 972 | Truncated and RIP-degenerated copies of the LTR retrotransposon are clustered in a pericentromeric region of the genome. <i>Fungal Genetics and Biology</i> , 2005, 42, 30-41.                              | 0.9 | 26        |
| 973 | Gene discovery and expression profiling in porcine Peyer's patch. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 301-315.  | 0.5 | 27        |
| 974 | 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.   | 1.3 | 5         |
| 975 | Fine mapping of radiation susceptibility and gene expression analysis of LEC congenic rat lines. <i>Genomics</i> , 2005, 86, 271-279.   | 1.3 | 4         |
| 976 | A physical map of the genome of Atlantic salmon, <i>Salmo salar</i> . <i>Genomics</i> , 2005, 86, 396-404.  | 1.3 | 97        |
| 977 | A high-resolution comparative map between pig chromosome 17 and human chromosomes 4, 8, and 20: Identification of synteny breakpoints. <i>Genomics</i> , 2005, 86, 405-413.                                 | 1.3 | 14        |
| 978 | Targeted, haplotype-resolved resequencing of long segments of the human genome. <i>Genomics</i> , 2005, 86, 759-766.  | 1.3 | 23        |
| 979 | Identification of different regions among strains of <i>Yersinia pestis</i> by suppression subtractive hybridization. <i>Research in Microbiology</i> , 2005, 156, 785-789.                                 | 1.0 | 15        |
| 980 | Identification and characterization of the <i>afsR</i> homologue regulatory gene from <i>Streptomyces peucetius</i> ATCC 27952. <i>Research in Microbiology</i> , 2005, 156, 707-712.                       | 1.0 | 45        |
| 981 | Multilocus Sequence Typing for Studying Genetic Relationships among <i>Yersinia</i> Species. <i>Journal of Clinical Microbiology</i> , 2005, 43, 2674-2684.   | 1.8 | 103       |
| 982 | Comprehensive Structural Analysis of the Genome of Red Clover ( <i>Trifolium pratense</i> L.). <i>DNA Research</i> , 2005, 12, 301-364.   | 1.5 | 145       |
| 983 | Protein interaction mapping: A <i>Drosophila</i> case study. <i>Genome Research</i> , 2005, 15, 376-384.  | 2.4 | 509       |
| 984 | Transcriptome comparison of winter and spring wheat responding to low temperature. <i>Genome</i> , 2005, 48, 913-923.   | 0.9 | 95        |
| 985 | TNF- $\alpha$ Promoter Polymorphisms and Susceptibility to Human Papillomavirus 16-associated Cervical Cancer. <i>Journal of Infectious Diseases</i> , 2005, 191, 969-976.                                  | 1.9 | 91        |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 986  | The efficacy of Cot-based gene enrichment in wheat ( <i>Triticum aestivum</i> L.). <i>Genome</i> , 2005, 48, 1120-1126.  | 0.9  | 40        |
| 987  | Phylogeny and the Evolution of Floral Diversity in <i>Pedicularis</i> (Orobanchaceae). <i>International Journal of Plant Sciences</i> , 2005, 166, 595-613.  | 0.6  | 103       |
| 988  | Functional Analysis of Three Plasmids from <i>Lactobacillus plantarum</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 1223-1230.   | 1.4  | 100       |
| 989  | Low levels of linkage disequilibrium in wild barley ( <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> ) despite high rates of self-fertilization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2442-2447. | 3.3  | 184       |
| 990  | Molecular signatures for sex in the Placozoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15518-15522.   | 3.3  | 63        |
| 991  | Second report on chicken genes and chromosomes 2005. <i>Cytogenetic and Genome Research</i> , 2005, 109, 415-479.  | 0.6  | 136       |
| 993  | <i>Pseudomonas fluorescens</i> . , 2005, , 45-66.  |      | 6         |
| 995  | Analysis of the <i>Macaca mulatta</i> transcriptome and the sequence divergence between <i>Macaca</i> and human. <i>Genome Biology</i> , 2005, 6, R60.   | 13.9 | 84        |
| 996  | Genomic sequence and analysis of a vaccinia virus isolate from a patient with a smallpox vaccine-related complication. <i>Virology Journal</i> , 2006, 3, 88.  | 1.4  | 24        |
| 997  | Comparison of dot chromosome sequences from <i>D. melanogaster</i> and <i>D. virilis</i> reveals an enrichment of DNA transposon sequences in heterochromatic domains. <i>Genome Biology</i> , 2006, 7, R15.   | 3.8  | 50        |
| 998  | <i>Statistical Methods in Serial Analysis of Gene Expression</i> (Sage). , 2006, , 209-233.  |      | 2         |
| 1002 | Molecular Basis of Plant Gene Expression During Aphid Invasion: Wheat <i>Pto</i> and <i>Pti</i> Like Sequences Are Involved in Interactions Between Wheat and Russian Wheat Aphid (Homoptera: Tj ETQq1 1 0.784314 rgBT /@erlock 10                             |      |           |
| 1003 | Single Nucleotide Polymorphism Discovery in the Avian Tapasin Gene. <i>Poultry Science</i> , 2006, 85, 606-612.  | 1.5  | 7         |
| 1004 | Evolution of the Terminal Regions of the <i>Streptomyces</i> Linear Chromosome. <i>Molecular Biology and Evolution</i> , 2006, 23, 2361-2369.  | 3.5  | 96        |
| 1006 | Rigorous performance evaluation in protein structure modelling and implications for computational biology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 453-458.   | 1.8  | 34        |
| 1007 | A hitchhiker's guide to expressed sequence tag (EST) analysis. <i>Briefings in Bioinformatics</i> , 2006, 8, 6-21.   | 3.2  | 235       |
| 1008 | The <i>Methanosarcina barkeri</i> Genome: Comparative Analysis with <i>Methanosarcina acetivorans</i> and <i>Methanosarcina mazei</i> Reveals Extensive Rearrangement within Methanosarcinal Genomes. <i>Journal of Bacteriology</i> , 2006, 188, 7922-7931.   | 1.0  | 158       |
| 1009 | Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. <i>American Journal of Human Genetics</i> , 2006, 79, 500-513.   | 2.6  | 261       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1010 | Gene expression profiles underlying alternative caste phenotypes in a highly eusocial bee, <i>Melipona quadrifasciata</i> . <i>Insect Molecular Biology</i> , 2006, 15, 33-44.  | 1.0 | 42        |
| 1011 | Comparative and functional genomics of <i>Listeria</i> spp.. <i>Journal of Biotechnology</i> , 2006, 126, 37-51.  | 1.9 | 86        |
| 1012 | Discovery, cloning and heterologous expression of secreted potato proteins reveal erroneous pre-mRNA splicing in <i>Aspergillus oryzae</i> . <i>Journal of Biotechnology</i> , 2006, 126, 265-276.                              | 1.9 | 15        |
| 1013 | Molecular Population Genetics of the Gene Encoding the Human Fertilization Protein Zonadhesin Reveals Rapid Adaptive Evolution. <i>American Journal of Human Genetics</i> , 2006, 79, 820-830.                                  | 2.6 | 48        |
| 1014 | Bioinformatics Packages for Sequence Analysis. <i>Applied Mycology and Biotechnology</i> , 2006, 6, 143-160.  | 0.3 | 8         |
| 1015 | The Consensus Coding Sequences of Human Breast and Colorectal Cancers. <i>Science</i> , 2006, 314, 268-274.   | 6.0 | 3,130     |
| 1016 | Generating Unigene Collections of Expressed Sequence Tag Sequences for Use in Mass Spectrometry Identification. , 2007, 367, 77-86.   |     | 4         |
| 1017 | Types and Rates of Sequence Evolution at the High-Molecular-Weight Glutenin Locus in Hexaploid Wheat and Its Ancestral Genomes. <i>Genetics</i> , 2006, 174, 1493-1504.   | 1.2 | 83        |
| 1018 | Fifteen-Year Study of the Changing Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>American Journal of Medicine</i> , 2006, 119, 943-951.   | 0.6 | 173       |
| 1019 | Molecular sequencing and morphological analysis of a nematode community. <i>Applied Soil Ecology</i> , 2006, 32, 325-337.   | 2.1 | 58        |
| 1020 | Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus <i>Penicillium marneffei</i> . <i>FEBS Letters</i> , 2006, 580, 3409-3416.  | 1.3 | 60        |
| 1021 | Whole-genome re-sequencing. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 545-552.   | 1.5 | 706       |
| 1022 | The Fanconi anemia gene network is conserved from zebrafish to human. <i>Gene</i> , 2006, 371, 211-223.   | 1.0 | 35        |
| 1023 | DNA barcoding: A molecular tool to identify Antarctic marine larvae. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2006, 53, 1053-1060.   | 0.6 | 89        |
| 1024 | Isolation and Characterization of a Cyanophage Infecting the Toxic Cyanobacterium <i>Microcystis aeruginosa</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 1239-1247.  | 1.4 | 126       |
| 1025 | Variants in candidate ALS modifier genes linked to Cu/Zn superoxide dismutase do not explain divergent survival phenotypes. <i>Neuroscience Letters</i> , 2006, 392, 52-57.   | 1.0 | 17        |
| 1026 | Gene expression in the gut of keratin-feeding clothes moths ( <i>Tineola</i> ) and keratin beetles ( <i>Trox</i> ) revealed by subtracted cDNA libraries. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 584-592. | 1.2 | 29        |
| 1027 | Purification, characterization and molecular cloning of the major chitinase from <i>Tenebrio molitor</i> larval midgut. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 789-800.                                   | 1.2 | 68        |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1028 | Macroarray expression analysis of barley susceptibility and nonhost resistance to <i>Blumeria graminis</i> . <i>Journal of Plant Physiology</i> , 2006, 163, 657-670.  | 1.6 | 24        |
| 1029 | Characterization of caprine herpesvirus 1 glycoprotein D gene and its translation product. <i>Virus Research</i> , 2006, 115, 112-121.   | 1.1 | 4         |
| 1030 | Utilization of a zebra finch BAC library to determine the structure of an avian androgen receptor genomic region. <i>Genomics</i> , 2006, 87, 181-190.   | 1.3 | 25        |
| 1031 | Defective repair of radiation-induced DNA damage is complemented by a CHORI-230-65K18 BAC clone on rat chromosome 4. <i>Genomics</i> , 2006, 87, 236-242.  | 1.3 | 2         |
| 1032 | An efficient and high-throughput approach for experimental validation of novel human gene predictions. <i>Genomics</i> , 2006, 87, 437-445.  | 1.3 | 6         |
| 1033 | ChickGCE: A novel germ cell EST database for studying the early developmental stage in chickens. <i>Genomics</i> , 2006, 88, 252-257.  | 1.3 | 10        |
| 1034 | Correlation of serpinâ€œprotease expression by comparative analysis of real-time PCR profiling data. <i>Genomics</i> , 2006, 88, 173-184.  | 1.3 | 17        |
| 1035 | Analysis of ESTs from <i>Lutzomyia longipalpis</i> sand flies and their contribution toward understanding the insectâ€œparasite relationship. <i>Genomics</i> , 2006, 88, 831-840.   | 1.3 | 62        |
| 1036 | Four specific isogenes of the anthocyanin metabolic pathway are systematically co-expressed with the red colour of grape berries. <i>Plant Science</i> , 2006, 170, 372-383.   | 1.7 | 176       |
| 1037 | Comparative EST profiles of leaf and root of <i>Leymus chinensis</i> , a xerophilous grass adapted to high pH sodic soil. <i>Plant Science</i> , 2006, 170, 1081-1086.   | 1.7 | 84        |
| 1038 | Sequencing and analysis of 14,842 expressed sequence tags of burma mangrove, <i>Bruguiera gymnorhiza</i> . <i>Plant Science</i> , 2006, 171, 234-241.  | 1.7 | 32        |
| 1039 | Enrichment of bermudagrass genes associated with tolerance to the spring dead spot fungus <i>Ophiostoma herpotricha</i> . <i>Physiological and Molecular Plant Pathology</i> , 2006, 68, 105-118.  | 1.3 | 5         |
| 1040 | Proteomic analysis of <i>Neisseria lactamica</i> and <i>N. meningitidis</i> outer membrane vesicle vaccine antigens. <i>Vaccine</i> , 2006, 24, 5277-5293.   | 1.7 | 43        |
| 1041 | A bacterial artificial chromosome library for <i>Biomphalaria glabrata</i> , intermediate snail host of <i>Schistosoma mansoni</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2006, 101, 167-177.   | 0.8 | 36        |
| 1042 | Comparative analysis of the paired immunoglobulin-like receptor (PILR) locus in six mammalian genomes: duplication, conversion, and the birth of new genes. <i>Physiological Genomics</i> , 2006, 27, 201-218.                                     | 1.0 | 27        |
| 1043 | The genome of the filamentous fungus <i>Ashbya gossypii</i> : annotation and evolutionary implications. , 0, , 197-232.  |     | 2         |
| 1044 | Gene expression and specificity in the mature zone of the lobster olfactory organ. <i>Physiological Genomics</i> , 2006, 25, 224-233.  | 1.0 | 33        |
| 1045 | Intraspecific variation in the first internal transcribed spacer (ITS1) of the nuclear ribosomal DNA in <i>Melipona subnitida</i> (Hymenoptera, Apidae), an endemic stingless bee from northeastern Brazil. <i>Apidologie</i> , 2006, 37, 376-386. | 0.9 | 14        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1046 | Brazilian coffee genome project: an EST-based genomic resource. <i>Brazilian Journal of Plant Physiology</i> , 2006, 18, 95-108.   | 0.5 | 112       |
| 1047 | Identification and molecular modeling of a family 5 endocellulase from <i>Thermus caldophilus</i> GK24, a cellulolytic strain of <i>Thermus thermophilus</i> . <i>International Journal of Molecular Sciences</i> , 2006, 7, 571-589.                  | 1.8 | 10        |
| 1050 | Expression Analysis and Physical Mapping of a cDNA Library of Fusarium Head Blight Infected Wheat Spikes. <i>Crop Science</i> , 2006, 46, S-15.  | 0.8 | 30        |
| 1051 | The Eight Amino-Acid Differences Within Three Leucine-Rich Repeats Between Pi2 and Piz-t Resistance Proteins Determine the Resistance Specificity to <i>Magnaporthe grisea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1216-1228.    | 1.4 | 357       |
| 1052 | H19-DMR allele-specific methylation analysis reveals epigenetic heterogeneity of CTCF binding site 6 but not of site 5 in head-and-neck carcinomas: A pilot case-control analysis. <i>International Journal of Molecular Medicine</i> , 2006, 17, 397. | 1.8 | 2         |
| 1053 | Chicken genomics resource: sequencing and annotation of 35,407 ESTs from single and multiple tissue cDNA libraries and CAP3 assembly of a chicken gene index. <i>Physiological Genomics</i> , 2006, 25, 514-524.                                       | 1.0 | 60        |
| 1055 | Glutathione-S-Transferase P1 Isoenzyme Polymorphisms, Platinum-Based Chemotherapy, and Non-small Cell Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2006, 1, 679-683.   | 0.5 | 20        |
| 1056 | Glutathione-S-Transferase P1 Isoenzyme Polymorphisms, Platinum-Based Chemotherapy, and Non-small Cell Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2006, 1, 679-683.   | 0.5 | 47        |
| 1057 | Bioinformatic analysis of expressed sequence tags from sporophyte of <i>Porphyra yezoensis</i> (Bagiaceae). <i>Tj ETQq0 0 0,rgBT /Overlock 10</i>  | 1.8 | 9         |
| 1060 | Prion gene haplotypes of U.S. cattle. <i>BMC Genetics</i> , 2006, 7, 51.   | 2.7 | 36        |
| 1061 | Isolation of germline cells from <i>Drosophila</i> embryos by flow cytometry. <i>Development Growth and Differentiation</i> , 2006, 48, 49-57.   | 0.6 | 36        |
| 1062 | Toward unraveling the structure of <i>Brassica rapa</i> genome. <i>Physiologia Plantarum</i> , 2006, 126, 060307071539002-???  | 2.6 | 8         |
| 1063 | Sequence analysis of three plasmids harboured in <i>Rhodococcus erythropolis</i> strain PR4. <i>Environmental Microbiology</i> , 2006, 8, 334-346.   | 1.8 | 139       |
| 1064 | Distribution of hepatitis B virus genotypes among patients with chronic infection. <i>Liver International</i> , 2006, 26, 636-642.   | 1.9 | 31        |
| 1065 | A bioinformatics pipeline for high-throughput microbial multilocus sequence typing (MLST) analyses. <i>Clinical Microbiology and Infection</i> , 2006, 12, 1144-1146.  | 2.8 | 17        |
| 1066 | Genetic determinants of normal variation in coagulation factor (F) IX levels: genome-wide scan and examination of the FIX structural gene. <i>Journal of Thrombosis and Haemostasis</i> , 2006, 4, 1537-1545.  | 1.9 | 22        |
| 1067 | ANALYSIS OF EXPRESSED SEQUENCE TAGS (ESTS) FROM THE POLAR DIATOM <i>FRAGILARIOPSIS CYLINDRUS</i> 1. <i>Journal of Phycology</i> , 2006, 42, 78-85.   | 1.0 | 46        |
| 1068 | Diffuse and segmental variants of cutaneous leiomyomatosis: novel mutations in the fumarate hydratase gene and review of the literature. <i>Experimental Dermatology</i> , 2006, 15, 735-741.  | 1.4 | 68        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1069 | Recurring HRAS mutation G12S in Dutch patients with Costello syndrome. <i>Experimental Dermatology</i> , 2006, 15, 731-734.   | 1.4 | 28        |
| 1070 | Sequencing and Analysis of a Genomic Fragment Provide an Insight into the <i>Dunaliella viridis</i> Genomic Sequence. <i>Acta Biochimica Et Biophysica Sinica</i> , 2006, 38, 812-820.  | 0.9 | 7         |
| 1071 | Draft Assembly and Annotation of the <i>Pneumocystis carinii</i> Genome. <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, S89-S91.   | 0.8 | 31        |
| 1072 | A novel ABCA12 mutation underlying a case of Harlequin ichthyosis. <i>British Journal of Dermatology</i> , 2006, 155, 204-206.  | 1.4 | 18        |
| 1073 | Phylogeography, phylogeny and hybridization in trichechid sirenians: implications for manatee conservation. <i>Molecular Ecology</i> , 2006, 15, 433-447.   | 2.0 | 102       |
| 1074 | Genomics of hybrid poplar ( <i>Populus trichocarpa</i> × <i>deltoides</i> ) interacting with forest tent caterpillars ( <i>Malacosoma disstria</i> ): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences. <i>Molecular Ecology</i> , 2006, 15, 1275-1297. | 2.0 | 183       |
| 1075 | Global patterns of diversity and community structure in marine bacterioplankton. <i>Molecular Ecology</i> , 2006, 16, 867-880.  | 2.0 | 410       |
| 1076 | The molecular ecologist's guide to expressed sequence tags. <i>Molecular Ecology</i> , 2006, 16, 907-924.   | 2.0 | 326       |
| 1077 | Direct repeat-mediated deletion of a type IV pilin gene results in major virulence attenuation of <i>Francisella tularensis</i> . <i>Molecular Microbiology</i> , 2006, 59, 1818-1830.  | 1.2 | 94        |
| 1078 | Lost in the middle of nowhere: the AvrLm1 avirulence gene of the Dothideomycete <i>Leptosphaeria maculans</i> . <i>Molecular Microbiology</i> , 2006, 60, 67-80.  | 1.2 | 243       |
| 1079 | Genomic structure and gene order of swine chromosome 7q1.1q1.2. <i>Animal Genetics</i> , 2006, 37, 10-16.   | 0.6 | 21        |
| 1080 | Comparative analysis of the bovine MHC class IIb sequence1 identifies inversion breakpoints and three unexpected genes. <i>Animal Genetics</i> , 2006, 37, 121-129.   | 0.6 | 37        |
| 1081 | Analysis of chicken embryonic gonad expressed sequenced tags. <i>Animal Genetics</i> , 2006, 37, 85-86.   | 0.6 | 5         |
| 1082 | Linkage mapping of gene-associated SNPs to pig chromosome 11. <i>Animal Genetics</i> , 2006, 37, 199-204.   | 0.6 | 5         |
| 1083 | Channel catfish BAC-end sequences for marker development and assessment of syntenic conservation with other fish species. <i>Animal Genetics</i> , 2006, 37, 321-326.   | 0.6 | 78        |
| 1084 | The maize viviparous15 locus encodes the molybdopterin synthase small subunit. <i>Plant Journal</i> , 2006, 45, 264-274.  | 2.8 | 50        |
| 1085 | Characterizing the composition and evolution of homoeologous genomes in hexaploid wheat through BAC-end sequencing on chromosome 3B. <i>Plant Journal</i> , 2006, 48, 463-474.  | 2.8 | 189       |
| 1086 | Annotation and expression profile analysis of 2073 full-length cDNAs from stress-induced maize ( <i>Zea mays</i> ) Tj ETQq1 1 0.784314 rgBT /Overl...<br>2.8 86   | 2.8 | 86        |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 1087 | Analysis of expressed sequence tags from <i>Rhynchosciara americana</i> salivary glands. <i>Insect Molecular Biology</i> , 2006, 15, 109-118.  | 1.0  | 10        |
| 1088 | Sweetness and light: illuminating the honey bee genome. <i>Insect Molecular Biology</i> , 2006, 15, 535-539.   | 1.0  | 23        |
| 1089 | Sequencing errors or SNPs at splice-acceptor guanines in dbSNP?. <i>Nature Biotechnology</i> , 2006, 24, 1068-1070.  | 9.4  | 8         |
| 1090 | Data integration gets 'Sloppy'. <i>Nature Biotechnology</i> , 2006, 24, 1070-1071.   | 9.4  | 17        |
| 1091 | Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium <i>Alcanivorax borkumensis</i> . <i>Nature Biotechnology</i> , 2006, 24, 997-1004.  | 9.4  | 417       |
| 1092 | Complete genome of the mutualistic, N <sub>2</sub> -fixing grass endophyte <i>Azoarcus</i> sp. strain BH72. <i>Nature Biotechnology</i> , 2006, 24, 1384-1390.   | 9.4  | 237       |
| 1093 | The genome and transcriptomes of the anti-tumor agent <i>Clostridium novyi</i> -NT. <i>Nature Biotechnology</i> , 2006, 24, 1573-1580.   | 9.4  | 128       |
| 1094 | Automating sequence-based detection and genotyping of SNPs from diploid samples. <i>Nature Genetics</i> , 2006, 38, 375-381.   | 9.4  | 145       |
| 1095 | Automating resequencing-based detection of insertion-deletion polymorphisms. <i>Nature Genetics</i> , 2006, 38, 1457-1462.   | 9.4  | 79        |
| 1096 | Molecular characterization of Ph1 as a major chromosome pairing locus in polyploid wheat. <i>Nature</i> , 2006, 439, 749-752.  | 13.7 | 495       |
| 1097 | Identification of novel genes and transcription factors involved in spleen, thymus and immunological development and function. <i>Genes and Immunity</i> , 2006, 7, 101-112.   | 2.2  | 11        |
| 1098 | The Rat Bloodâ€™ Brain Barrier Transcriptome. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2006, 26, 959-973.  | 2.4  | 176       |
| 1099 | ABCA12 Is the Major Harlequin Ichthyosis Gene. <i>Journal of Investigative Dermatology</i> , 2006, 126, 2408-2413.   | 0.3  | 88        |
| 1100 | Differential diagnosis of dog hookworms based on PCR-RFLP from the ITS region of their rDNA. <i>Veterinary Parasitology</i> , 2006, 140, 373-377.  | 0.7  | 28        |
| 1102 | The Complete Nucleotide Sequence and Genomic Organization of Citrus Leprosis Associated Virus, Cytoplasmatic type (CiLV-C). <i>Virus Genes</i> , 2006, 32, 289-298.  | 0.7  | 90        |
| 1103 | The chloroplast genome of mulberry: complete nucleotide sequence, gene organization and comparative analysis. <i>Tree Genetics and Genomes</i> , 2006, 3, 49-59.   | 0.6  | 55        |
| 1104 | Comparative analysis of genes expressed in regenerating intestine and non-eviscerated intestine of <i>Apostichopus japonicus</i> Selenka (Aspidochirotrida: Stichopodidae) and cloning of ependymin gene. <i>Hydrobiologia</i> , 2006, 571, 109-122. | 1.0  | 22        |
| 1105 | Comparative genomic analysis links karyotypic evolution with genomic evolution in the Indian Muntjac ( <i>Muntiacus muntjak vaginalis</i> ). <i>Chromosoma</i> , 2006, 115, 427-436.   | 1.0  | 6         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1106 | The <i>Macrostomum lignano</i> EST database as a molecular resource for studying platyhelminth development and phylogeny. <i>Development Genes and Evolution</i> , 2006, 216, 695-707.                                      | 0.4 | 25        |
| 1107 | A cluster of 11 CBF transcription factors is located at the frost tolerance locus Fr-A m 2 in <i>Triticum monococcum</i> . <i>Molecular Genetics and Genomics</i> , 2006, 275, 193-203.                                     | 1.0 | 146       |
| 1108 | Analysis of papaya BAC end sequences reveals first insights into the organization of a fruit tree genome. <i>Molecular Genetics and Genomics</i> , 2006, 276, 1-12.   | 1.0 | 61        |
| 1109 | Sequence diversity, natural selection and linkage disequilibrium in the human T cell receptor alpha/delta locus. <i>Human Genetics</i> , 2006, 119, 255-266.  | 1.8 | 19        |
| 1110 | Linkage disequilibrium across six prion gene regions spanning 20 kbp in U.S. sheep. <i>Mammalian Genome</i> , 2006, 17, 1121-1129.  | 1.0 | 6         |
| 1111 | HLA-E, HLA-F, and HLA-G polymorphism: genomic sequence defines haplotype structure and variation spanning the nonclassical class I genes. <i>Immunogenetics</i> , 2006, 58, 241-251.  | 1.2 | 53        |
| 1112 | Characterization of four <i>Rhodococcus</i> alcohol dehydrogenase genes responsible for the oxidation of aromatic alcohols. <i>Applied Microbiology and Biotechnology</i> , 2006, 71, 824-832.                              | 1.7 | 23        |
| 1113 | The complete DNA sequence of the mitochondrial genome of the dermatophyte fungus <i>Epidermophyton floccosum</i> . <i>Current Genetics</i> , 2006, 49, 302-308.   | 0.8 | 16        |
| 1114 | Structural variation and evolution of a defense-gene cluster in natural populations of <i>Aegilops tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2006, 112, 618-626.   | 1.8 | 17        |
| 1115 | Development of four phylogenetically-arrayed BAC libraries and sequence of the APA locus in <i>Phaseolus vulgaris</i> . <i>Theoretical and Applied Genetics</i> , 2006, 112, 987-998.                                       | 1.8 | 73        |
| 1116 | Complete chloroplast genome sequences of <i>Solanum bulbocastanum</i> , <i>Solanum lycopersicum</i> and comparative analyses with other Solanaceae genomes. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1503-1518. | 1.8 | 157       |
| 1117 | Construction of a watermelon BAC library and identification of SSRs anchored to melon or <i>Arabidopsis</i> genomes. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1553-1562.  | 1.8 | 49        |
| 1118 | EST sequencing and phylogenetic analysis of the model grass <i>Brachypodium distachyon</i> . <i>Theoretical and Applied Genetics</i> , 2006, 113, 186-195.  | 1.8 | 117       |
| 1119 | Sequence comparison of distal and proximal ribosomal DNA arrays in rice ( <i>Oryza sativa</i> L.) chromosome 9S and analysis of their flanking regions. <i>Theoretical and Applied Genetics</i> , 2006, 113, 419-428.       | 1.8 | 18        |
| 1120 | Comparative sequence and genetic analyses of asparagus BACs reveal no microsynteny with onion or rice. <i>Theoretical and Applied Genetics</i> , 2006, 114, 31-39.  | 1.8 | 13        |
| 1121 | Exploitation of pepper ESTs-SSRs and an SSR-based linkage map. <i>Theoretical and Applied Genetics</i> , 2006, 114, 113-130.  | 1.8 | 175       |
| 1122 | Topoisomerase II beta expression level correlates with doxorubicin-induced apoptosis in peripheral blood cells. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2006, 374, 21-30.                                   | 1.4 | 21        |
| 1123 | The genome of Epstein-Barr virus type 2 strain AG876. <i>Virology</i> , 2006, 350, 164-170.   | 1.1 | 116       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1124 | Complete nucleotide sequence of a P2 family lysogenic bacteriophage, $\phi$ MhaA1-PHL101, from <i>Mannheimia haemolytica</i> serotype A1. <i>Virology</i> , 2006, 350, 79-89.   | 1.1 | 18        |
| 1125 | Molecular phylogeny based on the 16S rRNA gene of elite rhizobial strains used in Brazilian commercial inoculants. <i>Systematic and Applied Microbiology</i> , 2006, 29, 315-332.  | 1.2 | 129       |
| 1126 | Should the draft chimpanzee sequence be finished?. <i>Trends in Genetics</i> , 2006, 22, 122-125.   | 2.9 | 19        |
| 1127 | Large-scale amplification, cloning and sequencing of near full-length HIV-1 subtype C genomes. <i>Journal of Virological Methods</i> , 2006, 136, 118-125.  | 1.0 | 88        |
| 1128 | Complete nucleotide sequence of pSCV50, the virulence plasmid of <i>Salmonella enterica</i> serovar <i>Choleraesuis</i> SC-B67. <i>Plasmid</i> , 2006, 55, 145-151.   | 0.4 | 18        |
| 1129 | Rapid and accurate pyrosequencing of angiosperm plastid genomes. <i>BMC Plant Biology</i> , 2006, 6, 17.  | 1.6 | 224       |
| 1130 | Ebbie: automated analysis and storage of small RNA cloning data using a dynamic web server. <i>BMC Bioinformatics</i> , 2006, 7, 185.   | 1.2 | 3         |
| 1131 | preAssemble: a tool for automatic sequencer trace data processing. <i>BMC Bioinformatics</i> , 2006, 7, 22.   | 1.2 | 11        |
| 1132 | SPODOBASE: an EST database for the lepidopteran crop pest Spodoptera. <i>BMC Bioinformatics</i> , 2006, 7, 322.   | 1.2 | 91        |
| 1133 | QualitySNP: a pipeline for detecting single nucleotide polymorphisms and insertions/deletions in EST data from diploid and polyploid species. <i>BMC Bioinformatics</i> , 2006, 7, 438.   | 1.2 | 127       |
| 1134 | SNP-PHAGE-High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006, 7, 468.   | 1.2 | 29        |
| 1135 | JUICE: a data management system that facilitates the analysis of large volumes of information in an EST project workflow. <i>BMC Bioinformatics</i> , 2006, 7, 513.   | 1.2 | 9         |
| 1136 | Phylogenetic analyses of <i>Vitis</i> (Vitaceae) based on complete chloroplast genome sequences: effects of taxon sampling and phylogenetic methods on resolving relationships among rosids. <i>BMC Evolutionary Biology</i> , 2006, 6, 32. | 3.2 | 230       |
| 1137 | Complete plastid genome sequences of <i>Drimys</i> , <i>Liriodendron</i> , and <i>Piper</i> : implications for the phylogenetic relationships of magnoliids. <i>BMC Evolutionary Biology</i> , 2006, 6, 77.                                 | 3.2 | 138       |
| 1138 | Construction of a nurse shark ( <i>Ginglymostoma cirratum</i> ) bacterial artificial chromosome (BAC) library and a preliminary genome survey. <i>BMC Genomics</i> , 2006, 7, 106.  | 1.2 | 27        |
| 1139 | LocustDB: a relational database for the transcriptome and biology of the migratory locust ( <i>Locusta</i> ) Tj ETQq1 1 0.784314 rgBT/Overl<br>1.2 59   | 1.2 | 59        |
| 1140 | A wing expressed sequence tag resource for <i>Bicyclus anynana</i> butterflies, an evo-devo model. <i>BMC Genomics</i> , 2006, 7, 130.  | 1.2 | 85        |
| 1141 | Wheat EST resources for functional genomics of abiotic stress. <i>BMC Genomics</i> , 2006, 7, 149.  | 1.2 | 100       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1142 | Gene identification and analysis of transcripts differentially regulated in fracture healing by EST sequencing in the domestic sheep. <i>BMC Genomics</i> , 2006, 7, 172.   | 1.2 | 23        |
| 1143 | Analysis of bacteria-challenged wild silkworm, <i>Antheraea mylitta</i> (Lepidoptera) transcriptome reveals potential immune genes. <i>BMC Genomics</i> , 2006, 7, 184.   | 1.2 | 48        |
| 1144 | Single nucleotide polymorphism (SNP) discovery in duplicated genomes: intron-primed exon-crossing (IPEC) as a strategy for avoiding amplification of duplicated loci in Atlantic salmon ( <i>Salmo salar</i> ) and other salmonid fishes. <i>BMC Genomics</i> , 2006, 7, 192. | 1.2 | 42        |
| 1145 | Generation, annotation and analysis of ESTs from <i>Trichoderma harzianum</i> CECT 2413. <i>BMC Genomics</i> , 2006, 7, 193.  | 1.2 | 60        |
| 1146 | Identification and analysis of gene families from the duplicated genome of soybean using EST sequences. <i>BMC Genomics</i> , 2006, 7, 204.   | 1.2 | 21        |
| 1147 | Gene expression profiling of chicken primordial germ cell ESTs. <i>BMC Genomics</i> , 2006, 7, 220.   | 1.2 | 26        |
| 1148 | Genomic organization and evolution of the ULBP genes in cattle. <i>BMC Genomics</i> , 2006, 7, 227.   | 1.2 | 23        |
| 1149 | Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , 2006, 7, 246.   | 1.2 | 173       |
| 1150 | Analysis and functional annotation of expressed sequence tags from the fall armyworm <i>Spodoptera frugiperda</i> . <i>BMC Genomics</i> , 2006, 7, 264.   | 1.2 | 16        |
| 1151 | Evolution and comparative analysis of the MHC Class III inflammatory region. <i>BMC Genomics</i> , 2006, 7, 281.  | 1.2 | 54        |
| 1152 | Generation and analysis of large-scale expressed sequence tags (ESTs) from a full-length enriched cDNA library of porcine backfat tissue. <i>BMC Genomics</i> , 2006, 7, 36.  | 1.2 | 28        |
| 1153 | Using pyrosequencing to shed light on deep mine microbial ecology. <i>BMC Genomics</i> , 2006, 7, 57.   | 1.2 | 405       |
| 1154 | A high-throughput screen identifying sequence and promiscuity characteristics of the loxP spacer region in Cre-mediated recombination. <i>BMC Genomics</i> , 2006, 7, 73.   | 1.2 | 60        |
| 1155 | Analysis of 10,000 ESTs from lymphocytes of the cynomolgus monkey to improve our understanding of its immune system. <i>BMC Genomics</i> , 2006, 7, 82.   | 1.2 | 13        |
| 1156 | Generation, annotation, and analysis of an extensive <i>Aspergillus niger</i> EST collection. <i>BMC Microbiology</i> , 2006, 6, 7.   | 1.3 | 34        |
| 1157 | Decoding the rice genome. <i>BioEssays</i> , 2006, 28, 421-432.   | 1.2 | 44        |
| 1158 | EST-based profiling and comparison of gene expression in the silkworm fat body during metamorphosis. <i>Archives of Insect Biochemistry and Physiology</i> , 2006, 61, 10-23.   | 0.6 | 30        |
| 1159 | Large-scale Pyrosequencing of synthetic DNA: A comparison with results from Sanger dideoxy sequencing. <i>Electrophoresis</i> , 2006, 27, 3042-3047.  | 1.3 | 22        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1160 | What is the future of electrophoresis in large-scale genomic sequencing?. <i>Electrophoresis</i> , 2006, 27, 3689-3702.   | 1.3 | 35        |
| 1161 | Xeroderma pigmentosum group D haplotype predicts for response, survival, and toxicity after platinum-based chemotherapy in advanced nonsmall cell lung cancer. <i>Cancer</i> , 2006, 106, 2421-2427.  | 2.0 | 46        |
| 1162 | Comparative genomics in vertebrate evolution and development. <i>Journal of Experimental Zoology Part A, Comparative Experimental Biology</i> , 2006, 305A, 672-682.  | 1.3 | 2         |
| 1163 | Modeling and base-calling for Dna Sequencing-By-Synthesis. , 0, , .   |     | 6         |
| 1164 | A RecA-mediated exon profiling method. <i>Nucleic Acids Research</i> , 2006, 34, e97-e97.   | 6.5 | 5         |
| 1165 | Imprinting of Opossum <i>Igf2r</i> in the Absence of Differential Methylation and Air. <i>Epigenetics</i> , 2006, 1, 50-55.   | 1.3 | 34        |
| 1166 | Direct detection of null alleles in SNP genotyping data. <i>Human Molecular Genetics</i> , 2006, 15, 1931-1937.   | 1.4 | 34        |
| 1167 | Phytome: a platform for plant comparative genomics. <i>Nucleic Acids Research</i> , 2006, 34, D724-D730.  | 6.5 | 35        |
| 1168 | HTPSELEX—a database of high-throughput SELEX libraries for transcription factor binding sites. <i>Nucleic Acids Research</i> , 2006, 34, D90-D94.   | 6.5 | 26        |
| 1169 | Organization of chromosome ends in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Nucleic Acids Research</i> , 2006, 34, 4685-4701.  | 6.5 | 98        |
| 1170 | Mouse microRNA profiles determined with a new and sensitive cloning method. <i>Nucleic Acids Research</i> , 2006, 34, e115-e115.  | 6.5 | 96        |
| 1171 | Position-dependent effects of locked nucleic acid (LNA) on DNA sequencing and PCR primers. <i>Nucleic Acids Research</i> , 2006, 34, e142-e142.   | 6.5 | 56        |
| 1172 | Color Polymorphism and Genetic Structure in the Sea Star <i>Pisaster ochraceus</i> . <i>Biological Bulletin</i> , 2006, 211, 248-262.   | 0.7 | 52        |
| 1173 | Adaptive Loss of an Old Duplicated Gene During Incipient Speciation. <i>Molecular Biology and Evolution</i> , 2006, 23, 401-410.  | 3.5 | 21        |
| 1174 | Construction and characterization of EST libraries from the porcelain crab, <i>Petrolisthes cinctipes</i> . <i>Integrative and Comparative Biology</i> , 2006, 46, 919-930.   | 0.9 | 21        |
| 1175 | Complete Nucleotide Sequence of pK245, a 98-Kilobase Plasmid Conferring Quinolone Resistance and Extended-Spectrum-β-Lactamase Activity in a Clinical <i>Klebsiella pneumoniae</i> Isolate. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 3861-3866. | 1.4 | 96        |
| 1176 | Identification of Endometrial Genes Regulated by Early Pregnancy, Progesterone, and Interferon Tau in the Ovine Uterus1. <i>Biology of Reproduction</i> , 2006, 74, 383-394.  | 1.2 | 162       |
| 1177 | Integrated Databasing and Analysis. , 2006, , 141-217.  |     | 12        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1178 | Divergent Haplotypes and Human History as Revealed in a Worldwide Survey of X-Linked DNA Sequence Variation. <i>Molecular Biology and Evolution</i> , 2006, 24, 687-698.  | 3.5 | 17        |
| 1179 | SAGE2Splice: Unmapped SAGE Tags Reveal Novel Splice Junctions. <i>PLoS Computational Biology</i> , 2006, 2, e34.  | 1.5 | 10        |
| 1180 | Who Ate Whom? Adaptive <i>Helicobacter</i> Genomic Changes That Accompanied a Host Jump from Early Humans to Large Felines. <i>PLoS Genetics</i> , 2006, 2, e120.   | 1.5 | 145       |
| 1181 | Pathways of Carbon Assimilation and Ammonia Oxidation Suggested by Environmental Genomic Analyses of Marine Crenarchaeota. <i>PLoS Biology</i> , 2006, 4, e95.  | 2.6 | 554       |
| 1182 | The Genome of Deep-Sea Vent Chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006, 4, e383.   | 2.6 | 144       |
| 1183 | Epigenetic regulation of maspin expression in the human placenta. <i>Molecular Human Reproduction</i> , 2006, 12, 611-617.  | 1.3 | 48        |
| 1184 | Refinement of optical map assemblies. <i>Bioinformatics</i> , 2006, 22, 1217-1224.  | 1.8 | 29        |
| 1185 | Water stress-responsive genes in loblolly pine ( <i>Pinus taeda</i> ) roots identified by analyses of expressed sequence tag libraries. <i>Tree Physiology</i> , 2006, 26, 1-16.  | 1.4 | 84        |
| 1186 | Crimean-Congo Hemorrhagic Fever Virus Genomics and Global Diversity. <i>Journal of Virology</i> , 2006, 80, 8834-8842.  | 1.5 | 227       |
| 1187 | Class 1 Integrons Potentially Predating the Association with Tn 402 -Like Transposition Genes Are Present in a Sediment Microbial Community. <i>Journal of Bacteriology</i> , 2006, 188, 5722-5730.   | 1.0 | 139       |
| 1188 | Development and Characterization of a Normalized Canine Retinal cDNA Library for Genomic and Expression Studies. , 2006, 47, 2632.  |     | 9         |
| 1189 | Application of Minimal Sequence Quality Values Prevents Misidentification of the blaSHV Type in Single Bacterial Isolates Carrying Different SHV Extended-Spectrum $\beta$ -Lactamase Genes. <i>Journal of Clinical Microbiology</i> , 2006, 44, 1896-1898. | 1.8 | 9         |
| 1190 | Plasmids from freshwater environments capable of IncQ retrotransfer are diverse and include pQKH54, a new IncP-1 subgroup archetype. <i>Microbiology (United Kingdom)</i> , 2006, 152, 2689-2701.   | 0.7 | 42        |
| 1191 | Whole-Genome Sequence of <i>Listeria welshimeri</i> Reveals Common Steps in Genome Reduction with <i>Listeria innocua</i> as Compared to <i>Listeria monocytogenes</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7405-7415.                             | 1.0 | 89        |
| 1192 | santa and valentine pattern concentric growth of cardiac myocardium in the zebrafish. <i>Development (Cambridge)</i> , 2006, 133, 3139-3146.  | 1.2 | 128       |
| 1193 | Living with Genome Instability: the Adaptation of Phytoplasmas to Diverse Environments of Their Insect and Plant Hosts. <i>Journal of Bacteriology</i> , 2006, 188, 3682-3696.  | 1.0 | 356       |
| 1194 | An initial map of insertion and deletion (INDEL) variation in the human genome. <i>Genome Research</i> , 2006, 16, 1182-1190.   | 2.4 | 548       |
| 1195 | Genetic Association of the Antiviral Restriction Factor TRIM5 $\alpha$ with Human Immunodeficiency Virus Type 1 Infection. <i>Journal of Virology</i> , 2006, 80, 2463-2471.  | 1.5 | 103       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1196 | TOPAAS, a Tomato and Potato Assembly Assistance System for Selection and Finishing of Bacterial Artificial Chromosomes. <i>Plant Physiology</i> , 2006, 140, 805-817.   | 2.3 | 13        |
| 1197 | Increased Abundance of IncP-1 $\beta$ Plasmids and Mercury Resistance Genes in Mercury-Polluted River Sediments: First Discovery of IncP-1 $\beta$ Plasmids with a Complex mer Transposon as the Sole Accessory Element. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7253-7259. | 1.4 | 83        |
| 1198 | The Evolution of Biased Codon and Amino Acid Usage in Nematode Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 2303-2315.   | 3.5 | 84        |
| 1199 | Genome-Wide Analysis of Epigenetic Silencing Identifies BEX1 and BEX2 as Candidate Tumor Suppressor Genes in Malignant Glioma. <i>Cancer Research</i> , 2006, 66, 6665-6674.  | 0.4 | 135       |
| 1200 | Potential Source of Francisella tularensis Live Vaccine Strain Attenuation Determined by Genome Comparison. <i>Infection and Immunity</i> , 2006, 74, 6895-6906.  | 1.0 | 83        |
| 1201 | Stolbur Phytoplasma Genome Survey Achieved Using a Suppression Subtractive Hybridization Approach with High Specificity. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3274-3283.   | 1.4 | 28        |
| 1202 | 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.  | 3.3 | 226       |
| 1203 | Evidence for Existence of "Mesotogas," Members of the Order Thermotogales Adapted to Low-Temperature Environments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5061-5068.   | 1.4 | 54        |
| 1204 | Truncated Gamma-Glutamyl Carboxylase in Rambouillet Sheep. <i>Veterinary Pathology</i> , 2006, 43, 430-437.   | 0.8 | 5         |
| 1205 | EST library sequencing of genes expressed during early limb regeneration in the fiddler crab and transcriptional responses to ecdysteroid exposure in limb bud explants. <i>Integrative and Comparative Biology</i> , 2006, 46, 948-964.  | 0.9 | 22        |
| 1207 | Sequence-Level Analysis of the Diploidization Process in the Triplicated FLOWERING LOCUS C Region of Brassica rapa. <i>Plant Cell</i> , 2006, 18, 1339-1347.  | 3.1 | 223       |
| 1209 | Physical map-assisted whole-genome shotgun sequence assemblies. <i>Genome Research</i> , 2006, 16, 768-775.   | 2.4 | 27        |
| 1210 | Scan of Human Genome Reveals No New Loci Under Ancient Balancing Selection. <i>Genetics</i> , 2006, 173, 2165-2177.   | 1.2 | 117       |
| 1211 | Prevalence, Spectrum, and Functional Characterization of Melanocortin-4 Receptor Gene Mutations in a Representative Population-Based Sample and Obese Adults from Germany. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2006, 91, 1761-1769.                                     | 1.8 | 181       |
| 1212 | Dense Taxonomic EST Sampling and Its Applications for Molecular Systematics of the Coleoptera (Beetles). <i>Molecular Biology and Evolution</i> , 2006, 23, 268-278.  | 3.5 | 86        |
| 1213 | A novel class of CoA-transferase involved in short-chain fatty acid metabolism in butyrate-producing human colonic bacteria. <i>Microbiology (United Kingdom)</i> , 2006, 152, 179-185.   | 0.7 | 76        |
| 1214 | X chromosomes and autosomes evolve at similar rates in Drosophila: No evidence for faster-X protein evolution. <i>Genome Research</i> , 2006, 16, 498-504.  | 2.4 | 67        |
| 1215 | Large-scale production of SAGE libraries from microdissected tissues, flow-sorted cells, and cell lines. <i>Genome Research</i> , 2006, 17, 108-116.  | 2.4 | 34        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1216 | Genome characteristics of facultatively symbiotic <i>Frankia</i> sp. strains reflect host range and host plant biogeography. <i>Genome Research</i> , 2006, 17, 7-15.   | 2.4 | 352       |
| 1217 | Sequence Analysis of the 144-Kilobase Accessory Plasmid pSmeSM11a, Isolated from a Dominant <i>Sinorhizobium meliloti</i> Strain Identified during a Long-Term Field Release Experiment. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3662-3672.   | 1.4 | 58        |
| 1218 | Genome of Horsepox Virus. <i>Journal of Virology</i> , 2006, 80, 9244-9258.   | 1.5 | 122       |
| 1219 | Antibodies Immunoreactive With Formalin-Fixed Tissue Antigens Recognize Linear Protein Epitopes. <i>American Journal of Clinical Pathology</i> , 2006, 125, 82-90.  | 0.4 | 49        |
| 1220 | Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , 2006, 16, 796-803.   | 2.4 | 73        |
| 1221 | Construction of a Single Nucleotide Polymorphism Linkage Map for the Silkworm, <i>Bombyx mori</i> , Based on Bacterial Artificial Chromosome End Sequences. <i>Genetics</i> , 2006, 173, 151-161.   | 1.2 | 76        |
| 1222 | Characterization of two whey protein genes in the Australian dasyurid marsupial, the stripe-faced dunnart ( <i>Sminthopsis macroura</i> ). <i>Cytogenetic and Genome Research</i> , 2006, 115, 62-69.   | 0.6 | 13        |
| 1223 | TRPV6 exhibits unusual patterns of polymorphism and divergence in worldwide populations. <i>Human Molecular Genetics</i> , 2006, 15, 2106-2113.   | 1.4 | 58        |
| 1224 | Distinctive Repertoire of Contingency Genes Conferring Mutation- Based Phase Variation and Combinatorial Expression of Surface Lipoproteins in <i>Mycoplasma capricolum</i> subsp. <i>capricolum</i> of the <i>Mycoplasma mycoides</i> Phylogenetic Cluster. <i>Journal of Bacteriology</i> , 2006, 188, 4926-4941. | 1.0 | 29        |
| 1225 | Machine Learning in Basecalling $\hat{\Delta}$ Decoding Trace Peak Behaviour. , 2006, , .   |     | 5         |
| 1226 | Naked corals: Skeleton loss in Scleractinia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9096-9100.   | 3.3 | 221       |
| 1227 | The Genome Sequence of the Obligately Chemolithoautotrophic, Facultatively Anaerobic Bacterium <i>Thiobacillus denitrificans</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1473-1488.   | 1.0 | 306       |
| 1228 | Acquisition and Evolution of the <i>exoU</i> Locus in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4037-4050.  | 1.0 | 95        |
| 1229 | The Broad-Spectrum Blast Resistance Gene <i>Pi9</i> Encodes a Nucleotide-Binding Site "Leucine-Rich Repeat Protein and Is a Member of a Multigene Family in Rice. <i>Genetics</i> , 2006, 172, 1901-1914.   | 1.2 | 479       |
| 1230 | Genome Rearrangements, Deletions, and Amplifications in the Natural Population of <i>Bartonella henselae</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7426-7439.   | 1.0 | 47        |
| 1231 | The <i>clc</i> Element of <i>Pseudomonas</i> sp. Strain B13, a Genomic Island with Various Catabolic Properties. <i>Journal of Bacteriology</i> , 2006, 188, 1999-2013.   | 1.0 | 153       |
| 1232 | Functional Classification, Genomic Organization, Putatively cis-Acting Regulatory Elements, and Relationship to Quantitative Trait Loci, of Sorghum Genes with Rhizome-Enriched Expression. <i>Plant Physiology</i> , 2006, 142, 1148-1159.   | 2.3 | 62        |
| 1233 | Sequence Analysis and Organization of the Neodiprion abietis Nucleopolyhedrovirus Genome. <i>Journal of Virology</i> , 2006, 80, 6952-6963.   | 1.5 | 38        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1234 | Widespread genome duplications throughout the history of flowering plants. <i>Genome Research</i> , 2006, 16, 738-749.  | 2.4 | 664       |
| 1235 | Multilocus Patterns of Nucleotide Diversity, Linkage Disequilibrium and Demographic History of Norway Spruce [ <i>Picea abies</i> (L.) Karst]. <i>Genetics</i> , 2006, 174, 2095-2105.  | 1.2 | 241       |
| 1236 | NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , 2006, 34, W394-W399.   | 6.5 | 918       |
| 1237 | Sequence analysis of the <i>Choristoneura occidentalis</i> granulovirus genome. <i>Journal of General Virology</i> , 2006, 87, 1917-1933.   | 1.3 | 53        |
| 1238 | Characterization of the first growth hormone gene sequence for a passerine bird—the pied flycatcher ( <i>Ficedula hypoleuca</i> ). <i>DNA Sequence</i> , 2006, 17, 401-406.   | 0.7 | 6         |
| 1239 | Genome of the most widely used viral biopesticide: <i>Anticarsia gemmatalis</i> multiple nucleopolyhedrovirus. <i>Journal of General Virology</i> , 2006, 87, 3233-3250.  | 1.3 | 76        |
| 1240 | Transcriptome Analysis of <i>Aspergillus nidulans</i> Exposed to Camptothecin-Induced DNA Damage. <i>Eukaryotic Cell</i> , 2006, 5, 1688-1704.  | 3.4 | 26        |
| 1241 | Genome reduction in <i>Leptospira borgpetersenii</i> reflects limited transmission potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14560-14565.                | 3.3 | 309       |
| 1242 | Inference of population genetic parameters in metagenomics: A clean look at messy data. <i>Genome Research</i> , 2006, 16, 1320-1327.   | 2.4 | 70        |
| 1243 | Genome Sequence of the Chemolithoautotrophic Nitrite-Oxidizing Bacterium <i>Nitrobacter winogradskyi</i> Nb-255. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2050-2063.   | 1.4 | 169       |
| 1244 | The Genome Sequence of <i>Mannheimia haemolytica</i> A1: Insights into Virulence, Natural Competence, and Pasteurellaceae Phylogeny. <i>Journal of Bacteriology</i> , 2006, 188, 7257-7266.                                   | 1.0 | 94        |
| 1245 | Application of a High-Density Oligonucleotide Microarray Approach To Study Bacterial Population Dynamics during Uranium Reduction and Reoxidation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6288-6298.       | 1.4 | 404       |
| 1246 | A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696.   | 1.2 | 285       |
| 1247 | Genome dynamics in a natural archaeal population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1883-1888.  | 3.3 | 123       |
| 1248 | Decoding Trace Peak Behaviour - A Neuro-Fuzzy Approach. <i>IEEE International Conference on Fuzzy Systems</i> , 2007, , .   | 0.0 | 3         |
| 1249 | Human Transcriptome Subtraction by Using Short Sequence Tags To Search for Tumor Viruses in Conjunctival Carcinoma. <i>Journal of Virology</i> , 2007, 81, 11332-11340.   | 1.5 | 105       |
| 1250 | Gene organization of the liverwort Y chromosome reveals distinct sex chromosome evolution in a haploid system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6472-6477. | 3.3 | 125       |
| 1251 | Transcriptome Analysis in Response to Heat Shock and Cadmium in the Aquatic Fungus <i>Blastocladiella emersonii</i> . <i>Eukaryotic Cell</i> , 2007, 6, 1053-1062.  | 3.4 | 29        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1252 | Genomics and Diversity of the Common Marmoset Monkey NK Complex. <i>Journal of Immunology</i> , 2007, 178, 7151-7161.   | 0.4 | 19        |
| 1253 | Insights into rubber biosynthesis from transcriptome analysis of <i>Hevea brasiliensis</i> latex. <i>Journal of Experimental Botany</i> , 2007, 58, 2429-2440.  | 2.4 | 163       |
| 1254 | Cloning and transcriptional analysis of <i>Crepis alpina</i> fatty acid desaturases affecting the biosynthesis of crepenynic acid. <i>Journal of Experimental Botany</i> , 2007, 58, 1421-1432.                     | 2.4 | 12        |
| 1255 | Urban aerosols harbor diverse and dynamic bacterial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 299-304.                                       | 3.3 | 593       |
| 1256 | Transcript profiles at different growth stages and tap-root zones identify correlated developmental and metabolic pathways of sugar beet. <i>Journal of Experimental Botany</i> , 2007, 58, 699-715.                | 2.4 | 30        |
| 1257 | Comparisons Among Two Fertile and Three Male-Sterile Mitochondrial Genomes of Maize. <i>Genetics</i> , 2007, 177, 1173-1192.  | 1.2 | 210       |
| 1258 | A Genomic Approach to Suberin Biosynthesis and Cork Differentiation. <i>Plant Physiology</i> , 2007, 144, 419-431.  | 2.3 | 147       |
| 1259 | Use of Sequence Analysis of the NS5B Region for Routine Genotyping of Hepatitis C Virus with Reference to C/E1 and 5' Untranslated Region Sequences. <i>Journal of Clinical Microbiology</i> , 2007, 45, 1102-1112. | 1.8 | 246       |
| 1260 | PolyScan: An automatic indel and SNP detection approach to the analysis of human resequencing data. <i>Genome Research</i> , 2007, 17, 659-666.   | 2.4 | 76        |
| 1261 | Gene Duplication and Adaptive Evolution of Digestive Proteases in <i>Drosophila arizonae</i> Female Reproductive Tracts. <i>PLoS Genetics</i> , 2007, 3, e148.  | 1.5 | 70        |
| 1262 | The Genographic Project Public Participation Mitochondrial DNA Database. <i>PLoS Genetics</i> , 2007, 3, e104.  | 1.5 | 99        |
| 1263 | Organization and Evolution of Primate Centromeric DNA from Whole-Genome Shotgun Sequence Data. <i>PLoS Computational Biology</i> , 2007, 3, e181.   | 1.5 | 80        |
| 1264 | Being Pathogenic, Plastic, and Sexual while Living with a Nearly Minimal Bacterial Genome. <i>PLoS Genetics</i> , 2007, 3, e75.   | 1.5 | 176       |
| 1265 | Transcriptional Regulation by Protein Kinase A in <i>Cryptococcus neoformans</i> . <i>PLoS Pathogens</i> , 2007, 3, e42.  | 2.1 | 92        |
| 1266 | A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53.   | 1.5 | 166       |
| 1267 | Comparative analysis of chicken chromosome 28 provides new clues to the evolutionary fragility of gene-rich vertebrate regions. <i>Genome Research</i> , 2007, 17, 1603-1613.                                       | 2.4 | 46        |
| 1268 | TXNIP Regulates Peripheral Glucose Metabolism in Humans. <i>PLoS Medicine</i> , 2007, 4, e158.  | 3.9 | 435       |
| 1269 | Comparative Physical Mapping Between <i>Oryza sativa</i> (AA Genome Type) and <i>O. punctata</i> (BB Genome) Tj ETQq1 1.0,784314,rgBT /Ove  | 1.2 | 49        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1270 | SNP mining porcine ESTs with MAVIANT, a novel tool for SNP evaluation and annotation. <i>Bioinformatics</i> , 2007, 23, i387-i391.   | 1.8 | 29        |
| 1271 | Chapter 11 Genome Sequencing and Assembly. <i>Perspectives in Bioanalysis</i> , 2007, , 327-355.   | 0.3 | 2         |
| 1272 | Comparative Genomics of Large Mitochondria in Placozoans. <i>PLoS Genetics</i> , 2007, 3, e13.   | 1.5 | 99        |
| 1273 | Mapping Human Genetic Ancestry. <i>Molecular Biology and Evolution</i> , 2007, 24, 2266-2276.  | 3.5 | 117       |
| 1274 | TBestDB: a taxonomically broad database of expressed sequence tags (ESTs). <i>Nucleic Acids Research</i> , 2007, 35, D445-D451.  | 6.5 | 81        |
| 1275 | ForestTreeDB: a database dedicated to the mining of tree transcriptomes. <i>Nucleic Acids Research</i> , 2007, 35, D888-D894.  | 6.5 | 22        |
| 1276 | Comparative Genetic Mapping in <i>Boechera stricta</i> , a Close Relative of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2007, 144, 286-298.  | 2.3 | 67        |
| 1277 | Patterns of Selection and Tissue-Specific Expression among Maize Domestication and Crop Improvement Loci. <i>Plant Physiology</i> , 2007, 144, 1642-1653.  | 2.3 | 17        |
| 1278 | Characterization and predictive discovery of evolutionarily conserved mammalian alternative promoters. <i>Genome Research</i> , 2007, 17, 145-155.   | 2.4 | 81        |
| 1279 | Diploid genome reconstruction of <i>Ciona intestinalis</i> and comparative analysis with <i>Ciona savignyi</i> . <i>Genome Research</i> , 2007, 17, 1101-1110.   | 2.4 | 65        |
| 1280 | SHARCGS, a fast and highly accurate short-read assembly algorithm for de novo genomic sequencing. <i>Genome Research</i> , 2007, 17, 1697-1706.  | 2.4 | 230       |
| 1281 | A comparative analysis of the <i>Lactuca</i> and <i>Helianthus</i> (Asteraceae) plastid genomes: identification of divergent regions and categorization of shared repeats. <i>American Journal of Botany</i> , 2007, 94, 302-312.  | 0.8 | 258       |
| 1282 | Machine learned regression for abductive DNA sequencing. , 2007, , .   |     | 3         |
| 1283 | Multilocus Sequence Typing Confirms the Close Genetic Interrelatedness of Three Distinct Flavescence DorA©e Phytoplasma Strain Clusters and Group 16SrV Phytoplasmas Infecting Grapevine and Alder in Europe. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4001-4010.         | 1.4 | 128       |
| 1284 | A Mutation in the Myostatin Gene Increases Muscle Mass and Enhances Racing Performance in Heterozygote Dogs. <i>PLoS Genetics</i> , 2007, 3, e79.  | 1.5 | 654       |
| 1285 | Evidence of Horizontal Transfer of Symbiotic Genes from a Bradyrhizobium japonicum Inoculant Strain to Indigenous Diazotrophs Sinorhizobium (Ensifer) fredii and Bradyrhizobium elkanii in a Brazilian Savannah Soil. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2635-2643. | 1.4 | 176       |
| 1286 | High-density yeast-tiling array reveals previously undiscovered introns and extensive regulation of meiotic splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1522-1527.   | 3.3 | 116       |
| 1287 | External Quality Assessment of a DNA Sequence-Based Scheme for Epidemiological Typing of <i>Legionella pneumophila</i> by an International Network of Laboratories. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3251-3256.   | 1.8 | 13        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1288 | PEDE (Pig EST Data Explorer) has been expanded into Pig Expression Data Explorer, including 10 147 porcine full-length cDNA sequences. <i>Nucleic Acids Research</i> , 2007, 35, D650-D653.   | 6.5 | 60        |
| 1289 | ESTpass: a web-based server for processing and annotating expressed sequence tag (EST) sequences. <i>Nucleic Acids Research</i> , 2007, 35, W159-W162.  | 6.5 | 30        |
| 1290 | Rapid evolution of an X-linked microRNA cluster in primates. <i>Genome Research</i> , 2007, 17, 612-617.  | 2.4 | 139       |
| 1291 | A comprehensive crop genome research project: the Superhybrid Rice Genome Project in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1023-1034.   | 1.8 | 10        |
| 1292 | Abortive Phage Resistance Mechanism AbiZ Speeds the Lysis Clock To Cause Premature Lysis of Phage-Infected <i>Lactococcus lactis</i> . <i>Journal of Bacteriology</i> , 2007, 189, 1417-1425.   | 1.0 | 81        |
| 1293 | Successful Gene Tagging in Lettuce Using the Tnt1 Retrotransposon from Tobacco. <i>Plant Physiology</i> , 2007, 144, 18-31.   | 2.3 | 46        |
| 1294 | Genetic Exchange Across a Species Boundary in the Archaeal Genus <i>Ferroplasma</i> . <i>Genetics</i> , 2007, 177, 407-416.   | 1.2 | 67        |
| 1295 | Phylogenomic Analysis Supports the Monophyly of Cryptophytes and Haptophytes and the Association of Rhizaria with Chromalveolates. <i>Molecular Biology and Evolution</i> , 2007, 24, 1702-1713.  | 3.5 | 218       |
| 1296 | Current progress in network research: toward reference networks for key model organisms. <i>Briefings in Bioinformatics</i> , 2007, 8, 318-332.   | 3.2 | 46        |
| 1297 | Serial Analysis of rRNA Genes and the Unexpected Dominance of Rare Members of Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4532-4542.   | 1.4 | 78        |
| 1298 | Nitrate reductase assay for the rapid detection of pyrazinamide resistance in <i>Mycobacterium tuberculosis</i> using nicotinamide. <i>Journal of Antimicrobial Chemotherapy</i> , 2007, 61, 123-127.                                       | 1.3 | 15        |
| 1299 | Comparative analysis of the <i>Corynebacterium glutamicum</i> group and complete genome sequence of strain R. <i>Microbiology (United Kingdom)</i> , 2007, 153, 1042-1058.  | 0.7 | 223       |
| 1300 | WASABI: An Automated Sequence Processing System for Multigene Phylogenies. <i>Systematic Biology</i> , 2007, 56, 523-531.   | 2.7 | 22        |
| 1301 | Comparative Genomic Analyses of Seventeen <i>Streptococcus pneumoniae</i> Strains: Insights into the Pneumococcal Supragenome. <i>Journal of Bacteriology</i> , 2007, 189, 8186-8195.   | 1.0 | 249       |
| 1302 | The Complete Plastid Genome Sequence of <i>Angiopteris evecta</i> (G. Forst.) Hoffm. (Marattiaceae). <i>American Fern Journal</i> , 2007, 97, 95-106.   | 0.2 | 44        |
| 1303 | MC1R: three novel variants identified in a malignant melanoma association study in the Spanish population. <i>Carcinogenesis</i> , 2007, 28, 1659-1664.   | 1.3 | 60        |
| 1304 | Transcriptome profiling of <i>Paracoccidioides brasiliensis</i> yeast-phase cells recovered from infected mice brings new insights into fungal response upon host interaction. <i>Microbiology (United Kingdom)</i> , 2007, 153, 4194-4207. | 0.7 | 86        |
| 1305 | Worldwide phylogeny of <i>Lactarius</i> section <i>Deliciosi</i> inferred from ITS and glyceraldehyde-3-phosphate dehydrogenase gene sequences. <i>Mycologia</i> , 2007, 99, 820-832.   | 0.8 | 24        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1306 | Accounting for Bias from Sequencing Error in Population Genetic Estimates. <i>Molecular Biology and Evolution</i> , 2007, 25, 199-206.  | 3.5 | 83        |
| 1307 | Assessing Bias in Experiment Design for Large Scale Mass Spectrometry-based Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1741-1748.   | 2.5 | 52        |
| 1308 | Analyses of the <i>hlyE</i> Gene Cluster in <i>Desulfococcus multivorans</i> : Homologous to the Virulence-Associated Locus of the Ovine Footrot Pathogen <i>Dichelobacter nodosus</i> ; Strain A198. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2007, 13, 156-164. | 1.0 | 1         |
| 1309 | Comparative Genomic Structure of Human, Dog, and Cat MHC: HLA, DLA, and FLA. <i>Journal of Heredity</i> , 2007, 98, 390-399.  | 1.0 | 54        |
| 1310 | Organization of the biosynthetic gene cluster in <i>Streptomyces</i> sp. DSM 4137 for the novel neuroprotectant polyketide meridamycin. <i>Microbiology (United Kingdom)</i> , 2007, 153, 631-631.  | 0.7 | 0         |
| 1311 | A New Binding Motif for the Transcriptional Repressor REST Uncovers Large Gene Networks Devoted to Neuronal Functions. <i>Journal of Neuroscience</i> , 2007, 27, 6729-6739.  | 1.7 | 210       |
| 1312 | Single Nucleotide Polymorphisms and Linkage Disequilibrium in Sunflower. <i>Genetics</i> , 2007, 177, 457-468.  | 1.2 | 77        |
| 1313 | Gene-Based Sequence Diversity Analysis of Field Pea ( <i>Pisum</i> ). <i>Genetics</i> , 2007, 177, 2263-2275.   | 1.2 | 74        |
| 1314 | Genomic analysis of the Mozambique strain of <i>Vibrio cholerae</i> O1 reveals the origin of El Tor strains carrying classical CTX prophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5151-5156.                           | 3.3 | 101       |
| 1315 | New <i>Trypanosoma cruzi</i> Repeated Element That Shows Site Specificity for Insertion. <i>Eukaryotic Cell</i> , 2007, 6, 1228-1238.   | 3.4 | 15        |
| 1316 | The genome size evolution of medaka ( <i>Oryzias latipes</i> ) and fugu ( <i>Takifugu rubripes</i> ). <i>Genes and Genetic Systems</i> , 2007, 82, 135-144.   | 0.2 | 16        |
| 1317 | Diversity and phylogenetic affinities of foliar fungal endophytes in loblolly pine inferred by culturing and environmental PCR. <i>Mycologia</i> , 2007, 99, 185-206.   | 0.8 | 178       |
| 1318 | Worldwide phylogeny of <i>Lactarius</i> section <i>Deliciosi</i> inferred from ITS and glyceraldehyde-3-phosphate dehydrogenase gene sequences. <i>Mycologia</i> , 2007, 99, 820-832.   | 0.8 | 29        |
| 1319 | The Genomic Dynamics and Evolutionary Mechanism of the Pi2/9 Locus in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 63-71.  | 1.4 | 73        |
| 1320 | Protein Accumulation in the Germinating <i>Uromyces appendiculatus</i> Uredospore. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 857-866.   | 1.4 | 37        |
| 1321 | Diversity of <i>Ralstonia solanacearum</i> Infecting Eggplant in the Philippines. <i>Phytopathology</i> , 2007, 97, 1467-1475.  | 1.1 | 38        |
| 1322 | A sequence variation scan of the coagulation factor VIII (FVIII) structural gene and associations with plasma FVIII activity levels. <i>Blood</i> , 2007, 109, 3713-3724.   | 0.6 | 86        |
| 1323 | The Genus <i>Machaerium</i> (Leguminosae) is More Closely Related to <i>Aeschynomene</i> Sect. <i>Ochopodium</i> than to <i>Dalbergia</i> : Inferences From Combined Sequence Data. <i>Systematic Botany</i> , 2007, 32, 762-771.   | 0.2 | 33        |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1324 | Genomic differences of Vaccinia virus clones from Dryvax smallpox vaccine: The Dryvax-like ACAM2000 and the mouse neurovirulent Clone-3. <i>Vaccine</i> , 2007, 25, 8807-8832.   | 1.7 | 40        |
| 1325 | The genomic sequence of the bovine T cell receptor gamma TRG loci and localization of the TRGC5 cassette. <i>Veterinary Immunology and Immunopathology</i> , 2007, 115, 346-356.   | 0.5 | 48        |
| 1326 | Analysis of the expression of immunoglobulins throughout lactation suggests two periods of immune transfer in the tammar wallaby ( <i>Macropus eugenii</i> ). <i>Veterinary Immunology and Immunopathology</i> , 2007, 120, 187-200.                               | 0.5 | 49        |
| 1327 | Molecular cloning and expression of channel catfish, <i>Ictalurus punctatus</i> , complement membrane attack complex inhibitor CD59. <i>Veterinary Immunology and Immunopathology</i> , 2007, 120, 246-253.  | 0.5 | 27        |
| 1328 | Porcine kallikrein gene family: Genomic structure, mapping, and differential expression analysis. <i>Genomics</i> , 2007, 89, 429-438.   | 1.3 | 8         |
| 1329 | P518/Qrfp sequence polymorphisms in SAMP6 osteopenic mouse. <i>Genomics</i> , 2007, 90, 629-635.   | 1.3 | 16        |
| 1330 | Identification by suppression subtractive hybridization and expression analysis of <i>Medicago truncatula</i> putative defence genes in response to <i>Orobanche crenata</i> parasitization. <i>Physiological and Molecular Plant Pathology</i> , 2007, 70, 49-59. | 1.3 | 37        |
| 1331 | Localization of Period 1 mRNA in the ruminant oocyte and investigations of its role in ovarian function. <i>Animal Reproduction Science</i> , 2007, 99, 93-105.  | 0.5 | 16        |
| 1332 | Serial analysis of gene expression (SAGE) in rat liver regeneration. <i>Biochemical and Biophysical Research Communications</i> , 2007, 360, 545-552.  | 1.0 | 13        |
| 1333 | Spidroins from the Brazilian spider <i>Nephilengys cruentata</i> (Araneae: Nephilidae). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2007, 147, 597-606.  | 0.7 | 22        |
| 1334 | Evolutionary history of the ABCB2 genomic region in teleosts. <i>Developmental and Comparative Immunology</i> , 2007, 31, 483-498.   | 1.0 | 15        |
| 1335 | The complete mitochondrial genomes of two common shrimps ( <i>Litopenaeus vannamei</i> and <i>Tigres</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 267   | 1.0 | 45        |
| 1336 | Generation of ESTs in <i>Vitis vinifera</i> wine grape (Cabernet Sauvignon) and table grape (Muscat) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267  | 1.0 | 45        |
| 1337 | Characterization of the porcine ATM gene: Towards the generation of a novel non-murine animal model for Ataxia-Telangiectasia. <i>Gene</i> , 2007, 405, 27-35.   | 1.0 | 11        |
| 1338 | A luminal breast cancer genome atlas: Progress and barriers. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2007, 106, 125-129.  | 1.2 | 7         |
| 1339 | Detection of HPV-2 and identification of novel mutations by whole genome sequencing from biopsies of two patients with multiple cutaneous horns. <i>Journal of Clinical Virology</i> , 2007, 39, 34-42.  | 1.6 | 16        |
| 1340 | Relationship between mitochondrial DNA mutations and clinical characteristics in human lung cancer. <i>Mitochondrion</i> , 2007, 7, 347-353.   | 1.6 | 42        |
| 1341 | Transcriptome analysis of the salivary glands of <i>Dermacentor andersoni</i> Stiles (Acari: Ixodidae). <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 48-71.  | 1.2 | 87        |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 1342 | The alternative complex III from <i>Rhodothermus marinus</i> – A prototype of a new family of quinol:electron acceptor oxidoreductases. <i>FEBS Letters</i> , 2007, 581, 4831-4835.   | 1.3  | 52        |
| 1343 | Evidence of Amino Acid Diversity – Enhancing Selection within Humans and among Primates at the Candidate Sperm-Receptor Gene PKDREJ. <i>American Journal of Human Genetics</i> , 2007, 81, 44-52.   | 2.6  | 48        |
| 1344 | Whole-Genome Analysis of the Methyl tert -Butyl Ether-Degrading Beta-Proteobacterium <i>Methylibium petroleiphilum</i> PM1. <i>Journal of Bacteriology</i> , 2007, 189, 1931-1945.  | 1.0  | 139       |
| 1345 | FepA- and TonB-Dependent Bacteriophage H8: Receptor Binding and Genomic Sequence. <i>Journal of Bacteriology</i> , 2007, 189, 5658-5674.  | 1.0  | 83        |
| 1346 | Distinct patterns of mutations occurring in de novo AML versus AML arising in the setting of severe congenital neutropenia. <i>Blood</i> , 2007, 110, 1648-1655.  | 0.6  | 88        |
| 1347 | Genome Sequences of Three Koi Herpesvirus Isolates Representing the Expanding Distribution of an Emerging Disease Threatening Koi and Common Carp Worldwide. <i>Journal of Virology</i> , 2007, 81, 5058-5065.                                    | 1.5  | 222       |
| 1348 | Single Nucleotide Polymorphism Discovery. , 2007, , 53-76.  |      | 31        |
| 1349 | Complete Genome Analysis of 33 Ecologically and Biologically Diverse Rift Valley Fever Virus Strains Reveals Widespread Virus Movement and Low Genetic Diversity due to Recent Common Ancestry. <i>Journal of Virology</i> , 2007, 81, 2805-2816. | 1.5  | 208       |
| 1350 | Assembling Genomic DNA Sequences with PHRAP. <i>Current Protocols in Bioinformatics</i> , 2007, 17, Unit11.4.   | 25.8 | 111       |
| 1351 | Global survey of diversity among environmental saltwater Bacterioviraceae. <i>Environmental Microbiology</i> , 2007, 9, 2441-2450.  | 1.8  | 59        |
| 1352 | High Altitude Adaptation and Phylogenetic Analysis of Tibetan Horse Based on the Mitochondrial Genome. <i>Journal of Genetics and Genomics</i> , 2007, 34, 720-729.   | 1.7  | 92        |
| 1353 | Distribution of Menin-Occupied Regions in Chromatin Specifies a Broad Role of Menin in Transcriptional Regulation. <i>Neoplasia</i> , 2007, 9, 101-107.   | 2.3  | 47        |
| 1354 | Accuracy and quality of massively parallel DNA pyrosequencing. <i>Genome Biology</i> , 2007, 8, R143.   | 13.9 | 1,060     |
| 1355 | Comparison of <i>Francisella tularensis</i> genomes reveals evolutionary events associated with the emergence of human pathogenic strains. <i>Genome Biology</i> , 2007, 8, R102.   | 13.9 | 245       |
| 1356 | Characterization and modeling of the <i>Haemophilus influenzae</i> core and supragenomes based on the complete genomic sequences of Rd and 12 clinical nontypeable strains. <i>Genome Biology</i> , 2007, 8, R103.                                | 13.9 | 228       |
| 1357 | LongSAGE profiling of nine human embryonic stem cell lines. <i>Genome Biology</i> , 2007, 8, R113.  | 13.9 | 21        |
| 1358 | LongSAGE analysis of skeletal muscle at three prenatal stages in Tongcheng and Landrace pigs. <i>Genome Biology</i> , 2007, 8, R115.  | 13.9 | 123       |
| 1359 | Porcine transcriptome analysis based on 97 non-normalized cDNA libraries and assembly of 1,021,891 expressed sequence tags. <i>Genome Biology</i> , 2007, 8, R45.   | 13.9 | 67        |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 1360 | Interrupted coding sequences in <i>Mycobacterium smegmatis</i> : authentic mutations or sequencing errors?. <i>Genome Biology</i> , 2007, 8, R20.   | 13.9 | 29        |
| 1361 | An annotated cDNA library and microarray for large-scale gene-expression studies in the ant <i>Solenopsis invicta</i> . <i>Genome Biology</i> , 2007, 8, R9.  | 13.9 | 47        |
| 1362 | Identification of early salt stress response genes in tomato root by suppression subtractive hybridization and microarray analysis. <i>Journal of Experimental Botany</i> , 2007, 58, 507-520.                                | 2.4  | 183       |
| 1363 | Genetic evidence for a second domestication of barley ( <i>Hordeum vulgare</i> ) east of the Fertile Crescent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3289-3294. | 3.3  | 331       |
| 1364 | Complete Genome Sequence of the Prototype Lactic Acid Bacterium <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363. <i>Journal of Bacteriology</i> , 2007, 189, 3256-3270.   | 1.0  | 362       |
| 1365 | Identification of stress-responsive genes in an indica rice ( <i>Oryza sativa</i> L.) using ESTs generated from drought-stressed seedlings. <i>Journal of Experimental Botany</i> , 2007, 58, 253-265.                        | 2.4  | 127       |
| 1366 | Expressed sequence tags from the halophyte <i>Limonium sinense</i> . <i>DNA Sequence</i> , 2007, 18, 61-67.   | 0.7  | 16        |
| 1367 | Diversity and phylogenetic affinities of foliar fungal endophytes in loblolly pine inferred by culturing and environmental PCR. <i>Mycologia</i> , 2007, 99, 185-206.   | 0.8  | 357       |
| 1368 | EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2259-2261.                    | 0.8  | 1,960     |
| 1369 | Characterization of an EST Database for the Perennial Weed Leafy Spurge: An Important Resource for Weed Biology Research. <i>Weed Science</i> , 2007, 55, 193-203.  | 0.8  | 51        |
| 1370 | Accuracy Assessment of Diploid Consensus Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 88-97.  | 1.9  | 10        |
| 1371 | The ribosomal database project (RDP-II): introducing myRDP space and quality controlled public data. <i>Nucleic Acids Research</i> , 2007, 35, D169-D172.   | 6.5  | 991       |
| 1372 | Loss of Bacterial Diversity during Antibiotic Treatment of Intubated Patients Colonized with <i>Pseudomonas aeruginosa</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 1954-1962.                                   | 1.8  | 166       |
| 1373 | Genetic and Haplotypic Structure in 14 European and African Cattle Breeds. <i>Genetics</i> , 2007, 177, 1059-1070.  | 1.2  | 133       |
| 1374 | Phylogeography of the Tree <i>Hymenaea stigonocarpa</i> (Fabaceae: Caesalpinioideae) and the Influence of Quaternary Climate Changes in the Brazilian Cerrado. <i>Annals of Botany</i> , 2007, 100, 1219-1228.                | 1.4  | 84        |
| 1376 | Phenotypic and genetic analysis of <i>Enterobacter</i> spp. from a Brazilian oligotrophic freshwater lake. <i>Canadian Journal of Microbiology</i> , 2007, 53, 983-991.   | 0.8  | 3         |
| 1377 | Congruence, Conflict, and Polyploidization Shown by Nuclear and Chloroplast Markers in the Monophyletic "Bristle Clade" (Paniceae, Panicoideae, Poaceae). <i>Systematic Botany</i> , 2007, 32, 531-544.                       | 0.2  | 39        |
| 1378 | The Complete Genome Sequence and Analysis of the Epsilonproteobacterium <i>Arcobacter butzleri</i> . <i>PLoS ONE</i> , 2007, 2, e1358.  | 1.1  | 203       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1379 | A North American <i>Yersinia pestis</i> Draft Genome Sequence: SNPs and Phylogenetic Analysis. PLoS ONE, 2007, 2, e220.   | 1.1 | 30        |
| 1380 | Analysis of Expressed Sequence Tags of the Cyclically Parthenogenetic Rotifer <i>Brachionus plicatilis</i> . PLoS ONE, 2007, 2, e671.   | 1.1 | 50        |
| 1381 | Molecular Correlates of Host Specialization in <i>Staphylococcus aureus</i> . PLoS ONE, 2007, 2, e1120.   | 1.1 | 203       |
| 1382 | The genome of <i>Hyperthermus butylicus</i> : a sulfur-reducing, peptide fermenting, neutrophilic Crenarchaeote growing up to 108 Å°C. Archaea, 2007, 2, 127-135.   | 2.3 | 41        |
| 1383 | Improved DNA sequencing quality and efficiency using an optimized fast cycle sequencing protocol. BioTechniques, 2007, 43, 58-62.   | 0.8 | 141       |
| 1384 | Gene projects: a genome web tool for ongoing mining and annotation applied to CitEST. Genetics and Molecular Biology, 2007, 30, 1030-1036.  | 0.6 | 8         |
| 1385 | A model for the RecA protein of <i>Mycoplasma synoviae</i> . Genetics and Molecular Biology, 2007, 30, 290-295.   | 0.6 | 1         |
| 1386 | Comparative analysis of differentially expressed sequence tags of sweet orange and mandarin infected with <i>Xylella fastidiosa</i> . Genetics and Molecular Biology, 2007, 30, 965-971.  | 0.6 | 19        |
| 1387 | Mitochondrial DNA corroborates the species distinctiveness of the Planalto ( <i>Thamnophilus pelzelni</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5   | 0.4 | 13        |
| 1388 | A basal phylogenetic placement for the salticid spider <i>Eupoa</i> , with descriptions of two new species (Araneae: Salticidae). Zootaxa, 2007, 1432, .  | 0.2 | 17        |
| 1390 | Novelty seeking and the dopamine D4 receptor gene (DRD4) revisited in Asians: Haplotype characterization and relevance of the 2-repeat allele. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 453-457. | 1.1 | 62        |
| 1391 | Variants of the ST6GALNAC2 promoter influence transcriptional activity and contribute to genetic susceptibility to IgA nephropathy. Human Mutation, 2007, 28, 950-957.  | 1.1 | 30        |
| 1392 | Comparative modeling of marsupial MHC class I molecules identifies structural polymorphisms affecting functional motifs. Journal of Experimental Zoology, 2007, 307A, 611-624.  | 1.2 | 3         |
| 1393 | Phylogenetic relationships, host affinity, and geographic structure of boreal and arctic endophytes from three major plant lineages. Molecular Phylogenetics and Evolution, 2007, 42, 543-555.  | 1.2 | 279       |
| 1394 | Development of bioinformatic tools to support EST-sequencing, in silico- and microarray-based transcriptome profiling in mycorrhizal symbioses. Phytochemistry, 2007, 68, 19-32.  | 1.4 | 49        |
| 1395 | Mutation screen and association studies in the Diacylglycerol O-acyltransferase homolog 2 gene (DGAT2), a positional candidate gene for early onset obesity on chromosome 11q13. BMC Genetics, 2007, 8, 17.                                 | 2.7 | 24        |
| 1396 | The mitochondrial genome from the thermal dimorphic fungus <i>Paracoccidioides brasiliensis</i> . Yeast, 2007, 24, 607-616.   | 0.8 | 33        |
| 1397 | Orthologous comparison in a gene-rich region among grasses reveals stability in the sugarcane polyploid genome. Plant Journal, 2007, 50, 574-585.   | 2.8 | 154       |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 1398 | Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . <i>Nature Biotechnology</i> , 2007, 25, 319-326.   | 9.4  | 449       |
| 1399 | Genomic analysis of <i>Bartonella</i> identifies type IV secretion systems as host adaptability factors. <i>Nature Genetics</i> , 2007, 39, 1469-1476.  | 9.4  | 120       |
| 1400 | Sequencing complete mitochondrial and plastid genomes. <i>Nature Protocols</i> , 2007, 2, 603-614.  | 5.5  | 84        |
| 1401 | Positive replication and linkage disequilibrium mapping of the chromosome 21q22.1 malaria susceptibility locus. <i>Genes and Immunity</i> , 2007, 8, 570-576.   | 2.2  | 27        |
| 1402 | Novel Mutations in the BHD Gene and Absence of Loss of Heterozygosity in Fibrofolliculomas of Birt-Hogg-Dubé Patients. <i>Journal of Investigative Dermatology</i> , 2007, 127, 588-593.  | 0.3  | 70        |
| 1403 | A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. <i>Nature</i> , 2007, 448, 1050-1053.  | 13.7 | 406       |
| 1404 | Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.   | 13.7 | 1,181     |
| 1405 | Vertical distribution of picoeukaryotic diversity in the Sargasso Sea. <i>Environmental Microbiology</i> , 2007, 9, 1233-1252.  | 1.8  | 181       |
| 1406 | Genome structure impacts molecular evolution at the <i>AvrLm1</i> avirulence locus of the plant pathogen <i>Leptosphaeria maculans</i> . <i>Environmental Microbiology</i> , 2007, 9, 2978-2992.                                  | 1.8  | 101       |
| 1407 | Whole-genome analysis of the ammonia-oxidizing bacterium, <i>Nitrosomonas eutropha</i> C91: implications for niche adaptation. <i>Environmental Microbiology</i> , 2007, 9, 2993-3007.  | 1.8  | 150       |
| 1408 | Rapidly evolving CRISPRs implicated in acquired resistance of microorganisms to viruses. <i>Environmental Microbiology</i> , 2008, 10, 200-207.   | 1.8  | 289       |
| 1409 | The localized adherence pattern of an atypical enteropathogenic <i>Escherichia coli</i> is mediated by intimin omicron and unexpectedly promotes HeLa cell invasion. <i>Cellular Microbiology</i> , 2007, 10, 071003010119002-??? | 1.1  | 50        |
| 1410 | Dismissal of Acoelomorpha: Acoela and Nemertodermatida are separate early bilaterian clades. <i>Zoologica Scripta</i> , 2007, 36, 509-523.  | 0.7  | 80        |
| 1411 | Evolutionary genetics of a defensive facultative symbiont of insects: exchange of toxin-encoding bacteriophage. <i>Molecular Ecology</i> , 2008, 17, 916-929.   | 2.0  | 126       |
| 1412 | Conservation and diversity in the immunity regions of wild phages with the immunity specificity of phage $\lambda$ . <i>Molecular Microbiology</i> , 2007, 64, 232-244.   | 1.2  | 20        |
| 1413 | Novel EBP gene mutations in Conradi-Häpplermann syndrome. <i>British Journal of Dermatology</i> , 2007, 157, 1225-1229.   | 1.4  | 27        |
| 1414 | Gene expression profiles of erythroid precursors characterise several mechanisms of the action of hydroxycarbamide in sickle cell anaemia. <i>British Journal of Haematology</i> , 2007, 136, 333-342.                            | 1.2  | 11        |
| 1415 | Both sulfate-reducing bacteria and Enterobacteriaceae take part in marine biocorrosion of carbon steel. <i>Journal of Applied Microbiology</i> , 2007, 102, 161-168.  | 1.4  | 72        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1416 | Characterization of the centromere and peri-centromere retrotransposons in <i>Brassica rapa</i> and their distribution in related <i>Brassica</i> species. <i>Plant Journal</i> , 2007, 49, 173-183.  | 2.8 | 116       |
| 1417 | Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton ( <i>Gossypium</i> ). <i>Plant Journal</i> , 2007, 50, 995-1006.   | 2.8 | 89        |
| 1418 | A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.  | 2.8 | 70        |
| 1419 | Identification of 10€882 porcine microsatellite sequences and virtual mapping of 4528 of these sequences. <i>Animal Genetics</i> , 2007, 38, 401-405.   | 0.6 | 8         |
| 1420 | Genes differentially expressed in <i>Theobroma cacao</i> associated with resistance to witches' broom disease caused by <i>Crinipellis pernicioso</i> . <i>Molecular Plant Pathology</i> , 2007, 8, 279-292.  | 2.0 | 48        |
| 1421 | Generation of a wheat leaf rust, <i>Puccinia triticina</i> , EST database from stage-specific cDNA libraries. <i>Molecular Plant Pathology</i> , 2007, 8, 451-467.  | 2.0 | 49        |
| 1422 | Generation and analysis of 5318 expressed sequence tags from the filamentous sporophyte of <i>Porphyra haitanensis</i> (Rhodophyta). <i>Journal of Phycology</i> , 2007, 43, 1287-1294.   | 1.0 | 55        |
| 1423 | Identification of <i>Legionella</i> spp. by 19 European reference laboratories: results of the European Working Group for <i>Legionella</i> Infections External Quality Assessment Scheme using DNA sequencing of the macrophage infectivity potentiator gene and dedicated online tools. <i>Clinical Microbiology and Infection</i> , 2007, 13, 1119-1124. | 2.8 | 20        |
| 1424 | Haplotype Structure of FSHB, the Beta-Subunit Gene for Fertility-Associated Follicle-Stimulating Hormone: Possible Influence of Balancing Selection. <i>Annals of Human Genetics</i> , 2007, 71, 18-28.   | 0.3 | 34        |
| 1425 | High-throughput species identification: from DNA isolation to bioinformatics. <i>Molecular Ecology Notes</i> , 2007, 7, 199-207.  | 1.7 | 69        |
| 1426 | DNA barcoding of Neotropical bats: species identification and discovery within Guyana. <i>Molecular Ecology Notes</i> , 2007, 7, 184-190.   | 1.7 | 261       |
| 1427 | BARCODING: bold: The Barcode of Life Data System ( <a href="http://www.barcodinglife.org">http://www.barcodinglife.org</a> ). <i>Molecular Ecology Notes</i> , 2007, 7, 355-364.  | 1.7 | 4,686     |
| 1428 | DNA pooling: a comprehensive, multi-stage association analysis of ACSL6 and SIRT5 polymorphisms in schizophrenia. <i>Genes, Brain and Behavior</i> , 2007, 6, 229-239.  | 1.1 | 16        |
| 1429 | Bacterial and fungal community structure in Arctic tundra tussock and shrub soils. <i>FEMS Microbiology Ecology</i> , 2007, 59, 428-435.  | 1.3 | 221       |
| 1430 | The transcriptional profile of <i>Paracoccidioides brasiliensis</i> yeast cells is influenced by human plasma. <i>FEMS Immunology and Medical Microbiology</i> , 2007, 51, 43-57.   | 2.7 | 37        |
| 1431 | Generation and annotation of lodgepole pine and oleoresin-induced expressed sequences from the blue-stain fungus <i>Ophiostoma clavigerum</i> , a Mountain Pine Beetle-associated pathogen. <i>FEMS Microbiology Letters</i> , 2007, 267, 151-158.  | 0.7 | 42        |
| 1432 | Aba3 oxygen reductase from the thermohalophilic bacterium <i>Rhodothermus marinus</i> . <i>FEMS Microbiology Letters</i> , 2007, 269, 41-47.  | 0.7 | 16        |
| 1433 | Sequence analysis of the 181-kb accessory plasmid pSmeSM11b, isolated from a dominant <i>Sinorhizobium melilotis</i> strain identified during a long-term field release experiment. <i>FEMS Microbiology Letters</i> , 2007, 271, 297-309.  | 0.7 | 27        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1434 | TAXONOMIC STATUS OF THE GENUS SOTALIA: SPECIES LEVEL RANKING FOR "TUCUXI" (SOTALIA FLUVIATILIS) AND "COSTERO" (SOTALIA GUIANENSIS) DOLPHINS. <i>Marine Mammal Science</i> , 2007, 23, 358-386.   | 0.9 | 107       |
| 1435 | Frequency, type, and distribution of EST-SSRs from three genotypes of <i>Lolium perenne</i> , and their conservation across orthologous sequences of <i>Festuca arundinacea</i> , <i>Brachypodium distachyon</i> , and <i>Oryza sativa</i> . <i>BMC Plant Biology</i> , 2007, 7, 36. | 1.6 | 60        |
| 1436 | An analysis of expressed sequence tags of developing castor endosperm using a full-length cDNA library. <i>BMC Plant Biology</i> , 2007, 7, 42.  | 1.6 | 51        |
| 1437 | Correlations of EGFR mutations and increases in EGFR and HER2 copy number to gefitinib response in a retrospective analysis of lung cancer patients. <i>BMC Cancer</i> , 2007, 7, 128.   | 1.1 | 36        |
| 1438 | A novel approach to sequence validating protein expression clones with automated decision making. <i>BMC Bioinformatics</i> , 2007, 8, 198.  | 1.2 | 6         |
| 1439 | miRAS: a data processing system for miRNA expression profiling study. <i>BMC Bioinformatics</i> , 2007, 8, 285.  | 1.2 | 1         |
| 1440 | Strainer: software for analysis of population variation in community genomic datasets. <i>BMC Bioinformatics</i> , 2007, 8, 398.   | 1.2 | 30        |
| 1441 | Minimus: a fast, lightweight genome assembler. <i>BMC Bioinformatics</i> , 2007, 8, 64.  | 1.2 | 354       |
| 1442 | Cloning, analysis and functional annotation of expressed sequence tags from the Earthworm <i>Eisenia fetida</i> . <i>BMC Bioinformatics</i> , 2007, 8, S7.   | 1.2 | 52        |
| 1443 | Global repeat discovery and estimation of genomic copy number in a large, complex genome using a high-throughput 454 sequence survey. <i>BMC Genomics</i> , 2007, 8, 132.  | 1.2 | 84        |
| 1444 | Comparative chloroplast genomics: analyses including new sequences from the angiosperms <i>Nuphar advena</i> and <i>Ranunculus macranthus</i> . <i>BMC Genomics</i> , 2007, 8, 174.  | 1.2 | 340       |
| 1445 | Generation and analysis of expressed sequence tags from the ciliate protozoan parasite <i>Ichthyophthirius multifiliis</i> . <i>BMC Genomics</i> , 2007, 8, 176.   | 1.2 | 29        |
| 1446 | Annotated Expressed Sequence Tags (ESTs) from pre-smolt Atlantic salmon ( <i>Salmo salar</i> ) in a searchable data resource. <i>BMC Genomics</i> , 2007, 8, 209.  | 1.2 | 51        |
| 1447 | A complete mitochondrial genome sequence of the wild two-humped camel ( <i>Camelus bactrianus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlode   | 1.2 | 69        |
| 1448 | Identification of unannotated exons of low abundance transcripts in <i>Drosophila melanogaster</i> and cloning of a new serine protease gene upregulated upon injury. <i>BMC Genomics</i> , 2007, 8, 249.  | 1.2 | 9         |
| 1449 | Genomic organization of duplicated major histocompatibility complex class I regions in Atlantic salmon ( <i>Salmo salar</i> ). <i>BMC Genomics</i> , 2007, 8, 251.   | 1.2 | 60        |
| 1450 | cDNA sequences reveal considerable gene prediction inaccuracy in the <i>Plasmodium falciparum</i> genome. <i>BMC Genomics</i> , 2007, 8, 255.  | 1.2 | 50        |
| 1451 | Expressed sequences tags of the anther smut fungus, <i>Microbotryum violaceum</i> , identify mating and pathogenicity genes. <i>BMC Genomics</i> , 2007, 8, 272.   | 1.2 | 30        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1452 | Analysis of 13000 unique Citrus clusters associated with fruit quality, production and salinity tolerance. BMC Genomics, 2007, 8, 31.  | 1.2 | 64        |
| 1453 | Characterization of the equine 2'-5' oligoadenylate synthetase 1 (OAS1) and ribonuclease L (RNASEL) innate immunity genes. BMC Genomics, 2007, 8, 313.   | 1.2 | 16        |
| 1454 | End-sequencing and characterization of silkworm ( <i>Bombyx mori</i> ) bacterial artificial chromosome libraries. BMC Genomics, 2007, 8, 314.  | 1.2 | 12        |
| 1455 | Optical mapping as a routine tool for bacterial genome sequence finishing. BMC Genomics, 2007, 8, 321.   | 1.2 | 104       |
| 1456 | Gene duplication and paleopolyploidy in soybean and the implications for whole genome sequencing. BMC Genomics, 2007, 8, 330.  | 1.2 | 132       |
| 1457 | Collebase: a repository for springtail genomics and soil quality assessment. BMC Genomics, 2007, 8, 341.   | 1.2 | 44        |
| 1458 | An optimized procedure greatly improves EST vector contamination removal. BMC Genomics, 2007, 8, 416.  | 1.2 | 74        |
| 1459 | Genomic resources for <i>Myzus persicae</i> : EST sequencing, SNP identification, and microarray design. BMC Genomics, 2007, 8, 423.   | 1.2 | 116       |
| 1460 | Discovery of novel alternatively spliced <i>C. elegans</i> transcripts by computational analysis of SAGE data. BMC Genomics, 2007, 8, 447.   | 1.2 | 6         |
| 1461 | Construction and characterization of an expressed sequenced tag library for the mosquito vector <i>Armigeres subalbatus</i> . BMC Genomics, 2007, 8, 462.  | 1.2 | 12        |
| 1462 | Diversity in conserved genes in tomato. BMC Genomics, 2007, 8, 465.  | 1.2 | 65        |
| 1463 | AphanoDB: a genomic resource for <i>Aphanomyces</i> pathogens. BMC Genomics, 2007, 8, 471.   | 1.2 | 43        |
| 1464 | Surviving extreme polar winters by desiccation: clues from Arctic springtail ( <i>Onychiurus arcticus</i> ) EST libraries. BMC Genomics, 2007, 8, 475.   | 1.2 | 61        |
| 1465 | The capsule polysaccharide structure and biogenesis for non-O1 <i>Vibrio cholerae</i> NRT36S: genes are embedded in the LPS region. BMC Microbiology, 2007, 7, 20.   | 1.3 | 42        |
| 1466 | The transcriptome analysis of early morphogenesis in <i>Paracoccidioides brasiliensis</i> mycelium reveals novel and induced genes potentially associated to the dimorphic process. BMC Microbiology, 2007, 7, 29. | 1.3 | 100       |
| 1467 | Analysis of <i>Chromobacterium</i> sp. natural isolates from different Brazilian ecosystems. BMC Microbiology, 2007, 7, 58.  | 1.3 | 51        |
| 1468 | The use of Tn5 transposable elements in a gene trapping strategy for the protozoan <i>Leishmania</i> . International Journal for Parasitology, 2007, 37, 735-742.  | 1.3 | 4         |
| 1469 | GRAT genome-scale rapid alignment tool. Computer Methods and Programs in Biomedicine, 2007, 86, 87-92.   | 2.6 | 3         |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1470 | Genes that may modulate longevity in <i>C. elegans</i> in both dauer larvae and long-lived <i>daf-2</i> adults. <i>Experimental Gerontology</i> , 2007, 42, 825-839.   | 1.2 | 26        |
| 1471 | Papillomatous digital dermatitis spirochetes suppress the bovine macrophage innate immune response. <i>Veterinary Microbiology</i> , 2007, 125, 256-264.   | 0.8 | 36        |
| 1472 | Complete genomic sequence and mass spectrometric analysis of highly diverse, atypical <i>Bacillus thuringiensis</i> phage 03051-8a. <i>Virology</i> , 2007, 368, 405-421.  | 1.1 | 65        |
| 1473 | Complete nucleotide sequence of pBMB67, a 67-kb plasmid from <i>Bacillus thuringiensis</i> strain YBT-1520. <i>Plasmid</i> , 2007, 57, 44-54.  | 0.4 | 21        |
| 1474 | Sequence of plasmid pBS228 and reconstruction of the IncP-1± phylogeny. <i>Plasmid</i> , 2007, 58, 76-83.  | 0.4 | 44        |
| 1475 | Complete nucleotide sequence of pLD-TEX-KL, a 66-kb plasmid of <i>Legionella dumoffii</i> TEX-KL strain. <i>Plasmid</i> , 2007, 58, 261-268.   | 0.4 | 6         |
| 1476 | Tolerance of Antarctic soil fungi to hydrocarbons. <i>Science of the Total Environment</i> , 2007, 372, 539-548.   | 3.9 | 60        |
| 1477 | Single nucleotide polymorphisms identification in expressed genes of <i>Schistosoma mansoni</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 154, 134-140.  | 0.5 | 22        |
| 1478 | Species delimitation and phylogenetic relationships in <i>Lactarius</i> section <i>Deliciosi</i> in Europe. <i>Mycological Research</i> , 2007, 111, 1285-1297.  | 2.5 | 24        |
| 1479 | Expressed sequence tags from wheat roots under hypoxia. <i>Russian Journal of Plant Physiology</i> , 2007, 54, 659-668.  | 0.5 | 7         |
| 1480 | Complete Nucleotide Sequence of the pCTX-M3 Plasmid and Its Involvement in Spread of the Extended-Spectrum β-Lactamase Gene <i>bla</i> <sub>CTX-M-3</sub> . <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3789-3795.  | 1.4 | 124       |
| 1481 | Erythromycin Resistance-Confering Plasmid pRSB105, Isolated from a Sewage Treatment Plant, Harbors a New Macrolide Resistance Determinant, an Integron-Containing Tn402-Like Element, and a Large Region of Unknown Function. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1952-1960. | 1.4 | 69        |
| 1482 | Construction and characterization of a full-length cDNA library for the wheat stripe rust pathogen ( <i>Puccinia striiformis</i> f. sp. <i>tritici</i> ). <i>BMC Genomics</i> , 2007, 8, 145.  | 1.2 | 60        |
| 1483 | Reaping the Benefits of SAGE. , 2007, 406, 365-386.  |     | 3         |
| 1484 | Automated Discovery of Single Nucleotide Polymorphism and Simple Sequence Repeat Molecular Genetic Markers. , 2007, 406, 473-494.  |     | 11        |
| 1485 | Discovery of cSNPs in pig using full-length enriched cDNA libraries of the Korean native pig as a source of genetic diversity. <i>Biotechnology and Bioprocess Engineering</i> , 2007, 12, 424-432.  | 1.4 | 3         |
| 1486 | Adaptive Evolution in an Avian Reproductive Protein: ZP3. <i>Journal of Molecular Evolution</i> , 2007, 65, 555-563.   | 0.8 | 22        |
| 1487 | High-Density Universal 16S rRNA Microarray Analysis Reveals Broader Diversity than Typical Clone Library When Sampling the Environment. <i>Microbial Ecology</i> , 2007, 53, 371-383.  | 1.4 | 416       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1488 | Long serial analysis of gene expression for transcriptome profiling during the initiation of ligninolytic enzymes production in <i>Phanerochaete chrysosporium</i> . <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 609-618.              | 1.7 | 16        |
| 1489 | Generation, annotation, and analysis of ESTs from four different <i>Trichoderma</i> strains grown under conditions related to biocontrol. <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 853-862.   | 1.7 | 39        |
| 1490 | Comparative genomics reveals functional transcriptional control sequences in the <i>Prop1</i> gene. <i>Mammalian Genome</i> , 2007, 18, 521-537.   | 1.0 | 21        |
| 1491 | Ancestral bias in the <i>Hras1</i> gene and distal Chromosome 7 among inbred mice. <i>Mammalian Genome</i> , 2007, 18, 732-738.  | 1.0 | 0         |
| 1492 | Analysis of DNA polymorphisms in sugar beet ( <i>Beta vulgaris</i> L.) and development of an SNP-based map of expressed genes. <i>Theoretical and Applied Genetics</i> , 2007, 115, 601-615.   | 1.8 | 60        |
| 1493 | Serial analysis of gene expression in sugarcane ( <i>Saccharum</i> spp.) leaves revealed alternative C4 metabolism and putative antisense transcripts. <i>Plant Molecular Biology</i> , 2007, 63, 745-762.   | 2.0 | 69        |
| 1494 | A collection of 10,096 indica rice full-length cDNAs reveals highly expressed sequence divergence between <i>Oryza sativa indica</i> and <i>japonica</i> subspecies. <i>Plant Molecular Biology</i> , 2007, 65, 403-415.                             | 2.0 | 55        |
| 1495 | Isolation and characterization of expressed sequence tags (ESTs) from subtracted cDNA libraries of <i>Pennisetum glaucum</i> seedlings. <i>Plant Molecular Biology</i> , 2007, 64, 713-732.  | 2.0 | 55        |
| 1496 | Analysis of expression profile of selected genes expressed during auxin-induced somatic embryogenesis in leaf base system of wheat ( <i>Triticum aestivum</i> ) and their possible interactions. <i>Plant Molecular Biology</i> , 2007, 65, 677-692. | 2.0 | 72        |
| 1497 | cDNA cloning, characterization, and expression analysis of channel catfish ( <i>Ictalurus punctatus</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10 0,9 18  |     |           |
| 1498 | A revision of the systematics of panther worms ( <i>Hofstenia</i> spp., Acoela), with notes on color variation and genetic variation within the genus. <i>Hydrobiologia</i> , 2007, 592, 439-454.  | 1.0 | 13        |
| 1499 | Characterization of a BAC Library from Channel Catfish <i>Ictalurus punctatus</i> : Indications of High Levels of Chromosomal Reshuffling Among Teleost Genomes. <i>Marine Biotechnology</i> , 2007, 9, 701-711.                                     | 1.1 | 39        |
| 1500 | The chloroplast genome from a lycophyte (microphylophyte), <i>Selaginella uncinata</i> , has a unique inversion, transpositions and many gene losses. <i>Journal of Plant Research</i> , 2007, 120, 281-290.   | 1.2 | 70        |
| 1501 | Organization of H locus conserved repeats in <i>Leishmania (Viannia) braziliensis</i> correlates with lack of gene amplification and drug resistance. <i>Parasitology Research</i> , 2007, 101, 667-676.   | 0.6 | 20        |
| 1502 | Genetic and physical maps around the sex-determining M-locus of the dioecious plant asparagus. <i>Molecular Genetics and Genomics</i> , 2007, 278, 221-234.  | 1.0 | 91        |
| 1503 | Molecular characterization of a retrotransposon in the <i>Rhynchosciara americana</i> genome and its association with telomere. <i>Chromosome Research</i> , 2008, 16, 729-742.  | 1.0 | 9         |
| 1504 | FISH mapping and molecular organization of the major repetitive sequences of tomato. <i>Chromosome Research</i> , 2008, 16, 919-933.   | 1.0 | 69        |
| 1505 | Gene expression in diplosporous and sexual <i>Eragrostis curvula</i> genotypes with differing ploidy levels. <i>Plant Molecular Biology</i> , 2008, 67, 11-23.   | 2.0 | 53        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1506 | Sugar levels modulate sorbitol dehydrogenase expression in maize. <i>Plant Molecular Biology</i> , 2008, 68, 203-213.   | 2.0 | 29        |
| 1507 | Development of ChillPeach genomic tools and identification of cold-responsive genes in peach fruit. <i>Plant Molecular Biology</i> , 2008, 68, 379-397.   | 2.0 | 80        |
| 1508 | BAC-derived markers for assaying the stem rust resistance gene, Sr2, in wheat breeding programs. <i>Molecular Breeding</i> , 2008, 22, 15-24.   | 1.0 | 36        |
| 1509 | Mariner-like elements in <i>Rhynchosciara americana</i> (Sciaridae) genome: molecular and cytological aspects. <i>Genetica</i> , 2008, 133, 137-145.  | 0.5 | 9         |
| 1510 | Extensive Rearrangements in the Chloroplast Genome of <i>Trachelium caeruleum</i> Are Associated with Repeats and tRNA Genes. <i>Journal of Molecular Evolution</i> , 2008, 66, 350-361.  | 0.8 | 257       |
| 1511 | Extensive Reorganization of the Plastid Genome of <i>Trifolium subterraneum</i> (Fabaceae) Is Associated with Numerous Repeated Sequences and Novel DNA Insertions. <i>Journal of Molecular Evolution</i> , 2008, 67, 696-704.                                | 0.8 | 217       |
| 1512 | Degree-day accumulation controlling allopatric and sympatric variations in the sociality of sweat bees, <i>Lasioglossum (Evyllaesus) baleicum</i> (Hymenoptera: Halictidae). <i>Behavioral Ecology and Sociobiology</i> , 2008, 62, 1239-1247.                | 0.6 | 39        |
| 1513 | The complete nucleotide sequence of the cassava ( <i>Manihot esculenta</i> ) chloroplast genome and the evolution of atpF in Malpighiales: RNA editing and multiple losses of a group II intron. <i>Theoretical and Applied Genetics</i> , 2008, 116, 723-37. | 1.8 | 96        |
| 1514 | Genetic analysis of opaque2 modifier loci in quality protein maize. <i>Theoretical and Applied Genetics</i> , 2008, 117, 157-170.   | 1.8 | 81        |
| 1515 | Analysis of genome organization, composition and microsynteny using 500Åkb BAC sequences in chickpea. <i>Theoretical and Applied Genetics</i> , 2008, 117, 449-458.   | 1.8 | 24        |
| 1516 | Positive correlation between recombination rate and nucleotide diversity is shown under domestication selection in the chicken genome. <i>Science Bulletin</i> , 2008, 53, 746-750.   | 1.7 | 40        |
| 1517 | Phylogenetic identification and microbial diversity in snow of the summit (8201 m) of Cho Oyu Mountain, Tibet. <i>Science Bulletin</i> , 2008, 53, 3317-3323.   | 4.3 | 2         |
| 1518 | BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean ( <i>Phaseolus vulgaris</i> L.) Genome. <i>Tropical Plant Biology</i> , 2008, 1, 40-48.   | 1.0 | 70        |
| 1519 | The shrunken genome of <i>Arabidopsis thaliana</i> . <i>Plant Systematics and Evolution</i> , 2008, 273, 257-271.   | 0.3 | 35        |
| 1520 | EST and Mitochondrial DNA Sequences Support a Distinct Pacific Form of Salmon Louse, <i>Lepeophtheirus salmonis</i> . <i>Marine Biotechnology</i> , 2008, 10, 741-749.  | 1.1 | 50        |
| 1521 | The nuclear genome of <i>Brachypodium distachyon</i> : analysis of BAC end sequences. <i>Functional and Integrative Genomics</i> , 2008, 8, 135-147.  | 1.4 | 83        |
| 1522 | Primary responses to salt stress in a halophyte, smooth cordgrass ( <i>Spartina alterniflora</i> Loisel.). <i>Functional and Integrative Genomics</i> , 2008, 8, 287-300.   | 1.4 | 87        |
| 1523 | Indonesian Kickxellales: two species of <i>Coemansia</i> and <i>Linderina</i> . <i>Mycoscience</i> , 2008, 49, 241-249.   | 0.3 | 10        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1524 | Unexpectedly large number of conserved noncoding regions within the ancestral chordate Hox cluster. <i>Development Genes and Evolution</i> , 2008, 218, 591-597.   | 0.4 | 19        |
| 1525 | Transcriptome analysis for <i>Caenorhabditis elegans</i> based on novel expressed sequence tags. <i>BMC Biology</i> , 2008, 6, 30.   | 1.7 | 46        |
| 1526 | Expressed sequence tags (ESTs) from immune tissues of turbot ( <i>Scophthalmus maximus</i> ) challenged with pathogens. <i>BMC Veterinary Research</i> , 2008, 4, 37.  | 0.7 | 61        |
| 1527 | Expression of Groucho/TLE proteins during pancreas development. <i>BMC Developmental Biology</i> , 2008, 8, 81.  | 2.1 | 29        |
| 1528 | Sequence variation in the human transcription factor gene POU5F1. <i>BMC Genetics</i> , 2008, 9, 15.   | 2.7 | 8         |
| 1529 | HaploSNPer: a web-based allele and SNP detection tool. <i>BMC Genetics</i> , 2008, 9, 23.  | 2.7 | 37        |
| 1530 | Detecting the effects of selection at the population level in six bovine immune genes. <i>BMC Genetics</i> , 2008, 9, 62.  | 2.7 | 10        |
| 1531 | Proteomic profiling of rice embryos from a hybrid rice cultivar and its parental lines. <i>Proteomics</i> , 2008, 8, 4808-4821.  | 1.3 | 48        |
| 1532 | The gap-filling sequence on the left arm of chromosome 2 in fission yeast <i>Schizosaccharomyces pombe</i> . <i>Yeast</i> , 2008, 25, 673-679.   | 0.8 | 9         |
| 1533 | Nucleotide sequence of plasmid pA387 of <i>Amycolatopsis benzoatilytica</i> and construction of a conjugative shuttle vector. <i>Journal of Basic Microbiology</i> , 2008, 48, 177-185.  | 1.8 | 8         |
| 1534 | Tauopathy with paired helical filaments in an aged chimpanzee. <i>Journal of Comparative Neurology</i> , 2008, 509, 259-270.   | 0.9 | 129       |
| 1535 | An optimized nested polymerase chain reaction (PCR) approach allows detection and characterization of human immunodeficiency virus type 1 (HIV-1) env and gag genes from clinical samples. <i>Journal of Clinical Laboratory Analysis</i> , 2008, 22, 106-113.                 | 0.9 | 2         |
| 1536 | SSCP markers provide a useful alternative to microsatellites in genotyping and estimating genetic diversity in populations and germplasm collections of plant specialty crops. <i>Electrophoresis</i> , 2008, 29, 4096-4108.   | 1.3 | 23        |
| 1537 | Large-scale microfabricated channel plates for high-throughput, fully automated DNA sequencing. <i>Electrophoresis</i> , 2008, 29, 4723-4732.  | 1.3 | 7         |
| 1538 | Molecular Analysis of the Kirromycin Biosynthetic Gene Cluster Revealed Î²-Alanine as Precursor of the Pyridone Moiety. <i>Chemistry and Biology</i> , 2008, 15, 175-188.  | 6.2 | 101       |
| 1539 | Mitochondrial DNA variation of the dog hookworm <i>Ancylostoma caninum</i> in Brazilian populations. <i>Veterinary Parasitology</i> , 2008, 151, 61-67.  | 0.7 | 28        |
| 1540 | Identification of gender-regulated genes in <i>Ancylostoma braziliense</i> by real-time RT-PCR. <i>Veterinary Parasitology</i> , 2008, 153, 277-284.   | 0.7 | 8         |
| 1541 | Molecular phylogenetics of <i>Alchemilla</i> , <i>Aphanes</i> and <i>Lachemilla</i> (Rosaceae) inferred from plastid and nuclear intron and spacer DNA sequences, with comments on generic classification. <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 1030-1044. | 1.2 | 62        |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 1542 | Reconstructing ordinal relationships in the Demospongiae using mitochondrial genomic data. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 111-124.  | 1.2  | 136       |
| 1543 | Molecular systematics of the genus <i>Artibeus</i> (Chiroptera: Phyllostomidae). <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 44-58.  | 1.2  | 75        |
| 1544 | DNA methylation and chromatin accessibility of the proximal <i>Cyp19</i> promoter region 1.5/2 correlate with expression levels in sheep placentomes. <i>Molecular Reproduction and Development</i> , 2008, 75, 1-7.              | 1.0  | 31        |
| 1545 | Genomic organization of the porcine dopachrome tautomerase (DCT) gene. <i>Animal Science Journal</i> , 2008, 79, 182-186.   | 0.6  | 4         |
| 1546 | Chloroplast genome sequencing analysis of <i>Heterosigma akashiwo</i> CCMP452 (West Atlantic) and NIES293 (West Pacific) strains. <i>BMC Genomics</i> , 2008, 9, 211.   | 1.2  | 52        |
| 1547 | Complete Genome Sequence of the Soil Actinomycete <i>Kocuria rhizophila</i> . <i>Journal of Bacteriology</i> , 2008, 190, 4139-4146.  | 1.0  | 79        |
| 1548 | Genomic and host range studies of <i>Maruca vitrata</i> nucleopolyhedrovirus. <i>Journal of General Virology</i> , 2008, 89, 2315-2330.   | 1.3  | 33        |
| 1549 | Exploiting an oil palm EST database for the development of gene-derived SSR markers and their exploitation for assessment of genetic diversity. <i>Biologia (Poland)</i> , 2008, 63, 227-235.                                     | 0.8  | 54        |
| 1550 | Global Identification of Significantly Expressed Genes in Developing Endosperm of Rice by Expression Sequence Tags and cDNA Array Approaches. <i>Journal of Integrative Plant Biology</i> , 2008, 50, 1078-1088.                  | 4.1  | 9         |
| 1551 | Lateral gene transfer of O1 serogroup encoding genes of <i>Vibrio cholerae</i> . <i>FEMS Microbiology Letters</i> , 2008, 286, 32-38.   | 0.7  | 20        |
| 1552 | Amazon River dolphin love fetishes: From folklore to molecular forensics. <i>Marine Mammal Science</i> , 2008, 24, 969-978.   | 0.9  | 18        |
| 1553 | A cDNA microarray for the three-spined stickleback, <i>Gasterosteus aculeatus</i> L., and analysis of the interactive effects of oestradiol and dibenzanthracene exposures. <i>Journal of Fish Biology</i> , 2008, 72, 2133-2153. | 0.7  | 34        |
| 1554 | Phylum Tardigrada: an "individual" approach. <i>Cladistics</i> , 2008, 24, 861-871.   | 1.5  | 105       |
| 1555 | Two levels of protection for the B cell genome during somatic hypermutation. <i>Nature</i> , 2008, 451, 841-845.  | 13.7 | 524       |
| 1556 | The complete genome of an individual by massively parallel DNA sequencing. <i>Nature</i> , 2008, 452, 872-876.  | 13.7 | 1,635     |
| 1557 | Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , 2008, 456, 53-59.   | 13.7 | 3,118     |
| 1558 | Rapid genome sequencing with short universal tiling probes. <i>Nature Biotechnology</i> , 2008, 26, 676-684.  | 9.4  | 43        |
| 1559 | Next-generation DNA sequencing. <i>Nature Biotechnology</i> , 2008, 26, 1135-1145.  | 9.4  | 3,609     |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1560 | Pyrobayes: an improved base caller for SNP discovery in pyrosequences. <i>Nature Methods</i> , 2008, 5, 179-181.  | 9.0 | 180       |
| 1561 | An examination of the Chiropteran HoxD locus from an evolutionary perspective. <i>Evolution &amp; Development</i> , 2008, 10, 657-670.  | 1.1 | 24        |
| 1562 | Characterisation of <i>Yersinia pestis</i> isolates from natural foci of plague in the Republic of Georgia, and their relationship to <i>Y. pestis</i> isolates from other countries. <i>Clinical Microbiology and Infection</i> , 2008, 14, 429-436. | 2.8 | 21        |
| 1563 | DNA BARCODING: Barcoding corals: limited by interspecific divergence, not intraspecific variation. <i>Molecular Ecology Resources</i> , 2008, 8, 247-255.   | 2.2 | 142       |
| 1564 | Extracting DNA from museum bird eggs, and whole genome amplification of archive DNA. <i>Molecular Ecology Resources</i> , 2008, 8, 551-560.   | 2.2 | 33        |
| 1565 | Molecular characterization of early colonizer bacteria from wastes in a steel plant. <i>Letters in Applied Microbiology</i> , 2008, 47, 241-249.  | 1.0 | 24        |
| 1566 | The occurrence of tissue-specific twitchin isoforms in the mussel <i>Mytilus galloprovincialis</i> . <i>Fisheries Science</i> , 2008, 74, 677-686.  | 0.7 | 7         |
| 1567 | Metabolic versatility of the <i>Riftia pachyptila</i> endosymbiont revealed through metagenomics. <i>Environmental Microbiology</i> , 2008, 10, 727-737.  | 1.8 | 143       |
| 1568 | Integron-associated gene cassettes in Halifax Harbour: assessment of a mobile gene pool in marine sediments. <i>Environmental Microbiology</i> , 2008, 10, 1024-1038.   | 1.8 | 59        |
| 1569 | Wide genetic diversity of picoplanktonic green algae (Chloroplastida) in the Mediterranean Sea uncovered by a phylum-biased PCR approach. <i>Environmental Microbiology</i> , 2008, 10, 1804-1822.  | 1.8 | 112       |
| 1570 | Viral communities associated with healthy and bleaching corals. <i>Environmental Microbiology</i> , 2008, 10, 2277-2286.  | 1.8 | 125       |
| 1571 | A locus for autosomal dominant progressive non-syndromic hearing loss, <i>DFNA27</i> , is on chromosome 4q12-13.1. <i>Clinical Genetics</i> , 2008, 73, 367-372.  | 1.0 | 17        |
| 1572 | Chanarin-Dorfman syndrome caused by a novel splice site mutation in ABHD5. <i>British Journal of Dermatology</i> , 2008, 158, 1378-1380.  | 1.4 | 20        |
| 1573 | A newly identified splice site mutation in ZMPSTE24 causes restrictive dermopathy in the Middle East. <i>British Journal of Dermatology</i> , 2008, 159, 961-967.   | 1.4 | 18        |
| 1574 | Reduced introgression of the Y chromosome between subspecies of the European rabbit ( <i>Oryctolagus cuniculus</i> ) in the Iberian Peninsula. <i>Molecular Ecology</i> , 2008, 17, 4489-4499.  | 2.0 | 45        |
| 1575 | Inferring the history of speciation in house mice from autosomal, X-linked and mitochondrial genes. <i>Molecular Ecology</i> , 2008, 17, 5349-5363.   | 2.0 | 219       |
| 1576 | Metabolic adaptation in <i>Cryptococcus neoformans</i> during early murine pulmonary infection. <i>Molecular Microbiology</i> , 2008, 69, 1456-1475.  | 1.2 | 147       |
| 1577 | Detection of SNPs in bovine immune-response genes that may mediate resistance to the cattle tick <i>Rhipicephalus</i> ( <i>Boophilus</i> ) <i>microplus</i> . <i>Animal Genetics</i> , 2008, 39, 328-329.   | 0.6 | 7         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1578 | Characterization of a 320â€kb region containing the <i>HEXA</i> gene on bovine chromosome 10 and analysis of its association with BSE susceptibility. <i>Animal Genetics</i> , 2008, 39, 400-406. | 0.6 | 4         |
| 1579 | Absence of <i>fumarate hydratase</i> mutation in a family with cutaneous leiomyosarcoma and renal cancer. <i>International Journal of Dermatology</i> , 2008, 47, 18-20.                           | 0.5 | 11        |
| 1580 | Using quality scores and longer reads improves accuracy of Solexa read mapping. <i>BMC Bioinformatics</i> , 2008, 9, 128.  | 1.2 | 261       |
| 1581 | DNAAlignEditor: DNA alignment editor tool. <i>BMC Bioinformatics</i> , 2008, 9, 154.   | 1.2 | 11        |
| 1582 | EST Express: PHP/MySQL based automated annotation of ESTs from expression libraries. <i>BMC Bioinformatics</i> , 2008, 9, 186.   | 1.2 | 5         |
| 1583 | Large-scale identification of polymorphic microsatellites using an in silico approach. <i>BMC Bioinformatics</i> , 2008, 9, 374.   | 1.2 | 65        |
| 1584 | XplorSeq: A software environment for integrated management and phylogenetic analysis of metagenomic sequence data. <i>BMC Bioinformatics</i> , 2008, 9, 420.                                       | 1.2 | 47        |
| 1585 | Probabilistic base calling of Solexa sequencing data. <i>BMC Bioinformatics</i> , 2008, 9, 431.  | 1.2 | 82        |
| 1586 | VarDetect: a nucleotide sequence variation exploratory tool. <i>BMC Bioinformatics</i> , 2008, 9, S9.  | 1.2 | 14        |
| 1587 | The complete plastid genome sequence of <i>Welwitschia mirabilis</i> : an unusually compact plastome with accelerated divergence rates. <i>BMC Evolutionary Biology</i> , 2008, 8, 130.            | 3.2 | 110       |
| 1588 | A genome-wide screen for noncoding elements important in primate evolution. <i>BMC Evolutionary Biology</i> , 2008, 8, 17.   | 3.2 | 90        |
| 1589 | Bayesian inference of population size history from multiple loci. <i>BMC Evolutionary Biology</i> , 2008, 8, 289.  | 3.2 | 658       |
| 1590 | Multiple expressed MHC class II loci in salmonids; details of one non-classical region in Atlantic salmon ( <i>Salmo salar</i> ). <i>BMC Genomics</i> , 2008, 9, 193.                              | 1.2 | 41        |
| 1591 | The abundant extrachromosomal DNA content of the <i>Spiroplasma citri</i> GII3-3X genome. <i>BMC Genomics</i> , 2008, 9, 195.  | 1.2 | 52        |
| 1592 | Genomics of an extreme psychrophile, <i>Psychromonas ingrahamii</i> . <i>BMC Genomics</i> , 2008, 9, 210.  | 1.2 | 114       |
| 1593 | Genomic and bioinformatics analysis of human adenovirus type 37: New insights into corneal tropism. <i>BMC Genomics</i> , 2008, 9, 213.  | 1.2 | 40        |
| 1594 | Insight into the sialome of the castor bean tick, <i>Ixodes ricinus</i> . <i>BMC Genomics</i> , 2008, 9, 233.  | 1.2 | 77        |
| 1595 | Improved annotation through genome-scale metabolic modeling of <i>Aspergillus oryzae</i> . <i>BMC Genomics</i> , 2008, 9, 245.   | 1.2 | 88        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1596 | Pyrosequencing as a method for SNP identification in the rhesus macaque ( <i>Macaca mulatta</i> ). <i>BMC Genomics</i> , 2008, 9, 256.  | 1.2 | 42        |
| 1597 | The genome of the versatile nitrogen fixer <i>Azorhizobium caulinodans</i> ORS571. <i>BMC Genomics</i> , 2008, 9, 271.  | 1.2 | 104       |
| 1598 | A genome-wide 20 K citrus microarray for gene expression analysis. <i>BMC Genomics</i> , 2008, 9, 318.  | 1.2 | 49        |
| 1599 | The mitochondrial genome of the hexactinellid sponge <i>Aphrocallistes vastus</i> : Evidence for programmed translational frameshifting. <i>BMC Genomics</i> , 2008, 9, 33.   | 1.2 | 49        |
| 1600 | Complete genome of <i>Phenylobacterium zucineum</i> – a novel facultative intracellular bacterium isolated from human erythroleukemia cell line K562. <i>BMC Genomics</i> , 2008, 9, 386.   | 1.2 | 12        |
| 1601 | Assessing the feasibility of GS FLX Pyrosequencing for sequencing the Atlantic salmon genome. <i>BMC Genomics</i> , 2008, 9, 404.   | 1.2 | 72        |
| 1602 | Development of genomic resources for <i>Citrus clementina</i> : Characterization of three deep-coverage BAC libraries and analysis of 46,000 BAC end sequences. <i>BMC Genomics</i> , 2008, 9, 423.                                   | 1.2 | 81        |
| 1603 | A conifer genomics resource of 200,000 spruce ( <i>Picea</i> spp.) ESTs and 6,464 high-quality, sequence-finished full-length cDNAs for Sitka spruce ( <i>Picea sitchensis</i> ). <i>BMC Genomics</i> , 2008, 9, 484.                 | 1.2 | 113       |
| 1604 | Genomic resources for a commercial flatfish, the Senegalese sole ( <i>Solea senegalensis</i> ): EST sequencing, oligo microarray design, and development of the bioinformatic platform Soleamold. <i>BMC Genomics</i> , 2008, 9, 508. | 1.2 | 70        |
| 1605 | Isolation, characterization and comparison of Atlantic and Chinook salmon growth hormone 1 and 2. <i>BMC Genomics</i> , 2008, 9, 522.   | 1.2 | 27        |
| 1606 | A salmonid EST genomic study: genes, duplications, phylogeny and microarrays. <i>BMC Genomics</i> , 2008, 9, 545.   | 1.2 | 145       |
| 1607 | Analysis of 4,664 high-quality sequence-finished poplar full-length cDNA clones and their utility for the discovery of genes responding to insect feeding. <i>BMC Genomics</i> , 2008, 9, 57.   | 1.2 | 68        |
| 1608 | Insights into the <i>Musa</i> genome: Syntenic relationships to rice and between <i>Musa</i> species. <i>BMC Genomics</i> , 2008, 9, 58.  | 1.2 | 105       |
| 1609 | Comparative genomic analysis of carbon and nitrogen assimilation mechanisms in three indigenous bioleaching bacteria: predictions and validations. <i>BMC Genomics</i> , 2008, 9, 581.  | 1.2 | 99        |
| 1610 | Coral life history and symbiosis: Functional genomic resources for two reef building Caribbean corals, <i>Acropora palmata</i> and <i>Montastraea faveolata</i> . <i>BMC Genomics</i> , 2008, 9, 97.                                  | 1.2 | 122       |
| 1611 | Characterization of new IS elements and studies of their dispersion in two subspecies of <i>Leifsonia xyli</i> . <i>BMC Microbiology</i> , 2008, 8, 127.  | 1.3 | 12        |
| 1612 | Universal ligation-detection-reaction microarray applied for compost microbes. <i>BMC Microbiology</i> , 2008, 8, 237.  | 1.3 | 29        |
| 1613 | Identification of a set of genes showing regionally enriched expression in the mouse brain. <i>BMC Neuroscience</i> , 2008, 9, 66.  | 0.8 | 25        |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1614 | Transcriptomic profiling of mature embryo from an elite super-hybrid rice LYP9 and its parental lines. <i>BMC Plant Biology</i> , 2008, 8, 114.  | 1.6 | 41        |
| 1615 | Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, <i>Thellungiella halophila</i> . <i>BMC Plant Biology</i> , 2008, 8, 115.  | 1.6 | 57        |
| 1616 | Identification of precursor transcripts for 6 novel miRNAs expands the diversity on the genomic organisation and expression of miRNA genes in rice. <i>BMC Plant Biology</i> , 2008, 8, 123.   | 1.6 | 46        |
| 1617 | A putative autonomous 20.5 kb-CACTA transposon insertion in an F3'H allele identifies a new CACTA transposon subfamily in <i>Glycine max</i> . <i>BMC Plant Biology</i> , 2008, 8, 124.  | 1.6 | 21        |
| 1618 | Oil palm ( <i>Elaeis guineensis</i> Jacq.) tissue culture ESTs: Identifying genes associated with callogenesis and embryogenesis. <i>BMC Plant Biology</i> , 2008, 8, 62.  | 1.6 | 83        |
| 1619 | Single nucleotide polymorphisms concordant with the horned/polled trait in Holsteins. <i>BMC Research Notes</i> , 2008, 1, 128.  | 0.6 | 18        |
| 1620 | Molecular phylogeny of Anthelidae and other bombycoid taxa (Lepidoptera: Bombycoidea). <i>Systematic Entomology</i> , 2008, 33, 190-209.   | 1.7 | 30        |
| 1621 | <i>Eimeria tenella</i> : Analysis of differentially expressed genes in the monensin- and maduramicin-resistant lines using cDNA array. <i>Experimental Parasitology</i> , 2008, 119, 264-271.  | 0.5 | 14        |
| 1622 | Identification of a <i>Leishmania infantum</i> gene mediating resistance to $\alpha$ and SbIII. <i>International Journal for Parasitology</i> , 2008, 38, 1411-1423.   | 1.3 | 57        |
| 1623 | Screening isolates from antibody phage-display libraries. <i>Drug Discovery Today</i> , 2008, 13, 318-324.   | 3.2 | 39        |
| 1624 | Complete nucleotide sequence of plasmid plca36 isolated from <i>Lactobacillus casei</i> Zhang. <i>Plasmid</i> , 2008, 60, 131-135.   | 0.4 | 27        |
| 1625 | Evidence for novel viruses by analysis of nucleic acids in virus-like particle fractions from <i>Ambrosia psilotachya</i> . <i>Journal of Virological Methods</i> , 2008, 152, 49-55.  | 1.0 | 46        |
| 1626 | Cold hardening processes in the Antarctic springtail, <i>Cryptopygus antarcticus</i> : Clues from a microarray. <i>Journal of Insect Physiology</i> , 2008, 54, 1356-1362.   | 0.9 | 39        |
| 1627 | Genomic panorama of <i>Bradyrhizobium japonicum</i> CPAC 15, a commercial inoculant strain largely established in Brazilian soils and belonging to the same serogroup as USDA 123. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2743-2753. | 4.2 | 17        |
| 1628 | Bacterial communities and biogeochemical transformations of iron and sulfur in a high saltmarsh soil profile. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2854-2864.  | 4.2 | 17        |
| 1629 | Geographic locality and host identity shape fungal endophyte communities in cupressaceous trees. <i>Mycological Research</i> , 2008, 112, 331-344.   | 2.5 | 207       |
| 1630 | The mitochondrial genome of the phytopathogenic basidiomycete <i>Moniliophthora perniciosa</i> is 109kb in size and contains a stable integrated plasmid. <i>Mycological Research</i> , 2008, 112, 1136-1152.                                  | 2.5 | 87        |
| 1631 | Computer-Assisted Reading of DNA Sequences. <i>Methods in Molecular Medicine</i> , 2008, 141, 177-197.   | 0.8 | 4         |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 1632 | Genomic organization and characterization of two vomeronasal 1 receptor-like genes ( <i>ora1</i> and <i>ora2</i> ) in Atlantic salmon <i>Salmo salar</i> . <i>Marine Genomics</i> , 2008, 1, 23-31.                             | 0.4  | 22        |
| 1633 | Exploring Microbial Diversity and Taxonomy Using SSU rRNA Hypervariable Tag Sequencing. <i>PLoS Genetics</i> , 2008, 4, e1000255.   | 1.5  | 779       |
| 1634 | Genotypic and phenotypic diversity of <i>Bacillus</i> spp. isolated from steel plant waste. <i>BMC Research Notes</i> , 2008, 1, 92.  | 0.6  | 47        |
| 1635 | Molecular bacterial diversity and distribution in waste from a steel plant. <i>Canadian Journal of Microbiology</i> , 2008, 54, 996-1005.   | 0.8  | 6         |
| 1636 | Overview of DNA Sequencing Strategies. <i>Current Protocols in Molecular Biology</i> , 2008, 81, Unit 7.1.  | 2.9  | 43        |
| 1637 | Genomics of Tropical Crop Plants. , 2008, , .   |      | 13        |
| 1638 | Identification of transcripts with enriched expression in the developing and adult pancreas. <i>Genome Biology</i> , 2008, 9, R99.  | 13.9 | 33        |
| 1639 | Functions, structure, and read-through alternative splicing of feline APOBEC3 genes. <i>Genome Biology</i> , 2008, 9, R48.  | 13.9 | 116       |
| 1640 | Genome assembly forensics: finding the elusive mis-assembly. <i>Genome Biology</i> , 2008, 9, R55.  | 13.9 | 248       |
| 1641 | Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008, 18, 1851-1858.   | 2.4  | 2,275     |
| 1643 | A new class of ice-binding proteins discovered in a salt-stress-induced cDNA library of the psychrophilic diatom <i>Fragilariopsis cylindrus</i> (Bacillariophyceae). <i>European Journal of Phycology</i> , 2008, 43, 423-433. | 0.9  | 56        |
| 1644 | A Phylogenomic Investigation into the Origin of Metazoa. <i>Molecular Biology and Evolution</i> , 2008, 25, 664-672.  | 3.5  | 259       |
| 1646 | Structure, processing and midgut secretion of putative peritrophic membrane ancillary protein (PMAP) from <i>Tenebrio molitor</i> larvae. <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 233-243.                 | 1.2  | 9         |
| 1647 | Pyrosequence analysis of expressed sequence tags for <i>Manduca sexta</i> hemolymph proteins involved in immune responses. <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 677-682.                                | 1.2  | 64        |
| 1648 | A simple binomial test for estimating sequencing errors in public repository 16S rRNA sequences. <i>Journal of Microbiological Methods</i> , 2008, 72, 166-179.   | 0.7  | 3         |
| 1649 | Functional adaptive diversity of the Atlantic salmon T-cell receptor gamma locus. <i>Molecular Immunology</i> , 2008, 45, 2150-2157.  | 1.0  | 46        |
| 1650 | Phylogeography of Japanese water crowfoot based on chloroplast DNA haplotypes. <i>Aquatic Botany</i> , 2008, 89, 1-8.   | 0.8  | 28        |
| 1651 | Hepatitis D and B virus genotypes in chronically infected patients from the Eastern Amazon Basin. <i>Acta Tropica</i> , 2008, 106, 149-155.   | 0.9  | 36        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1652 | The Dawn of Human Matrilineal Diversity. <i>American Journal of Human Genetics</i> , 2008, 82, 1130-1140.   | 2.6 | 392       |
| 1653 | Viral diversity and dynamics in an infant gut. <i>Research in Microbiology</i> , 2008, 159, 367-373.  | 1.0 | 288       |
| 1654 | Molecular diversity of Brazilian strains of porcine circovirus type 2 (PCV-2). <i>Research in Veterinary Science</i> , 2008, 85, 197-200.   | 0.9 | 10        |
| 1655 | Characterisation of the cellulose-binding protein Mj-cbp-1 of the root knot nematode, <i>Meloidogyne javanica</i> . <i>Physiological and Molecular Plant Pathology</i> , 2008, 72, 21-28.   | 1.3 | 26        |
| 1656 | Laser capture microdissection and expressed sequence tag analysis of uredinia formed by <i>Phakopsora pachyrhizi</i> , the causal agent of Asian soybean rust. <i>Physiological and Molecular Plant Pathology</i> , 2008, 73, 163-174.                    | 1.3 | 21        |
| 1657 | Channel catfish, <i>Ictalurus punctatus</i> , cyclophilin A and B cDNA characterization and expression analysis. <i>Veterinary Immunology and Immunopathology</i> , 2008, 121, 370-377.   | 0.5 | 29        |
| 1658 | Molecular cloning, sequencing and characterization of channel catfish ( <i>Ictalurus punctatus</i> ), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 T  | 0.5 | 24        |
| 1659 | Large-insert genome analysis technology detects structural variation in <i>Pseudomonas aeruginosa</i> clinical strains from cystic fibrosis patients. <i>Genomics</i> , 2008, 91, 530-537.  | 1.3 | 22        |
| 1660 | Genome sequences of <i>Halobacterium</i> species. <i>Genomics</i> , 2008, 91, 548-552.  | 1.3 | 15        |
| 1661 | Applications of next-generation sequencing technologies in functional genomics. <i>Genomics</i> , 2008, 92, 255-264.  | 1.3 | 1,013     |
| 1662 | A distinctive repertoire of cathepsins is expressed by juvenile invasive <i>Fasciola hepatica</i> . <i>Biochimie</i> , 2008, 90, 1461-1475.   | 1.3 | 90        |
| 1663 | Comparative analysis of ESTs in response to drought stress in chickpea ( <i>C. arietinum</i> L.). <i>Biochemical and Biophysical Research Communications</i> , 2008, 376, 578-583.  | 1.0 | 46        |
| 1664 | Identification and analysis of a prepro-chicken gonadotropin releasing hormone II (preprocGnRH-II) precursor in the Asian seabass, <i>Lates calcarifer</i> , based on an EST-based assessment of its brain transcriptome. <i>Gene</i> , 2008, 411, 77-86. | 1.0 | 8         |
| 1665 | Characterization of duplicated <i>Dunaliella viridis</i> SPT1 genes provides insights into early gene divergence after duplication. <i>Gene</i> , 2008, 423, 36-42.   | 1.0 | 10        |
| 1666 | The mitochondrial view of <i>Blastocladiella emersonii</i> . <i>Gene</i> , 2008, 424, 33-39.  | 1.0 | 14        |
| 1667 | Striking antigen recognition diversity in the Atlantic salmon T-cell receptor $\hat{\pm}/\hat{\iota}$ locus. <i>Developmental and Comparative Immunology</i> , 2008, 32, 204-212.   | 1.0 | 53        |
| 1668 | Functional genomic analysis of the response of Atlantic cod ( <i>Gadus morhua</i> ) spleen to the viral mimic polyriboinosinic polyribocytidylic acid (pIC). <i>Developmental and Comparative Immunology</i> , 2008, 32, 916-931.                         | 1.0 | 90        |
| 1669 | Evolution of polydom-like molecules: Identification and characterization of cnidarian polydom ( <i>Cnpolydom</i> ) in the basal metazoan <i>Hydractinia</i> . <i>Developmental and Comparative Immunology</i> , 2008, 32, 1192-1210.                      | 1.0 | 13        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1670 | Phylogenetic Analysis of Brine Shrimp ( <i>Artemia</i> ) in China Using DNA Barcoding. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 155-162.  | 3.0 | 20        |
| 1671 | Complete Genome Sequence of <i>Nitrobacter hamburgensis</i> X14 and Comparative Genomic Analysis of Species within the Genus <i>Nitrobacter</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 2852-2863.   | 1.4 | 115       |
| 1672 | Quality scores and SNP detection in sequencing-by-synthesis systems. <i>Genome Research</i> , 2008, 18, 763-770.   | 2.4 | 232       |
| 1673 | Identification of human enteric pathogens in gull feces at Southwestern Lake Michigan bathing beaches. <i>Canadian Journal of Microbiology</i> , 2008, 54, 1006-1015.  | 0.8 | 55        |
| 1674 | Generation and Analysis of 10,443 ESTs from Cephalothorax of <i>Fenneropenaeus Chinensis</i> . , 2008, , .   |     | 5         |
| 1675 | A low-complexity probabilistic genome assembly based on hashing functions with SNP detection. , 2008, , .  |     | 0         |
| 1676 | Population genomics of the wild yeast <i>Saccharomyces paradoxus</i> : Quantifying the life cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4957-4962.  | 3.3 | 287       |
| 1677 | Complete Genome Sequence of the Mosquitocidal Bacterium <i>Bacillus sphaericus</i> C3-41 and Comparison with Those of Closely Related <i>Bacillus</i> Species. <i>Journal of Bacteriology</i> , 2008, 190, 2892-2902.  | 1.0 | 80        |
| 1678 | Molecular Cytogenetic Evidence of Rearrangements on the Y Chromosome of the Threespine Stickleback Fish. <i>Genetics</i> , 2008, 179, 2173-2182.   | 1.2 | 89        |
| 1679 | Bacteriophage 2851 Is a Prototype Phage for Dissemination of the Shiga Toxin Variant Gene 2c in <i>Escherichia coli</i> O157:H7. <i>Infection and Immunity</i> , 2008, 76, 5466-5477.  | 1.0 | 64        |
| 1680 | What's Driving False Discovery Rates?. <i>Journal of Proteome Research</i> , 2008, 7, 45-46.   | 1.8 | 53        |
| 1681 | Genetic Analysis of Fenhexamid-Resistant Field Isolates of the Phytopathogenic Fungus <i>Botrytis cinerea</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 3933-3940.  | 1.4 | 97        |
| 1682 | Applying Rapid Genome Sequencing Technologies To Characterize Pathogen Genomes. <i>Analytical Chemistry</i> , 2008, 80, 520-528.   | 3.2 | 17        |
| 1683 | Cloning and Characterization of Monacolin K Biosynthetic Gene Cluster from <i>Monascus pilosus</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 5639-5646.  | 2.4 | 91        |
| 1684 | Scrapie Resistance in ARQ Sheep. <i>Journal of Virology</i> , 2008, 82, 10318-10320.   | 1.5 | 36        |
| 1685 | Genetic and functional characterization of the gene cluster directing the biosynthesis of putisolvin I and II in <i>Pseudomonas putida</i> strain PCL1445. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2070-2083.  | 0.7 | 51        |
| 1686 | Phylogenetic relationships amongst the saltwater members of the genus <i>Bacteriovorax</i> using <i>rpoB</i> sequences and reclassification of <i>Bacteriovorax stolpii</i> as <i>Bacteriolyticum stolpii</i> gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 1203-1209. | 0.8 | 45        |
| 1687 | The Whole-genome Sequencing of the Obligate Intracellular Bacterium <i>Orientia tsutsugamushi</i> Revealed Massive Gene Amplification During Reductive Genome Evolution. <i>DNA Research</i> , 2008, 15, 185-199.  | 1.5 | 166       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1688 | Isolation of New <i>Stenotrophomonas</i> Bacteriophages and Genomic Characterization of Temperate Phage S1. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7552-7560.   | 1.4 | 36        |
| 1689 | The Native Bacterioplankton Community in the Central Baltic Sea Is Influenced by Freshwater Bacterial Species. <i>Applied and Environmental Microbiology</i> , 2008, 74, 503-515.  | 1.4 | 118       |
| 1690 | A Common Virulence Plasmid in Biotype 2 <i>Vibrio vulnificus</i> and Its Dissemination Aided by a Conjugal Plasmid. <i>Journal of Bacteriology</i> , 2008, 190, 1638-1648.   | 1.0 | 70        |
| 1691 | Differential Accumulation of Retroelements and Diversification of NB-LRR Disease Resistance Genes in Duplicated Regions following Polyploidy in the Ancestor of Soybean. <i>Plant Physiology</i> , 2008, 148, 1740-1759.       | 2.3 | 140       |
| 1692 | Molecular Analysis Reveals a Distinctive Fungal Endophyte Community Associated with Foliage of Montane Oaks in Southeastern Arizona. <i>Journal of the Arizona-Nevada Academy of Science</i> , 2008, 40, 91-100.               | 0.1 | 13        |
| 1693 | Bacteriophage Prevalence in the Genus <i>Azospirillum</i> and Analysis of the First Genome Sequence of an <i>Azospirillum brasilense</i> Integrative Phage. <i>Applied and Environmental Microbiology</i> , 2008, 74, 861-874. | 1.4 | 25        |
| 1694 | Recurrent Deletion and Gene Presence/Absence Polymorphism: Telomere Dynamics Dominate Evolution at the Tip of 3L in <i>Drosophila melanogaster</i> and <i>D. simulans</i> . <i>Genetics</i> , 2008, 179, 1021-1027.            | 1.2 | 30        |
| 1695 | A simple algorithm for quantifying DNA methylation levels on multiple independent CpG sites in bisulfite genomic sequencing electropherograms. <i>Nucleic Acids Research</i> , 2008, 36, e64-e64.                              | 6.5 | 37        |
| 1696 | Tracing the Geographic Origins of Major Avocado Cultivars. <i>Journal of Heredity</i> , 2008, 100, 56-65.  | 1.0 | 126       |
| 1697 | Cytogenetic and molecular analysis of MLL rearrangements in acute lymphoblastic leukaemia survivors. <i>Mutagenesis</i> , 2008, 24, 153-160.   | 1.0 | 11        |
| 1698 | High-Resolution Melting Curve Analysis of Genomic and Whole-Genome Amplified DNA. <i>Clinical Chemistry</i> , 2008, 54, 2055-2058.   | 1.5 | 33        |
| 1699 | Chloroplast DNA phylogeography in long-lived Huon pine, a Tasmanian rain forest conifer. <i>Canadian Journal of Forest Research</i> , 2008, 38, 1576-1589.   | 0.8 | 10        |
| 1700 | Nested Patch PCR enables highly multiplexed mutation discovery in candidate genes. <i>Genome Research</i> , 2008, 18, 1844-1850.   | 2.4 | 55        |
| 1701 | Putative identification of expressed genes associated with attachment of the zebra mussel ( <i>Dreissena</i> ) Tj ETQq1 1 0.784314, rgBT /Over   | 0.8 | 29        |
| 1702 | Comparative genomic analysis of the whale ( <i>Pseudorca crassidens</i> ) <i>PRNP</i> locus. <i>Genome</i> , 2008, 51, 452-464.  | 0.9 | 6         |
| 1703 | High-throughput single-nucleotide structural mapping by capillary automated footprinting analysis. <i>Nucleic Acids Research</i> , 2008, 36, e63-e63.  | 6.5 | 89        |
| 1704 | Tetrameric and Homodimeric Camelid IgGs Originate from the Same IgH Locus. <i>Journal of Immunology</i> , 2008, 181, 2001-2009.  | 0.4 | 64        |
| 1705 | A Single <i>Banana Streak Virus</i> Integration Event in the Banana Genome as the Origin of Infectious Endogenous Pararetrovirus. <i>Journal of Virology</i> , 2008, 82, 6697-6710.  | 1.5 | 109       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1706 | Complete nucleotide sequence of pKP96, a 67 850 bp multiresistance plasmid encoding qnrA1, aac(6â€²)-Ib-cr and blaCTX-M-24 from <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 62, 1252-1256. | 1.3 | 57        |
| 1707 | Genome of the Epsilonproteobacterial Chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 1145-1156.  | 1.4 | 228       |
| 1708 | A Catalog of Neutral and Deleterious Polymorphism in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000183.  | 1.5 | 212       |
| 1709 | Genome Sequence of <i>Thermophilum pendens</i> Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. <i>Journal of Bacteriology</i> , 2008, 190, 2957-2965.   | 1.0 | 53        |
| 1710 | Functional Gene Losses Occur with Minimal Size Reduction in the Plastid Genome of the Parasitic Liverwort <i>Aneura mirabilis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 393-401.                                    | 3.5 | 108       |
| 1711 | Collection and Comparative Analysis of 1888 Full-length cDNAs from Wild Rice <i>Oryza rufipogon</i> Griff. W1943. <i>DNA Research</i> , 2008, 15, 285-295.   | 1.5 | 34        |
| 1712 | Mutation and Evolutionary Rates in AdÃ©lie Penguins from the Antarctic. <i>PLoS Genetics</i> , 2008, 4, e1000209.  | 1.5 | 79        |
| 1713 | The effect of sequence quality on sequence alignment. <i>Bioinformatics</i> , 2008, 24, 897-900.   | 1.8 | 17        |
| 1714 | A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1415-1428.   | 3.5 | 57        |
| 1715 | The Genome of <i>Borrelia recurrentis</i> , the Agent of Deadly Louse-Borne Relapsing Fever, Is a Degraded Subset of Tick-Borne <i>Borrelia duttonii</i> . <i>PLoS Genetics</i> , 2008, 4, e1000185.                               | 1.5 | 146       |
| 1716 | Sepsid even-skipped Enhancers Are Functionally Conserved in <i>Drosophila</i> Despite Lack of Sequence Conservation. <i>PLoS Genetics</i> , 2008, 4, e1000106.   | 1.5 | 262       |
| 1717 | Metagenomic Analysis of Human Diarrhea: Viral Detection and Discovery. <i>PLoS Pathogens</i> , 2008, 4, e1000011.  | 2.1 | 317       |
| 1718 | Ma-LMM01 Infecting Toxic <i>Microcystis aeruginosa</i> Illuminates Diverse Cyanophage Genome Strategies. <i>Journal of Bacteriology</i> , 2008, 190, 1762-1772.  | 1.0 | 124       |
| 1719 | An Empirical Test for Branch-Specific Positive Selection. <i>Genetics</i> , 2008, 179, 2183-2193.  | 1.2 | 10        |
| 1720 | Identification of ancient remains through genomic sequencing. <i>Genome Research</i> , 2008, 18, 1347-1353.  | 2.4 | 47        |
| 1721 | Saprolegniaceae identified on amphibian eggs throughout the Pacific Northwest, USA, by internal transcribed spacer sequences and phylogenetic analysis. <i>Mycologia</i> , 2008, 100, 171-180.                                     | 0.8 | 28        |
| 1722 | Rapid Evolution of Yeast Centromeres in the Absence of Drive. <i>Genetics</i> , 2008, 178, 2161-2167.  | 1.2 | 57        |
| 1723 | Diverse Phage-Encoded Toxins in a Protective Insect Endosymbiont. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6782-6791.   | 1.4 | 184       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1724 | New <i>VAPB</i> deletion variant and exclusion of <i>VAPB</i> mutations in familial ALS. <i>Neurology</i> , 2008, 70, 1179-1185.   | 1.5 | 50        |
| 1725 | Sequencing and Analysis of Approximately 40 000 Soybean cDNA Clones from a Full-Length-Enriched cDNA Library. <i>DNA Research</i> , 2008, 15, 333-346.   | 1.5 | 98        |
| 1726 | Drug-sensitive <i>FGFR2</i> mutations in endometrial carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8713-8717.   | 3.3 | 329       |
| 1727 | Adaptive Functional Divergence Among Triplicated $\beta$ -Globin Genes in Rodents. <i>Genetics</i> , 2008, 178, 1623-1638.   | 1.2 | 29        |
| 1728 | Variation in HLA Class I Antigen-Processing Genes and Susceptibility to Human Papillomavirus Type 16-Associated Cervical Cancer. <i>Journal of Infectious Diseases</i> , 2008, 197, 371-381.   | 1.9 | 28        |
| 1729 | Estimation of Nucleotide Diversity, Disequilibrium Coefficients, and Mutation Rates from High-Coverage Genome-Sequencing Projects. <i>Molecular Biology and Evolution</i> , 2008, 25, 2409-2419.   | 3.5 | 112       |
| 1730 | Dietary Change and Adaptive Evolution of <i>enamelin</i> in Humans and Among Primates. <i>Genetics</i> , 2008, 178, 1595-1603.   | 1.2 | 47        |
| 1731 | Evidence that the gene encoding insulin degrading enzyme influences human lifespan. <i>Human Molecular Genetics</i> , 2008, 17, 2370-2378.   | 1.4 | 9         |
| 1732 | Comparative Analysis of Testis Protein Evolution in Rodents. <i>Genetics</i> , 2008, 179, 2075-2089.   | 1.2 | 67        |
| 1733 | The new paradigm of flow cell sequencing: Table 1.. <i>Genome Research</i> , 2008, 18, 839-846.  | 2.4 | 185       |
| 1734 | Nucleotide Diversity and Linkage Disequilibrium in Wild Avocado ( <i>Persea americana</i> Mill.). <i>Journal of Heredity</i> , 2008, 99, 382-389.  | 1.0 | 44        |
| 1735 | Transcriptome analysis and identification of regulators for long-term plasticity in <i>Aplysia kurodai</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18602-18607.            | 3.3 | 25        |
| 1736 | The Genome Sequence of the Tomato-Pathogenic Actinomycete <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB382 Reveals a Large Island Involved in Pathogenicity. <i>Journal of Bacteriology</i> , 2008, 190, 2138-2149. | 1.0 | 153       |
| 1737 | Genome Sequence of the Fish Pathogen <i>Renibacterium salmoninarum</i> Suggests Reductive Evolution away from an Environmental <i>Arthrobacter</i> Ancestor. <i>Journal of Bacteriology</i> , 2008, 190, 6970-6982.                      | 1.0 | 55        |
| 1738 | An MCMC algorithm for haplotype assembly from whole-genome sequence data. <i>Genome Research</i> , 2008, 18, 1336-1346.  | 2.4 | 114       |
| 1739 | Molecular epidemiology of the African horse sickness virus S10 gene. <i>Journal of General Virology</i> , 2008, 89, 1159-1168.   | 1.3 | 31        |
| 1740 | Cross-Kingdom Amplification Using <i>Bacteria</i> -Specific Primers: Complications for Studies of Coral Microbial Ecology. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7828-7831.  | 1.4 | 156       |
| 1741 | Molecular Evolution of a Primate-Specific microRNA Family. <i>Molecular Biology and Evolution</i> , 2008, 25, 1493-1502.   | 3.5 | 150       |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 1742 | DNA Methylation of Placenta-specific Cyp19 Promoters of Cattle and Sheep. <i>Experimental and Clinical Endocrinology and Diabetes</i> , 2008, 116, 437-442.  | 0.6  | 25        |
| 1743 | Determination of the Genome Sequence of <i>Porphyromonas gingivalis</i> Strain ATCC 33277 and Genomic Comparison with Strain W83 Revealed Extensive Genome Rearrangements in <i>P. gingivalis</i> . <i>DNA Research</i> , 2008, 15, 215-225.   | 1.5  | 243       |
| 1744 | Comparative Analysis of the MIR319a MicroRNA Locus in <i>Arabidopsis</i> and Related Brassicaceae. <i>Molecular Biology and Evolution</i> , 2008, 25, 892-902.   | 3.5  | 67        |
| 1745 | Haplotype sorting using human fosmid clone end-sequence pairs. <i>Genome Research</i> , 2008, 18, 2016-2023.   | 2.4  | 25        |
| 1746 | Complete Structure, Genomic Organization, and Expression of Channel Catfish ( <i>Ictalurus punctatus</i> ), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 72, 702-714.   | 0.6  | 20        |
| 1747 | Bioinformatics and Its Relevance to Weed Science. <i>Weed Science</i> , 2008, 56, 297-305.   | 0.8  | 3         |
| 1748 | Joint base-calling of two DNA sequences with factor graphs. <i>Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing</i> , 2008, , .  | 1.8  | 1         |
| 1749 | Development of an <i>Adonis aestivalis</i> expressed sequence tag population as a resource for genes of the carotenoid pathway. <i>Genome</i> , 2008, 51, 888-896.   | 0.9  | 4         |
| 1750 | Isolation of microsatellites from unknown genomes using known genomes as enrichment templates. <i>Limnology and Oceanography: Methods</i> , 2008, 6, 412-426.  | 1.0  | 31        |
| 1751 | Microsatellite markers derived from <i>Quercus mongolica</i> var. <i>crispula</i> (Fagaceae) inner bark expressed sequence tags. <i>Genes and Genetic Systems</i> , 2008, 83, 179-187.   | 0.2  | 41        |
| 1752 | BAC library construction and BAC end sequencing of five <i>Drosophila</i> species: the comparative map with the <i>D. melanogaster</i> genome. <i>Genes and Genetic Systems</i> , 2008, 83, 245-256.   | 0.2  | 4         |
| 1753 | Molecular characterization of <i>Giardia intestinalis</i> haplotypes in marine animals: variation and zoonotic potential. <i>Diseases of Aquatic Organisms</i> , 2008, 81, 39-51.  | 0.5  | 51        |
| 1754 | Statistical analysis of electrophoresis time series for improving basecalling in DNA sequencing. <i>International Journal of Signal and Imaging Systems Engineering</i> , 2008, 1, 36.   | 0.6  | 0         |
| 1755 | Analysis of Expressed Sequence Tags from <i>Uromyces appendiculatus</i> Hyphae and Haustoria and Their Comparison to Sequences from Other Rust Fungi. <i>Phytopathology</i> , 2008, 98, 1126-1135.   | 1.1  | 40        |
| 1756 | Saprolegniaceae identified on amphibian eggs throughout the Pacific Northwest, USA, by internal transcribed spacer sequences and phylogenetic analysis. <i>Mycologia</i> , 2008, 100, 171-180.   | 0.8  | 23        |
| 1757 | PolyPhred Analysis Software for Mutation Detection from Fluorescence-Based Sequence Data. <i>Current Protocols in Human Genetics</i> , 2008, 59, Unit 7.16.  | 3.5  | 9         |
| 1758 | cDNA Sequences for Transcription Factors and Signaling Proteins of the Hemichordate <i>Saccoglossus kowalevskii</i> : Efficacy of the Expressed Sequence Tag (EST) Approach for Evolutionary and Developmental Studies of a New Organism. <i>Biological Bulletin</i> , 2008, 214, 284-302. | 0.7  | 47        |
| 1759 | Salticid spider phylogeny revisited, with the discovery of a large Australasian clade (Araneae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 0.52 67   | 0.52 | 67        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1760 | Structural Features of the Endogenous <i>CHS</i> Silencing and Target Loci in the Soybean Genome. <i>Crop Science</i> , 2008, 48, S-49.   | 0.8 | 40        |
| 1761 | Transcriptome analysis of leaf tissue from Bermudagrass ( <i>Cynodon dactylon</i> ) using a normalised cDNA library. <i>Functional Plant Biology</i> , 2008, 35, 585.   | 1.1 | 20        |
| 1762 | High-Precision, Whole-Genome Sequencing of Laboratory Strains Facilitates Genetic Studies. <i>PLoS Genetics</i> , 2008, 4, e1000139.  | 1.5 | 202       |
| 1763 | Transcriptional Changes in the Hookworm, <i>Ancylostoma caninum</i> , during the Transition from a Free-Living to a Parasitic Larva. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e130.                 | 1.3 | 72        |
| 1764 | On the Extent and Origins of Genic Novelty in the Phylum Nematoda. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e258.   | 1.3 | 68        |
| 1765 | The Airborne Metagenome in an Indoor Urban Environment. <i>PLoS ONE</i> , 2008, 3, e1862.   | 1.1 | 192       |
| 1766 | Environmental Adaptation: Genomic Analysis of the Piezotolerant and Psychrotolerant Deep-Sea Iron Reducing Bacterium <i>Shewanella piezotolerans</i> WP3. <i>PLoS ONE</i> , 2008, 3, e1937.                   | 1.1 | 123       |
| 1767 | Sequences, Annotation and Single Nucleotide Polymorphism of the Major Histocompatibility Complex in the Domestic Cat. <i>PLoS ONE</i> , 2008, 3, e2674.   | 1.1 | 39        |
| 1768 | Molecular characterization of the NSP4 gene of human group A rotavirus samples from the West Central region of Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2008, 103, 288-294.                        | 0.8 | 18        |
| 1769 | Development in Rice Genome Research Based on Accurate Genome Sequence. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-9.  | 2.2 | 8         |
| 1770 | Seasonal Cholera from Multiple Small Outbreaks, Rural Bangladesh. <i>Emerging Infectious Diseases</i> , 2008, 14, 831-833.  | 2.0 | 73        |
| 1771 | Identificari3n of contaminant bacteria in cacha3sa yeast by 16s rDNA gene sequencing. <i>Scientia Agricola</i> , 2008, 65, 508-515.   | 0.6 | 10        |
| 1772 | Construction of an <i>Amaranthus hypochondriacus</i> Bacterial Artificial Chromosome Library and Genomic Sequencing of Herbicide Target Genes. <i>Crop Science</i> , 2008, 48, S-85.                          | 0.8 | 23        |
| 1773 | Identificaci3n de algunos genes asociados al proceso de germinaci3n de la conidia al micelio en <i>Paracoccidioides brasiliensis</i> . <i>Biomedica</i> , 2009, 29, 403.                                      | 0.3 | 5         |
| 1776 | Molecular Marker Discovery and Genetic Map Visualisation. , 2009, , 165-189.  |     | 9         |
| 1777 | Confirmation of quantitative trait loci using a low-density single nucleotide polymorphism map for twinning and ovulation rate on bovine chromosome 51,2. <i>Journal of Animal Science</i> , 2009, 87, 46-56. | 0.2 | 37        |
| 1778 | MLL leukemia-associated rearrangements in peripheral blood lymphocytes from healthy individuals. <i>Genetics and Molecular Biology</i> , 2009, 32, 234-241.   | 0.6 | 10        |
| 1779 | Analysis of expressed sequence tags derived from inflorescence shoot of <i>Tectona grandis</i> (teak). <i>African Journal of Biotechnology</i> , 2009, 8, 5633-5640.  | 0.3 | 0         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1780 | SplinkBES: a splinkerette-based method for generating long end sequences from large insert DNA libraries. <i>BioTechniques</i> , 2009, 47, 681-690.  | 0.8 | 1         |
| 1781 | Run-Off Replication of Host-Adaptability Genes Is Associated with Gene Transfer Agents in the Genome of Mouse-Infecting <i>Bartonella grahamii</i> . <i>PLoS Genetics</i> , 2009, 5, e1000546.   | 1.5 | 87        |
| 1782 | Giant Panda Genomic Data Provide Insight into the Birth-and-Death Process of Mammalian Major Histocompatibility Complex Class II Genes. <i>PLoS ONE</i> , 2009, 4, e4147.  | 1.1 | 32        |
| 1783 | Big Genomes Facilitate the Comparative Identification of Regulatory Elements. <i>PLoS ONE</i> , 2009, 4, e4688.  | 1.1 | 41        |
| 1784 | A "Shallow Phylogeny" of Shallow Barnacles ( <i>Chthamalus</i> ). <i>PLoS ONE</i> , 2009, 4, e5567.  | 1.1 | 43        |
| 1785 | MUEGANO: A divide and conquer algorithm to overcome memory limitations when assembling shotgun projects. <i>Nature Precedings</i> , 2009, , .  | 0.1 | 0         |
| 1786 | Quantitative Proteomic Analysis of Bean Plants Infected by a Virulent and Avirulent Obligate Rust Fungus. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 19-31.   | 2.5 | 61        |
| 1787 | Meta-analysis of small RNA-sequencing errors reveals ubiquitous post-transcriptional RNA modifications. <i>Nucleic Acids Research</i> , 2009, 37, 2461-2470.   | 6.5 | 196       |
| 1788 | SNP detection for massively parallel whole-genome resequencing. <i>Genome Research</i> , 2009, 19, 1124-1132.  | 2.4 | 855       |
| 1789 | Big and Slow: Phylogenetic Estimates of Molecular Evolution in Baleen Whales (Suborder Mysticeti). <i>Molecular Biology and Evolution</i> , 2009, 26, 2427-2440.   | 3.5 | 73        |
| 1790 | Complete Genome Sequence of the Ethanol Producer <i>Zymomonas mobilis</i> NCIMB 11163. <i>Journal of Bacteriology</i> , 2009, 191, 7140-7141.  | 1.0 | 39        |
| 1791 | Effect of inulin on the human gut microbiota: stimulation of <i>Bifidobacterium adolescentis</i> and <i>Faecalibacterium prausnitzii</i> . <i>British Journal of Nutrition</i> , 2009, 101, 541-550.   | 1.2 | 675       |
| 1792 | Molecular Population Genetics and Evolution of <i>Drosophila</i> Meiosis Genes. <i>Genetics</i> , 2009, 181, 177-185.  | 1.2 | 35        |
| 1793 | Novel Genetic Environment of the Carbapenem-Hydrolyzing $\beta$ -Lactamase KPC-2 among <i>Enterobacteriaceae</i> in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 4333-4338.   | 1.4 | 173       |
| 1794 | <i>Hamiltonella defensa</i> , genome evolution of protective bacterial endosymbiont from pathogenic ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9063-9068.                  | 3.3 | 214       |
| 1795 | Isolation and Characterization of AaWRKY1, an <i>Artemisia annua</i> Transcription Factor that Regulates the Amorpha-4,11-diene Synthase Gene, a Key Gene of Artemisinin Biosynthesis. <i>Plant and Cell Physiology</i> , 2009, 50, 2146-2161. | 1.5 | 307       |
| 1796 | TrichOME: A Comparative Omics Database for Plant Trichomes. <i>Plant Physiology</i> , 2009, 152, 44-54.  | 2.3 | 98        |
| 1797 | Genome Sequencing and Comparative Analysis of <i>Klebsiella pneumoniae</i> NTUH-K2044, a Strain Causing Liver Abscess and Meningitis. <i>Journal of Bacteriology</i> , 2009, 191, 4492-4501.   | 1.0 | 300       |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 1798 | The <i>Magnaporthe oryzae</i> Avirulence Gene <i>AvrPiz-t</i> Encodes a Predicted Secreted Protein That Triggers the Immunity in Rice Mediated by the Blast Resistance Gene <i>Piz-t</i> . <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 411-420.  | 1.4  | 240       |
| 1799 | Rapid Access to Genes of Biotechnologically Useful Enzymes by Partial Genome Sequencing: The Thermoalkaliphile <i>Anaerobranca gottschalkii</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 16, 81-90.  | 1.0  | 7         |
| 1800 | Repetitive sequence variation and dynamics in the ribosomal DNA array of <i>Saccharomyces cerevisiae</i> as revealed by whole-genome resequencing. <i>Genome Research</i> , 2009, 19, 626-635.   | 2.4  | 82        |
| 1801 | Possible Diversifying Selection in the Imprinted Gene, MEDEA, in Arabidopsis. <i>Molecular Biology and Evolution</i> , 2009, 26, 843-857.  | 3.5  | 43        |
| 1802 | Bacteroidales Diversity in Ring-Billed Gulls ( <i>Larus delawarensis</i> ) Residing at Lake Michigan Beaches. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1525-1533.   | 1.4  | 31        |
| 1803 | Analysis of the Genome of the <i>Escherichia coli</i> O157:H7 2006 Spinach-Associated Outbreak Isolate Indicates Candidate Genes That May Enhance Virulence. <i>Infection and Immunity</i> , 2009, 77, 3713-3721.  | 1.0  | 163       |
| 1804 | Genome Sequence of the Anaerobic, Thermophilic, and Cellulolytic Bacterium <i>Anaerocellum thermophilum</i> DSM 6725. <i>Journal of Bacteriology</i> , 2009, 191, 3760-3761.   | 1.0  | 78        |
| 1805 | The mosaic genome structure of the <i>Wolbachia w</i> Ri strain infecting <i>Drosophila simulans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5725-5730.  | 3.3  | 236       |
| 1806 | Transcriptome analysis of <i>Schistosoma mansoni</i> larval development using serial analysis of gene expression (SAGE). <i>Parasitology</i> , 2009, 136, 469-485.   | 0.7  | 32        |
| 1807 | Genetic diversity of capsular polysaccharide biosynthesis in <i>Klebsiella pneumoniae</i> clinical isolates. <i>Microbiology (United Kingdom)</i> , 2009, 155, 4170-4183.  | 0.7  | 124       |
| 1808 | Trimeric Autotransporters of <i>Haemophilus parasuis</i> : Generation of an Extensive Passenger Domain Repertoire Specific for Pathogenic Strains. <i>Journal of Bacteriology</i> , 2009, 191, 576-587.  | 1.0  | 53        |
| 1809 | Considerations for the development of a reference method for sequencing of haploid DNA – an opinion paper on behalf of the IFCC Committee on Molecular Diagnostics. <i>International Federation of Clinical Chemistry and Laboratory Medicine. Clinical Chemistry and Laboratory Medicine</i> , 2009, 47, 1343-50. | 1.4  | 9         |
| 1810 | Genomic Organization and Evolution of the Vomeronasal Type 2 Receptor-Like (OlfC) Gene Clusters in Atlantic Salmon, <i>Salmo salar</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 1117-1125.   | 3.5  | 25        |
| 1811 | Molecular Genetic Markers: Discovery, Applications, Data Storage and Visualisation. <i>Current Bioinformatics</i> , 2009, 4, 16-27.  | 0.7  | 121       |
| 1812 | Mitochondrial DNA Variation and Range Expansion in Western Bean Cutworm (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 7 274-280.  | 0.7  | 17        |
| 1813 | Inhibitors of Factor VIII in Black Patients with Hemophilia. <i>New England Journal of Medicine</i> , 2009, 360, 1618-1627.  | 13.9 | 177       |
| 1814 | Stimulation of growth and changes in the hepatic transcriptome by 17 $\beta$ -estradiol in the yellow perch ( <i>Perca flavescens</i> ). <i>Physiological Genomics</i> , 2009, 38, 261-280.  | 1.0  | 29        |
| 1815 | Efficient frequency-based de novo short-read clustering for error trimming in next-generation sequencing. <i>Genome Research</i> , 2009, 19, 1309-1315.  | 2.4  | 53        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1816 | Analysis of Exonic Elastin Variants in Severe, Early-Onset Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2009, 40, 751-755.                                   | 1.4 | 17        |
| 1817 | Processing and population genetic analysis of multigenic datasets with ProSeq3 software. <i>Bioinformatics</i> , 2009, 25, 3189-3190.  | 1.8 | 83        |
| 1818 | Characterization of Chromosome Ends in the Filamentous Fungus <i>Neurospora crassa</i> . <i>Genetics</i> , 2009, 181, 1129-1145.   | 1.2 | 52        |
| 1819 | Genomic Survey of the Non-Cultivable Opportunistic Human Pathogen, <i>Enterocytozoon bieneusi</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000261.   | 2.1 | 119       |
| 1820 | FLYSNPdb: a high-density SNP database of <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2009, 37, D567-D570.   | 6.5 | 12        |
| 1821 | Inference of Microbial Recombination Rates from Metagenomic Data. <i>PLoS Genetics</i> , 2009, 5, e1000674.  | 1.5 | 31        |
| 1822 | Meningococcus genome informatics platform: a system for analyzing multilocus sequence typing data. <i>Nucleic Acids Research</i> , 2009, 37, W606-W611.  | 6.5 | 11        |
| 1823 | BayesCall: A model-based base-calling algorithm for high-throughput short-read sequencing. <i>Genome Research</i> , 2009, 19, 1884-1895.   | 2.4 | 80        |
| 1824 | Phylogeny and Biogeography of <i>Primula</i> sect. <i>Parryi</i> (Primulaceae). <i>International Journal of Plant Sciences</i> , 2009, 170, 93-106.  | 0.6 | 10        |
| 1825 | Analysis of <i>FUS</i> gene mutation in familial amyotrophic lateral sclerosis within an Italian cohort. <i>Neurology</i> , 2009, 73, 1180-1185.   | 1.5 | 139       |
| 1826 | Programmed loss of millions of base pairs from a vertebrate genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11212-11217.                                       | 3.3 | 151       |
| 1827 | Degenerate Tetraploidy Was Established Before Bdelloid Rotifer Families Diverged. <i>Molecular Biology and Evolution</i> , 2009, 26, 375-383.  | 3.5 | 55        |
| 1828 | Fine-Scale Variation and Genetic Determinants of Alternative Splicing across Individuals. <i>PLoS Genetics</i> , 2009, 5, e1000766.  | 1.5 | 81        |
| 1829 | High-Resolution Mapping of Evolutionary Trajectories in a Phage. <i>Genome Biology and Evolution</i> , 2009, 1, 294-307.   | 1.1 | 10        |
| 1830 | <i>Kosmotoga olearia</i> gen. nov., sp. nov., a thermophilic, anaerobic heterotroph isolated from an oil production fluid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2991-3000. | 0.8 | 112       |
| 1831 | Not any two will do: DNA divergence and interpopulation reproductive compatibility in the simultaneous hermaphroditic shrimp <i>Lysmata wurdemanni</i> . <i>Marine Ecology - Progress Series</i> , 2009, 388, 185-195.     | 0.9 | 7         |
| 1832 | Striking Diversity of <i>vmp1</i> , a Variable Gene Encoding a Putative Membrane Protein of the Stolbur Phytoplasma. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2951-2957.                                  | 1.4 | 94        |
| 1833 | Draft Genome Sequencing of <i>Giardia intestinalis</i> Assemblage B Isolate GS: Is Human Giardiasis Caused by Two Different Species?. <i>PLoS Pathogens</i> , 2009, 5, e1000560.   | 2.1 | 236       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1834 | Population Genetic Inference From Resequencing Data. <i>Genetics</i> , 2009, 181, 187-197.   | 1.2 | 42        |
| 1835 | Genetic polymorphism, linkage disequilibrium, haplotype structure and novel allele analysis of CYP2C19 and CYP2D6 in Han Chinese. <i>Pharmacogenomics Journal</i> , 2009, 9, 380-394.  | 0.9 | 54        |
| 1836 | Functional Genomic Analysis of Two <i>Staphylococcus aureus</i> Phages Isolated from the Dairy Environment. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7663-7673.   | 1.4 | 46        |
| 1837 | Population Genomic Analysis of ALMS1 in Humans Reveals a Surprisingly Complex Evolutionary History. <i>Molecular Biology and Evolution</i> , 2009, 26, 1357-1367.  | 3.5 | 27        |
| 1838 | Clinical, Experimental, and Genomic Differences between Intermediately Pathogenic, Highly Pathogenic, and Epidemic <i>Streptococcus suis</i> . <i>Journal of Infectious Diseases</i> , 2009, 199, 97-107.  | 1.9 | 126       |
| 1839 | Genome Sequences of Three <i>Agrobacterium</i> Biovars Help Elucidate the Evolution of Multichromosome Genomes in Bacteria. <i>Journal of Bacteriology</i> , 2009, 191, 2501-2511.   | 1.0 | 220       |
| 1840 | Targeted resequencing of two genes, RAGE and POLL, confirms findings from a genome-wide scan for adaptive evolution and provides evidence for positive selection in additional populations. <i>Human Molecular Genetics</i> , 2009, 18, 779-784. | 1.4 | 7         |
| 1841 | Analysis of the <i>Nicotiana tabacum</i> Stigma/Style Transcriptome Reveals Gene Expression Differences between Wet and Dry Stigma Species Å Å. <i>Plant Physiology</i> , 2009, 149, 1211-1230.  | 2.3 | 65        |
| 1842 | Genome Sequence of <i>Azotobacter vinelandii</i> , an Obligate Aerobe Specialized To Support Diverse Anaerobic Metabolic Processes. <i>Journal of Bacteriology</i> , 2009, 191, 4534-4545.   | 1.0 | 265       |
| 1843 | Genomic organization and expression profile of the mucin-associated surface protein (masp) family of the human pathogen <i>Trypanosoma cruzi</i> . <i>Nucleic Acids Research</i> , 2009, 37, 3407-3417.  | 6.5 | 111       |
| 1844 | Whole-genome analyses reveal genetic instability of <i>Acetobacter pasteurianus</i> . <i>Nucleic Acids Research</i> , 2009, 37, 5768-5783.   | 6.5 | 164       |
| 1845 | Swift: primary data analysis for the Illumina Solexa sequencing platform. <i>Bioinformatics</i> , 2009, 25, 2194-2199.   | 1.8 | 83        |
| 1846 | Linkage Disequilibrium and Demographic History of Wild and Domestic Canids. <i>Genetics</i> , 2009, 181, 1493-1505.  | 1.2 | 129       |
| 1847 | Complete Genome Sequence of <i>Lactobacillus johnsonii</i> F19785, a Competitive Exclusion Agent against Pathogens in Poultry. <i>Journal of Bacteriology</i> , 2009, 191, 7142-7143.  | 1.0 | 31        |
| 1848 | The apolipoprotein L family of programmed cell death and immunity genes rapidly evolved in primates at discrete sites of host-pathogen interactions. <i>Genome Research</i> , 2009, 19, 850-858.   | 2.4 | 135       |
| 1849 | Xylanases from <i>Cryptococcus flavus</i> isolate I-11: Enzymatic profile, isolation and heterologous expression of CfXYN1 in <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2009, 59, 52-57.            | 1.8 | 28        |
| 1850 | Diversity and evolutionary origins of fungi associated with seeds of a neotropical pioneer tree: a case study for analysing fungal environmental samples. <i>Mycological Research</i> , 2009, 113, 432-449.                                      | 2.5 | 131       |
| 1851 | Complete sequence of three plasmids from <i>Bacillus thuringiensis</i> INTA-FR7-4 environmental isolate and comparison with related plasmids from the <i>Bacillus cereus</i> group. <i>Plasmid</i> , 2009, 62, 172-182.                          | 0.4 | 16        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1852 | Incremental generation of an EST set for the analysis of scrapie pathogenesis. <i>Small Ruminant Research</i> , 2009, 81, 75-78.   | 0.6 | 0         |
| 1853 | Effects of simulated light regimes on gene expression in Antarctic krill ( <i>Euphausia superba</i> Dana). <i>Journal of Experimental Marine Biology and Ecology</i> , 2009, 381, 57-64.           | 0.7 | 29        |
| 1854 | Local alignment of two-base encoded DNA sequence. <i>BMC Bioinformatics</i> , 2009, 10, 175.   | 1.2 | 32        |
| 1855 | CNV-seq, a new method to detect copy number variation using high-throughput sequencing. <i>BMC Bioinformatics</i> , 2009, 10, 80.  | 1.2 | 495       |
| 1856 | Finding optimal threshold for correction error reads in DNA assembling. <i>BMC Bioinformatics</i> , 2009, 10, S15.   | 1.2 | 11        |
| 1857 | Crystallizing short-read assemblies around seeds. <i>BMC Bioinformatics</i> , 2009, 10, S16.   | 1.2 | 35        |
| 1859 | Complete chloroplast genome sequence of a tree fern <i>Alsophila spinulosa</i> : insights into evolutionary changes in fern chloroplast genomes. <i>BMC Evolutionary Biology</i> , 2009, 9, 130.   | 3.2 | 130       |
| 1860 | On the phylogenetic position of Myzostomida: Can 77 genes get it wrong?. <i>BMC Evolutionary Biology</i> , 2009, 9, 150.   | 3.2 | 52        |
| 1861 | HaMStR: Profile hidden markov model based search for orthologs in ESTs. <i>BMC Evolutionary Biology</i> , 2009, 9, 157.  | 3.2 | 269       |
| 1862 | An EST screen from the annelid <i>Pomatoceros lamarckii</i> reveals patterns of gene loss and gain in animals. <i>BMC Evolutionary Biology</i> , 2009, 9, 240.                                     | 3.2 | 40        |
| 1863 | Positive selection for the male functionality of a co-retroposed gene in the hominoids. <i>BMC Evolutionary Biology</i> , 2009, 9, 252.  | 3.2 | 14        |
| 1864 | Discovering genes associated with dormancy in the monogonont rotifer <i>Brachionus plicatilis</i> . <i>BMC Genomics</i> , 2009, 10, 108.   | 1.2 | 84        |
| 1865 | A close phylogenetic relationship between Sipuncula and Annelida evidenced from the complete mitochondrial genome sequence of <i>Phascolosoma esculenta</i> . <i>BMC Genomics</i> , 2009, 10, 136. | 1.2 | 60        |
| 1866 | The complete genome sequence of <i>Staphylothermus marinus</i> reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. <i>BMC Genomics</i> , 2009, 10, 145.                    | 1.2 | 26        |
| 1867 | Genome evolution driven by host adaptations results in a more virulent and antimicrobial-resistant <i>Streptococcus pneumoniae</i> serotype 14. <i>BMC Genomics</i> , 2009, 10, 158.               | 1.2 | 63        |
| 1868 | Genetic diversity of canine olfactory receptors. <i>BMC Genomics</i> , 2009, 10, 21.   | 1.2 | 51        |
| 1869 | Recent dermatophyte divergence revealed by comparative and phylogenetic analysis of mitochondrial genomes. <i>BMC Genomics</i> , 2009, 10, 238.  | 1.2 | 46        |
| 1870 | Analysis of salivary transcripts and antigens of the sand fly <i>Phlebotomus arabicus</i> . <i>BMC Genomics</i> , 2009, 10, 282.   | 1.2 | 79        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 1871 | Comprehensive EST analysis of the symbiotic sea anemone, <i>Anemonia viridis</i> . BMC Genomics, 2009, 10, 333.  | 1.2 | 43        |
| 1872 | Metabolic analysis of the soil microbe <i>Dechloromonas aromatica</i> str. RCB: indications of a surprisingly complex life-style and cryptic anaerobic pathways for aromatic degradation. BMC Genomics, 2009, 10, 351.   | 1.2 | 155       |
| 1873 | <i>Brucella microti</i> : the genome sequence of an emerging pathogen. BMC Genomics, 2009, 10, 352.  | 1.2 | 77        |
| 1874 | Comparative genomic analyses of <i>Streptococcus mutans</i> provide insights into chromosomal shuffling and species-specific content. BMC Genomics, 2009, 10, 358.   | 1.2 | 72        |
| 1875 | Genomic analysis of a sexually-selected character: EST sequencing and microarray analysis of eye-antennal imaginal discs in the stalk-eyed fly <i>Teleopsis dalmanni</i> (Diopsidae). BMC Genomics, 2009, 10, 361.   | 1.2 | 20        |
| 1876 | Grapevine cell early activation of specific responses to DIMEB, a resveratrol elicitor. BMC Genomics, 2009, 10, 363.   | 1.2 | 54        |
| 1877 | Generation, annotation, and analysis of ESTs from midgut tissue of adult female <i>Anopheles stephensi</i> mosquitoes. BMC Genomics, 2009, 10, 386.  | 1.2 | 8         |
| 1878 | Mining for single nucleotide polymorphisms in pig genome sequence data. BMC Genomics, 2009, 10, 4.   | 1.2 | 32        |
| 1879 | Comparative EST transcript profiling of peach fruits under different post-harvest conditions reveals candidate genes associated with peach fruit quality. BMC Genomics, 2009, 10, 423.   | 1.2 | 63        |
| 1880 | A first generation BAC-based physical map of the rainbow trout genome. BMC Genomics, 2009, 10, 462.  | 1.2 | 41        |
| 1881 | Identification of novel androgen-responsive genes by sequencing of LongSAGE libraries. BMC Genomics, 2009, 10, 476.  | 1.2 | 75        |
| 1882 | A gene catalogue for post-diapause development of an anhydrobiotic arthropod <i>Artemia franciscana</i> . BMC Genomics, 2009, 10, 52.  | 1.2 | 36        |
| 1883 | De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. BMC Genomics, 2009, 10, 547.   | 1.2 | 69        |
| 1884 | The mitochondrial genomes of sponges provide evidence for multiple invasions by Repetitive Hairpin-forming Elements (RHE). BMC Genomics, 2009, 10, 591.  | 1.2 | 39        |
| 1885 | Comparative analysis of catfish BAC end sequences with the zebrafish genome. BMC Genomics, 2009, 10, 592.  | 1.2 | 40        |
| 1886 | Desiccation survival in an Antarctic nematode: molecular analysis using expressed sequenced tags. BMC Genomics, 2009, 10, 69.  | 1.2 | 76        |
| 1887 | COMUS: Clinician-Oriented locus-specific MUtation detection and deposition System. BMC Genomics, 2009, 10, S35.  | 1.2 | 2         |
| 1888 | Targeted isolation, sequence assembly and characterization of two white spruce ( <i>Picea glauca</i> ) BAC clones for terpenoid synthase and cytochrome P450 genes involved in conifer defence reveal insights into a conifer genome. BMC Plant Biology, 2009, 9, 106. | 1.6 | 55        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1889 | Sampling nucleotide diversity in cotton. <i>BMC Plant Biology</i> , 2009, 9, 125.   | 1.6 | 72        |
| 1890 | Linkage mapping of putative regulator genes of barley grain development characterized by expression profiling. <i>BMC Plant Biology</i> , 2009, 9, 4.   | 1.6 | 10        |
| 1891 | Evolution of ribosomal DNA-derived satellite repeat in tomato genome. <i>BMC Plant Biology</i> , 2009, 9, 42.   | 1.6 | 46        |
| 1892 | Screening and association testing of common coding variation in steroid hormone receptor co-activator and co-repressor genes in relation to breast cancer risk: the Multiethnic Cohort. <i>BMC Cancer</i> , 2009, 9, 43.                              | 1.1 | 24        |
| 1893 | Characterization of an Atlantic cod ( <i>Gadus morhua</i> ) embryonic stem cell cDNA library. <i>BMC Research Notes</i> , 2009, 2, 74.  | 0.6 | 4         |
| 1894 | Molecular characterization of avian polyomavirus isolated from psittacine birds based on the whole genome sequence analysis. <i>Veterinary Microbiology</i> , 2009, 138, 69-77.   | 0.8 | 15        |
| 1895 | Molecular characterization of the genome of duck enteritis virus. <i>Virology</i> , 2009, 391, 151-161.   | 1.1 | 79        |
| 1896 | New hypotheses on the function of the avian shell gland derived from microarray analysis comparing tissue from juvenile and sexually mature hens. <i>General and Comparative Endocrinology</i> , 2009, 163, 225-232.                                  | 0.8 | 45        |
| 1897 | <i>Trypanosoma cruzi</i> : Multiplex PCR to detect and classify strains according to groups I and II. <i>Experimental Parasitology</i> , 2009, 123, 283-291.  | 0.5 | 10        |
| 1898 | Analysis of the complete genome sequence of the lactococcal bacteriophage b1BB29. <i>International Journal of Food Microbiology</i> , 2009, 131, 52-61.   | 2.1 | 18        |
| 1899 | The missense mutation G12D in connexin30.3 can cause both erythrokeratoderma variabilis of Mendes da Costa and progressive symmetric erythrokeratoderma of Gottron. <i>American Journal of Medical Genetics, Part A</i> , 2009, 149A, 657-661.        | 0.7 | 54        |
| 1900 | Novel missense mutations in the <i>FOXC2</i> gene alter transcriptional activity. <i>Human Mutation</i> , 2009, 30, E1002-E1009.  | 1.1 | 39        |
| 1901 | Bacterial artificial chromosome library for genome-wide analysis of Chinese hamster ovary cells. <i>Biotechnology and Bioengineering</i> , 2009, 104, 986-994.  | 1.7 | 34        |
| 1902 | Characterization of a deep-coverage carrot ( <i>Daucus carota</i> L.) BAC library and initial analysis of BAC-end sequences. <i>Molecular Genetics and Genomics</i> , 2009, 281, 273-288.   | 1.0 | 41        |
| 1903 | EST sequencing of blood-fed and <i>Leishmania</i> -infected midgut of <i>Lutzomyia longipalpis</i> , the principal visceral leishmaniasis vector in the Americas. <i>Molecular Genetics and Genomics</i> , 2009, 282, 307-317.                        | 1.0 | 27        |
| 1904 | Functional Annotation and Analysis of Expressed Sequence Tags from the Hepatopancreas of Mitten Crab ( <i>Eriocheir sinensis</i> ). <i>Marine Biotechnology</i> , 2009, 11, 317-326.  | 1.1 | 68        |
| 1905 | Identification of Genes Involved in Immune Response, Microsatellite, and SNP Markers from Expressed Sequence Tags Generated from Hemocytes of Freshwater Pearl Mussel ( <i>Hyriopsis cumingii</i> ). <i>Marine Biotechnology</i> , 2009, 11, 520-530. | 1.1 | 38        |
| 1906 | Protistan community patterns within the brine and halocline of deep hypersaline anoxic basins in the eastern Mediterranean Sea. <i>Extremophiles</i> , 2009, 13, 151-167.   | 0.9 | 84        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1907 | Full-Length Enriched cDNA Library Construction from Tissues Related to Energy Metabolism in Pigs. <i>Molecules and Cells</i> , 2009, 28, 529-536.   | 1.0 | 7         |
| 1908 | Patterns of nucleotide diversity in wild and cultivated rice. <i>Plant Systematics and Evolution</i> , 2009, 281, 97-106.   | 0.3 | 13        |
| 1909 | Organization of a $\hat{\mu}^2$ and $\hat{\mu}^{\pm}$ Globin Gene Set in the Teleost Atlantic Cod, <i>Gadus morhua</i> . <i>Biochemical Genetics</i> , 2009, 47, 817-830.   | 0.8 | 7         |
| 1910 | Familial hypertrophic cardiomyopathy: Basic concepts and future molecular diagnostics. <i>Clinical Biochemistry</i> , 2009, 42, 755-765.  | 0.8 | 26        |
| 1911 | The R2 mobile element of <i>Rhynchosciara americana</i> : Molecular, cytological and dynamic aspects. <i>Chromosome Research</i> , 2009, 17, 455-467.   | 1.0 | 6         |
| 1912 | Molecular characterization of a putative heat shock protein cognate gene in <i>Rhynchosciara americana</i> . <i>Chromosome Research</i> , 2009, 17, 935-945.  | 1.0 | 6         |
| 1913 | Construction, Characterization, and Expressed Sequence Tag (EST) Analysis of Normalized cDNA Library of Thermo-Photoperiod-Sensitive Genic Male Sterile (TPGMS) Wheat from Spike Developmental Stages. <i>Plant Molecular Biology Reporter</i> , 2009, 27, 117-125. | 1.0 | 10        |
| 1914 | A complete mitochondrial genome of wheat ( <i>Triticum aestivum</i> cv. Chinese Yumai), and fast evolving mitochondrial genes in higher plants. <i>Journal of Genetics</i> , 2009, 88, 299-307.   | 0.4 | 29        |
| 1915 | Computational Biology Methods and Their Application to the Comparative Genomics of Endocellular Symbiotic Bacteria of Insects. <i>Biological Procedures Online</i> , 2009, 11, 52-78.   | 1.4 | 6         |
| 1916 | EST, COSII, and arbitrary gene markers give similar estimates of nucleotide diversity in cultivated tomato ( <i>Solanum lycopersicum</i> L.). <i>Theoretical and Applied Genetics</i> , 2009, 118, 1005-1014.   | 1.8 | 23        |
| 1917 | Single nucleotide polymorphism genotyping in polyploid wheat with the Illumina GoldenGate assay. <i>Theoretical and Applied Genetics</i> , 2009, 119, 507-517.  | 1.8 | 257       |
| 1918 | Genetic differences between <i>Bradyrhizobium japonicum</i> variant strains contrasting in N <sub>2</sub> -fixation efficiency revealed by representational difference analysis. <i>Archives of Microbiology</i> , 2009, 191, 113-122.                              | 1.0 | 17        |
| 1919 | Synopsis of a new collection of sea spiders (Arthropoda: Pycnogonida) from the Ross Sea, Antarctica. <i>Polar Biology</i> , 2009, 32, 1147-1155.  | 0.5 | 12        |
| 1921 | The Pig Genome Database (PiGenome): an integrated database for pig genome research. <i>Mammalian Genome</i> , 2009, 20, 60-66.  | 1.0 | 14        |
| 1922 | Removal of Noisy Characters from Chloroplast Genome-Scale Data Suggests Revision of Phylogenetic Placements of <i>Amborella</i> and <i>Ceratophyllum</i> . <i>Journal of Molecular Evolution</i> , 2009, 68, 197-204.   | 0.8 | 28        |
| 1923 | Contrasting Patterns of Sequence Evolution at the Functionally Redundant <i>bric-Å-brac</i> Paralogs in <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 2009, 69, 194-202.   | 0.8 | 5         |
| 1924 | Multiple Antimicrobial Resistance of Gram-Negative Bacteria from Natural Oligotrophic Lakes Under Distinct Anthropogenic Influence in a Tropical Region. <i>Microbial Ecology</i> , 2009, 58, 762-772.  | 1.4 | 42        |
| 1925 | Differences in distribution of single nucleotide polymorphisms among intracellular pattern recognition receptors in pigs. <i>Immunogenetics</i> , 2009, 61, 153-160.  | 1.2 | 18        |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 1926 | Contrasting evolution of diversity at two disease-associated chicken genes. <i>Immunogenetics</i> , 2009, 61, 303-314.   | 1.2  | 13        |
| 1927 | Comparative genomic analysis of the major histocompatibility complex class I region in the teleost genus <i>Oryzias</i> . <i>Immunogenetics</i> , 2009, 61, 385-399.   | 1.2  | 20        |
| 1928 | Identification and characterisation of a novel immune-type receptor (NITR) gene cluster in the European sea bass, <i>Dicentrarchus labrax</i> , reveals recurrent gene expansion and diversification by positive selection. <i>Immunogenetics</i> , 2009, 61, 773-788. | 1.2  | 18        |
| 1929 | The conserved WW-domain binding sites in Dystroglycan C-terminus are essential but partially redundant for Dystroglycan function. <i>BMC Developmental Biology</i> , 2009, 9, 18.  | 2.1  | 10        |
| 1930 | Automated DNA mutation detection using universal conditions direct sequencing: application to ten muscular dystrophy genes. <i>BMC Genetics</i> , 2009, 10, 66.  | 2.7  | 13        |
| 1931 | Haplotypes of the porcine peroxisome proliferator-activated receptor delta gene are associated with backfat thickness. <i>BMC Genetics</i> , 2009, 10, 76.   | 2.7  | 15        |
| 1932 | Loss of the insulator protein CTCF during nematode evolution. <i>BMC Molecular Biology</i> , 2009, 10, 84.   | 3.0  | 78        |
| 1933 | Genetic variation in the NBS1, MRE11, RAD50 and BLM genes and susceptibility to non-Hodgkin lymphoma. <i>BMC Medical Genetics</i> , 2009, 10, 117.   | 2.1  | 27        |
| 1934 | Genetic determinants of mate recognition in <i>Brachionus manjavacas</i> (Rotifera). <i>BMC Biology</i> , 2009, 7, 60.   | 1.7  | 26        |
| 1935 | Tissue-specific variation in DNA methylation levels along human chromosome 1. <i>Epigenetics and Chromatin</i> , 2009, 2, 7.   | 1.8  | 54        |
| 1936 | Identification of an active LTR retrotransposon in rice. <i>Plant Journal</i> , 2009, 58, 754-765.   | 2.8  | 60        |
| 1937 | Asymmetric allele-specific expression in relation to developmental variation and drought stress in barley hybrids. <i>Plant Journal</i> , 2009, 59, 14-26.   | 2.8  | 56        |
| 1938 | Structural and functional responses of sewage microbial communities used for the treatment of a complex mixture of volatile organic compounds (VOCs). <i>Journal of Applied Microbiology</i> , 2009, 107, 85-96.   | 1.4  | 22        |
| 1939 | Variation in neighbouring genes of the dopaminergic and serotonergic systems affects feather pecking behaviour of laying hens. <i>Animal Genetics</i> , 2009, 40, 192-199.   | 0.6  | 65        |
| 1940 | Monophyletic origin of domestic bactrian camel ( <i>Camelus bactrianus</i> ) and its evolutionary relationship with the extant wild camel ( <i>Camelus bactrianus ferus</i> ). <i>Animal Genetics</i> , 2009, 40, 377-382.   | 0.6  | 111       |
| 1941 | A high-density transcript linkage map of barley derived from a single population. <i>Heredity</i> , 2009, 103, 110-117.  | 1.2  | 119       |
| 1942 | Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . <i>ISME Journal</i> , 2009, 3, 512-521.  | 4.4  | 364       |
| 1943 | PEP1 regulates perennial flowering in <i>Arabis alpina</i> . <i>Nature</i> , 2009, 459, 423-427.   | 13.7 | 325       |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 1944 | The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , 2009, 460, 345-351.  | 13.7 | 635       |
| 1945 | Targeted capture and massively parallel sequencing of 12 human exomes. <i>Nature</i> , 2009, 461, 272-276.  | 13.7 | 1,801     |
| 1946 | Genetic Exchange Within and Between Assemblages of <i>Giardia duodenalis</i> . <i>Journal of Eukaryotic Microbiology</i> , 2009, 56, 504-518.   | 0.8  | 75        |
| 1947 | An awkward introduction: phylogeography of <i>Notropis lutipinnis</i> in its native range and the Little Tennessee River. <i>Ecology of Freshwater Fish</i> , 2009, 18, 538-549.  | 0.7  | 7         |
| 1948 | Temporal and spatial variability in nearshore bacterioplankton communities of Lake Michigan. <i>FEMS Microbiology Ecology</i> , 2009, 67, 511-522.  | 1.3  | 86        |
| 1949 | Diversity of bacteria associated with grassland soil nematodes of different feeding groups. <i>FEMS Microbiology Ecology</i> , 2009, 69, 53-61.   | 1.3  | 36        |
| 1950 | Confirmed expression of MHC class I and class II genes in the New Zealand endemic Hector's dolphin ( <i>Cephalorhynchus hectori</i> ). <i>Marine Mammal Science</i> , 2009, 25, 68-90.  | 0.9  | 16        |
| 1951 | Evolutionary dynamics of transferrin in <i>Notropis</i> . <i>Journal of Fish Biology</i> , 2009, 74, 1056-1069.   | 0.7  | 3         |
| 1952 | Discovering genetic polymorphisms in next-generation sequencing data. <i>Plant Biotechnology Journal</i> , 2009, 7, 312-317.  | 4.1  | 118       |
| 1953 | Single nucleotide polymorphism discovery in barley using autoSNPdb. <i>Plant Biotechnology Journal</i> , 2009, 7, 326-333.  | 4.1  | 56        |
| 1954 | Characterization of the crustose red alga <i>Peyssonnelia japonica</i> (Rhodophyta, Gigartinales) and its taxonomic relationship with <i>Peyssonnelia boudouresquei</i> based on morphological and molecular data. <i>Phycological Research</i> , 2009, 57, 74-86.              | 0.8  | 15        |
| 1955 | Reporting 678 putative cSNPs from full-length enriched cDNA sequences of the Korean native pig. <i>Journal of Animal Breeding and Genetics</i> , 2009, 126, 127-133.  | 0.8  | 6         |
| 1956 | Allele-specific SNP markers for the new low linolenic mutant genotype of winter oilseed rape. <i>Plant Breeding</i> , 2009, 129, 502.   | 1.0  | 7         |
| 1957 | Association of canine anal furunculosis with TNFA is secondary to linkage disequilibrium with DLA-DRB1*. <i>Tissue Antigens</i> , 2009, 73, 218-224.  | 1.0  | 15        |
| 1958 | Overdominant maintenance of diversity in the sea star <i>Pisaster ochraceus</i> . <i>Journal of Evolutionary Biology</i> , 2009, 22, 80-87.   | 0.8  | 5         |
| 1959 | Effect of PCR amplicon size on assessments of clone library microbial diversity and community structure. <i>Environmental Microbiology</i> , 2009, 11, 1292-1302.   | 1.8  | 133       |
| 1960 | The genome of <i>Polaromonas naphthalenivorans</i> strain CJ2, isolated from coal tar-contaminated sediment, reveals physiological and metabolic versatility and evolution through extensive horizontal gene transfer. <i>Environmental Microbiology</i> , 2009, 11, 2253-2270. | 1.8  | 90        |
| 1961 | Microbial diversity in chronic open wounds. <i>Wound Repair and Regeneration</i> , 2009, 17, 163-172.   | 1.5  | 96        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1962 | Combining Microarray-based Genomic Selection (MGS) with the Illumina Genome Analyzer Platform to Sequence Diploid Target Regions. <i>Annals of Human Genetics</i> , 2009, 73, 502-513.  | 0.3 | 16        |
| 1963 | Nucleotide diversity among natural populations of a North American poplar ( <i>Populus trichocarpa</i> ). <i>Genetics</i> , 2009, 183, 1071-1080.   | 3.5 | 21        |
| 1964 | Quasispecies of hepatitis C virus genotype 1 and treatment outcome with Peginterferon and Ribavirin. <i>Infection, Genetics and Evolution</i> , 2009, 9, 689-698.   | 1.0 | 21        |
| 1965 | Identification of host immune regulation candidate genes of <i>Toxascaris leonina</i> by expression sequenced tags (ESTs) analysis. <i>Veterinary Parasitology</i> , 2009, 164, 242-247.  | 0.7 | 6         |
| 1966 | Allopolyploidy in <i>Fragariinae</i> (Rosaceae): Comparing four DNA sequence regions, with comments on classification. <i>Molecular Phylogenetics and Evolution</i> , 2009, 51, 269-280.  | 1.2 | 32        |
| 1967 | Phylogenetic analyses of complete mitochondrial genome of <i>Urechis unicinctus</i> (Echiura) support that echiurans are derived annelids. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 558-562.  | 1.2 | 27        |
| 1968 | The Sequence Analysis and Management System "SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. <i>Journal of Biotechnology</i> , 2009, 140, 3-12. | 1.9 | 37        |
| 1969 | Sequence assembly. <i>Computational Biology and Chemistry</i> , 2009, 33, 121-136.  | 1.1 | 39        |
| 1970 | Generation de marqueurs de séquences exprimées et développement de marqueurs microsatellites pour <i>Castanopsis sieboldii</i> var. <i>sieboldii</i> (Fagaceae). <i>Annals of Forest Science</i> , 2009, 66, 509-509.                                     | 0.8 | 20        |
| 1971 | TriFLDB: A Database of Clustered Full-Length Coding Sequences from Triticeae with Applications to Comparative Grass Genomics. <i>Plant Physiology</i> , 2009, 150, 1135-1146.   | 2.3 | 86        |
| 1972 | GENE EXPRESSION PROFILING IN ATLANTIC COD ( <i>GADUS MORHUA</i> L.) FROM TWO CONTAMINATED SITES USING A CUSTOM-MADE cDNA MICROARRAY. <i>Environmental Toxicology and Chemistry</i> , 2009, 28, 1711.  | 2.2 | 31        |
| 1973 | Remarkably Little Variation in Proteins Encoded by the Y Chromosome's Single-Copy Genes, Implying Effective Purifying Selection. <i>American Journal of Human Genetics</i> , 2009, 85, 923-928.   | 2.6 | 39        |
| 1974 | Canine Distemper Virus in a Crab-eating Fox ( <i>Cerdocyon thous</i> ) in Brazil: Case Report and Phylogenetic Analyses. <i>Journal of Wildlife Diseases</i> , 2009, 45, 527-530.   | 0.3 | 28        |
| 1975 | Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. <i>Genome Research</i> , 2009, 19, 1270-1278.   | 2.4 | 266       |
| 1976 | Fine Mapping and Marker Development for the Crossability Gene SKr on Chromosome 5BS of Hexaploid Wheat ( <i>Triticum aestivum</i> L.). <i>Genetics</i> , 2009, 183, 469-481.  | 1.2 | 43        |
| 1977 | The complete mitochondrial genome of the clam <i>Meretrix petechialis</i> (Mollusca: Bivalvia: Veneridae). <i>Mitochondrial DNA</i> , 2009, 20, 78-87.  | 0.6 | 30        |
| 1978 | Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12741-12746.  | 3.3 | 72        |
| 1979 | Genetic diagnosis by whole exome capture and massively parallel DNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19096-19101.  | 3.3 | 1,167     |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1980 | Pyrosequencing of the Chaperonin-60 Universal Target as a Tool for Determining Microbial Community Composition. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2889-2898.  | 1.4 | 102       |
| 1981 | Recombination and Speciation: Loci Near Centromeres Are More Differentiated Than Loci Near Telomeres Between Subspecies of the European Rabbit ( <i>Oryctolagus cuniculus</i> ). <i>Genetics</i> , 2009, 181, 593-606.  | 1.2 | 92        |
| 1982 | Phylogeographical Structure of the Neotropical Forest Tree <i>Hymenaea courbaril</i> (Leguminosae:). <i>Journal of Heredity</i> , 2009, 100, 206-216.   | 1.0 | 47        |
| 1983 | Identification of an Atlantic salmon IFN multigene cluster encoding three IFN subtypes with very different expression properties. <i>Developmental and Comparative Immunology</i> , 2009, 33, 547-558.  | 1.0 | 140       |
| 1984 | Genomic structure of the whole C clusters and the upstream region coding V segments of the TRB locus in pig. <i>Developmental and Comparative Immunology</i> , 2009, 33, 1111-1119.   | 1.0 | 33        |
| 1985 | Structural organization of the <i>glnBA</i> region of the <i>Azospirillum brasilense</i> genome. <i>European Journal of Soil Biology</i> , 2009, 45, 100-105.   | 1.4 | 5         |
| 1986 | Gene discovery from an ovary cDNA library of oriental river prawn <i>Macrobrachium nipponense</i> by ESTs annotation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 111-120.  | 0.4 | 27        |
| 1987 | Transcriptomic profiling of <i>Ichthyophthirius multifiliis</i> reveals polyadenylation of the large subunit ribosomal RNA. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 179-186.                                  | 0.4 | 3         |
| 1988 | Chasing relationships between nutrition and reproduction: A comparative transcriptome analysis of hepatopancreas and testis from <i>Eriocheir sinensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 227-234. | 0.4 | 42        |
| 1989 | Channel catfish, <i>Ictalurus punctatus</i> , cysteine proteinases: Cloning, characterisation and expression of cathepsin H and L. <i>Fish and Shellfish Immunology</i> , 2009, 26, 332-338.  | 1.6 | 37        |
| 1990 | Identification of immune related genes in Atlantic halibut ( <i>Hippoglossus hippoglossus</i> L.) following in vivo antigenic and in vitro mitogenic stimulation. <i>Fish and Shellfish Immunology</i> , 2009, 27, 729-738.                                     | 1.6 | 17        |
| 1991 | The complete mitochondrial genome of the large yellow croaker, <i>Larimichthys crocea</i> (Perciformes). <i>Gene</i> , 2009, 432, 33-43.  | 1.0 | 103       |
| 1992 | The complete mitochondrial genome of the ridgetail white prawn <i>Exopalaemon carinicauda</i> Holthuis, 1950 (Crustacean: Decapoda: Palaemonidae) revealed a novel rearrangement of tRNA genes. <i>Gene</i> , 2009, 437, 1-8.                                   | 1.0 | 42        |
| 1993 | The complete mitochondrial genome of <i>Watersipora subtorquata</i> (Bryozoa, Gymnolaemata). <i>Gene</i> , 2009, 432, 33-43.  | 1.0 | 15        |
| 1994 | Complete mitochondrial genome of the sea cucumber <i>Apostichopus japonicus</i> (Echinodermata): ground pattern. <i>Gene</i> , 2009, 439, 79-86.  | 1.0 | 35        |
| 1995 | Harnessing genomics for evolutionary insights. <i>Trends in Ecology and Evolution</i> , 2009, 24, 192-200.  | 4.2 | 124       |
| 1996 | Channel catfish, <i>Ictalurus punctatus</i> Rafinesque 1818, tetraspanin membrane protein family: Characterization and expression analysis of CD81 cDNA. <i>Veterinary Immunology and Immunopathology</i> , 2009, 128, 431-436.                                 | 0.5 | 7         |
| 1997 | Genetic characterization of the complete coding regions of genotype 3 hepatitis E virus isolated from Spanish swine herds. <i>Virus Research</i> , 2009, 139, 111-116.  | 1.1 | 25        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 1998 | Genome-wide analysis reveals increased levels of transcripts related with infectivity in peanut lectin non-agglutinated promastigotes of <i>Leishmania infantum</i> . <i>Genomics</i> , 2009, 93, 551-564.        | 1.3 | 50        |
| 1999 | Comparative sequence analysis of the SALT OVERLY SENSITIVE1 orthologous region in <i>Thellungiella halophila</i> and <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2009, 94, 196-203.                           | 1.3 | 17        |
| 2000 | Functional expression of five <i>Arabidopsis</i> fatty acyl-CoA reductase genes in <i>Escherichia coli</i> . <i>Journal of Plant Physiology</i> , 2009, 166, 787-796.   | 1.6 | 110       |
| 2001 | 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. | 1.2 | 5         |
| 2002 | Sequence and function of lysosomal and digestive cathepsin D-like proteinases of <i>Musca domestica</i> midgut. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 782-791.                             | 1.2 | 54        |
| 2003 | Purification, characterization and sequencing of the major $\beta$ -1,3-glucanase from the midgut of <i>Tenebrio molitor</i> larvae. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 861-874.        | 1.2 | 53        |
| 2004 | Male-enriched transcription of genes encoding ASPs and Kunitz-type protease inhibitors in <i>Ancylostoma</i> species. <i>Molecular and Cellular Probes</i> , 2009, 23, 298-303.                                   | 0.9 | 9         |
| 2005 | Genomic sequence encoding diversity segments of the pig TCR $\beta$ chain gene demonstrates productivity of highly diversified repertoire. <i>Molecular Immunology</i> , 2009, 46, 1212-1221.                     | 1.0 | 25        |
| 2006 | DNA sequence analysis of the conserved region around the SOD1 gene locus in recessively inherited ALS. <i>Neuroscience Letters</i> , 2009, 463, 64-69.  | 1.0 | 6         |
| 2007 | Inter- and intrapopulation genetic variability of <i>Tityus serrulatus</i> (Scorpiones, Buthidae). <i>Acta Tropica</i> , 2009, 112, 97-100.   | 0.9 | 2         |
| 2008 | Analysis of the genome sequences of three <i>Drosophila melanogaster</i> spontaneous mutation accumulation lines. <i>Genome Research</i> , 2009, 19, 1195-1201.   | 2.4 | 343       |
| 2009 | Next-Generation Sequencing Methods: Impact of Sequencing Accuracy on SNP Discovery. <i>Methods in Molecular Biology</i> , 2009, 578, 95-111.  | 0.4 | 41        |
| 2010 | The complete mitochondrial genome sequence of the cutlassfish <i>Trichiurus japonicus</i> (Perciformes). <i>TJ ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> 133-142.  | 0.4 | 47        |
| 2011 | Multiple linked $\beta$ and $\alpha$ globin genes in Atlantic cod: A PCR based strategy of genomic exploration. <i>Marine Genomics</i> , 2009, 2, 169-181.  | 0.4 | 6         |
| 2012 | Genomic organization of Atlantic salmon ( <i>Salmo salar</i> ) fatty acid binding protein (fabp2) genes reveals independent loss of duplicate loci in teleosts. <i>Marine Genomics</i> , 2009, 2, 193-200.        | 0.4 | 13        |
| 2013 | 15-P003 An EST screen from the annelid <i>Pomatoceros lamarckii</i> reveals patterns of gene loss and gain in animals. <i>Mechanisms of Development</i> , 2009, 126, S247-S248.                                   | 1.7 | 1         |
| 2014 | Mining SNPs from DNA Sequence Data; Computational Approaches to SNP Discovery and Analysis. <i>Methods in Molecular Biology</i> , 2009, 578, 73-91.   | 0.4 | 16        |
| 2015 | Large-Scale Sequencing and Analytical Processing of ESTs. <i>Methods in Molecular Biology</i> , 2009, 533, 153-187.   | 0.4 | 11        |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 2016 | Sequencing and modular analysis of the hybrid non-ribosomal peptide synthase-polyketide synthase gene cluster from the marine sponge <i>Hymeniacidon perleве-associated</i> bacterium <i>Pseudoalteromonas</i> sp. strain NJ631. <i>Canadian Journal of Microbiology</i> , 2009, 55, 219-227.                              | 0.8  | 3         |
| 2017 | Genome analysis and genetic enhancement of tomato. <i>Critical Reviews in Biotechnology</i> , 2009, 29, 152-181.   | 5.1  | 16        |
| 2018 | Epigenetically reprogramming metastatic tumor cells with an embryonic microenvironment. <i>Epigenomics</i> , 2009, 1, 387-398.   | 1.0  | 77        |
| 2019 | Phylogeny and taxonomy of a diverse collection of <i>Bradyrhizobium</i> strains based on multilocus sequence analysis of the 16S rRNA gene, ITS region and <i>glnII</i> , <i>recA</i> , <i>atpD</i> and <i>dnaK</i> genes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2934-2950. | 0.8  | 154       |
| 2020 | Transcriptome analysis of <i>Taenia solium</i> cysticerci using Open Reading Frame ESTs (ORESTES). <i>Parasites and Vectors</i> , 2009, 2, 35.   | 1.0  | 24        |
| 2021 | Heuristic Reusable Dynamic Programming: Efficient Updates of Local Sequence Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 570-582.  | 1.9  | 5         |
| 2022 | Next-Generation Sequencing: From Basic Research to Diagnostics. <i>Clinical Chemistry</i> , 2009, 55, 641-658.   | 1.5  | 668       |
| 2023 | The <i>Bifidobacterium dentium</i> Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.   | 1.5  | 141       |
| 2024 | Single Nucleotide Polymorphisms. <i>Methods in Molecular Biology</i> , 2009, , .   | 0.4  | 44        |
| 2025 | Applications of Ultra-high-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2009, 553, 79-108.   | 0.4  | 72        |
| 2026 | New Technologies for Ultra-High Throughput Genotyping in Plants. <i>Methods in Molecular Biology</i> , 2009, 513, 19-39.   | 0.4  | 107       |
| 2027 | Genetics and Genomics of Cotton. , 2009, , .   |      | 23        |
| 2028 | A novel allele of <i>HWP1</i> , isolated from a clinical strain of <i>Candida albicans</i> with defective hyphal growth and biofilm formation, has deletions of Gln/Pro and Ser/Thr repeats involved in cellular adhesion. <i>Medical Mycology</i> , 2009, 47, 824-835.  | 0.3  | 19        |
| 2029 | A Phylogeny of <i>Setaria</i> (Poaceae, Panicoideae, Paniceae) and Related Genera Based on the Chloroplast <i>GenDhF</i> . <i>International Journal of Plant Sciences</i> , 2009, 170, 117-131.  | 0.6  | 47        |
| 2030 | Population structure analyses and demographic history of the malaria vector <i>Anopheles albimanus</i> from the Caribbean and the Pacific regions of Colombia. <i>Malaria Journal</i> , 2009, 8, 259.  | 0.8  | 37        |
| 2032 | Mining for SNPs and SSRs Using SNPServer, dbSNP and SSR Taxonomy Tree. <i>Methods in Molecular Biology</i> , 2009, 537, 303-321.   | 0.4  | 20        |
| 2033 | Transcriptome analysis of functional differentiation between haploid and diploid cells of <i>Emiliania huxleyi</i> , a globally significant photosynthetic calcifying cell. <i>Genome Biology</i> , 2009, 10, R114.  | 13.9 | 105       |
| 2034 | ALLPATHS 2: small genomes assembled accurately and with high continuity from short paired reads. <i>Genome Biology</i> , 2009, 10, R103.   | 13.9 | 151       |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 2035 | Genome-wide comparative analysis of the <i>Brassica rapa</i> gene space reveals genome shrinkage and differential loss of duplicated genes after whole genome triplication. <i>Genome Biology</i> , 2009, 10, R111. | 13.9 | 183       |
| 2036 | Improved base calling for the Illumina Genome Analyzer using machine learning strategies. <i>Genome Biology</i> , 2009, 10, R83.  | 13.9 | 212       |
| 2037 | Genome analysis and genome-wide proteomics of <i>Thermococcus gammatolerans</i> , the most radioresistant organism known amongst the Archaea. <i>Genome Biology</i> , 2009, 10, R70.                                | 13.9 | 125       |
| 2038 | Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. <i>Genome Biology</i> , 2009, 10, R25.   | 13.9 | 19,212    |
| 2040 | Bacteriophages. <i>Methods in Molecular Biology</i> , 2009, , .   | 0.4  | 35        |
| 2041 | Epigenetic Silencing of CRABP2 and MX1 in Head and Neck Tumors. <i>Neoplasia</i> , 2009, 11, 1329-IN9.  | 2.3  | 70        |
| 2042 | Genome assembly reborn: recent computational challenges. <i>Briefings in Bioinformatics</i> , 2009, 10, 354-366.  | 3.2  | 291       |
| 2043 | Estimation of Allele Frequencies From High-Coverage Genome-Sequencing Projects. <i>Genetics</i> , 2009, 182, 295-301.   | 1.2  | 89        |
| 2044 | An overview of recent developments in genomics and associated statistical methods. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2009, 367, 4313-4337.             | 1.6  | 27        |
| 2045 | Comparative Assessment of DNA Assemblers for Assembling Expressed Sequence Tags. , 2009, , .  |      | 1         |
| 2046 | The ClinSeq Project: Piloting large-scale genome sequencing for research in genomic medicine. <i>Genome Research</i> , 2009, 19, 1665-1674.   | 2.4  | 236       |
| 2047 | Cloning and Characterization of Full-length Triticin cDNA and Genes from Wheat Varieties K-68 and Chinese Spring. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2009, 18, 21-28.                         | 0.9  | 0         |
| 2048 | Functional and geographical differentiation of candidate balanced polymorphisms in <i>Arabidopsis thaliana</i> . <i>Molecular Ecology</i> , 2009, 18, 2844-2855.  | 2.0  | 8         |
| 2049 | Identification of candidate genome regions controlling disease resistance in <i>Arachis</i> . <i>BMC Plant Biology</i> , 2009, 9, 112.  | 1.6  | 118       |
| 2050 | Complete Genome Sequence of the Chemolithoautotrophic Marine Magnetotactic Coccus Strain MC-1. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4835-4852.   | 1.4  | 114       |
| 2051 | Genetic diversity and structure in semiwild and domesticated chiles ( <i>Capsicum annuum</i> ); Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5<br>0.8 163   |      |           |
| 2052 | Isolation and characterization of 145 polymorphic microsatellite loci for the common frog ( <i>Rana</i> ); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5<br>2.2 17  |      |           |
| 2053 | Characterization of canthaxanthin biosynthesis genes from an uncultured marine bacterium. <i>Environmental Microbiology Reports</i> , 2009, 1, 524-534.   | 1.0  | 5         |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2054 | A Phylogenetic Estimation of Trophic Transition Networks for Ascomycetous Fungi: Are Lichens Cradles of Symbiotrophic Fungal Diversification?. <i>Systematic Biology</i> , 2009, 58, 283-297.  | 2.7 | 321       |
| 2055 | Toward Cloning of the Magnetotactic Metagenome: Identification of Magnetosome Island Gene Clusters in Uncultivated Magnetotactic Bacteria from Different Aquatic Sediments. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3972-3979. | 1.4 | 96        |
| 2056 | Fine Mapping a Locus Controlling Leg Morphology in the Domestic Dog. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2009, 74, 327-333.   | 2.0 | 15        |
| 2057 | Identification and analysis of differentially expressed genes in immune tissues of Atlantic cod stimulated with formalin-killed, atypical <i>Aeromonas salmonicida</i> . <i>Physiological Genomics</i> , 2009, 37, 149-163.                      | 1.0 | 86        |
| 2058 | Analysis of SINE and LINE repeat content of Y chromosomes in the platypus, <i>Ornithorhynchus anatinus</i> . <i>Reproduction, Fertility and Development</i> , 2009, 21, 964.   | 0.1 | 13        |
| 2060 | Restricted gene flow in Chilean barnacles reflects an oceanographic and biogeographic transition zone. <i>Marine Ecology - Progress Series</i> , 2009, 394, 165-177.   | 0.9 | 49        |
| 2061 | RECOUNT: EXPECTATION MAXIMIZATION BASED ERROR CORRECTION TOOL FOR NEXT GENERATION SEQUENCING DATA. , 2009, , .   |     | 12        |
| 2062 | Predominant modifier of extreme liver cancer susceptibility in C57BR/cdJ female mice localized to 6 Mb on chromosome 17. <i>Carcinogenesis</i> , 2009, 30, 879-885.  | 1.3 | 10        |
| 2063 | Extraction and Quality Control of CAGE Tags. , 2009, , 83-91.  |     | 0         |
| 2064 | Distinct Amino Acids of the <i>Phytophthora infestans</i> Effector AVR3a Condition Activation of R3a Hypersensitivity and Suppression of Cell Death. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 269-281.                            | 1.4 | 65        |
| 2065 | Identification of salt-induced genes from <i>Salicornia brachiata</i> , an extreme halophyte through expressed sequence tags analysis. <i>Genes and Genetic Systems</i> , 2009, 84, 111-120.   | 0.2 | 61        |
| 2066 | Correcting short reads with high error rates for improved sequencing result. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 224.  | 0.1 | 3         |
| 2067 | Complete genome sequence of <i>Methanoculleus marisnigri</i> Romesser et al. 1981 type strain JR1. <i>Standards in Genomic Sciences</i> , 2009, 1, 189-196.  | 1.5 | 34        |
| 2068 | Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.   | 1.5 | 100       |
| 2069 | Evidence of balanced diversity at the chicken interleukin 4 receptor alpha chain locus. <i>BMC Evolutionary Biology</i> , 2009, 9, 136.  | 3.2 | 13        |
| 2070 | Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). <i>Standards in Genomic Sciences</i> , 2009, 1, 133-140.   | 1.5 | 25        |
| 2071 | Positional Cloning in Mice and Its Use For Molecular Dissection of Inflammatory Arthritis. <i>Current Pharmaceutical Biotechnology</i> , 2009, 10, 252-260.  | 0.9 | 2         |
| 2072 | Electronic DNA Sequencing. <i>Current Pharmaceutical Analysis</i> , 2009, 5, 91-100.   | 0.3 | 0         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2073 | Transcriptomic and proteomic analysis of global ischemia and cardioprotection in the rabbit heart. <i>Physiological Genomics</i> , 2009, 38, 125-137.   | 1.0 | 19        |
| 2074 | Computational Finishing of Large Sequence Contigs Reveals Interspersed Nested Repeats and Gene Islands in the <i>rfl1</i> -Associated Region of Maize $\Delta$ . <i>Plant Physiology</i> , 2009, 151, 483-495.                | 2.3 | 9         |
| 2075 | Human dopamine beta-hydroxylase (DBH) regulatory polymorphism that influences enzymatic activity, autonomic function, and blood pressure. <i>Journal of Hypertension</i> , 2010, 28, 76-86.                                   | 0.3 | 48        |
| 2076 | Quantitative Gene Expression Profiles in Real Time From Expressed Sequence Tag Databases. <i>Gene Expression</i> , 2010, 14, 321-336.   | 0.5 | 4         |
| 2077 | Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer</i> ( <i>Sinorhizobium</i> ) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010, 2, 77-86.                                    | 1.5 | 100       |
| 2078 | The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. <i>Standards in Genomic Sciences</i> , 2010, 2, 229-237.  | 1.5 | 55        |
| 2079 | SeqTrim07: a pipeline for preprocessing sequence reads. <i>International Journal of Computational Intelligence in Bioinformatics and Systems Biology</i> , 2010, 1, 370.  | 0.1 | 0         |
| 2080 | A quality management system application to investigate and troubleshoot process failures. <i>Clinical Governance</i> , 2010, 15, 102-112.   | 0.4 | 0         |
| 2081 | Impact of asymptomatic nodavirus carrier state and intraperitoneal viral mimic injection on brain transcript expression in Atlantic cod ( <i>Gadus morhua</i> ). <i>Physiological Genomics</i> , 2010, 42, 266-280.           | 1.0 | 53        |
| 2083 | A Polymerase Chain Reaction Assay for the Detection of <i>Xanthomonas campestris</i> pv. <i>musacearum</i> in Banana. <i>Plant Disease</i> , 2010, 94, 109-114.   | 0.7 | 26        |
| 2084 | Phylogeography and historical demography of the neotropical stingless bee <i>Melipona quadrifasciata</i> (Hymenoptera, Apidae): incongruence between morphology and mitochondrial DNA. <i>Apidologie</i> , 2010, 41, 534-547. | 0.9 | 78        |
| 2085 | Gene expression profiling of the endophytic fungus <i>Neotyphodium lolii</i> in association with its host plant perennial ryegrass. <i>Australasian Plant Pathology</i> , 2010, 39, 467.                                      | 0.5 | 16        |
| 2086 | De novo assembly of short sequence reads. <i>Briefings in Bioinformatics</i> , 2010, 11, 457-472.   | 3.2 | 167       |
| 2087 | Highly Punctuated Patterns of Population Structure on the X Chromosome and Implications for African Evolutionary History. <i>American Journal of Human Genetics</i> , 2010, 86, 34-44.  | 2.6 | 24        |
| 2088 | Replication Strategies for Rare Variant Complex Trait Association Studies via Next-Generation Sequencing. <i>American Journal of Human Genetics</i> , 2010, 87, 790-801.  | 2.6 | 53        |
| 2089 | Current Progress in Static and Dynamic Modeling of Biological Networks. <i>Systems Biology</i> , 2010, , 13-73.   | 0.1 | 4         |
| 2090 | Genetic variation at <i>bx1</i> controls DIMBOA content in maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 721-734.   | 1.8 | 49        |
| 2091 | Genomic structure and evolution of the <i>Pi2/9</i> locus in wild rice species. <i>Theoretical and Applied Genetics</i> , 2010, 121, 295-309.   | 1.8 | 25        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2092 | The Mitochondrial Genomes of Two Scallops, <i>Argopecten irradians</i> and <i>Chlamys farreri</i> (Mollusca: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Evolution, 2010, 70, 57-68.   | 0.8 | 38        |
| 2093 | Implications of the Plastid Genome Sequence of <i>Typha</i> (Typhaceae, Poales) for Understanding Genome Evolution in Poaceae. <i>Journal of Molecular Evolution</i> , 2010, 70, 149-166.   | 0.8 | 196       |
| 2094 | Functional Diversification and Evolution of Antifreeze Proteins in the Antarctic Fish <i>Lycodichthys dearborni</i> . <i>Journal of Molecular Evolution</i> , 2010, 71, 111-118.  | 0.8 | 11        |
| 2095 | Community Analysis Reveals Close Affinities Between Endophytic and Endolichenic Fungi in Mosses and Lichens. <i>Microbial Ecology</i> , 2010, 60, 340-353.  | 1.4 | 191       |
| 2096 | Short template amplicon and multiplex megaprimer-enabled relay (STAMMER) sequencing, a simultaneous approach to higher throughput sequence-based typing of polymorphic genes. <i>Immunogenetics</i> , 2010, 62, 253-260.              | 1.2 | 0         |
| 2097 | An expression analysis of 57 transcription factors derived from ESTs of developing seeds in Maize ( <i>Zea</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50  | 2.8 | 24        |
| 2098 | Analysis of expressed sequence tags from the <i>Ulva prolifera</i> (Chlorophyta). <i>Chinese Journal of Oceanology and Limnology</i> , 2010, 28, 26-36.   | 0.7 | 9         |
| 2099 | Construction and characterization of a normalized cDNA library of <i>Nannochloropsis oculata</i> (Eustigmatophyceae). <i>Chinese Journal of Oceanology and Limnology</i> , 2010, 28, 802-807.   | 0.7 | 3         |
| 2100 | Development and analysis of a germline BAC resource for the sea lamprey, a vertebrate that undergoes substantial chromatin diminution. <i>Chromosoma</i> , 2010, 119, 381-389.  | 1.0 | 44        |
| 2101 | Comparative Analysis of Expressed Sequence Tags from the White-Rot Fungi (Phanerochaete) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50  | 1.6 | 1         |
| 2102 | A genomics resource for investigating regulation of essential oil production in <i>Lavandula angustifolia</i> . <i>Planta</i> , 2010, 231, 835-845.   | 1.6 | 87        |
| 2103 | Genome-wide discovery of DNA polymorphism in <i>Brassica rapa</i> . <i>Molecular Genetics and Genomics</i> , 2010, 283, 135-145.  | 1.0 | 60        |
| 2104 | Identification of Immune Genes of the Agamaki Clam ( <i>Sinonovacula constricta</i> ) by Sequencing and Bioinformatic Analysis of ESTs. <i>Marine Biotechnology</i> , 2010, 12, 282-291.  | 1.1 | 35        |
| 2105 | Control of flowering time and spike development in cereals: the earliness per se Eps-1 region in wheat, rice, and <i>Brachypodium</i> . <i>Functional and Integrative Genomics</i> , 2010, 10, 293-306.                               | 1.4 | 71        |
| 2106 | Recruitment of closely linked genes for divergent functions: the seed storage protein (Glu-3) and powdery mildew (Pm3) genes in wheat ( <i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , 2010, 10, 241-251. | 1.4 | 6         |
| 2107 | A 9-bp Deletion Homoplasmy in Women with Polycystic Ovary Syndrome Revealed by Mitochondrial Genome-Mutation Screen. <i>Biochemical Genetics</i> , 2010, 48, 157-163.   | 0.8 | 26        |
| 2108 | Intrapopulational genetic diversity of <i>Araucaria angustifolia</i> (Bertol.) Kuntze is different when assessed on the basis of chloroplast or nuclear markers. <i>Plant Systematics and Evolution</i> , 2010, 284, 111-122.         | 0.3 | 16        |
| 2109 | Identification and molecular cloning of a novel porcine parvovirus. <i>Archives of Virology</i> , 2010, 155, 801-806.   | 0.9 | 99        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2110 | PCR screening and sequence analysis of iol clusters in <i>Lactobacillus casei</i> strains isolated from koumiss. <i>Folia Microbiologica</i> , 2010, 55, 603-606.  | 1.1 | 3         |
| 2111 | Comparative Phylogeography of North American Atlantic Salt Marsh Communities. <i>Estuaries and Coasts</i> , 2010, 33, 828-839.   | 1.0 | 31        |
| 2112 | Assessment of soil fungal communities using pyrosequencing. <i>Journal of Microbiology</i> , 2010, 48, 284-289.  | 1.3 | 116       |
| 2113 | Expressed sequence tag analysis generated from a normalized full-length cDNA library of the root-knot nematode ( <i>Meloidogyne incognita</i> ). <i>Genes and Genomics</i> , 2010, 32, 553-562.  | 0.5 | 7         |
| 2114 | Sequencing, annotation and comparative analysis of nine BACs of giant panda ( <i>Ailuropoda</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T   | 2.3 | 6         |
| 2115 | Genome research profile of two <i>Cordyceps sinensis</i> cDNA libraries. <i>Science Bulletin</i> , 2010, 55, 1403-1411.  | 1.7 | 5         |
| 2116 | Mining, characterization, and exploitation of EST-derived microsatellites in <i>Gossypium barbadense</i> . <i>Science Bulletin</i> , 2010, 55, 1889-1893.  | 1.7 | 19        |
| 2117 | Bioinformatics "Mining the genome for information. <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2010, 5, 391-404.   | 0.6 | 0         |
| 2118 | Interaction between organochlorines and the AHR gene, and risk of non-Hodgkin lymphoma. <i>Cancer Causes and Control</i> , 2010, 21, 11-22.  | 0.8 | 36        |
| 2119 | Utilization of next-generation sequencing platforms in plant genomics and genetic variant discovery. <i>Molecular Breeding</i> , 2010, 25, 553-570.  | 1.0 | 112       |
| 2120 | Genic markers for wild abortive (WA) cytoplasm based male sterility and its fertility restoration in rice. <i>Molecular Breeding</i> , 2010, 26, 275-292.  | 1.0 | 52        |
| 2121 | Characterization and tissue expression of channel catfish ( <i>Ictalurus punctatus</i> Rafinesque, 1818) ubiquitin carboxyl-terminal hydrolase L5 (UCHL5) cDNA. <i>Molecular Biology Reports</i> , 2010, 37, 1229-1234.                    | 1.0 | 3         |
| 2122 | The mitochondrial genome of <i>Euphausia superba</i> (Prydz Bay) (Crustacea: Malacostraca: Euphausiacea) reveals a novel gene arrangement and potential molecular markers. <i>Molecular Biology Reports</i> , 2010, 37, 771-784.           | 1.0 | 35        |
| 2123 | Complete mitochondrial genome of the Asian paddle crab <i>Charybdis japonica</i> (Crustacea: Decapoda:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 582 T decapods. <i>Molecular Biology Reports</i> , 2010, 37, 2559-2569.                | 1.0 | 51        |
| 2124 | The complete mitochondrial genomes of the whistling duck ( <i>Dendrocygna javanica</i> ) and black swan ( <i>Cygnus atratus</i> ): dating evolutionary divergence in Galloanserae. <i>Molecular Biology Reports</i> , 2010, 37, 3001-3015. | 1.0 | 21        |
| 2125 | The EgMUR3 xyloglucan galactosyltransferase from <i>Eucalyptus grandis</i> complements the mur3 cell wall phenotype in <i>Arabidopsis thaliana</i> . <i>Tree Genetics and Genomes</i> , 2010, 6, 745-756.                                  | 0.6 | 16        |
| 2126 | Evaluating <i>Theobroma grandiflorum</i> for comparative genomic studies with <i>Theobroma cacao</i> . <i>Tree Genetics and Genomes</i> , 2010, 6, 783-792.  | 0.6 | 16        |
| 2127 | Identification of novel members in sweet orange carotenoid biosynthesis gene families. <i>Tree Genetics and Genomes</i> , 2010, 6, 905-914.  | 0.6 | 27        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2128 | Development and mapping of peach candidate genes involved in fruit quality and their transferability and potential use in other Rosaceae species. <i>Tree Genetics and Genomes</i> , 2010, 6, 995-1012.  | 0.6 | 23        |
| 2129 | An ordered EST catalogue and gene expression profiles of cassava ( <i>Manihot esculenta</i> ) at key growth stages. <i>Plant Molecular Biology</i> , 2010, 74, 573-590.  | 2.0 | 24        |
| 2130 | â€Candidatus <i>Phlomobacter fragariae</i> â€™ and the proteobacterium associated with the low sugar content syndrome of sugar beet are related to bacteria of the arsenophonus clade detected in hemipteran insects. <i>European Journal of Plant Pathology</i> , 2010, 126, 123-127. | 0.8 | 12        |
| 2131 | Identification of <i>Colletotrichum</i> species associated with anthracnose disease of coffee in Vietnam. <i>European Journal of Plant Pathology</i> , 2010, 127, 73-87.   | 0.8 | 40        |
| 2132 | Investigation of highly unsaturated fatty acid metabolism in the Asian sea bass, <i>Lates calcarifer</i> . <i>Fish Physiology and Biochemistry</i> , 2010, 36, 827-843.  | 0.9 | 103       |
| 2133 | Rapidly developing functional genomics in ecological model systems via 454 transcriptome sequencing. <i>Genetica</i> , 2010, 138, 433-451.   | 0.5 | 119       |
| 2134 | Survey of genome organization and gene content of <i>Corynebacterium pseudotuberculosis</i> . <i>Microbiological Research</i> , 2010, 165, 312-320.  | 2.5 | 17        |
| 2135 | Transcript analysis of parasitic females of the sedentary semi-endoparasitic nematode <i>Rotylenchulus reniformis</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 172, 31-40.  | 0.5 | 24        |
| 2136 | Transcriptomic analyses of the avirulent protozoan parasite <i>Trypanosoma rangeli</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 174, 18-25.   | 0.5 | 32        |
| 2137 | Development and optimisation of a duplex real-time reverse transcription quantitative PCR assay targeting the VP7 and NS2 genes of African horse sickness virus. <i>Journal of Virological Methods</i> , 2010, 167, 45-52.   | 1.0 | 36        |
| 2138 | Phylogenetic analysis of small ruminant lentiviruses from Northern Brazil. <i>Small Ruminant Research</i> , 2010, 94, 205-209.   | 0.6 | 10        |
| 2139 | SeqTrim: a high-throughput pipeline for pre-processing any type of sequence read. <i>BMC Bioinformatics</i> , 2010, 11, 38.  | 1.2 | 180       |
| 2140 | Reanalyze unassigned reads in Sanger based metagenomic data using conserved gene adjacency. <i>BMC Bioinformatics</i> , 2010, 11, 565.   | 1.2 | 8         |
| 2141 | Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , 2010, 11, 94.   | 1.2 | 1,421     |
| 2142 | The evolution of euhermaphroditism in caridean shrimps: a molecular perspective of sexual systems and systematics. <i>BMC Evolutionary Biology</i> , 2010, 10, 297.  | 3.2 | 31        |
| 2143 | Unusual conservation of mitochondrial gene order in <i>Crassostrea</i> oysters: evidence for recent speciation in Asia. <i>BMC Evolutionary Biology</i> , 2010, 10, 394.   | 3.2 | 119       |
| 2144 | Genomic organization of duplicated short wave-sensitive and long wave-sensitive opsin genes in the green swordtail, <i>Xiphophorus helleri</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 87.   | 3.2 | 32        |
| 2145 | Identification and analysis of in planta expressed genes of <i>Magnaporthe oryzae</i> . <i>BMC Genomics</i> , 2010, 11, 104.   | 1.2 | 37        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2146 | Genomic sequencing and analyses of <i>Lymantria xyli</i> multiple nucleopolyhedrovirus. BMC Genomics, 2010, 11, 116.  | 1.2 | 29        |
| 2147 | Hyper-expansion of large DNA segments in the genome of kuruma shrimp, <i>Marsupenaeus japonicus</i> . BMC Genomics, 2010, 11, 141.  | 1.2 | 33        |
| 2148 | Genome dynamics of <i>Bartonella grahamii</i> in micro-populations of woodland rodents. BMC Genomics, 2010, 11, 152.  | 1.2 | 18        |
| 2149 | Comprehensive analysis of MHC class I genes from the U-, S-, and Z-lineages in Atlantic salmon. BMC Genomics, 2010, 11, 154.  | 1.2 | 50        |
| 2150 | Transcriptome survey of the anhydrobiotic tardigrade <i>Milnesium tardigradum</i> in comparison with <i>Hypsibius dujardini</i> and <i>Richtersius coronifer</i> . BMC Genomics, 2010, 11, 168.         | 1.2 | 49        |
| 2151 | Novel insights into the genomic basis of citrus canker based on the genome sequences of two strains of <i>Xanthomonas fuscans</i> subsp. <i>aurantifolii</i> . BMC Genomics, 2010, 11, 238.             | 1.2 | 102       |
| 2152 | <i>Salmo salar</i> and <i>Esox lucius</i> full-length cDNA sequences reveal changes in evolutionary pressures on a post-tetraploidization genome. BMC Genomics, 2010, 11, 279.                          | 1.2 | 163       |
| 2153 | Powdery mildew fungal effector candidates share N-terminal Y/F/WxC-motif. BMC Genomics, 2010, 11, 317.  | 1.2 | 177       |
| 2154 | Understanding the evolutionary relationships and major traits of <i>Bacillus</i> through comparative genomics. BMC Genomics, 2010, 11, 332.   | 1.2 | 143       |
| 2155 | From array-based hybridization of <i>Helicobacter pylori</i> isolates to the complete genome sequence of an isolate associated with MALT lymphoma. BMC Genomics, 2010, 11, 368.                         | 1.2 | 47        |
| 2156 | Genome size evolution in pufferfish: an insight from BAC clone-based <i>Diodon holocanthus</i> genome sequencing. BMC Genomics, 2010, 11, 396.  | 1.2 | 16        |
| 2157 | Light whole genome sequence for SNP discovery across domestic cat breeds. BMC Genomics, 2010, 11, 406.  | 1.2 | 51        |
| 2158 | The <i>Pinus taeda</i> genome is characterized by diverse and highly diverged repetitive sequences. BMC Genomics, 2010, 11, 420.  | 1.2 | 144       |
| 2159 | Full-length cDNA sequences from Rhesus monkey placenta tissue: analysis and utility for comparative mapping. BMC Genomics, 2010, 11, 427.   | 1.2 | 3         |
| 2160 | Deep sequencing-based transcriptome profiling analysis of bacteria-challenged <i>Lateolabrax japonicus</i> reveals insight into the immune-relevant genes in marine fish. BMC Genomics, 2010, 11, 472.  | 1.2 | 189       |
| 2161 | Evolution of duplicated IgH loci in Atlantic salmon, <i>Salmo salar</i> . BMC Genomics, 2010, 11, 486.  | 1.2 | 75        |
| 2162 | The genome of <i>Geobacter bemidjiensis</i> , exemplar for the subsurface clade of <i>Geobacter</i> species that predominate in Fe(III)-reducing subsurface environments.. BMC Genomics, 2010, 11, 490. | 1.2 | 52        |
| 2163 | Gene discovery for the bark beetle-vectored fungal tree pathogen <i>Grosmannia clavigera</i> . BMC Genomics, 2010, 11, 536.   | 1.2 | 25        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2164 | Genomic organization and evolution of the Atlantic salmon hemoglobin repertoire. BMC Genomics, 2010, 11, 539.  | 1.2 | 25        |
| 2165 | Genome analysis and comparative genomics of a Giardia intestinalis assemblage E isolate. BMC Genomics, 2010, 11, 543.  | 1.2 | 125       |
| 2166 | Insights into metazoan evolution from alvinella pompejana cDNAs. BMC Genomics, 2010, 11, 634.  | 1.2 | 46        |
| 2167 | Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. BMC Genomics, 2010, 11, 650.  | 1.2 | 82        |
| 2168 | A genome-wide study of PDZ-domain interactions in C. elegans reveals a high frequency of non-canonical binding. BMC Genomics, 2010, 11, 671.   | 1.2 | 39        |
| 2169 | The European sea bass Dicentrarchus labrax genome puzzle: comparative BAC-mapping and low coverage shotgun sequencing. BMC Genomics, 2010, 11, 68.   | 1.2 | 60        |
| 2170 | Unprecedented loss of ammonia assimilation capability in a urease-encoding bacterial mutualist. BMC Genomics, 2010, 11, 687.   | 1.2 | 39        |
| 2171 | Genomic organisation analysis of novel immunoglobulin-like transcripts in Atlantic salmon (Salmo Tj ETQq1 1 0.784314 rgBT <sub>11</sub> /Overlo  | 1.2 | 11        |
| 2172 | Heat-shock responsive genes identified and validated in Atlantic cod (Gadus morhua) liver, head kidney and skeletal muscle using genomic techniques. BMC Genomics, 2010, 11, 72.   | 1.2 | 72        |
| 2173 | Transcriptome analysis of the Cryptocaryon irritans tomont stage identifies potential genes for the detection and control of cryptocaryonosis. BMC Genomics, 2010, 11, 76.   | 1.2 | 38        |
| 2174 | Systematic overrepresentation of DNA termini and underrepresentation of subterminal regions among sequencing templates prepared from hydrodynamically sheared linear DNA molecules. BMC Genomics, 2010, 11, 87.  | 1.2 | 5         |
| 2175 | Transcriptional profiling reveals the expression of novel genes in response to various stimuli in the human dermatophyte Trichophyton rubrum. BMC Microbiology, 2010, 10, 39.  | 1.3 | 49        |
| 2176 | Genome-wide characterization of the biggest grass, bamboo, based on 10,608 putative full-length cDNA sequences. BMC Plant Biology, 2010, 10, 116.  | 1.6 | 81        |
| 2177 | Single nucleotide polymorphisms for assessing genetic diversity in castor bean (Ricinus communis). BMC Plant Biology, 2010, 10, 13.  | 1.6 | 95        |
| 2178 | Delineating the structural, functional and evolutionary relationships of sucrose phosphate synthase gene family II in wheat and related grasses. BMC Plant Biology, 2010, 10, 134.   | 1.6 | 14        |
| 2179 | Analysis of gene expression in response to water deficit of chickpea (Cicer arietinum L.) varieties differing in drought tolerance. BMC Plant Biology, 2010, 10, 24.   | 1.6 | 90        |
| 2180 | Functionally relevant microsatellites in sugarcane unigenes. BMC Plant Biology, 2010, 10, 251.   | 1.6 | 52        |
| 2181 | Analysis of expressed sequence tags from a single wheat cultivar facilitates interpretation of tandem mass spectrometry data and discrimination of gamma gliadin proteins that may play different functional roles in flour. BMC Plant Biology, 2010, 10, 7. | 1.6 | 45        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2182 | Uncovering the evolutionary origin of plant molecular processes: comparison of Coleochaete (Coleochaetales) and Spirogyra (Zygnematales) transcriptomes. <i>BMC Plant Biology</i> , 2010, 10, 96.  | 1.6 | 91        |
| 2183 | A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. <i>BMC Plant Biology</i> , 2010, 10, 98.  | 1.6 | 16        |
| 2184 | Wheat beta-expansin (EXPB11) genes: Identification of the expressed gene on chromosome 3BS carrying a pollen allergen domain. <i>BMC Plant Biology</i> , 2010, 10, 99.   | 1.6 | 17        |
| 2185 | Maternal gene expression in Atlantic halibut ( <i>Hippoglossus hippoglossus</i> L.) and its relation to egg quality. <i>BMC Research Notes</i> , 2010, 3, 138.   | 0.6 | 45        |
| 2186 | A direct comparison of the KBâ„¢ Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. <i>BMC Research Notes</i> , 2010, 3, 257.   | 0.6 | 9         |
| 2187 | An efficient method for developing SNP markers based on EST data combined with high resolution melting (HRM) analysis. <i>BMC Research Notes</i> , 2010, 3, 51.  | 0.6 | 17        |
| 2188 | The identification of a new <i>Giardia duodenalis</i> assemblage in marine vertebrates and a preliminary analysis of <i>G. duodenalis</i> population biology in marine systems. <i>International Journal for Parasitology</i> , 2010, 40, 1063-1074. | 1.3 | 176       |
| 2189 | Rabies virus in insectivorous bats: Implications of the diversity of the nucleoprotein and glycoprotein genes for molecular epidemiology. <i>Virology</i> , 2010, 405, 352-360.  | 1.1 | 52        |
| 2190 | Genetic diagnosis of familial breast cancer using clonal sequencing. <i>Human Mutation</i> , 2010, 31, 484-491.  | 1.1 | 75        |
| 2191 | Distinct troponin C isoform requirements in cardiac and skeletal muscle. <i>Developmental Dynamics</i> , 2010, 239, 3115-3123.   | 0.8 | 24        |
| 2192 | Identification of Polymorphic Markers for Genetic Mapping. , 2010, , 33-48.  |     | 0         |
| 2193 | High-throughput DNA sequencing " concepts and limitations. <i>BioEssays</i> , 2010, 32, 524-536.   | 1.2 | 490       |
| 2194 | Molecular characterization, distribution, and dynamics of hepatitis C virus genotypes in blood donors in Colombia. <i>Journal of Medical Virology</i> , 2010, 82, 1889-1898.   | 2.5 | 23        |
| 2195 | Sequence analysis and PCR-RFLP profiling of the hsp70 gene as a valuable tool for identifying <i>Leishmania</i> species associated with human leishmaniasis in Brazil. <i>Infection, Genetics and Evolution</i> , 2010, 10, 77-83.                   | 1.0 | 70        |
| 2196 | Epidemiologic aspects of an outbreak of <i>Trypanosoma vivax</i> in a dairy cattle herd in Minas Gerais state, Brazil. <i>Veterinary Parasitology</i> , 2010, 169, 320-326.  | 0.7 | 34        |
| 2197 | Biogeographic history of the species complex <i>Basileuterus culicivorus</i> (Aves, Parulidae) in the Neotropics. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 585-597.  | 1.2 | 15        |
| 2198 | Geographic and phylogenetic patterns in <i>Silene</i> section <i>Melandrium</i> (Caryophyllaceae) as inferred from chloroplast and nuclear DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 978-991.                          | 1.2 | 93        |
| 2199 | Conservation of MAP kinase activity and MSP genes in parthenogenetic nematodes. <i>BMC Developmental Biology</i> , 2010, 10, 51.   | 2.1 | 10        |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2200 | Population genetics of foxtail millet and its wild ancestor. <i>BMC Genetics</i> , 2010, 11, 90.   | 2.7 | 53        |
| 2201 | Genetic diversity of NS5A protein from hepatitis C virus genotype 3a and its relationship to therapy response. <i>BMC Infectious Diseases</i> , 2010, 10, 36.  | 1.3 | 14        |
| 2202 | The IGF1small dog haplotype is derived from Middle Eastern grey wolves. <i>BMC Biology</i> , 2010, 8, 16.  | 1.7 | 58        |
| 2203 | Generation and analysis of expressed sequence tags from a cDNA library of the fruiting body of <i>Ganoderma lucidum</i> . <i>Chinese Medicine</i> , 2010, 5, 9.  | 1.6 | 15        |
| 2204 | Captive-born intergeneric hybrid of a Guiana and bottlenose dolphin: <i>Sotalia guianensis</i> — <i>Tursiops truncatus</i> . <i>Zoo Biology</i> , 2010, 29, 647-657.   | 0.5 | 16        |
| 2205 | Proteomic analysis of the <i>Echinococcus granulosus</i> metacestode during infection of its intermediate host. <i>Proteomics</i> , 2010, 10, 1985-1999.   | 1.3 | 117       |
| 2206 | ANALYSES OF THE COMPLETE CHLOROPLAST GENOME SEQUENCES OF TWO MEMBERS OF THE PELAGOPHYCEAE: <i>AUREOCOCCUS ANOPHAGEFFERENS</i> CCMP1984 AND <i>AUREOUMBRA LAGUNENSIS</i> CCMP1507 <sup>1</sup> . <i>Journal of Phycology</i> , 2010, 46, 602-615. | 1.0 | 32        |
| 2207 | Genetic Diversity of the Fragile X Syndrome Gene ( <i>FMR1</i> ) in a Large Sub-Saharan West African Population. <i>Annals of Human Genetics</i> , 2010, 74, 316-325.  | 0.3 | 14        |
| 2208 | FEMALE HETEROGAMETY AND SPECIATION: REDUCED INTROGRESSION OF THE Z CHROMOSOME BETWEEN TWO SPECIES OF NIGHTINGALES. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 456-471.   | 1.1 | 113       |
| 2209 | SPECIATION IN THE EUROPEAN RABBIT ( <i>ORYCTOLAGUS CLUNICULUS</i> ): ISLANDS OF DIFFERENTIATION ON THE X CHROMOSOME AND AUTOSOMES. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3443-3460.                           | 1.1 | 71        |
| 2210 | Genetic analysis of three important genes in pigmentation and melanoma susceptibility: <i>CDKN2A</i> , <i>MC1R</i> and <i>HERC2/OCA2</i> . <i>Experimental Dermatology</i> , 2010, 19, 836-844.  | 1.4 | 28        |
| 2211 | High diversity of polyketide synthase genes and the melanin biosynthesis gene cluster in <i>Penicillium marneffeii</i> . <i>FEBS Journal</i> , 2010, 277, 3750-3758.   | 2.2 | 105       |
| 2212 | Identifications of expressed sequence tags from Pacific threadfin ( <i>Polydactylus sexfilis</i> ) skeletal muscle cDNA library. <i>Aquaculture Research</i> , 2010, 41, 572-578.  | 0.9 | 1         |
| 2213 | Discovery of host defence genes in the Japanese scallop <i>Mizuhopecten yessoensis</i> Jay by expressed sequence tag analysis of kidney tissue. <i>Aquaculture Research</i> , 2010, 41, 1602-1613.   | 0.9 | 18        |
| 2214 | Finding candidate genes under positive selection in Non-model species: examples of genes involved in host specialization in pathogens. <i>Molecular Ecology</i> , 2010, 19, 292-306.   | 2.0 | 44        |
| 2215 | A genetic basis for the phenotypic differentiation between siscowet and lean lake trout ( <i>Salvelinus</i> ) TJ ETQq1 1 0.784314 pgBT /Over 190   | 2.0 | 190       |
| 2216 | mLRho – a program for estimating the population mutation and recombination rates from shotgun-sequenced diploid genomes. <i>Molecular Ecology</i> , 2010, 19, 277-284.   | 2.0 | 88        |
| 2217 | Transcriptome divergence between the hexaploid salt-marsh sister species <i>Spartina maritima</i> and <i>Spartina alterniflora</i> (Poaceae). <i>Molecular Ecology</i> , 2010, 19, 2050-2063.  | 2.0 | 34        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2218 | Rapid diversification by recombination in <i>Bartonella grahamii</i> from wild rodents in Asia contrasts with low levels of genomic divergence in Northern Europe and America. <i>Molecular Ecology</i> , 2010, 19, 2241-2255.     | 2.0 | 34        |
| 2219 | Phylogeographical analyses of domestic and wild yaks based on mitochondrial DNA: new data and reappraisal. <i>Journal of Biogeography</i> , 2010, 37, 2332-2344.   | 1.4 | 66        |
| 2220 | New insights on the speciation history and nucleotide diversity of three boreal spruce species and a Tertiary relict. <i>Heredity</i> , 2010, 104, 3-14.   | 1.2 | 74        |
| 2221 | Community shifts of soybean stem-associated bacteria responding to different nodulation phenotypes and N levels. <i>ISME Journal</i> , 2010, 4, 315-326.   | 4.4 | 63        |
| 2222 | Comparative community genomics in the Dead Sea: an increasingly extreme environment. <i>ISME Journal</i> , 2010, 4, 399-407.   | 4.4 | 101       |
| 2223 | The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. <i>ISME Journal</i> , 2010, 4, 61-77.  | 4.4 | 244       |
| 2224 | Transcript profiles of <i>Panax quinquefolius</i> from flower, leaf and root bring new insights into genes related to ginsenosides biosynthesis and transcriptional regulation. <i>Physiologia Plantarum</i> , 2010, 138, 134-149. | 2.6 | 46        |
| 2225 | Parallel, tag-directed assembly of locally derived short sequence reads. <i>Nature Methods</i> , 2010, 7, 119-122.   | 9.0 | 144       |
| 2226 | Visualizing genomes: techniques and challenges. <i>Nature Methods</i> , 2010, 7, S5-S15.   | 9.0 | 146       |
| 2227 | Defining transcribed regions using RNA-seq. <i>Nature Protocols</i> , 2010, 5, 255-266.  | 5.5 | 70        |
| 2228 | Generation and analysis of 10 000 ESTs from the half-smooth tongue sole <i>Cynoglossus semilaevis</i> and identification of microsatellite and SNP markers. <i>Journal of Fish Biology</i> , 2010, 76, 1190-1204.                  | 0.7 | 27        |
| 2229 | Ironing out the wrinkles in the rare biosphere through improved OTU clustering. <i>Environmental Microbiology</i> , 2010, 12, 1889-1898.   | 1.8 | 1,226     |
| 2230 | Expression-based identification of genetic determinants of the bacterial symbiosis of <i>Chlorochromatium aggregatum</i> . <i>Environmental Microbiology</i> , 2010, 12, 2259-2276.  | 1.8 | 11        |
| 2231 | Cultivation-independent characterization of <i>Candidatus Magnetobacterium bavaricum</i> via ultrastructural, geochemical and metagenomic methods. <i>Environmental Microbiology</i> , 2010, 12, 2466-2478.                        | 1.8 | 69        |
| 2232 | The genome of <i>Syntrophomonas wolfei</i> : new insights into syntrophic metabolism and biohydrogen production. <i>Environmental Microbiology</i> , 2010, 12, 2289-2301.  | 1.8 | 158       |
| 2233 | The genome of the Gram-positive metal- and sulfate-reducing bacterium <i>Desulfotomaculum reducens</i> strain MI-1. <i>Environmental Microbiology</i> , 2010, 12, 2738-2754.   | 1.8 | 60        |
| 2234 | Hepatitis B genotype G and high frequency of lamivudine-resistance mutations among human immunodeficiencyvirus/hepatitis B virus co-infected patients in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2010, 105, 770-778.   | 0.8 | 16        |
| 2235 | Genomics, Bioinformatics, and Computational Biology. , 2010, , 641-661.  |     | 1         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2236 | The Genome Sequence of <i>Methanohalophilus mahii</i> SLP <sup>T</sup> Reveals Differences in the Energy Metabolism among Members of the <i>Methanosarcinaceae</i> Inhabiting Freshwater and Saline Environments. <i>Archaea</i> , 2010, 2010, 1-16. | 2.3 | 35        |
| 2237 | Designing Efficient Spaced Seeds for SOLiD Read Mapping. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-12.   | 5.7 | 5         |
| 2238 | An Insect Herbivore Microbiome with High Plant Biomass-Degrading Capacity. <i>PLoS Genetics</i> , 2010, 6, e1001129.   | 1.5 | 213       |
| 2239 | Sequence Analysis of pKF3-70 in <i>Klebsiella pneumoniae</i> : Probable Origin from R100-Like Plasmid of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2010, 5, e8601.   | 1.1 | 29        |
| 2240 | Genetic Variation at Nuclear Loci Fails to Distinguish Two Morphologically Distinct Species of <i>Aquilegia</i> . <i>PLoS ONE</i> , 2010, 5, e8655.  | 1.1 | 23        |
| 2241 | The Smallest Known Genomes of Multicellular and Toxic Cyanobacteria: Comparison, Minimal Gene Sets for Linked Traits and the Evolutionary Implications. <i>PLoS ONE</i> , 2010, 5, e9235.  | 1.1 | 168       |
| 2242 | Rapid Multi-Locus Sequence Typing Using Microfluidic Biochips. <i>PLoS ONE</i> , 2010, 5, e10595.  | 1.1 | 12        |
| 2243 | Sequencing, Analysis, and Annotation of Expressed Sequence Tags for <i>Camelus dromedarius</i> . <i>PLoS ONE</i> , 2010, 5, e10720.  | 1.1 | 40        |
| 2244 | Random X Inactivation and Extensive Mosaicism in Human Placenta Revealed by Analysis of Allele-Specific Gene Expression along the X Chromosome. <i>PLoS ONE</i> , 2010, 5, e10947.   | 1.1 | 113       |
| 2245 | Identification of Mendel's <i>White Flower</i> Character. <i>PLoS ONE</i> , 2010, 5, e13230.   | 1.1 | 135       |
| 2246 | Molecular analysis of the bacterial diversity in a specialized consortium for diesel oil degradation. <i>Revista Brasileira De Ciencia Do Solo</i> , 2010, 34, 773-781.  | 0.5 | 14        |
| 2247 | Normal and defective mariner-like elements in <i>Rhynchosciara</i> species (Sciaridae, Diptera). <i>Genetics and Molecular Research</i> , 2010, 9, 849-857.  | 0.3 | 5         |
| 2248 | Phylogenetic analysis of <i>Biomphalaria tenagophila</i> (Orbigny, 1835) (Mollusca: Gastropoda). <i>Memorias Do Instituto Oswaldo Cruz</i> , 2010, 105, 504-511.   | 0.8 | 11        |
| 2249 | Complete Nucleotide Sequence and Comparative Analysis of pPR9, a 41.7-Kilobase Conjugative Staphylococcal Multiresistance Plasmid Conferring High-Level Mupirocin Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 2252-2257.    | 1.4 | 39        |
| 2250 | Genetic determinants of HSP70 gene expression following heat shock. <i>Human Molecular Genetics</i> , 2010, 19, 4939-4947.   | 1.4 | 21        |
| 2251 | Genome Sequence of <i>Kitasatospora setae</i> NBRC 14216T: An Evolutionary Snapshot of the Family Streptomycetaceae. <i>DNA Research</i> , 2010, 17, 393-406.  | 1.5 | 62        |
| 2252 | Intra- and Interhost Evolutionary Dynamics of Equine Influenza Virus. <i>Journal of Virology</i> , 2010, 84, 6943-6954.  | 1.5 | 97        |
| 2253 | Genome Sequence of the Polysaccharide-Degrading, Thermophilic Anaerobe <i>Spirochaeta thermophila</i> DSM 6192. <i>Journal of Bacteriology</i> , 2010, 192, 6492-6493.   | 1.0 | 19        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2254 | Genome-Wide Evidence for Efficient Positive and Purifying Selection in <i>Capsella grandiflora</i> , a Plant Species with a Large Effective Population Size. <i>Molecular Biology and Evolution</i> , 2010, 27, 1813-1821.                       | 3.5 | 153       |
| 2255 | Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. <i>Bioinformatics</i> , 2010, 26, 1277-1283.  | 1.8 | 98        |
| 2256 | Megabase Level Sequencing Reveals Contrasted Organization and Evolution Patterns of the Wheat Gene and Transposable Element Spaces. <i>Plant Cell</i> , 2010, 22, 1686-1701.   | 3.1 | 258       |
| 2257 | Completed Genome Sequence of the Anaerobic Iron-Oxidizing Bacterium <i>Acidovorax ebreus</i> Strain TPSY. <i>Journal of Bacteriology</i> , 2010, 192, 1475-1476.   | 1.0 | 83        |
| 2258 | Phylogenetic relationship of <i>Parmelia lindmanii</i> (Parmeliaceae) inferred by analysis of its nuITS rDNA sequence. <i>Lichenologist</i> , 2010, 42, 423-428.   | 0.5 | 4         |
| 2259 | Genome-wide Screening Reveals the Genetic Determinants of an Antibiotic Insecticide in <i>Bacillus thuringiensis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 39191-39200.  | 1.6 | 55        |
| 2260 | Genotypes of chicken major histocompatibility complex B locus associated with regression of Rous sarcoma virus J-strain tumors. <i>Poultry Science</i> , 2010, 89, 651-657.  | 1.5 | 12        |
| 2261 | Partial Chromosome Sequence of <i>Spiroplasma citri</i> Reveals Extensive Viral Invasion and Important Gene Decay. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3420-3426.  | 1.4 | 57        |
| 2262 | Analysis of the complete mitochondrial genome sequences of the soybean rust pathogens <i>Phakopsora pachyrhizi</i> and <i>P. meibomia</i> . <i>Mycologia</i> , 2010, 102, 887-897.   | 0.8 | 23        |
| 2263 | <i>Sawyeria marylandensis</i> (Heterolobosea) Has a Hydrogenosome with Novel Metabolic Properties. <i>Eukaryotic Cell</i> , 2010, 9, 1913-1924.  | 3.4 | 40        |
| 2264 | Conserved Symbiotic Plasmid DNA Sequences in the Multireplicon Pangenomic Structure of <i>Rhizobium etli</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 1604-1614.  | 1.4 | 86        |
| 2265 | Cattle demographic history modelled from autosomal sequence variation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 2531-2539.   | 1.8 | 69        |
| 2266 | Identification of genes associated with bud dormancy release in <i>Prunus persica</i> by suppression subtractive hybridization. <i>Tree Physiology</i> , 2010, 30, 655-666.  | 1.4 | 102       |
| 2267 | Complete genome sequence and taxonomic position of anguillid herpesvirus 1. <i>Journal of General Virology</i> , 2010, 91, 880-887.  | 1.3 | 68        |
| 2268 | Complete Genome Sequence of the Cellulolytic Thermophile <i>Caldicellulosiruptor obsidiansis</i> OB47 <sup>T</sup> . <i>Journal of Bacteriology</i> , 2010, 192, 6099-6100.  | 1.0 | 39        |
| 2269 | Comparative genomics of clinical and environmental <i>Vibrio mimicus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21134-21139.  | 3.3 | 52        |
| 2270 | Low Frequency Nonnucleoside Reverse Transcriptase Inhibitor Resistant Variants Contribute to Failure of Efavirenz-Containing Regimens in Treatment Experienced Patients. <i>Journal of Infectious Diseases</i> , 2010, 201, 100126095936095-000. | 1.9 | 84        |
| 2271 | Genome Sequence of Hybrid <i>Vibrio cholerae</i> O1 MJ-1236, B-33, and CIRS101 and Comparative Genomics with <i>V. cholerae</i> . <i>Journal of Bacteriology</i> , 2010, 192, 3524-3533.   | 1.0 | 101       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2272 | ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. <i>Genomics Insights</i> , 2010, 3, GEI.S4340.  | 3.0 | 26        |
| 2273 | Evolutionary constraint facilitates interpretation of genetic variation in resequenced human genomes. <i>Genome Research</i> , 2010, 20, 301-310.   | 2.4 | 77        |
| 2274 | The Human Nasal Microbiota and <i>Staphylococcus aureus</i> Carriage. <i>PLoS ONE</i> , 2010, 5, e10598.  | 1.1 | 337       |
| 2275 | Molecular epidemiology and genetic diversity of hepatitis B virus genotype E in an isolated Afro-Colombian community. <i>Journal of General Virology</i> , 2010, 91, 501-508.   | 1.3 | 39        |
| 2276 | Demographic histories of four spruce ( <i>Picea</i> ) species of the Qinghai-Tibetan Plateau and neighboring areas inferred from multiple nuclear loci. <i>Molecular Biology and Evolution</i> , 2010, 27, 1001-1014.                         | 3.5 | 113       |
| 2277 | Unlocking Short Read Sequencing for Metagenomics. <i>PLoS ONE</i> , 2010, 5, e11840.  | 1.1 | 157       |
| 2278 | Molecular evidence of horizontal transmission of hepatitis C virus within couples. <i>Journal of General Virology</i> , 2010, 91, 691-696.  | 1.3 | 14        |
| 2279 | Complete Genome Sequence of the Electricity-Producing <i>Thermincola potens</i> Strain JR. <i>Journal of Bacteriology</i> , 2010, 192, 4078-4079.   | 1.0 | 38        |
| 2280 | Diverse Bacteria Inhabit Living Hyphae of Phylogenetically Diverse Fungal Endophytes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4063-4075.  | 1.4 | 234       |
| 2281 | Optimization analyses of Velvet algorithm based on RBF Neural Network. , 2010, , .  |     | 0         |
| 2282 | The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. <i>Nucleic Acids Research</i> , 2010, 38, 1767-1771.  | 6.5 | 1,340     |
| 2283 | Genome Sequence of the Dioxin-Mineralizing Bacterium <i>Sphingomonas wittichii</i> RW1. <i>Journal of Bacteriology</i> , 2010, 192, 6101-6102.  | 1.0 | 93        |
| 2284 | Application of Molecular Techniques To Elucidate the Influence of Cellulosic Waste on the Bacterial Community Structure at a Simulated Low-Level-Radioactive-Waste Site. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3106-3115. | 1.4 | 39        |
| 2285 | Genomic Analysis of Wild Tomato Introgressions Determining Metabolism- and Yield-Associated Traits. <i>Plant Physiology</i> , 2010, 152, 1772-1786.   | 2.3 | 57        |
| 2286 | Rumen Microbial Population Dynamics during Adaptation to a High-Grain Diet. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7482-7490.  | 1.4 | 574       |
| 2287 | Complete Genome Sequence of <i>Listeria seeligeri</i> , a Nonpathogenic Member of the Genus <i>Listeria</i> . <i>Journal of Bacteriology</i> , 2010, 192, 1473-1474.  | 1.0 | 23        |
| 2288 | STATISTICAL COMPARISON OF METHODS TO ESTIMATE THE ERROR PROBABILITY IN SHORT-READ ILLUMINA SEQUENCING. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 579-591.  | 0.3 | 11        |
| 2289 | Virus discovery by deep sequencing and assembly of virus-derived small silencing RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1606-1611.   | 3.3 | 419       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2290 | Biochemical Characterization of a Novel Indole Prenyltransferase from <i>Streptomyces</i> sp. SN-593. <i>Journal of Bacteriology</i> , 2010, 192, 2839-2851.  | 1.0 | 64        |
| 2291 | Antibody Repertoire Development in Fetal and Neonatal Piglets. XI. The Relationship of Variable Heavy Chain Gene Usage and the Genomic Organization of the Variable Heavy Chain Locus. <i>Journal of Immunology</i> , 2010, 184, 3734-3742. | 0.4 | 44        |
| 2292 | A Small, Variable, and Irregular Killer Cell Ig-Like Receptor Locus Accompanies the Absence of <i>MHC-C</i> and <i>MHC-G</i> in Gibbons. <i>Journal of Immunology</i> , 2010, 184, 1379-1391.   | 0.4 | 38        |
| 2293 | Genome assembly quality: Assessment and improvement using the neutral indel model. <i>Genome Research</i> , 2010, 20, 675-684.  | 2.4 | 44        |
| 2294 | Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10578-10583.            | 3.3 | 299       |
| 2295 | Complete Genome Sequence of the Representative $\hat{3}$ -Hexachlorocyclohexane-Degrading Bacterium <i>Sphingobium japonicum</i> UT26. <i>Journal of Bacteriology</i> , 2010, 192, 5852-5853.   | 1.0 | 66        |
| 2296 | Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. <i>Bioinformatics</i> , 2010, 26, i350-i357.  | 1.8 | 190       |
| 2297 | Generation and Analysis of Expressed Sequence Tags from <i>Olea europaea</i> L.. <i>Comparative and Functional Genomics</i> , 2010, 2010, 1-9.  | 2.0 | 16        |
| 2298 | SoDA2: a Hidden Markov Model approach for identification of immunoglobulin rearrangements. <i>Bioinformatics</i> , 2010, 26, 867-872.   | 1.8 | 65        |
| 2299 | Molecular authentication of the traditional Chinese medicinal plant <i>Angelica sinensis</i> based on internal transcribed spacer of nrDNA. <i>Electronic Journal of Biotechnology</i> , 2010, 13, .  | 1.2 | 2         |
| 2300 | Analyses of an Expressed Sequence Tag Library from <i>Taenia solium</i> , <i>Cysticercus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e919.   | 1.3 | 12        |
| 2301 | A Survey of Genomic Traces Reveals a Common Sequencing Error, RNA Editing, and DNA Editing. <i>PLoS Genetics</i> , 2010, 6, e1000954.   | 1.5 | 40        |
| 2302 | The Mating Type Locus (MAT) and Sexual Reproduction of <i>Cryptococcus heveanensis</i> : Insights into the Evolution of Sex and Sex-Determining Chromosomal Regions in Fungi. <i>PLoS Genetics</i> , 2010, 6, e1000961.                     | 1.5 | 69        |
| 2303 | A Human-Specific De Novo Protein-Coding Gene Associated with Human Brain Functions. <i>PLoS Computational Biology</i> , 2010, 6, e1000734.  | 1.5 | 107       |
| 2304 | Gene expression analysis in cadmium-stressed roots of a low cadmium-accumulating solanaceous plant, <i>Solanum torvum</i> . <i>Journal of Experimental Botany</i> , 2010, 61, 423-437.  | 2.4 | 101       |
| 2305 | Family-based association analysis of 42 hereditary prostate cancer families identifies the Apolipoprotein L3 region on chromosome 22q12 as a risk locus. <i>Human Molecular Genetics</i> , 2010, 19, 3852-3862.                             | 1.4 | 21        |
| 2306 | Comparative Metagenomics and Population Dynamics of the Gut Microbiota in Mother and Infant. <i>Genome Biology and Evolution</i> , 2010, 2, 53-66.  | 1.1 | 202       |
| 2307 | Genomic characterisation of the ichthyotoxic prymnesiophyte <i>Chrysochromulina polylepis</i> and the expression of polyketide synthase genes in synchronized cultures. <i>European Journal of Phycology</i> , 2010, 45, 215-229.           | 0.9 | 21        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2308 | Molecular Characterization of the Archaeal Community in an Amazonian Wetland Soil and Culture-Dependent Isolation of Methanogenic Archaea. <i>Diversity</i> , 2010, 2, 1026-1047.   | 0.7 | 28        |
| 2309 | Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology. <i>Bioinformatics</i> , 2010, 26, 1704-1707.   | 1.8 | 212       |
| 2310 | First Identification of Canine Distemper Virus in Hoary Fox ( <i>Lycalopex vetulus</i> ): Pathologic Aspects and Virus Phylogeny. <i>Journal of Wildlife Diseases</i> , 2010, 46, 303-305.  | 0.3 | 26        |
| 2311 | A unified index of sequence quality and contig overlap for DNA barcoding. <i>Bioinformatics</i> , 2010, 26, 2780-2781.  | 1.8 | 15        |
| 2312 | A SNP discovery method to assess variant allele probability from next-generation resequencing data. <i>Genome Research</i> , 2010, 20, 273-280.   | 2.4 | 168       |
| 2313 | Multiple Mechanisms Influence Regulation of the Cystic Fibrosis Transmembrane Conductance Regulator Gene Promoter. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2010, 43, 334-341.                             | 1.4 | 21        |
| 2314 | Next-Generation Sequencing Techniques for Eukaryotic Microorganisms: Sequencing-Based Solutions to Biological Problems. <i>Eukaryotic Cell</i> , 2010, 9, 1300-1310.  | 3.4 | 120       |
| 2315 | Rapid Identification of Genetic Modifications in <i>Bacillus anthracis</i> Using Whole Genome Draft Sequences Generated by 454 Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e12397.   | 1.1 | 27        |
| 2316 | The biotechnological potential of the extreme halophilic archaea <i>Haloterrigena</i> sp. H13 in xenobiotic metabolism using a comparative genomics approach. <i>Environmental Technology (United Kingdom)</i> , 2010, 31, 1087-1097. | 0.0 | 0         |
| 2317 | Transcription profiling of acute temperature stress in the Antarctic plunderfish <i>Harpagifer antarcticus</i> . <i>Marine Genomics</i> , 2010, 3, 35-44.   | 0.4 | 58        |
| 2318 | Using DNA barcoding and phylogenetics to identify Antarctic invertebrate larvae: Lessons from a large scale study. <i>Marine Genomics</i> , 2010, 3, 165-177.   | 0.4 | 54        |
| 2319 | Gilthead sea bream ( <i>Sparus auratus</i> ) and European sea bass ( <i>Dicentrarchus labrax</i> ) expressed sequence tags: Characterization, tissue-specific expression and gene markers. <i>Marine Genomics</i> , 2010, 3, 179-191. | 0.4 | 25        |
| 2320 | A window into third-generation sequencing. <i>Human Molecular Genetics</i> , 2010, 19, R227-R240.   | 1.4 | 761       |
| 2321 | Characterization of Hepatitis B virus (HBV) genotypes in patients from Rondônia, Brazil. <i>Virology Journal</i> , 2010, 7, 315.  | 1.4 | 43        |
| 2322 | Molecular Epidemiology of Avian Infectious Bronchitis in Brazil from 2007 to 2008 in Breeders, Broilers, and Layers. <i>Avian Diseases</i> , 2010, 54, 894-898.   | 0.4 | 34        |
| 2323 | Genetic Characterization of <i>Vibrio vulnificus</i> Strains from Tilapia Aquaculture in Bangladesh. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4890-4895.   | 1.4 | 37        |
| 2324 | DNA barcoding: a six-question tour to improve users' awareness about the method. <i>Briefings in Bioinformatics</i> , 2010, 11, 440-453.  | 3.2 | 129       |
| 2325 | Applied Conservation Genetics and the Need for Quality Control and Reporting of Genetic Data Used in Fisheries and Wildlife Management. <i>Journal of Heredity</i> , 2010, 101, 1-10.   | 1.0 | 73        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2326 | Algorithms in Bioinformatics. Lecture Notes in Computer Science, 2010, , .   | 1.0 | 0         |
| 2327 | Accurate and simple sizing of primer extension products using a non-radioactive approach facilitates identification of transcription initiation sites. <i>Journal of Microbiological Methods</i> , 2010, 81, 256-258.  | 0.7 | 7         |
| 2328 | Balanced polymorphism in bottlenecked populations: The case of the CCR5 5â€² cis-regulatory region in Amazonian Amerindians. <i>Human Immunology</i> , 2010, 71, 922-928.  | 1.2 | 6         |
| 2329 | Characterization of a Î²-1,3-glucanase active in the alkaline midgut of <i>Spodoptera frugiperda</i> larvae and its relation to Î²-glucan-binding proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2010, 40, 861-872.  | 1.2 | 56        |
| 2330 | Identification of immune genes of the miiuy croaker ( <i>Miichthys miiuy</i> ) by sequencing and bioinformatic analysis of ESTs. <i>Fish and Shellfish Immunology</i> , 2010, 29, 1099-1105.   | 1.6 | 55        |
| 2331 | Accumulation, functional annotation, and comparative analysis of expressed sequence tags in eggplant ( <i>Solanum melongena</i> L.), the third pole of the genus <i>Solanum</i> species after tomato and potato. <i>Gene</i> , 2010, 450, 76-84.   | 1.0 | 39        |
| 2332 | Preliminary assessment of COSII gene diversity in lulo and a relative species: Initial identification of genes potentially associated with domestication. <i>Gene</i> , 2010, 458, 27-36.  | 1.0 | 7         |
| 2333 | Isolation of the lysolipin gene cluster of <i>Streptomyces tendae</i> TÃ¼ 4042. <i>Gene</i> , 2010, 461, 5-14.   | 1.0 | 42        |
| 2334 | Cell homeostasis in a <i>Leishmania major</i> mutant overexpressing the spliced leader RNA is maintained by an increased proteolytic activity. <i>International Journal of Biochemistry and Cell Biology</i> , 2010, 42, 1661-1671.  | 1.2 | 4         |
| 2335 | Phylogenetic diversity and evolutionary relatedness of alkenone-producing haptophyte algae in lakes: Implications for continental paleotemperature reconstructions. <i>Earth and Planetary Science Letters</i> , 2010, 300, 311-320.   | 1.8 | 119       |
| 2336 | EST analysis and identification of gonad-related genes from the normalized cDNA library of large yellow croaker, <i>Larimichthys crocea</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 89-97.   | 0.4 | 10        |
| 2337 | Identification of immune-relevant genes by expressed sequence tag analysis of head kidney from grass carp ( <i>Ctenopharyngodon idella</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 116-123.   | 0.4 | 11        |
| 2338 | The transcriptome of the early life history stages of the California Sea Hare <i>Aplysia californica</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 165-170.  | 0.4 | 28        |
| 2339 | The complete mitochondrial genome of the mantid shrimp <i>Oratosquilla oratoria</i> (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 ff<br>Stomatopoda. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 190-198.  | 0.4 | 12        |
| 2340 | Analysis and functional annotation of expressed sequence tags from in vitro cell lines of elasmobranchs: Spiny dogfish shark ( <i>Squalus acanthias</i> ) and little skate ( <i>Leucoraja erinacea</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 199-206. | 0.4 | 11        |
| 2341 | Complete mtDNA of <i>Meretrix lusoria</i> (Bivalvia: Veneridae) reveals the presence of an <i>atp8</i> gene, length variation and heteroplasmy in the control region. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 256-264.                                     | 0.4 | 18        |
| 2342 | A MaSp2-like gene found in the Amazon mygalomorph spider <i>Avicularia juruensis</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2010, 155, 419-426.   | 0.7 | 18        |
| 2343 | Transporters involved in glucose and water absorption in the <i>Dysdercus peruvianus</i> (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 ff<br><i>Molecular Biology</i> , 2010, 157, 1-9.  | 0.7 | 25        |



| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 2344 | The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. <i>Cell</i> , 2010, 140, 631-642.   | 13.5 | 399       |
| 2345 | Identification and expression analysis of genes associated with the early berry development in the seedless grapevine ( <i>Vitis vinifera</i> L.) cultivar Sultanine. <i>Plant Science</i> , 2010, 179, 510-519.   | 1.7  | 15        |
| 2346 | Assembly algorithms for next-generation sequencing data. <i>Genomics</i> , 2010, 95, 315-327.  | 1.3  | 957       |
| 2347 | Allele-specific PCR can improve the efficiency of experimental resolution of heterozygotes in resequencing studies. <i>Molecular Ecology Resources</i> , 2010, 10, 647-658.  | 2.2  | 4         |
| 2348 | Effort required to finish shotgun-generated genome sequences differs significantly among vertebrates. <i>BMC Genomics</i> , 2010, 11, 21.  | 1.2  | 10        |
| 2349 | SNP discovery by amplicon sequencing and multiplex SNP genotyping in the allopolyploid species <i>Brassica napus</i> This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 948-956. | 0.9  | 53        |
| 2350 | Gene expression analysis of <i>Paracoccidioides brasiliensis</i> transition from conidium to yeast cell. <i>Medical Mycology</i> , 2010, 48, 147-154.  | 0.3  | 19        |
| 2351 | Genomics " Bacterial Genome Sequencing and Annotation. ", 2010, , 4265-4280.   |      | 0         |
| 2352 | Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , 2010, 11, R94.   | 13.9 | 66        |
| 2353 | Genomic characterization of the <i>Yersinia</i> genus. <i>Genome Biology</i> , 2010, 11, R1.   | 13.9 | 103       |
| 2354 | Assembly of 500,000 inter-specific catfish expressed sequence tags and large scale gene-associated marker development for whole genome association studies. <i>Genome Biology</i> , 2010, 11, R8.  | 13.9 | 83        |
| 2355 | Complete genome sequence and comparative analysis of <i>Shewanella violacea</i> , a psychrophilic and piezophilic bacterium from deep sea floor sediments. <i>Molecular BioSystems</i> , 2010, 6, 1216.  | 2.9  | 42        |
| 2356 | Identification of Genes Potentially Involved in Pearl Formation by Expressed Sequence Tag Analysis of Mantle from Freshwater Pearl Mussel ( <i>Hyriopsis cumingii</i> Lea). <i>Journal of Shellfish Research</i> , 2010, 29, 527-534.  | 0.3  | 8         |
| 2357 | In search of true reads: A classification approach to next generation sequencing data selection. , 2010, , ,   |      | 0         |
| 2358 | Genomic Structure of an Economically Important Cyanobacterium, <i>Arthrospira (Spirulina) platensis</i> NIES-39. <i>DNA Research</i> , 2010, 17, 85-103.   | 1.5  | 107       |
| 2359 | Abundance and Diversity of Archaeal Ammonia Oxidizers in a Coastal Groundwater System. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7938-7948.  | 1.4  | 37        |
| 2360 | Population genetic inference from genomic sequence variation. <i>Genome Research</i> , 2010, 20, 291-300.  | 2.4  | 200       |
| 2361 | DNA Methylation Is Not Involved in Preovulatory Down-Regulation of CYP11A1, HSD3B1, and CYP19A1 in Bovine Follicles but May Have a Role in Permanent Silencing of CYP19A1 in Large Granulosa Lutein Cells. <i>Biology of Reproduction</i> , 2010, 82, 289-298.   | 1.2  | 49        |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 2362 | Comparative genomic analysis of the false killer whale ( <i>Pseudorca crassidens</i> ) <i>LMBR1</i> locus. <i>Genome</i> , 2010, 53, 658-666.   | 0.9  | 1         |
| 2363 | Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. , 2011, , .   |      | 0         |
| 2364 | naiveBayesCall: An Efficient Model-Based Base-Calling Algorithm for High-Throughput Sequencing. <i>Journal of Computational Biology</i> , 2011, 18, 365-377.  | 0.8  | 18        |
| 2365 | Analysis of CYP3A4 genetic polymorphisms in Han Chinese. <i>Journal of Human Genetics</i> , 2011, 56, 415-422.  | 1.1  | 36        |
| 2366 | Comparative analysis of algorithms for next-generation sequencing read alignment. <i>Bioinformatics</i> , 2011, 27, 2790-2796.  | 1.8  | 195       |
| 2367 | Inference of subgenomic origin of BACs in an interspecific hybrid sugarcane cultivar by overlapping oligonucleotide hybridizations. <i>Genome</i> , 2011, 54, 727-737.                              | 0.9  | 7         |
| 2368 | Competition between ADAR and RNAi pathways for an extensive class of RNA targets. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1094-1101.   | 3.6  | 73        |
| 2369 | The Awesome Power of Yeast Evolutionary Genetics: New Genome Sequences and Strain Resources for the <i>Saccharomyces sensu stricto</i> Genus. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 11-25. | 0.8  | 348       |
| 2370 | Bacterial Community Reconstruction Using Compressed Sensing. <i>Journal of Computational Biology</i> , 2011, 18, 1723-1741.   | 0.8  | 26        |
| 2371 | Complete Genome of the Cellulolytic Ruminal Bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , 2011, 193, 5574-5575.   | 1.0  | 87        |
| 2372 | The Genetic Structure of Domestic Rabbits. <i>Molecular Biology and Evolution</i> , 2011, 28, 1801-1816.  | 3.5  | 101       |
| 2373 | HiTRACE: high-throughput robust analysis for capillary electrophoresis. <i>Bioinformatics</i> , 2011, 27, 1798-1805.  | 1.8  | 86        |
| 2375 | GeneScreen: a program for high-throughput mutation detection in DNA sequence electropherograms. <i>Journal of Medical Genetics</i> , 2011, 48, 123-130.   | 1.5  | 20        |
| 2376 | Construction of random sheared fosmid library from Chinese cabbage and its use for <i>Brassica rapa</i> genome sequencing project. <i>Journal of Genetics and Genomics</i> , 2011, 38, 47-53.       | 1.7  | 6         |
| 2377 | <i>Neonothopanus gardneri</i> : a new combination for a bioluminescent agaric from Brazil. <i>Mycologia</i> , 2011, 103, 1433-1440.   | 0.8  | 19        |
| 2378 | An integrated semiconductor device enabling non-optical genome sequencing. <i>Nature</i> , 2011, 475, 348-352.  | 13.7 | 1,891     |
| 2380 | Newly developed primers for complete <i>ycf1</i> amplification in <i>Pinus</i> (Pinaceae) chloroplasts with possible family-wide utility. <i>American Journal of Botany</i> , 2011, 98, e185-8.     | 0.8  | 10        |
| 2382 | Systematics and Taxonomy of Great Striped-Faced Bats of the Genus <i>Vampyroides</i> Thomas, 1900 (Chiroptera: Phyllostomidae). <i>American Museum Novitates</i> , 2011, 3710, 1-35.                | 0.2  | 20        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2384 | Crawling through time: Transition of snails to slugs dating back to the Paleozoic, based on mitochondrial phylogenomics. <i>Marine Genomics</i> , 2011, 4, 51-59.   | 0.4 | 52        |
| 2385 | A transcriptomic scan for positively selected genes in two closely related marine fishes: <i>Sebastes caurinus</i> and <i>S. rastrelliger</i> . <i>Marine Genomics</i> , 2011, 4, 93-98.  | 0.4 | 11        |
| 2386 | Complete mitochondrial genome of <i>Tubulipora flabellaris</i> (Bryozoa: Stenolaemata): The first representative from the class Stenolaemata with unique gene order. <i>Marine Genomics</i> , 2011, 4, 159-165.                                   | 0.4 | 8         |
| 2387 | Mitogenome of the small abalone <i>Haliotis diversicolor</i> Reeve and phylogenetic analysis within Gastropoda. <i>Marine Genomics</i> , 2011, 4, 253-262.  | 0.4 | 19        |
| 2388 | Complete mtDNA of the <i>Meretrix lamarckii</i> (Bivalvia: Veneridae) and molecular identification of suspected <i>M. lamarckii</i> based on the whole mitochondrial genome. <i>Marine Genomics</i> , 2011, 4, 263-271.                           | 0.4 | 19        |
| 2389 | “First Generation” Automated DNA Sequencing Technology. <i>Current Protocols in Molecular Biology</i> , 2011, 96, Unit7.2.  | 2.9 | 29        |
| 2390 | Genome wide SNP discovery, analysis and evaluation in mallard ( <i>Anas platyrhynchos</i> ). <i>BMC Genomics</i> , 2011, 12, 150.   | 1.2 | 63        |
| 2391 | The complexity of <i>Rhipicephalus (Boophilus) microplus</i> genome characterised through detailed analysis of two BAC clones. <i>BMC Research Notes</i> , 2011, 4, 254.  | 0.6 | 6         |
| 2392 | Benchmarking Short Sequence Mapping Tools. , 2011, , .  |     | 5         |
| 2393 | Analysis of a Clonal Lineage of HIV-1 Envelope V2/V3 Conformational Epitope-Specific Broadly Neutralizing Antibodies and Their Inferred Unmutated Common Ancestors. <i>Journal of Virology</i> , 2011, 85, 9998-10009.                            | 1.5 | 393       |
| 2394 | Initial antibodies binding to HIV-1 gp41 in acutely infected subjects are polyreactive and highly mutated. <i>Journal of Experimental Medicine</i> , 2011, 208, 2237-2249.  | 4.2 | 198       |
| 2395 | The <i>Drosophila</i> Gene Disruption Project: Progress Using Transposons With Distinctive Site Specificities. <i>Genetics</i> , 2011, 188, 731-743.  | 1.2 | 330       |
| 2396 | A Bioinformatics Pipeline for Sequence-Based Analyses of Fungal Biodiversity. <i>Methods in Molecular Biology</i> , 2011, 722, 141-155.   | 0.4 | 22        |
| 2397 | High-Throughput Sequencing. , 2011, , 461-478.  |     | 8         |
| 2398 | Differences in bacterial community composition in Baltic Sea sediment in response to fish farming. <i>Aquaculture</i> , 2011, 313, 15-23.   | 1.7 | 51        |
| 2399 | Wild captured crab, <i>Chasmagnathus granulata</i> (Dana, 1851), a new host for white spot syndrome virus (WSSV). <i>Aquaculture</i> , 2011, 318, 20-24.  | 1.7 | 16        |
| 2400 | Identification of genes involved in immune response of Atlantic salmon ( <i>Salmo salar</i> ) to IPN virus infection, using expressed sequence tag (EST) analysis. <i>Aquaculture</i> , 2011, 318, 54-60.   | 1.7 | 32        |
| 2401 | The complete mitochondrial genome sequence of <i>Whitmania pigra</i> (Annelida, Hirudinea): The first representative from the class Hirudinea. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 133-138. | 0.4 | 12        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2402 | EST analysis on the gonad development related organs and microarray screen for differentially expressed genes in mature ovary and testis of <i>Scylla paramamosain</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 150-157. | 0.4 | 15        |
| 2403 | Multiple isoforms of immune-related genes from hemocytes and eyestalk cDNA libraries of swimming crab <i>Portunus trituberculatus</i> . <i>Fish and Shellfish Immunology</i> , 2011, 31, 29-42.   | 1.6 | 35        |
| 2404 | Over-expression, purification and immune responses to <i>Aeromonas hydrophila</i> AL09-73 flagellar proteins. <i>Fish and Shellfish Immunology</i> , 2011, 31, 1278-1283.   | 1.6 | 18        |
| 2405 | The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.   | 6.0 | 794       |
| 2406 | Improved molecular methods to characterise <i>Serpula lacrymans</i> and other Basidiomycetes involved in wood decay. <i>Journal of Microbiological Methods</i> , 2011, 84, 208-215.   | 0.7 | 16        |
| 2407 | Rapid hybrid de novo assembly of a microbial genome using only short reads: <i>Corynebacterium pseudotuberculosis</i> I19 as a case study. <i>Journal of Microbiological Methods</i> , 2011, 86, 218-223.   | 0.7 | 40        |
| 2408 | Identification and tissue distribution of odorant binding protein genes in the lucerne plant bug <i>Adelphocoris lineolatus</i> (Goeze). <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 254-263.  | 1.2 | 125       |
| 2409 | Rapid divergence of repetitive DNAs in <i>Brassica</i> relatives. <i>Genomics</i> , 2011, 97, 173-185.  | 1.3 | 46        |
| 2410 | Genomic analysis of bacteriophage $\phi$ AB1, a $\phi$ KMV-like virus infecting multidrug-resistant <i>Acinetobacter baumannii</i> . <i>Genomics</i> , 2011, 97, 249-255.   | 1.3 | 27        |
| 2411 | Directed sequencing and annotation of three <i>Dicentrarchus labrax</i> L. chromosomes by applying Sanger- and pyrosequencing technologies on pooled DNA of comparatively mapped BAC clones. <i>Genomics</i> , 2011, 98, 202-212.   | 1.3 | 15        |
| 2412 | EST profiling of resistant and susceptible <i>Hevea</i> infected by <i>Microcyclus ulei</i> . <i>Physiological and Molecular Plant Pathology</i> , 2011, 76, 126-136.   | 1.3 | 22        |
| 2413 | The complete mitochondrial genome sequence of <i>Euphausia pacifica</i> (Malacostraca: Tj ETQq1 1 0.784314 r9BT /Overlock 10 Tj   | 0.9 | 20        |
| 2414 | Single Nucleotide Polymorphism (SNP) Panels for Rapid Positional Cloning in Zebrafish. <i>Methods in Cell Biology</i> , 2011, 104, 219-235.   | 0.5 | 6         |
| 2415 | Transcriptome sequencing and high-resolution melt analysis advance single nucleotide polymorphism discovery in duplicated salmonids. <i>Molecular Ecology Resources</i> , 2011, 11, 335-348.  | 2.2 | 57        |
| 2416 | Identification of single nucleotide polymorphisms in candidate genes for growth and reproduction in a nonmodel organism; the Atlantic cod, <i>Gadus morhua</i> . <i>Molecular Ecology Resources</i> , 2011, 11, 71-80.  | 2.2 | 42        |
| 2417 | SNP discovery in black cottonwood ( <i>Populus trichocarpa</i> ) by population transcriptome resequencing. <i>Molecular Ecology Resources</i> , 2011, 11, 81-92.  | 2.2 | 104       |
| 2418 | De novo transcriptome characterization and development of genomic tools for <i>Scabiosa columbaria</i> L. using next-generation sequencing techniques. <i>Molecular Ecology Resources</i> , 2011, 11, 662-674.  | 2.2 | 44        |
| 2419 | Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. <i>Genome Biology</i> , 2011, 12, R59.  | 3.8 | 93        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2420 | Evidence for Reductive Genome Evolution and Lateral Acquisition of Virulence Functions in Two <i>Corynebacterium pseudotuberculosis</i> Strains. <i>PLoS ONE</i> , 2011, 6, e18551.  | 1.1 | 75        |
| 2421 | Bacterial Communities of Diverse <i>Drosophila</i> Species: Ecological Context of a Host-Microbe Model System. <i>PLoS Genetics</i> , 2011, 7, e1002272.   | 1.5 | 650       |
| 2422 | Developmental Transcriptomic Features of the Carcinogenic Liver Fluke, <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1208.  | 1.3 | 72        |
| 2423 | Chemical Constituents of the New Endophytic Fungus <i>Mycosphaerella</i> sp. nov. and Their Anti-parasitic Activity. <i>Natural Product Communications</i> , 2011, 6, 1934578X1100600.   | 0.2 | 26        |
| 2424 | Phylogenetic relationships within <i>Silene</i> ( <i>Caryophyllaceae</i> ) section <i>Physolychnis</i> . <i>Taxon</i> , 2011, 60, 953-968.   | 0.4 | 36        |
| 2425 | Association between Knops blood group polymorphisms and susceptibility to malaria in an endemic area of the Brazilian Amazon. <i>Genetics and Molecular Biology</i> , 2011, 34, 539-545.   | 0.6 | 12        |
| 2426 | Survey of the genetic information carried in the genome of <i>Eucalyptus camaldulensis</i> . <i>Plant Biotechnology</i> , 2011, 28, 471-480.   | 0.5 | 33        |
| 2427 | Limited vegetative compatibility as a cause of somatic recombination in <i>Trichoderma pseudokoningii</i> . <i>Brazilian Journal of Microbiology</i> , 2011, 42, 1625-1637.  | 0.8 | 3         |
| 2429 | Comparison of bacterial communities in the Solimões and Negro River tributaries of the Amazon River based on small subunit rRNA gene sequences. <i>Genetics and Molecular Research</i> , 2011, 10, 3783-3793.  | 0.3 | 8         |
| 2430 | A rapid and cost-effective method for sequencing pooled cDNA clones by using a combination of transposon insertion and Gateway technology. <i>BioTechniques</i> , 2011, 51, 195-197.   | 0.8 | 3         |
| 2431 | Genetic and biological characterization of a densovirus isolate that affects dengue virus infection. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2011, 106, 285-292.   | 0.8 | 23        |
| 2432 | Phylogeographic studies of Brazilian <i>œcampo-rupestre</i> species: <i>Wunderlichia mirabilis</i> Riedel ex Baker ( <i>Asteraceae</i> ). <i>Biotemas</i> , 2011, 22, 17.  | 0.2 | 8         |
| 2433 | Soybean Rust: Five Years of Research. , 0, , .   |     | 0         |
| 2434 | The Information Systems for DNA Barcode Data. , 2011, , .  |     | 1         |
| 2435 | Phylogenetic relationships within <i>Chamaecrista</i> sect. <i>Xerocalyx</i> ( <i>Leguminosae</i> , <i>Caesalpinioideae</i> ) inferred from the cpDNA <i>trnE-trnT</i> intergenic spacer and nrDNA ITS sequences. <i>Genetics and Molecular Biology</i> , 2011, 34, 244-251. | 0.6 | 13        |
| 2436 | Functional characterization of three cDNA libraries from the diploid wheat <i>Triticum monoccocum</i> (AmAm) with different growth habits. <i>Cereal Research Communications</i> , 2011, 39, 475-486.  | 0.8 | 0         |
| 2437 | The Barley Microarray. A Community Vision and Application to Abiotic Stress. <i>Czech Journal of Genetics and Plant Breeding</i> , 2005, 41, 144-152.  | 0.4 | 7         |
| 2438 | Structured Multiple Endosymbiosis of Bacteria and Archaea in a Ciliate from Marine Sulfidic Sediments: A Survival Mechanism in Low Oxygen, Sulfidic Sediments?. <i>Frontiers in Microbiology</i> , 2011, 2, 55.  | 1.5 | 53        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2439 | Population structure and demographic inferences concerning the endangered onychophoran species <i>Epiperipatus acacioi</i> (Onychophora: Peripatidae). <i>Genetics and Molecular Research</i> , 2011, 10, 2775-2785. | 0.3 | 4         |
| 2440 | Removal of PCR Error Products and Unincorporated Primers by Metal-Chelate Affinity Chromatography. <i>PLoS ONE</i> , 2011, 6, e14512.  | 1.1 | 2         |
| 2441 | Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont <i>Piriformospora indica</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002290.                                   | 2.1 | 361       |
| 2442 | Genomic Signatures of Strain Selection and Enhancement in <i>Bacillus atrophaeus</i> var. <i>globigii</i> , a Historical Biowarfare Simulant. <i>PLoS ONE</i> , 2011, 6, e17836.                                     | 1.1 | 41        |
| 2443 | Comprehensive Analysis of MGMT Promoter Methylation: Correlation with MGMT Expression and Clinical Response in GBM. <i>PLoS ONE</i> , 2011, 6, e16146.   | 1.1 | 89        |
| 2444 | Error and Error Mitigation in Low-Coverage Genome Assemblies. <i>PLoS ONE</i> , 2011, 6, e17034.   | 1.1 | 33        |
| 2445 | Transcriptome Analysis of the Desert Locust Central Nervous System: Production and Annotation of a <i>Schistocerca gregaria</i> EST Database. <i>PLoS ONE</i> , 2011, 6, e17274.                                     | 1.1 | 90        |
| 2446 | Classification of Plant Associated Bacteria Using RIF, a Computationally Derived DNA Marker. <i>PLoS ONE</i> , 2011, 6, e18496.  | 1.1 | 31        |
| 2447 | The Fat Body Transcriptomes of the Yellow Fever Mosquito <i>Aedes aegypti</i> , Pre- and Post- Blood Meal. <i>PLoS ONE</i> , 2011, 6, e22573.  | 1.1 | 77        |
| 2448 | Generation, Annotation and Analysis of First Large-Scale Expressed Sequence Tags from Developing Fiber of <i>Gossypium barbadense</i> L. <i>PLoS ONE</i> , 2011, 6, e22758.  | 1.1 | 25        |
| 2449 | Meraculous: De Novo Genome Assembly with Short Paired-End Reads. <i>PLoS ONE</i> , 2011, 6, e23501.  | 1.1 | 191       |
| 2450 | Comparative Genomics Study of Multi-Drug-Resistance Mechanisms in the Antibiotic-Resistant <i>Streptococcus suis</i> R61 Strain. <i>PLoS ONE</i> , 2011, 6, e24988.  | 1.1 | 36        |
| 2451 | H3N2 Influenza Infection Elicits More Cross-Reactive and Less Clonally Expanded Anti-Hemagglutinin Antibodies Than Influenza Vaccination. <i>PLoS ONE</i> , 2011, 6, e25797.   | 1.1 | 158       |
| 2452 | The Entomopathogenic Bacterial Endosymbionts <i>Xenorhabdus</i> and <i>Photorhabdus</i> : Convergent Lifestyles from Divergent Genomes. <i>PLoS ONE</i> , 2011, 6, e27909.   | 1.1 | 161       |
| 2453 | Generation of ESTs for Flowering Gene Discovery and SSR Marker Development in Upland Cotton. <i>PLoS ONE</i> , 2011, 6, e28676.  | 1.1 | 17        |
| 2454 | Differences in Genotype and Virulence among Four Multidrug-Resistant <i>Streptococcus pneumoniae</i> Isolates Belonging to the PMEN1 Clone. <i>PLoS ONE</i> , 2011, 6, e28850.                                       | 1.1 | 23        |
| 2455 | The Reproductive Biology of Siscowet and Lean Lake Trout in Southern Lake Superior. <i>Transactions of the American Fisheries Society</i> , 2011, 140, 1472-1491.  | 0.6 | 30        |
| 2456 | Complete genome sequence of <i>Staphylothermus hellenicus</i> P8T. <i>Standards in Genomic Sciences</i> , 2011, 5, 12-20.  | 1.5 | 7         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2457 | Complete genome sequence of <i>Enterobacter lignolyticus</i> SCF1. Standards in Genomic Sciences, 2011, 5, 69-85.  | 1.5 | 76        |
| 2458 | Complete genome sequence of <i>Parvibaculum lavamentivorans</i> type strain (DS-1T). Standards in Genomic Sciences, 2011, 5, 298-310.  | 1.5 | 37        |
| 2459 | Complete genome sequence of <i>Allochromatium vinosum</i> DSM 180T. Standards in Genomic Sciences, 2011, 5, 311-330.   | 1.5 | 65        |
| 2460 | Complete genome sequence of <i>Desulfurispirillum indicum</i> strain S5T. Standards in Genomic Sciences, 2011, 5, 371-378.   | 1.5 | 11        |
| 2461 | Differences in phosphorus demand among detritivorous chironomid larvae reflect intraspecific adaptations to differences in food resource stoichiometry across lowland tropical streams. Limnology and Oceanography, 2011, 56, 268-278. | 1.6 | 19        |
| 2462 | Genetic Mapping in Conifers. , 2011, , 224-266.  |     | 10        |
| 2464 | Marine subsurface eukaryotes: the fungal majority. Environmental Microbiology, 2011, 13, 172-183.  | 1.8 | 200       |
| 2465 | Energy metabolism and multiple respiratory pathways revealed by genome sequencing of <i>Desulfurispirillum indicum</i> strain S5. Environmental Microbiology, 2011, 13, 1611-1621.   | 1.8 | 24        |
| 2466 | Molecular phylogeny of <i>Potamogetrygonocotyle</i> (Monogenea, Monocotylidae) challenges the validity of some of its species. Zoologica Scripta, 2011, 40, 638-658.   | 0.7 | 12        |
| 2467 | Microsatellite Markers Reveal Genetic Variation within <i>Sclerotinia sclerotiorum</i> Populations in Irrigated Dry Bean Crops in Brazil. Journal of Phytopathology, 2011, 159, 94-99.   | 0.5 | 28        |
| 2468 | Multiresistance, beta-lactamase-encoding genes and bacterial diversity in hospital wastewater in Rio de Janeiro, Brazil. Journal of Applied Microbiology, 2011, 111, 572-581.  | 1.4 | 135       |
| 2469 | Large-scale detection of rare variants via pooled multiplexed next-generation sequencing: towards next-generation Ecotilling. Plant Journal, 2011, 67, 736-745.  | 2.8 | 81        |
| 2470 | Development of genetic markers in abalone through construction of a SNP database. Animal Genetics, 2011, 42, 309-315.  | 0.6 | 7         |
| 2471 | Narrowing down the apricot <i>Plum pox virus</i> resistance locus and comparative analysis with the peach genome syntenic region. Molecular Plant Pathology, 2011, 12, 535-547.  | 2.0 | 28        |
| 2472 | Higher differentiation among subspecies of the house mouse ( <i>Mus musculus</i> ) in genomic regions with low recombination. Molecular Ecology, 2011, 20, 4722-4736.  | 2.0 | 124       |
| 2473 | Characterization of a <i>Chromobacterium haemolyticum</i> population from a natural tropical lake. Letters in Applied Microbiology, 2011, 52, 642-650.   | 1.0 | 23        |
| 2474 | Bioinformatic analysis and annotation of expressed sequence tags (ESTs) generated from <i>Anopheles sinensis</i> mosquitoes challenged with apoptosis-inducing chemical, actinomycin D. Entomological Research, 2011, 41, 53-59.       | 0.6 | 2         |
| 2475 | Microbial consortia of gorgonian corals from the Aleutian islands. FEMS Microbiology Ecology, 2011, 76, 109-120.   | 1.3 | 68        |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 2476 | Characterization of culturable bacteria isolated from the cold-water coral <i>Lophelia pertusa</i> . <i>FEMS Microbiology Ecology</i> , 2011, 77, 333-346.  | 1.3  | 37        |
| 2477 | A framework for variation discovery and genotyping using next-generation DNA sequencing data. <i>Nature Genetics</i> , 2011, 43, 491-498.   | 9.4  | 10,018    |
| 2478 | Genotype and SNP calling from next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2011, 12, 443-451.  | 7.7  | 1,238     |
| 2479 | Phylogeography of the endangered rosewood <i>Dalbergia nigra</i> (Fabaceae): insights into the evolutionary history and conservation of the Brazilian Atlantic Forest. <i>Heredity</i> , 2011, 106, 46-57.                            | 1.2  | 81        |
| 2480 | Identity of epibiotic bacteria on symbiontid euglenozoans in O <sub>2</sub> -depleted marine sediments: evidence for symbiont and host co-evolution. <i>ISME Journal</i> , 2011, 5, 231-243.  | 4.4  | 44        |
| 2481 | Protistan microbial observatory in the Cariaco Basin, Caribbean. I. Pyrosequencing vs Sanger insights into species richness. <i>ISME Journal</i> , 2011, 5, 1344-1356.  | 4.4  | 211       |
| 2482 | Protistan microbial observatory in the Cariaco Basin, Caribbean. II. Habitat specialization. <i>ISME Journal</i> , 2011, 5, 1357-1373.  | 4.4  | 79        |
| 2483 | Experimental niche evolution alters the strength of the diversity-productivity relationship. <i>Nature</i> , 2011, 469, 89-92.  | 13.7 | 200       |
| 2484 | CREBBP mutations in relapsed acute lymphoblastic leukaemia. <i>Nature</i> , 2011, 471, 235-239.   | 13.7 | 542       |
| 2485 | The sequence of the pYV virulence plasmid from <i>Yersinia enterocolitica</i> strain WA-314 biogroup 1B serotype O:8. <i>Plasmid</i> , 2011, 65, 20-24.   | 0.4  | 3         |
| 2486 | Presence of the oral bacterium <i>Capnocytophaga canimorsus</i> in the tooth plaque of canines. <i>Veterinary Microbiology</i> , 2011, 149, 437-445.  | 0.8  | 16        |
| 2487 | Antioxidant defense is one of the mechanisms by which mosquito cells survive dengue 2 viral infection. <i>Virology</i> , 2011, 410, 410-417.  | 1.1  | 59        |
| 2488 | De novo sequence assembly and characterization of the floral transcriptome in cross- and self-fertilizing plants. <i>BMC Genomics</i> , 2011, 12, 298.  | 1.2  | 86        |
| 2489 | Sequencing of bovine herpesvirus 4 v.test strain reveals important genome features. <i>Virology Journal</i> , 2011, 8, 406.   | 1.4  | 16        |
| 2490 | Assessment of replicate bias in 454 pyrosequencing and a multi-purpose read-filtering tool. <i>BMC Research Notes</i> , 2011, 4, 149.   | 0.6  | 43        |
| 2491 | Phred-Phrap package to analyses tools: a pipeline to facilitate population genetics re-sequencing studies. <i>Investigative Genetics</i> , 2011, 2, 3.  | 3.3  | 42        |
| 2492 | Genomic organization and genomic structural rearrangements of <i>Sphingobium japonicum</i> UT26, an archetypal <sup>13</sup> C-hexachlorocyclohexane-degrading bacterium. <i>Enzyme and Microbial Technology</i> , 2011, 49, 499-508. | 1.6  | 47        |
| 2493 | Bacteria and Archaea community structure in the rumen microbiome of goats ( <i>Capra hircus</i> ) from the semiarid region of Brazil. <i>Anaerobe</i> , 2011, 17, 118-124.  | 1.0  | 81        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2494 | Involvement of <i>Clostridium gasigenes</i> and <i>C. algidicarnis</i> in 'blown pack' spoilage of Brazilian vacuum-packed beef. <i>International Journal of Food Microbiology</i> , 2011, 148, 156-63.           | 2.1 | 33        |
| 2495 | Microbial community response to addition of polylactate compounds to stimulate hexavalent chromium reduction in groundwater. <i>Chemosphere</i> , 2011, 85, 660-665.  | 4.2 | 50        |
| 2496 | How the Worm Got its Pharynx: Phylogeny, Classification and Bayesian Assessment of Character Evolution in Acoela. <i>Systematic Biology</i> , 2011, 60, 845-871.  | 2.7 | 66        |
| 2497 | Complete Genome Sequence and Immunoproteomic Analyses of the Bacterial Fish Pathogen <i>Streptococcus parauberis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3356-3366.                                     | 1.0 | 44        |
| 2498 | Comparative studies of <i>de novo</i> assembly tools for next-generation sequencing technologies. <i>Bioinformatics</i> , 2011, 27, 2031-2037.  | 1.8 | 109       |
| 2499 | Comparative analysis of expressed sequence tags (ESTs) between normal group and softness syndrome group in <i>Halocynthia roretzi</i> . <i>Molecular and Cellular Toxicology</i> , 2011, 7, 357-365.              | 0.8 | 2         |
| 2501 | In Silico Tools for Gene Discovery. <i>Methods in Molecular Biology</i> , 2011, , .   | 0.4 | 5         |
| 2502 | Effects of short-term starvation on ghrelin, GH-IGF system, and IGF-binding proteins in Atlantic salmon. <i>Fish Physiology and Biochemistry</i> , 2011, 37, 217-232.   | 0.9 | 89        |
| 2503 | Molecular evolution of the membrane associated progesterone receptor in the <i>Brachionus plicatilis</i> (Rotifera, Monogononta) species complex. <i>Hydrobiologia</i> , 2011, 662, 99-106.                       | 1.0 | 9         |
| 2504 | EST Analysis Predicts Putatively Causative Genes Underlying the Pharmaceutical Application of <i>Glycyrrhiza uralensis</i> Fisch. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 814-824.                    | 1.0 | 6         |
| 2505 | Development of single nucleotide polymorphism markers in <i>Theobroma cacao</i> and comparison to simple sequence repeat markers for genotyping of Cameroon clones. <i>Molecular Breeding</i> , 2011, 27, 93-106. | 1.0 | 33        |
| 2506 | Complete mitochondrial genome of the Chinese spiny lobster <i>Panulirus stimpsoni</i> (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 10) <i>2011, 38, 403-410.</i>  | 1.0 | 37        |
| 2507 | Identification of host-defense genes and development of microsatellite markers from ESTs of hard clam <i>Meretrix meretrix</i> . <i>Molecular Biology Reports</i> , 2011, 38, 769-775.                            | 1.0 | 37        |
| 2508 | Species delineation in <i>Pampus</i> (Perciformes) and the phylogenetic status of the Stromateoidei based on mitogenomics. <i>Molecular Biology Reports</i> , 2011, 38, 1103-1114.                                | 1.0 | 13        |
| 2509 | Genes Potentially Relevant in the Parasitic Phase of the Fungal Pathogen <i>Paracoccidioides brasiliensis</i> . <i>Mycopathologia</i> , 2011, 171, 1-9.   | 1.3 | 22        |
| 2510 | Phylogenetic and physiological characterization of organic waste-degrading bacterial communities. <i>World Journal of Microbiology and Biotechnology</i> , 2011, 27, 245-252.                                     | 1.7 | 16        |
| 2511 | Nucleotide diversity and linkage disequilibrium in <i>Populus nigra</i> cinnamyl alcohol dehydrogenase (CAD4) gene. <i>Tree Genetics and Genomes</i> , 2011, 7, 1011-1023.  | 0.6 | 138       |
| 2512 | A potato skin SSH library yields new candidate genes for suberin biosynthesis and periderm formation. <i>Planta</i> , 2011, 233, 933-945.   | 1.6 | 39        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2513 | EST analysis of functional genes associated with cell wall biosynthesis and modification in the secondary xylem of the yellow poplar ( <i>Liriodendron tulipifera</i> ) stem during early stage of tension wood formation. <i>Planta</i> , 2011, 234, 959-977.        | 1.6 | 37        |
| 2514 | Comparative sequence analysis of <i>VRN1</i> alleles of <i>Lolium perenne</i> with the co-linear regions in barley, wheat, and rice. <i>Molecular Genetics and Genomics</i> , 2011, 286, 433-447.   | 1.0 | 25        |
| 2515 | An Integrated Approach to Gene Discovery and Marker Development in Atlantic Cod ( <i>Gadus morhua</i> ). <i>Marine Biotechnology</i> , 2011, 13, 242-255.   | 1.1 | 37        |
| 2516 | Construction and Characterization of the BAC Library for Common Carp <i>Cyprinus Carpio</i> L. And Establishment of Microsynteny with Zebrafish <i>Danio Rerio</i> . <i>Marine Biotechnology</i> , 2011, 13, 706-712.   | 1.1 | 39        |
| 2517 | Major chimpanzee-specific structural changes in sperm development-associated genes. <i>Functional and Integrative Genomics</i> , 2011, 11, 507-517.   | 1.4 | 6         |
| 2518 | Comparative biogeography of <i>Chromobacterium</i> from the neotropics. <i>Antonie Van Leeuwenhoek</i> , 2011, 99, 355-370.   | 0.7 | 11        |
| 2519 | Generation and analysis of expressed sequence tags from a normalized cDNA library of young leaf from Ma bamboo ( <i>Dendrocalamus latiflorus</i> Munro). <i>Plant Cell Reports</i> , 2011, 30, 2045-2057.   | 2.8 | 24        |
| 2520 | Metagenome of microorganisms associated with the toxic Cyanobacteria <i>Microcystis aeruginosa</i> analyzed using the 454 sequencing platform. <i>Chinese Journal of Oceanology and Limnology</i> , 2011, 29, 505-513.  | 0.7 | 43        |
| 2521 | Downy mildew (PI 8 and PI 14 ) and rust (R Adv ) resistance genes reside in close proximity to tandemly duplicated clusters of non-TIR-like NBS-LRR-encoding genes on sunflower chromosomes 1 and 13. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1211-1221. | 1.8 | 60        |
| 2522 | Gene Duplication and Divergence of Long Wavelength-Sensitive Opsin Genes in the Guppy, <i>Poecilia reticulata</i> . <i>Journal of Molecular Evolution</i> , 2011, 72, 240-252.  | 0.8 | 47        |
| 2523 | Haplotypes of the bovine IgG2 heavy gamma chain in tick-resistant and tick-susceptible breeds of cattle. <i>Immunogenetics</i> , 2011, 63, 319-324.   | 1.2 | 10        |
| 2524 | Comparative genome analysis of the major histocompatibility complex (MHC) class I B/C segments in primates elucidated by genomic sequencing in common marmoset ( <i>Callithrix jacchus</i> ). <i>Immunogenetics</i> , 2011, 63, 485-499.                              | 1.2 | 21        |
| 2525 | Construction of Japanese BAC library Yamato-2 (JY2): a set of 330K clone resources of damage-minimized DNA taken from a genetically established Japanese individual. <i>Human Cell</i> , 2011, 24, 135-145.   | 1.2 | 1         |
| 2526 | Gene expression analysis of green tide alga <i>Ulva prolifera</i> (Chlorophyta) in China. <i>Genes and Genomics</i> , 2011, 33, 173-178.  | 0.5 | 9         |
| 2527 | Analysis of BAC-end sequences (BESs) and development of BES-SSR markers for genetic mapping and hybrid purity assessment in pigeonpea ( <i>Cajanus spp.</i> ). <i>BMC Plant Biology</i> , 2011, 11, 56.   | 1.6 | 121       |
| 2528 | Distribution of hepatitis c virus (hcv) genotypes in patients with chronic infection from Rondônia, Brazil. <i>Virology Journal</i> , 2011, 8, 165.   | 1.4 | 9         |
| 2529 | Sequencing of BAC pools by different next generation sequencing platforms and strategies. <i>BMC Research Notes</i> , 2011, 4, 411.   | 0.6 | 13        |
| 2530 | Linkage disequilibrium based genotype calling from low-coverage shotgun sequencing reads. <i>BMC Bioinformatics</i> , 2011, 12, S53.  | 1.2 | 9         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2531 | Molecular evolution of the vertebrate TLR1 gene family - a complex history of gene duplication, gene conversion, positive selection and co-evolution. <i>BMC Evolutionary Biology</i> , 2011, 11, 149.                        | 3.2 | 66        |
| 2532 | The mitochondrial genome of <i>Sinentomon erythranum</i> (Arthropoda: Hexapoda: Protura): an example of highly divergent evolution. <i>BMC Evolutionary Biology</i> , 2011, 11, 246.  | 3.2 | 28        |
| 2533 | Genomic lineages of <i>Rhizobium etli</i> revealed by the extent of nucleotide polymorphisms and low recombination. <i>BMC Evolutionary Biology</i> , 2011, 11, 305.  | 3.2 | 40        |
| 2534 | The Enhancer of split complex arose prior to the diversification of schizophoran flies and is strongly conserved between <i>Drosophila</i> and stalk-eyed flies (Diopsidae). <i>BMC Evolutionary Biology</i> , 2011, 11, 354. | 3.2 | 16        |
| 2535 | Identification of errors introduced during high throughput sequencing of the T cell receptor repertoire. <i>BMC Genomics</i> , 2011, 12, 106.   | 1.2 | 65        |
| 2536 | Comparative analysis of mitochondrial genomes between a wheat K-type cytoplasmic male sterility (CMS) line and its maintainer line. <i>BMC Genomics</i> , 2011, 12, 163.  | 1.2 | 73        |
| 2537 | A first generation integrated map of the rainbow trout genome. <i>BMC Genomics</i> , 2011, 12, 180.   | 1.2 | 51        |
| 2538 | Genomic insight into the common carp ( <i>Cyprinus carpio</i> ) genome by sequencing analysis of BAC-end sequences. <i>BMC Genomics</i> , 2011, 12, 188.  | 1.2 | 56        |
| 2539 | The midgut transcriptome of <i>Phlebotomus (Larrousius) perniciosus</i> , a vector of <i>Leishmania infantum</i> : comparison of sugar fed and blood fed sand flies. <i>BMC Genomics</i> , 2011, 12, 223.                     | 1.2 | 30        |
| 2540 | Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2011, 12, 235.   | 1.2 | 97        |
| 2541 | Fosmid library end sequencing reveals a rarely known genome structure of marine shrimp <i>Penaeus monodon</i> . <i>BMC Genomics</i> , 2011, 12, 242.  | 1.2 | 39        |
| 2542 | Comprehensive assessment of sequence variation within the copy number variable defensin cluster on 8p23 by target enriched in-depth 454 sequencing. <i>BMC Genomics</i> , 2011, 12, 243.                                      | 1.2 | 7         |
| 2543 | Regulation and expression of sexual differentiation factors in embryonic and extragonadal tissues of Atlantic salmon. <i>BMC Genomics</i> , 2011, 12, 31.   | 1.2 | 28        |
| 2544 | Analysis of BAC-end sequences in rainbow trout: Content characterization and assessment of synteny between trout and other fish genomes. <i>BMC Genomics</i> , 2011, 12, 314.   | 1.2 | 23        |
| 2545 | Complete genome sequence of the filamentous anoxygenic phototrophic bacterium <i>Chloroflexus aurantiacus</i> . <i>BMC Genomics</i> , 2011, 12, 334.  | 1.2 | 90        |
| 2546 | Sequencing of a QTL-rich region of the <i>Theobroma cacao</i> genome using pooled BACs and the identification of trait specific candidate genes. <i>BMC Genomics</i> , 2011, 12, 379.   | 1.2 | 20        |
| 2547 | A comparative physical map reveals the pattern of chromosomal evolution between the turkey ( <i>Meleagris gallopavo</i> ) and chicken ( <i>Gallus gallus</i> ) genomes. <i>BMC Genomics</i> , 2011, 12, 447.                  | 1.2 | 24        |
| 2548 | An attenuated strain of <i>Bacillus anthracis</i> (CDC 684) has a large chromosomal inversion and altered growth kinetics. <i>BMC Genomics</i> , 2011, 12, 477.   | 1.2 | 24        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2549 | De novo sequence assembly of <i>Albugo candida</i> reveals a small genome relative to other biotrophic oomycetes. <i>BMC Genomics</i> , 2011, 12, 503.  | 1.2 | 123       |
| 2550 | Conjugating effects of symbionts and environmental factors on gene expression in deep-sea hydrothermal vent mussels. <i>BMC Genomics</i> , 2011, 12, 530.   | 1.2 | 24        |
| 2551 | Sequence of the hyperplastic genome of the naturally competent <i>Thermus scotoductus</i> SA-01. <i>BMC Genomics</i> , 2011, 12, 577.   | 1.2 | 49        |
| 2552 | The maternal and early embryonic transcriptome of the milkweed bug <i>Oncopeltus fasciatus</i> . <i>BMC Genomics</i> , 2011, 12, 61.  | 1.2 | 110       |
| 2553 | Distinctive mitochondrial genome of Calanoid copepod <i>Calanus sinicus</i> with multiple large non-coding regions and reshuffled gene order: Useful molecular markers for phylogenetic and population studies. <i>BMC Genomics</i> , 2011, 12, 73. | 1.2 | 37        |
| 2554 | Comparative analysis of pepper and tomato reveals euchromatin expansion of pepper genome caused by differential accumulation of Ty3/Gypsy-like elements. <i>BMC Genomics</i> , 2011, 12, 85.  | 1.2 | 34        |
| 2555 | Structural variation in the chicken genome identified by paired-end next-generation DNA sequencing of reduced representation libraries. <i>BMC Genomics</i> , 2011, 12, 94.   | 1.2 | 25        |
| 2556 | The conjugative plasmid of a bean-nodulating <i>Sinorhizobium fredii</i> strain is assembled from sequences of two <i>Rhizobium</i> plasmids and the chromosome of a <i>Sinorhizobium</i> strain. <i>BMC Microbiology</i> , 2011, 11, 149.          | 1.3 | 39        |
| 2557 | Rare variants in the <i>CYP27B1</i> gene are associated with multiple sclerosis. <i>Annals of Neurology</i> , 2011, 70, 881-886.  | 2.8 | 204       |
| 2558 | Confounded by sequencing depth in association studies of rare alleles. <i>Genetic Epidemiology</i> , 2011, 35, 261-268.   | 0.6 | 28        |
| 2559 | Characterization of feather-degrading bacteria from Brazilian soils. <i>International Biodeterioration and Biodegradation</i> , 2011, 65, 102-107.  | 1.9 | 27        |
| 2560 | Molecular characterization of the Hepatitis B virus genotypes in Colombia: A Bayesian inference on the genotype F. <i>Infection, Genetics and Evolution</i> , 2011, 11, 103-108.  | 1.0 | 48        |
| 2561 | Dynamics of Hepatitis D (delta) virus genotype 3 in the Amazon region of South America. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1462-1468.   | 1.0 | 38        |
| 2562 | A gustatory receptor involved in host plant recognition for oviposition of a swallowtail butterfly. <i>Nature Communications</i> , 2011, 2, 542.  | 5.8 | 83        |
| 2563 | Characterization of genetic variation and natural selection at the arylamine <i>N</i> -acetyltransferase genes in global human populations. <i>Pharmacogenomics</i> , 2011, 12, 1545-1558.  | 0.6 | 38        |
| 2564 | Exhaustive T-cell repertoire sequencing of human peripheral blood samples reveals signatures of antigen selection and a directly measured repertoire size of at least 1 million clonotypes. <i>Genome Research</i> , 2011, 21, 790-797.             | 2.4 | 312       |
| 2565 | Fourteen-Genome Comparison Identifies DNA Markers for Severe-Disease-Associated Strains of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2011, 49, 2230-2238.  | 1.8 | 43        |
| 2566 | Genetic Structure and Demographic History of New World Screwworm Across Its Current Geographic Range. <i>Journal of Medical Entomology</i> , 2011, 48, 280-290.   | 0.9 | 20        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2567 | Genome Sequence of <i>Streptomyces griseus</i> Strain XylebKG-1, an Ambrosia Beetle-Associated Actinomycete. <i>Journal of Bacteriology</i> , 2011, 193, 2890-2891.   | 1.0 | 35        |
| 2568 | Expressed Sequence Tag Analysis of <i>Physa acuta</i> : A Freshwater Pulmonate in Korea. <i>Journal of Shellfish Research</i> , 2011, 30, 127-132.  | 0.3 | 6         |
| 2569 | High-quality draft assemblies of mammalian genomes from massively parallel sequence data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1513-1518.                              | 3.3 | 1,476     |
| 2570 | Complete Genome Sequence of the Metabolically Versatile Plant Growth-Promoting Endophyte <i>Variovorax paradoxus</i> S110. <i>Journal of Bacteriology</i> , 2011, 193, 1183-1190.   | 1.0 | 156       |
| 2571 | Genetic Diversity of O-Antigen Biosynthesis Regions in <i>Vibrio cholerae</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 2247-2253.  | 1.4 | 34        |
| 2572 | Complete Genome Sequence of <i>Weissella koreensis</i> KACC 15510, Isolated from Kimchi. <i>Journal of Bacteriology</i> , 2011, 193, 5534-5534.   | 1.0 | 18        |
| 2573 | Genome Sequence of the Repetitive-Sequence-Rich <i>Mycoplasma fermentans</i> Strain M64. <i>Journal of Bacteriology</i> , 2011, 193, 4302-4303.   | 1.0 | 9         |
| 2574 | Complete Genome Sequence of the Cellulose-Degrading Bacterium <i>Cellulosilyticum lentocellum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 2357-2358.  | 1.0 | 28        |
| 2575 | Genome Sequence of the Arctic Methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , 2011, 193, 6418-6419.  | 1.0 | 78        |
| 2576 | Efficient storage of high throughput DNA sequencing data using reference-based compression. <i>Genome Research</i> , 2011, 21, 734-740.   | 2.4 | 329       |
| 2577 | Genome Sequence of <i>Thermotoga</i> sp. Strain RQ2, a Hyperthermophilic Bacterium Isolated from a Geothermally Heated Region of the Seafloor near Ribeira Quente, the Azores. <i>Journal of Bacteriology</i> , 2011, 193, 5869-5870. | 1.0 | 16        |
| 2578 | GAMES identifies and annotates mutations in next-generation sequencing projects. <i>Bioinformatics</i> , 2011, 27, 9-13.  | 1.8 | 28        |
| 2579 | Complete Genome Sequence of the Pathogenic Bacterium <i>Riemerella anatipestifer</i> Strain RA-GD. <i>Journal of Bacteriology</i> , 2011, 193, 2896-2897.   | 1.0 | 28        |
| 2580 | Draft Genome Sequence of <i>Penicillium marneffei</i> Strain PM1. <i>Eukaryotic Cell</i> , 2011, 10, 1740-1741.   | 3.4 | 42        |
| 2581 | Microbial Diversity of a Brazilian Coastal Region Influenced by an Upwelling System and Anthropogenic Activity. <i>PLoS ONE</i> , 2011, 6, e16553.  | 1.1 | 47        |
| 2582 | Detection of Minority Resistance during Early HIV-1 Infection: Natural Variation and Spurious Detection rather than Transmission and Evolution of Multiple Viral Variants. <i>Journal of Virology</i> , 2011, 85, 8359-8367.          | 1.5 | 86        |
| 2583 | An Extended Domain of <i>Kcnq1ot1</i> Silencing Revealed by an Imprinted Fluorescent Reporter. <i>Molecular and Cellular Biology</i> , 2011, 31, 2827-2837.   | 1.1 | 12        |
| 2584 | Multilocus sequence analysis reveals the genetic diversity of European fruit tree phytoplasmas and supports the existence of inter-species recombination. <i>Microbiology (United Kingdom)</i> , 2011, 157, 438-450.                  | 0.7 | 62        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2585 | Phylogeny of Pilobolaceae. <i>Mycologia</i> , 2011, 103, 36-44.   | 0.8 | 8         |
| 2586 | Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> 119, a Strain Isolated from a Cow in Israel with Bovine Mastitis. <i>Journal of Bacteriology</i> , 2011, 193, 323-324.  | 1.0 | 45        |
| 2587 | Complete Genome Sequence of the Thermophilic Bacterium <i>Exiguobacterium</i> sp. AT1b. <i>Journal of Bacteriology</i> , 2011, 193, 2880-2881.  | 1.0 | 47        |
| 2588 | Sequence Analysis of the Segmental Duplication Responsible for Paris Sex-Ratio Drive in <i>Drosophila simulans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 401-410.  | 0.8 | 29        |
| 2589 | Complete Genome Sequence of the Polycyclic Aromatic Hydrocarbon-Degrading Bacterium <i>Alteromonas</i> sp. Strain SN2. <i>Journal of Bacteriology</i> , 2011, 193, 4292-4293.   | 1.0 | 54        |
| 2590 | A Comparative BAC Map for the Gilthead Sea Bream ( <i>Sparus aurata</i> L.). <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-7.   | 3.0 | 13        |
| 2591 | Phototransduction and clock gene expression in the troglobiont beetle <i>Ptomaphagus hirtus</i> of Mammoth cave. <i>Journal of Experimental Biology</i> , 2011, 214, 3532-3541.   | 0.8 | 61        |
| 2592 | Detection and Molecular Characterization of Human Group C Rotavirus in Brazil. <i>Intervirology</i> , 2011, 54, 261-267.  | 1.2 | 10        |
| 2593 | Genomic Potential of <i>Marinobacter aquaeolei</i> , a Biogeochemical <i>Opportunitroph</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 2763-2771.  | 1.4 | 120       |
| 2594 | Complete Genome Sequence of <i>Methanosaeta concilii</i> , a Specialist in Aceticlastic Methanogenesis. <i>Journal of Bacteriology</i> , 2011, 193, 3668-3669.  | 1.0 | 57        |
| 2595 | Genome Sequence of <i>Nitrosomonas</i> sp. Strain AL212, an Ammonia-Oxidizing Bacterium Sensitive to High Levels of Ammonia. <i>Journal of Bacteriology</i> , 2011, 193, 5047-5048.   | 1.0 | 35        |
| 2596 | Complete Genome Sequence of <i>Leuconostoc kimchii</i> Strain C2, Isolated from Kimchi. <i>Journal of Bacteriology</i> , 2011, 193, 5548-5548.  | 1.0 | 17        |
| 2597 | Genome Sequence of <i>Kosmotoga olearia</i> Strain TBF 19.5.1, a Thermophilic Bacterium with a Wide Growth Temperature Range, Isolated from the Troll B Oil Platform in the North Sea. <i>Journal of Bacteriology</i> , 2011, 193, 5566-5567. | 1.0 | 19        |
| 2598 | ECHO: A reference-free short-read error correction algorithm. <i>Genome Research</i> , 2011, 21, 1181-1192.   | 2.4 | 95        |
| 2599 | Complete Genome Sequence of <i>Lactobacillus kefiranofaciens</i> ZW3. <i>Journal of Bacteriology</i> , 2011, 193, 4280-4281.  | 1.0 | 28        |
| 2600 | Complete Genome Sequences of <i>Mycobacterium tuberculosis</i> Strains CCDC5079 and CCDC5080, Which Belong to the Beijing Family. <i>Journal of Bacteriology</i> , 2011, 193, 5591-5592.  | 1.0 | 34        |
| 2601 | Extreme Reconfiguration of Plastid Genomes in the Angiosperm Family Geraniaceae: Rearrangements, Repeats, and Codon Usage. <i>Molecular Biology and Evolution</i> , 2011, 28, 583-600.  | 3.5 | 338       |
| 2602 | Analysis of the workers head transcriptome of the Asian subterranean termite, <i>Coptotermes gestroi</i> . <i>Bulletin of Entomological Research</i> , 2011, 101, 383-391.  | 0.5 | 15        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2603 | Genome Sequence of the Ethanol-Producing <i>Zymomonas mobilis</i> subsp. <i>pomaceae</i> Lectotype Strain ATCC 29192. <i>Journal of Bacteriology</i> , 2011, 193, 5049-5050.  | 1.0 | 22        |
| 2604 | Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. <i>Plant Cell</i> , 2011, 23, 4221-4233.  | 3.1 | 189       |
| 2605 | Complete Genome Sequences for the Anaerobic, Extremely Thermophilic Plant Biomass-Degrading Bacteria <i>Caldicellulosiruptor hydrothermalis</i> , <i>Caldicellulosiruptor kristjanssonii</i> , <i>Caldicellulosiruptor kronotskyensis</i> , <i>Caldicellulosiruptor owensensis</i> , and <i>Caldicellulosiruptor lactoaceticus</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1483-1484. | 1.0 | 54        |
| 2606 | Call for a Quality Standard for Sequence-Based Assays in Clinical Microbiology: Necessity for Quality Assessment of Sequences Used in Microbial Identification and Typing. <i>Journal of Clinical Microbiology</i> , 2011, 49, 23-26.   | 1.8 | 20        |
| 2607 | Complete Genome Sequence of the Cellulolytic Thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011, 193, 2906-2907.  | 1.0 | 66        |
| 2608 | Complete Genome Sequence of the Marine Cellulose- and Xylan-Degrading Bacterium <i>Glaciecolasp.</i> Strain 4H-3-7+YE-5. <i>Journal of Bacteriology</i> , 2011, 193, 4547-4548.   | 1.0 | 30        |
| 2609 | Complete Genome Sequence of the Ureolytic <i>Streptococcus salivarius</i> Strain 57.I. <i>Journal of Bacteriology</i> , 2011, 193, 5596-5597.   | 1.0 | 14        |
| 2610 | Complete Genome Sequence of <i>Bifidobacterium longum</i> subsp. <i>longum</i> BBMN68, a New Strain from a Healthy Chinese Centenarian. <i>Journal of Bacteriology</i> , 2011, 193, 787-788.  | 1.0 | 31        |
| 2611 | <i>Stacks</i> : Building and Genotyping Loci <i>De Novo</i> From Short-Read Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 171-182.  | 0.8 | 1,643     |
| 2612 | <i>Bacillus anthracis</i> comparative genome analysis in support of the Amerithrax investigation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5027-5032.  | 3.3 | 152       |
| 2613 | Complete Genome Sequence of the Dog Commensal and Human Pathogen <i>Capnocytophaga canimorsus</i> Strain 5. <i>Journal of Bacteriology</i> , 2011, 193, 5558-5559.  | 1.0 | 18        |
| 2614 | Autoregulation of Nodulation Interferes with Impacts of Nitrogen Fertilization Levels on the Leaf-Associated Bacterial Community in Soybeans. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1973-1980.  | 1.4 | 50        |
| 2615 | Complete Plastid Genome Sequences of Three Rosids ( <i>Castanea</i> , <i>Prunus</i> , <i>Theobroma</i> ): Evidence for At Least Two Independent Transfers of <i>rpl22</i> to the Nucleus. <i>Molecular Biology and Evolution</i> , 2011, 28, 835-847.   | 3.5 | 203       |
| 2616 | Evolution of the PEBP Gene Family in Plants: Functional Diversification in Seed Plant Evolution. <i>Plant Physiology</i> , 2011, 156, 1967-1977.  | 2.3 | 238       |
| 2617 | Dengue Virus Type 3 Isolated from a Fatal Case with Visceral Complications Induces Enhanced Proinflammatory Responses and Apoptosis of Human Dendritic Cells. <i>Journal of Virology</i> , 2011, 85, 5374-5383.   | 1.5 | 42        |
| 2618 | Evolution of the <i>S</i> -Locus Region in <i>Arabidopsis</i> Relatives. <i>Plant Physiology</i> , 2011, 157, 937-946.  | 2.3 | 80        |
| 2619 | Whole-Genome Sequencing of Sake Yeast <i>Saccharomyces cerevisiae</i> Kyokai no. 7. <i>DNA Research</i> , 2011, 18, 423-434.  | 1.5 | 150       |
| 2620 | Genome-Wide Comparison of Nucleotide-Binding Site-Leucine-Rich Repeat-Encoding Genes in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2011, 157, 757-769.  | 2.3 | 175       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2621 | The Bacteriophage T4 Rapid-Lysis Genes and Their Mutational Proclivities. <i>Journal of Bacteriology</i> , 2011, 193, 3537-3545.  | 1.0 | 12        |
| 2622 | Generation of expressed sequence tags, development of microsatellite and single nucleotide polymorphism markers in <i>Primula sieboldii</i> E. Morren (Primulaceae) for analysis of genetic diversity in natural and horticultural populations. <i>Breeding Science</i> , 2011, 61, 234-243.                                      | 0.9 | 4         |
| 2623 | Complete Genome Sequence of <i>Alicyclobacillus acidocaldarius</i> Strain Tc-4-1. <i>Journal of Bacteriology</i> , 2011, 193, 5602-5603.  | 1.0 | 19        |
| 2624 | Development of a PCR-Restriction Fragment Length Polymorphism Protocol for Rapid Detection and Differentiation of Four Cockroach Vectors (Group I "Dirty 22" Species) Responsible for Food Contamination and Spreading of Foodborne Pathogens: Public Health Importance. <i>Journal of Food Protection</i> , 2011, 74, 1883-1890. | 0.8 | 20        |
| 2625 | A White Spruce Gene Catalog for Conifer Genome Analyses. <i>Plant Physiology</i> , 2011, 157, 14-28.  | 2.3 | 143       |
| 2626 | Digenic Inheritance of Mutations in the Coproporphyrinogen Oxidase and Porphobilinogen Oxidase Genes in a Unique Type of Porphyria. <i>Journal of Investigative Dermatology</i> , 2011, 131, 2249-2254.   | 0.3 | 5         |
| 2627 | Developing Molecular Amplification Methods for Rapid Diagnosis of Respiratory Tract Infections Caused by Bacterial Pathogens. <i>Clinical Infectious Diseases</i> , 2011, 52, S338-S345.  | 2.9 | 31        |
| 2628 | The <i>Lymantria dispar</i> IPLB-Ld652Y Cell Line Transcriptome Comprises Diverse Virus-Associated Transcripts. <i>Viruses</i> , 2011, 3, 2339-2350.  | 1.5 | 16        |
| 2629 | A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. <i>PLoS Genetics</i> , 2011, 7, e1002236.  | 1.5 | 278       |
| 2630 | Predisposition to Cancer Caused by Genetic and Functional Defects of Mammalian Atad5. <i>PLoS Genetics</i> , 2011, 7, e1002245.   | 1.5 | 73        |
| 2631 | Extreme mitochondrial evolution in the ctenophore <i>Mnemiopsis leidyi</i> : Insight from mtDNA and the nuclear genome. <i>Mitochondrial DNA</i> , 2011, 22, 130-142.   | 0.6 | 81        |
| 2632 | A Diverse Population of <i>Cryptococcus gattii</i> Molecular Type VGIII in Southern Californian HIV/AIDS Patients. <i>PLoS Pathogens</i> , 2011, 7, e1002205.   | 2.1 | 95        |
| 2633 | A Simple Strain Typing Assay for <i>Trypanosoma cruzi</i> : Discrimination of Major Evolutionary Lineages from a Single Amplification Product. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1777.  | 1.3 | 64        |
| 2634 | Development of expressed sequence tag and expressed sequence tag "simple sequence repeat marker resources for <i>Musa acuminata</i> . <i>AoB PLANTS</i> , 2012, 2012, pls030.   | 1.2 | 21        |
| 2635 | A Natural System of Chromosome Transfer in <i>Yersinia pseudotuberculosis</i> . <i>PLoS Genetics</i> , 2012, 8, e1002529.   | 1.5 | 31        |
| 2636 | DaizuBase, an integrated soybean genome database including BAC-based physical maps. <i>Breeding Science</i> , 2012, 61, 661-664.  | 0.9 | 18        |
| 2637 | A Platform-Independent Method for Detecting Errors in Metagenomic Sequencing Data: DRISSEE. <i>PLoS Computational Biology</i> , 2012, 8, e1002541.  | 1.5 | 83        |
| 2638 | Salivary Gland Transcriptomes and Proteomes of <i>Phlebotomus tobbi</i> and <i>Phlebotomus sergenti</i> , Vectors of Leishmaniasis. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1660.   | 1.3 | 66        |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2639 | Diversity of a Chlorine-Resistant <i>Bacillus</i> Population Isolated from a Wastewater Treatment Station. <i>Water Environment Research</i> , 2012, 84, 274-281.  | 1.3 | 19        |
| 2640 | Reduced Lentivirus Susceptibility in Sheep with TMEM154 Mutations. <i>PLoS Genetics</i> , 2012, 8, e1002467.   | 1.5 | 78        |
| 2641 | A redescription of the leggiest animal, the millipede <i>Illacme plenipes</i> , with notes on its natural history and biogeography (Diplopoda, Siphonophorida, Siphonorhinidae). <i>ZooKeys</i> , 2012, 241, 77-112.   | 0.5 | 30        |
| 2642 | Persisting Viral Sequences Shape Microbial CRISPR-based Immunity. <i>PLoS Computational Biology</i> , 2012, 8, e1002475.   | 1.5 | 136       |
| 2643 | Antibody-Dependent Cellular Cytotoxicity-Mediating Antibodies from an HIV-1 Vaccine Efficacy Trial Target Multiple Epitopes and Preferentially Use the VH1 Gene Family. <i>Journal of Virology</i> , 2012, 86, 11521-11532.  | 1.5 | 357       |
| 2644 | Mapping of Micro-Tom BAC-End Sequences to the Reference Tomato Genome Reveals Possible Genome Rearrangements and Polymorphisms. <i>International Journal of Plant Genomics</i> , 2012, 2012, 1-8.  | 2.2 | 13        |
| 2645 | Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765 <sup>T</sup> , <i>Desulfosporosinus youngiae</i> DSM17734 <sup>T</sup> , <i>Desulfosporosinus meridiei</i> DSM13257 <sup>T</sup> , and <i>Desulfosporosinus acidiphilus</i> DSM22704 <sup>T</sup> . <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301. | 1.0 | 73        |
| 2646 | Cultivation-Independent Methods Reveal Differences among Bacterial Gut Microbiota in Triatomine Vectors of Chagas Disease. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1631.   | 1.3 | 92        |
| 2647 | Finished bacterial genomes from shotgun sequence data. <i>Genome Research</i> , 2012, 22, 2270-2277.   | 2.4 | 205       |
| 2648 | Transformations for the compression of FASTQ quality scores of next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 628-635.   | 1.8 | 45        |
| 2649 | Bacteriophages $\phi$ MR299-2 and $\phi$ NH-4 Can Eliminate <i>Pseudomonas aeruginosa</i> in the Murine Lung and on Cystic Fibrosis Lung Airway Cells. <i>MBio</i> , 2012, 3, e00029-12.   | 1.8 | 218       |
| 2650 | Genetic Basis of a Violation of Dollo's Law: Re-Evolution of Rotating Sex Combs in <i>Drosophila bipectinata</i> . <i>Genetics</i> , 2012, 192, 1465-1475.   | 1.2 | 13        |
| 2651 | Comparative Analysis of Benzoxazinoid Biosynthesis in Monocots and Dicots: Independent Recruitment of Stabilization and Activation Functions. <i>Plant Cell</i> , 2012, 24, 915-928.   | 3.1 | 58        |
| 2652 | Automating HIV Drug Resistance Genotyping with RECall, a Freely Accessible Sequence Analysis Tool. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1936-1942.  | 1.8 | 156       |
| 2653 | Joint genotyping on the fly: Identifying variation among a sequenced panel of inbred lines. <i>Genome Research</i> , 2012, 22, 966-974.  | 2.4 | 24        |
| 2654 | SCALCE: boosting sequence compression algorithms using locally consistent encoding. <i>Bioinformatics</i> , 2012, 28, 3051-3057.   | 1.8 | 129       |
| 2655 | Complete Genome Sequence of <i>Lactococcus lactis</i> IO-1, a Lactic Acid Bacterium That Utilizes Xylose and Produces High Levels of <i>scpA</i> -Lactic Acid. <i>Journal of Bacteriology</i> , 2012, 194, 2102-2103.  | 1.0 | 49        |
| 2656 | Genomic Comparison of <i>Escherichia coli</i> O104:H4 Isolates from 2009 and 2011 Reveals Plasmid, and Prophage Heterogeneity, Including Shiga Toxin Encoding Phage <i>stx2</i> . <i>PLoS ONE</i> , 2012, 7, e48228.   | 1.1 | 118       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2657 | Comparative Genetic Mapping and Discovery of Linkage Disequilibrium Across Linkage Groups in White Clover ( <i>Trifolium repens</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 607-617.           | 0.8 | 28        |
| 2658 | Transcriptome Analysis Using a High-Density Oligomicroarray under Drought Stress in Various Genotypes of Cassava: An Important Tropical Crop. <i>DNA Research</i> , 2012, 19, 335-345.                     | 1.5 | 101       |
| 2659 | Complete Genome Sequence of the BTEX-Degrading Bacterium <i>Pseudoxanthomonas spadix</i> BD-a59. <i>Journal of Bacteriology</i> , 2012, 194, 544-544.  | 1.0 | 23        |
| 2660 | A mostly traditional approach improves alignment of bisulfite-converted DNA. <i>Nucleic Acids Research</i> , 2012, 40, e100-e100.  | 6.5 | 55        |
| 2661 | A systematic study of gene expression variation at single-nucleotide resolution reveals widespread regulatory roles for uAUGs. <i>Genome Research</i> , 2012, 22, 1089-1097.                               | 2.4 | 28        |
| 2662 | Complete Genome Sequence of <i>Leuconostoc gelidum</i> Strain JB7, Isolated from Kimchi. <i>Journal of Bacteriology</i> , 2012, 194, 6665-6665.  | 1.0 | 13        |
| 2663 | Complete Genome Sequence of <i>Rahnella</i> sp. Strain Y9602, a Gammaproteobacterium Isolate from Metal- and Radionuclide-Contaminated Soil. <i>Journal of Bacteriology</i> , 2012, 194, 2113-2114.        | 1.0 | 12        |
| 2664 | Dynamic Intra-Japonica Subspecies Variation and Resource Application. <i>Molecular Plant</i> , 2012, 5, 218-230.   | 3.9 | 23        |
| 2665 | Design and Analytical Validation of Clinical DNA Sequencing Assays. <i>Archives of Pathology and Laboratory Medicine</i> , 2012, 136, 41-46.   | 1.2 | 35        |
| 2666 | Genome Sequence and Assembly of <i>Bos indicus</i> . <i>Journal of Heredity</i> , 2012, 103, 342-348.  | 1.0 | 106       |
| 2667 | Genome Sequence of <i>Edwardsiella ictaluri</i> 93-146, a Strain Associated with a Natural Channel Catfish Outbreak of Enteric Septicemia of Catfish. <i>Journal of Bacteriology</i> , 2012, 194, 740-741. | 1.0 | 46        |
| 2668 | ANALYSIS OF CONTEXT-DEPENDENT ERRORS FOR ILLUMINA SEQUENCING. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1241005.  | 0.3 | 16        |
| 2670 | Complete Genome Sequence of <i>Rahnella aquatilis</i> CIP 78.65. <i>Journal of Bacteriology</i> , 2012, 194, 3020-3021.  | 1.0 | 18        |
| 2671 | Complete Genome Sequence of <i>Sphingobium</i> sp. Strain SYK-6, a Degrader of Lignin-Derived Biaryls and Monoaryls. <i>Journal of Bacteriology</i> , 2012, 194, 534-535.                                  | 1.0 | 58        |
| 2672 | Comparative Transcriptomic and Proteomic Analyses of <i>Trichomonas vaginalis</i> following Adherence to Fibronectin. <i>Infection and Immunity</i> , 2012, 80, 3900-3911.                                 | 1.0 | 41        |
| 2673 | Complete Genome Sequence of <i>Klebsiella oxytoca</i> KCTC 1686, Used in Production of 2,3-Butanediol. <i>Journal of Bacteriology</i> , 2012, 194, 2371-2372.  | 1.0 | 27        |
| 2674 | Complete Genome Sequence of <i>Clostridium</i> sp. Strain BNL1100, a Cellulolytic Mesophile Isolated from Corn Stover. <i>Journal of Bacteriology</i> , 2012, 194, 6982-6983.                              | 1.0 | 15        |
| 2675 | HIV-1 gp120 Vaccine Induces Affinity Maturation in both New and Persistent Antibody Clonal Lineages. <i>Journal of Virology</i> , 2012, 86, 7496-7507.   | 1.5 | 76        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2676 | Genomic and antigenic characterization of monomeric autotransporters of <i>Haemophilus parasuis</i> : an ongoing process of reductive evolution. <i>Microbiology (United Kingdom)</i> , 2012, 158, 436-447.        | 0.7 | 5         |
| 2677 | Complete Genome Sequence of <i>Leuconostoc carnosum</i> Strain JB16, Isolated from Kimchi. <i>Journal of Bacteriology</i> , 2012, 194, 6672-6673.  | 1.0 | 18        |
| 2678 | CloudMap: A Cloud-Based Pipeline for Analysis of Mutant Genome Sequences. <i>Genetics</i> , 2012, 192, 1249-1269.  | 1.2 | 281       |
| 2679 | The Whole Genome Sequence of <i>Sphingobium chlorophenicum</i> L-1: Insights into the Evolution of the Pentachlorophenol Degradation Pathway. <i>Genome Biology and Evolution</i> , 2012, 4, 184-198.              | 1.1 | 73        |
| 2680 | A powerful test for multiple rare variants association studies that incorporates sequencing qualities. <i>Nucleic Acids Research</i> , 2012, 40, e60-e60.  | 6.5 | 26        |
| 2681 | A Bioinformatics Procedure to Identify and Annotate Somatic Mutations in Whole-Exome Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2012, , 73-82.  | 1.0 | 0         |
| 2682 | Next generation sequencing technologies and the changing landscape of phage genomics. <i>Bacteriophage</i> , 2012, 2, 190-199.   | 1.9 | 57        |
| 2683 | Characterization of a thermostable extracellular tannase produced under submerged fermentation by <i>Aspergillus ochraceus</i> . <i>Electronic Journal of Biotechnology</i> , 2012, 15, .                          | 1.2 | 5         |
| 2684 | Recruitment of Members from the Rare Biosphere of Marine Bacterioplankton Communities after an Environmental Disturbance. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1361-1369.                     | 1.4 | 102       |
| 2685 | Indel-tolerant read mapping with trinucleotide frequencies using cache-oblivious kd-trees. <i>Bioinformatics</i> , 2012, 28, i325-i332.  | 1.8 | 3         |
| 2686 | Altered Pattern of Immunoglobulin Hypermutation in Mice Deficient in Slip-GC Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 31856-31865.   | 1.6 | 7         |
| 2687 | Draft Genome Sequence of the Anaerobic, Nitrate-Dependent, Fe(II)-Oxidizing Bacterium <i>Pseudogulbenkiania ferrooxidans</i> Strain 2002. <i>Journal of Bacteriology</i> , 2012, 194, 2400-2401.                   | 1.0 | 22        |
| 2688 | Complete Genome Sequence of <i>Brucella abortus</i> A13334, a New Strain Isolated from the Fetal Gastric Fluid of Dairy Cattle. <i>Journal of Bacteriology</i> , 2012, 194, 5444-5444.                             | 1.0 | 8         |
| 2689 | Complete Genome Sequence of <i>Brucella canis</i> Strain HSK A52141, Isolated from the Blood of an Infected Dog. <i>Journal of Bacteriology</i> , 2012, 194, 5134-5134.  | 1.0 | 9         |
| 2690 | Draft Genome Sequence of <i>Fusobacterium nucleatum</i> subsp. <i>fusiforme</i> ATCC 51190 <sup>T</sup>. <i>Journal of Bacteriology</i> , 2012, 194, 5445-5446.  | 1.0 | 9         |
| 2691 | Complete Genome Sequence of <i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> Strain J18, Isolated from Kimchi. <i>Journal of Bacteriology</i> , 2012, 194, 730-731.                                    | 1.0 | 31        |
| 2692 | Complete Genome Sequence of the Beer Spoilage Organism <i>Pediococcus claussenii</i> ATCC BAA-344T. <i>Journal of Bacteriology</i> , 2012, 194, 1271-1272.   | 1.0 | 40        |
| 2693 | Nucleotide Sequence Diversity of Floral Pigment Genes in Mexican Populations of <i>Ipomoea purpurea</i> (Morning Glory) Accord with a Neutral Model of Evolution. <i>Journal of Heredity</i> , 2012, 103, 863-872. | 1.0 | 4         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2694 | Genome Sequence of <i>Francisella tularensis</i> subspecies <i>holarctica</i> Strain FSC200, Isolated from a Child with Tularemia. <i>Journal of Bacteriology</i> , 2012, 194, 6965-6966.   | 1.0 | 34        |
| 2695 | Genome Sequence of <i>Amycolatopsis</i> sp. Strain ATCC 39116, a Plant Biomass-Degrading Actinomycete. <i>Journal of Bacteriology</i> , 2012, 194, 2396-2397.   | 1.0 | 37        |
| 2696 | Laboratory evolution of new lactate transporter genes in a <i>jen1</i> <sup>Δ</sup> mutant of <i>Saccharomyces cerevisiae</i> and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. <i>FEMS Yeast Research</i> , 2012, 12, n/a-n/a. | 1.1 | 33        |
| 2697 | Complete genome sequence of <i>Paenibacillus</i> sp. strain JDR-2. <i>Standards in Genomic Sciences</i> , 2012, 6, 1-10.  | 1.5 | 15        |
| 2698 | Complete genome sequence of the melanogenic marine bacterium <i>Marinomonas mediterranea</i> type strain (MMB-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 63-73.   | 1.5 | 21        |
| 2699 | Complete genome sequence of <i>Dehalogenimonas lykanthroporepellens</i> type strain (BL-DC-9T) and comparison to <i>Dehalococcoides</i> strains. <i>Standards in Genomic Sciences</i> , 2012, 6, 251-264.   | 1.5 | 51        |
| 2700 | Complete genome sequence of <i>Oscillibacter valericigenes</i> Sjm18-20T (=NBRC 101213T). <i>Standards in Genomic Sciences</i> , 2012, 6, 406-414.  | 1.5 | 36        |
| 2701 | Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012, 6, 325-335.   | 1.5 | 53        |
| 2702 | Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <i>Standards in Genomic Sciences</i> , 2012, 6, 165-173.  | 1.5 | 19        |
| 2703 | Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012, 7, 22-30.   | 1.5 | 22        |
| 2704 | Complete genome sequence of <i>Marinomonas posidonica</i> type strain (IVIA-Po-181T). <i>Standards in Genomic Sciences</i> , 2012, 7, 31-43.  | 1.5 | 10        |
| 2705 | Complete genome sequence of <i>Syntrophobacter fumaroxidans</i> strain (MPOBT). <i>Standards in Genomic Sciences</i> , 2012, 7, 91-106.   | 1.5 | 55        |
| 2706 | Genome sequence of the halotolerant bacterium <i>Corynebacterium halotolerans</i> type strain YIM 70093T (= DSM 44683T). <i>Standards in Genomic Sciences</i> , 2012, 7, 284-293.   | 1.5 | 9         |
| 2707 | Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6T). <i>Standards in Genomic Sciences</i> , 2012, 6, 31-42.  | 1.5 | 9         |
| 2708 | Complete Genome Sequence of <i>Clostridium clariflavum</i> DSM 19732. <i>Standards in Genomic Sciences</i> , 2012, 6, 104-115.  | 1.5 | 48        |
| 2709 | Complete genome sequence of <i>Terriglobus saanensis</i> type strain SP1PR4T, an Acidobacteria from tundra soil. <i>Standards in Genomic Sciences</i> , 2012, 7, 59-69.   | 1.5 | 20        |
| 2710 | Complete genome sequence of the motile actinomycete <i>Actinoplanes missouriensis</i> 431T (= NBRC) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5   | 1.5 | 28        |
| 2711 | Challenges and opportunities in estimating viral genetic diversity from next-generation sequencing data. <i>Frontiers in Microbiology</i> , 2012, 3, 329.   | 1.5 | 204       |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 2712 | Comparative genomics of the Hedgehog loci in chordates and the origins of Shh regulatory novelties. <i>Scientific Reports</i> , 2012, 2, 433.   | 1.6  | 29        |
| 2713 | Molecular detection and species identification of <i>Alexandrium</i> (Dinophyceae) causing harmful algal blooms along the Chilean coastline. <i>AoB PLANTS</i> , 2012, 2012, pls033.  | 1.2  | 17        |
| 2714 | Complete Genome Sequence of <i>Bradyrhizobium</i> , sp. S23321: Insights into Symbiosis Evolution in Soil Oligotrophs. <i>Microbes and Environments</i> , 2012, 27, 306-315.  | 0.7  | 76        |
| 2715 | Cultured fungal associates from the deep-sea coral <i>Lophelia pertusa</i> . <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2012, 67, 12-20.  | 0.6  | 18        |
| 2716 | Population Genomic Analysis of Model and Nonmodel Organisms Using Sequenced RAD Tags. <i>Methods in Molecular Biology</i> , 2012, 888, 235-260.   | 0.4  | 56        |
| 2717 | Extensive variation in surface lipoprotein gene content and genomic changes associated with virulence during evolution of a novel North American house finch epizootic strain of <i>Mycoplasma gallisepticum</i> . <i>Microbiology (United Kingdom)</i> , 2012, 158, 2073-2088. | 0.7  | 43        |
| 2718 | Genomic Libraries: II. Subcloning, Sequencing, and Assembling Large-Insert Genomic DNA Clones. <i>Methods in Molecular Biology</i> , 2012, 772, 59-81.  | 0.4  | 1         |
| 2719 | The sunflower ( <i>Helianthus annuus</i> L.) genome reflects a recent history of biased accumulation of transposable elements. <i>Plant Journal</i> , 2012, 72, 142-153.  | 2.8  | 88        |
| 2720 | CUSHAW: a CUDA compatible short read aligner to large genomes based on the Burrows-Wheeler transform. <i>Bioinformatics</i> , 2012, 28, 1830-1837.  | 1.8  | 131       |
| 2721 | The <i>Littorina</i> sequence database (LSD) – an online resource for genomic data. <i>Molecular Ecology Resources</i> , 2012, 12, 142-148.   | 2.2  | 15        |
| 2722 | Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. <i>BMC Genomics</i> , 2012, 13, S6.   | 1.2  | 38        |
| 2723 | All your base: a fast and accurate probabilistic approach to base calling. <i>Genome Biology</i> , 2012, 13, R13.   | 13.9 | 39        |
| 2724 | Genetic Consequences of Programmed Genome Rearrangement. <i>Current Biology</i> , 2012, 22, 1524-1529.  | 1.8  | 101       |
| 2725 | Telomere-Targeted Retrotransposons in the Rice Blast Fungus <i>Magnaporthe oryzae</i> : Agents of Telomere Instability. <i>Genetics</i> , 2012, 191, 389-406.   | 1.2  | 48        |
| 2726 | Construction and analysis of EST libraries of the trans-polyisoprene producing plant, <i>Eucommia ulmoides</i> Oliver. <i>Planta</i> , 2012, 236, 1405-1417.  | 1.6  | 33        |
| 2727 | Occurrence and phylogenetic characterization of a baculovirus isolated from <i>Culex quinquefasciatus</i> in São Paulo State, Brazil. <i>Archives of Virology</i> , 2012, 157, 1741-1745.   | 0.9  | 4         |
| 2728 | HEV infection in swine from Eastern Brazilian Amazon: Evidence of co-infection by different subtypes. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2012, 35, 477-485.  | 0.7  | 40        |
| 2729 | Origin of pisatin demethylase (PDA) in the genus <i>Fusarium</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 933-942.  | 0.9  | 26        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2730 | Genetic diversity of <i>Flavobacterium psychrophilum</i> isolated from rainbow trout in France: Predominance of a clonal complex. <i>Veterinary Microbiology</i> , 2012, 161, 169-178.  | 0.8 | 41        |
| 2731 | Distribution and molecular characterization of hepatitis C virus (HCV) genotypes in patients with chronic infection from Pernambuco State, Brazil. <i>Virus Research</i> , 2012, 169, 8-12.   | 1.1 | 6         |
| 2732 | Complete Genome Sequence of the Ethanol-Producing <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> Centrotype ATCC 29191. <i>Journal of Bacteriology</i> , 2012, 194, 5966-5967.  | 1.0 | 36        |
| 2733 | The <i>MTAP-CDKN2A</i> Locus Confers Susceptibility to a Naturally Occurring Canine Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1019-1027.   | 1.1 | 79        |
| 2734 | Comparative transcriptome analysis of <i>Paracoccidioides brasiliensis</i> during <i>in vitro</i> adhesion to type I collagen and fibronectin: identification of potential adhesins. <i>Research in Microbiology</i> , 2012, 163, 182-191.          | 1.0 | 19        |
| 2735 | PRNP haplotype and genotype frequencies in Brazilian sheep: Issues for conservation and breeding programs. <i>Research in Veterinary Science</i> , 2012, 93, 219-225.   | 0.9 | 19        |
| 2736 | Development and characterization of cDNA library based novel EST-SSR marker in radish ( <i>Raphanus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5   | 2.7 | 18        |
| 2737 | Biochemical characterization and identification of a cinnamyl alcohol dehydrogenase from <i>Artemisia annua</i> . <i>Plant Science</i> , 2012, 193-194, 85-95.  | 1.7 | 24        |
| 2738 | Phylogenetically diverse TT virus viremia among pregnant women. <i>Virology</i> , 2012, 432, 427-434.   | 1.1 | 26        |
| 2740 | Exome sequencing identifies a novel multiple sclerosis susceptibility variant in the <i>TYK2</i> gene. <i>Neurology</i> , 2012, 79, 406-411.  | 1.5 | 56        |
| 2741 | A Parameterization Study of Short Read Assembly Using the Velvet Assembler. <i>Advances in Intelligent and Soft Computing</i> , 2012, , 179-186.  | 0.2 | 0         |
| 2742 | Population-Based Variation in Cardiomyopathy Genes. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 391-399.   | 5.1 | 126       |
| 2743 | Rapid Whole-Genome Sequencing for Genetic Disease Diagnosis in Neonatal Intensive Care Units. <i>Science Translational Medicine</i> , 2012, 4, 154ra135.  | 5.8 | 534       |
| 2744 | DNA Pooling and Statistical Tests for the Detection of Single Nucleotide Polymorphisms. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 1.  | 0.2 | 2         |
| 2745 | Bacterial polycyclic aromatic hydrocarbon ring-hydroxylating dioxygenases (PAH-RHD) encoding genes in different soils from King George Bay, Antarctic Peninsula. <i>Applied Soil Ecology</i> , 2012, 55, 1-9.                                       | 2.1 | 57        |
| 2746 | Transcriptome and full-length cDNA resources for the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major insect pest of pine forests. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 525-536.                       | 1.2 | 93        |
| 2747 | Automated sequence analysis and editing software for HIV drug resistance testing. <i>Journal of Clinical Virology</i> , 2012, 54, 30-35.  | 1.6 | 5         |
| 2748 | Identification of differentially transcribed genes in shrimp <i>Litopenaeus vannamei</i> exposed to osmotic stress and challenged with WSSV virus. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 73-81. | 0.4 | 8         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2749 | Characterizing short read sequencing for gene discovery and RNA-Seq analysis in <i>Crassostrea gigas</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 94-99.           | 0.4 | 21        |
| 2750 | Culturing of the first 37:4 predominant lacustrine haptophyte: Geochemical, biochemical, and genetic implications. <i>Geochimica Et Cosmochimica Acta</i> , 2012, 78, 51-64.  | 1.6 | 49        |
| 2751 | Differences in mtDNA whole sequence between Tibetan and Han populations suggesting adaptive selection to high altitude. <i>Gene</i> , 2012, 496, 37-44.   | 1.0 | 45        |
| 2752 | Error-correcting properties of the SOLiD Exact Call Chemistry. <i>BMC Bioinformatics</i> , 2012, 13, 145.   | 1.2 | 10        |
| 2753 | Slim-Filter: an interactive windows-based application for illumina genome analyzer data assessment and manipulation. <i>BMC Bioinformatics</i> , 2012, 13, 166.   | 1.2 | 9         |
| 2754 | Estimation of sequencing error rates in short reads. <i>BMC Bioinformatics</i> , 2012, 13, 185.   | 1.2 | 61        |
| 2755 | ReQON: a Bioconductor package for recalibrating quality scores from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2012, 13, 221.   | 1.2 | 19        |
| 2756 | Improved base-calling and quality scores for 454 sequencing based on a Hurdle Poisson model. <i>BMC Bioinformatics</i> , 2012, 13, 303.   | 1.2 | 15        |
| 2757 | The phylogenetics of Anguillicolidae (Nematoda: Anguillicoidea), swimbladder parasites of eels. <i>BMC Evolutionary Biology</i> , 2012, 12, 60.   | 3.2 | 56        |
| 2758 | The complete genome sequence of the acarbose producer <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2012, 13, 112.  | 1.2 | 69        |
| 2759 | A second generation framework for the analysis of microsatellites in expressed sequence tags and the development of EST-SSR markers for a conifer, <i>Cryptomeria japonica</i> . <i>BMC Genomics</i> , 2012, 13, 136. | 1.2 | 69        |
| 2760 | A transcriptome map of perennial ryegrass ( <i>Lolium perenne</i> L.). <i>BMC Genomics</i> , 2012, 13, 140.   | 1.2 | 60        |
| 2761 | Oomycete transcriptomics database: A resource for oomycete transcriptomes. <i>BMC Genomics</i> , 2012, 13, 303.   | 1.2 | 7         |
| 2762 | Maternal 3'UTRs: from egg to onset of zygotic transcription in Atlantic cod. <i>BMC Genomics</i> , 2012, 13, 443.   | 1.2 | 17        |
| 2763 | Comparative genomics of the classical <i>Bordetella</i> subspecies: the evolution and exchange of virulence-associated diversity amongst closely related pathogens. <i>BMC Genomics</i> , 2012, 13, 545.              | 1.2 | 99        |
| 2764 | Large-scale sequencing based on full-length-enriched cDNA libraries in pigs: contribution to annotation of the pig genome draft sequence. <i>BMC Genomics</i> , 2012, 13, 581.  | 1.2 | 15        |
| 2765 | Genome-derived insights into the biology of the hepatotoxic bloom-forming cyanobacterium <i>Anabaena</i> sp. strain 90. <i>BMC Genomics</i> , 2012, 13, 613.  | 1.2 | 52        |
| 2766 | Evolution and phylogeny of the mud shrimps (Crustacea: Decapoda) revealed from complete mitochondrial genomes. <i>BMC Genomics</i> , 2012, 13, 631.   | 1.2 | 62        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2767 | The genome of <i>Pelobacter carbinolicus</i> reveals surprising metabolic capabilities and physiological features. <i>BMC Genomics</i> , 2012, 13, 690.   | 1.2 | 35        |
| 2768 | Co-occurrence of resistance to different antibiotics among aquatic bacteria. <i>BMC Microbiology</i> , 2012, 12, 225.   | 1.3 | 29        |
| 2769 | Evidence of cryptic introgression in tomato ( <i>Solanum lycopersicum</i> L.) based on wild tomato species alleles. <i>BMC Plant Biology</i> , 2012, 12, 133.   | 1.6 | 34        |
| 2770 | Targeted massive parallel sequencing: the effective detection of novel causative mutations associated with hearing loss in small families. <i>Orphanet Journal of Rare Diseases</i> , 2012, 7, 60.  | 1.2 | 75        |
| 2771 | Integrated pathway modules using time-course metabolic profiles and EST data from <i>Milnesium tardigradum</i> . <i>BMC Systems Biology</i> , 2012, 6, 72.  | 3.0 | 11        |
| 2772 | Genomic organization and sequence dynamics of the <i>AvrPiz-t</i> locus in <i>Magnaporthe oryzae</i> . <i>Journal of Zhejiang University: Science B</i> , 2012, 13, 452-464.  | 1.3 | 6         |
| 2773 | Phylogeography of an Atlantic forest passerine reveals demographic stability through the last glacial maximum. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 892-902.  | 1.2 | 79        |
| 2774 | How Conserved Are the Bacterial Communities Associated With Aphids? A Detailed Assessment of the <i>Brevicoryne brassicae</i> (Hemiptera: Aphididae) Using 16S rDNA. <i>Environmental Entomology</i> , 2012, 41, 1386-1397.                       | 0.7 | 17        |
| 2775 | The biogeography and age of salticid spider radiations (Araneae: Salticidae). <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 213-240.   | 1.2 | 66        |
| 2776 | New Virologic Tools for Management of Chronic Hepatitis B and C. <i>Gastroenterology</i> , 2012, 142, 1303-1313.e1.   | 0.6 | 109       |
| 2777 | The Importance of Changes to Microrna in the Evolution of <i>Homo Neanderthalensis</i> and <i>Homo Denisova</i> . <i>Archaeology, Ethnology and Anthropology of Eurasia</i> , 2012, 40, 22-30.  | 0.1 | 3         |
| 2778 | Bioinformatic analysis of the <i>Acinetobacter baumannii</i> phage AB1 genome. <i>Gene</i> , 2012, 507, 125-134.  | 1.0 | 33        |
| 2779 | Complete genome sequence of the rapeseed plant-growth promoting <i>Serratia plymuthica</i> strain AS9. <i>Standards in Genomic Sciences</i> , 2012, 6, 54-62.   | 1.5 | 27        |
| 2780 | Association study of genetic polymorphisms of drug transporters, <i>SLCO1B1</i> , <i>SLCO1B3</i> and <i>ABCC2</i> , in African-Americans, Hispanics and Caucasians and olmesartan exposure. <i>Journal of Human Genetics</i> , 2012, 57, 531-544. | 1.1 | 7         |
| 2782 | Haplotype Analysis and Linkage Disequilibrium at Five Loci in <i>Eragrostis tef</i>. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 407-419.  | 0.8 | 12        |
| 2783 | Genome-enabled transcriptomics reveals archaeal populations that drive nitrification in a deep-sea hydrothermal plume. <i>ISME Journal</i> , 2012, 6, 2269-2279.  | 4.4 | 100       |
| 2784 | Identification of potential target genes of cardioprotection against ischemiaâ€“reperfusion injury by express sequence tags analysis in rat hearts. <i>Journal of Cardiology</i> , 2012, 60, 98-110.  | 0.8 | 26        |
| 2786 | Complete mitochondrial genome of the Japanese snapping shrimp <i>Alpheus japonicus</i> (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlode<br>2012, 55, 591-598.   | 2.3 | 32        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2787 | Exploring the diploid wheat ancestral A genome through sequence comparison at the high-molecular-weight glutenin locus region. <i>Molecular Genetics and Genomics</i> , 2012, 287, 855-866.                                 | 1.0 | 7         |
| 2788 | Genomic Approaches for Interrogating the Biochemistry of Medicinal Plant Species. <i>Methods in Enzymology</i> , 2012, 517, 139-159.  | 0.4 | 46        |
| 2789 | Next Generation Sequence Analysis and Computational Genomics Using Graphical Pipeline Workflows. <i>Genes</i> , 2012, 3, 545-575.   | 1.0 | 45        |
| 2790 | RNA Abundance Analysis. <i>Methods in Molecular Biology</i> , 2012, , .   | 0.4 | 3         |
| 2791 | Genomic Variation in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2012, 192, 533-598.  | 1.2 | 325       |
| 2792 | A missense mutation (c.1963A<math>\rightarrow</math>G) of the complementary component 2 (C2) gene is associated with serum Ca <sup>++</sup> concentrations in pigs. <i>Molecular Biology Reports</i> , 2012, 39, 9291-9297. | 1.0 | 1         |
| 2793 | Comparative Nucleotide Diversity Across North American and European <i>Populus</i> Species. <i>Journal of Molecular Evolution</i> , 2012, 74, 257-272.  | 0.8 | 25        |
| 2794 | Analyses of expressed sequence tags in <i>Neurospora</i> reveal rapid evolution of genes associated with the early stages of sexual reproduction in fungi. <i>BMC Evolutionary Biology</i> , 2012, 12, 229.                 | 3.2 | 12        |
| 2795 | PyroTRF-ID: a novel bioinformatics methodology for the affiliation of terminal-restriction fragments using 16S rRNA gene pyrosequencing data. <i>BMC Microbiology</i> , 2012, 12, 306.                                      | 1.3 | 23        |
| 2796 | AdapterRemoval: easy cleaning of next-generation sequencing reads. <i>BMC Research Notes</i> , 2012, 5, 337.  | 0.6 | 548       |
| 2797 | Gene Transfer in <i>Leptolyngbya</i> sp. Strain BL0902, a Cyanobacterium Suitable for Production of Biomass and Bioproducts. <i>PLoS ONE</i> , 2012, 7, e30901.   | 1.1 | 59        |
| 2798 | Isolation of a 97-kb Minimal Essential MHC B Locus from a New Reverse-4D BAC Library of the Golden Pheasant. <i>PLoS ONE</i> , 2012, 7, e32154.   | 1.1 | 28        |
| 2799 | Accelerated Evolution of Mitochondrial but Not Nuclear Genomes of Hymenoptera: New Evidence from Crabronid Wasps. <i>PLoS ONE</i> , 2012, 7, e32826.  | 1.1 | 55        |
| 2800 | A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 2012, 7, e33892.   | 1.1 | 50        |
| 2801 | The Mitochondrial Genome of the Lycophyte <i>Huperzia squarrosa</i> : The Most Archaic Form in Vascular Plants. <i>PLoS ONE</i> , 2012, 7, e35168.  | 1.1 | 42        |
| 2802 | Identification of 34 Novel Proinflammatory Proteins in a Genome-Wide Macrophage Functional Screen. <i>PLoS ONE</i> , 2012, 7, e42388.   | 1.1 | 9         |
| 2803 | High-Throughput Sequencing and Characterization of the Small RNA Transcriptome Reveal Features of Novel and Conserved MicroRNAs in <i>Panax ginseng</i> . <i>PLoS ONE</i> , 2012, 7, e44385.                                | 1.1 | 59        |
| 2804 | The Use of Next Generation Sequencing and Junction Sequence Analysis Bioinformatics to Achieve Molecular Characterization of Crops Improved Through Modern Biotechnology. <i>Plant Genome</i> , 2012, 5, .                  | 1.6 | 84        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2805 | Evidence for Horizontal Gene Transfer of Anaerobic Carbon Monoxide Dehydrogenases. <i>Frontiers in Microbiology</i> , 2012, 3, 132.  | 1.5 | 82        |
| 2806 | Multilocus sequence analysis (MLSA) of Bradyrhizobium strains: revealing high diversity of tropical diazotrophic symbiotic bacteria. <i>Brazilian Journal of Microbiology</i> , 2012, 43, 698-710.   | 0.8 | 63        |
| 2807 | Hot Start 7-Deaza-dGTP Improves Sanger Dideoxy Sequencing Data of GC-Rich Targets. , 0, , .  |     | 0         |
| 2808 | Distribution of QPY and RAH haplotypes of granzyme B gene in distinct Brazilian populations. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2012, 45, 496-499.  | 0.4 | 0         |
| 2809 | SeqTrace: A Graphical Tool for Rapidly Processing DNA Sequencing Chromatograms. <i>Journal of Biomolecular Techniques</i> , 2012, 23, 90-93.   | 0.8 | 226       |
| 2810 | Two sequential PCR amplifications for detection of <i>Schistosoma mansoni</i> in stool samples with low parasite load. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2012, 54, 245-248.  | 0.5 | 9         |
| 2811 | Mitochondrial genetic variability of <i>Didelphis albiventris</i> (Didelphimorphia, Didelphidae) in Brazilian localities. <i>Genetics and Molecular Biology</i> , 2012, 35, 522-529.   | 0.6 | 10        |
| 2812 | Feminizing <i>Wolbachia</i> : a transcriptomics approach with insights on the immune response genes in <i>Armadillidium vulgare</i> . <i>BMC Microbiology</i> , 2012, 12, S1.  | 1.3 | 48        |
| 2813 | Host gene response to endosymbiont and pathogen in the cereal weevil <i>Sitophilus oryzae</i> . <i>BMC Microbiology</i> , 2012, 12, S14.   | 1.3 | 42        |
| 2814 | Influence of <i>Wolbachia</i> on host gene expression in an obligatory symbiosis. <i>BMC Microbiology</i> , 2012, 12, S7.  | 1.3 | 63        |
| 2815 | Contribution of Intra- and Interhost Dynamics to Norovirus Evolution. <i>Journal of Virology</i> , 2012, 86, 3219-3229.  | 1.5 | 109       |
| 2816 | Phylogenetic Relationships of <i>Silene multinervia</i> and <i>Silene</i> Section <i>Conoimorpha</i> (Caryophyllaceae). <i>Systematic Botany</i> , 2012, 37, 226-237.  | 0.2 | 50        |
| 2817 | Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 434-439.  | 9.4 | 1,226     |
| 2818 | Plant genome sequencing. , 2012, , 83-97.  |     | 3         |
| 2819 | Host and geographic structure of endophytic and endolichenic fungi at a continental scale. <i>American Journal of Botany</i> , 2012, 99, 898-914.  | 0.8 | 304       |
| 2820 | Construction and characterization of a full-length cDNA library and identification of genes involved in salinity stress in wild eggplant ( <i>Solanum torvum</i> Swartz). <i>Horticulture Environment and Biotechnology</i> , 2012, 53, 158-166.             | 0.7 | 4         |
| 2821 | Transcript Profiling Using ESTs from <i>Paracoccidioides brasiliensis</i> in Models of Infection. <i>Methods in Molecular Biology</i> , 2012, 845, 381-396.  | 0.4 | 4         |
| 2822 | De Novo Assembly of the Manila Clam <i>Ruditapes philippinarum</i> Transcriptome Provides New Insights into Expression Bias, Mitochondrial Doubly Uniparental Inheritance and Sex Determination. <i>Molecular Biology and Evolution</i> , 2012, 29, 771-786. | 3.5 | 98        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2823 | Accurate Imputation of Rare and Common Variants in a Founder Population From a Small Number of Sequenced Individuals. <i>Genetic Epidemiology</i> , 2012, 36, 312-319.   | 0.6 | 19        |
| 2824 | Mutation spectrum of and founder effects affecting the PTS gene in East Asian populations. <i>Journal of Human Genetics</i> , 2012, 57, 145-152.   | 1.1 | 34        |
| 2825 | Base-Calling for Bioinformaticians. , 2012, , 67-83.   |     | 2         |
| 2826 | Short-Read Mapping. , 2012, , 107-125.   |     | 2         |
| 2827 | Genome-scale metabolic representation of <i>Amycolatopsis balhimycina</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1798-1807.  | 1.7 | 19        |
| 2828 | SEQuel: improving the accuracy of genome assemblies. <i>Bioinformatics</i> , 2012, 28, i188-i196.  | 1.8 | 56        |
| 2829 | Analysis of High-Throughput Ancient DNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 840, 197-228.   | 0.4 | 177       |
| 2830 | OnlineCall: fast online parameter estimation and base calling for illumina's next-generation sequencing. <i>Bioinformatics</i> , 2012, 28, 1677-1683.  | 1.8 | 22        |
| 2831 | Computational Analysis of RNA-seq. <i>Methods in Molecular Biology</i> , 2012, 883, 201-219.   | 0.4 | 11        |
| 2832 | Retention of triplicated phytoene synthase (PSY) genes in <i>Brassica napus</i> L. and its diploid progenitors during the evolution of the Brassicaceae. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1215-1228. | 1.8 | 21        |
| 2833 | Characterization of active miniature inverted-repeat transposable elements in the peanut genome. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1429-1438.   | 1.8 | 76        |
| 2834 | The complete mitochondrial genome of the verongid sponge <i>Aplysina cauliformis</i> : implications for DNA barcoding in demosponges. <i>Hydrobiologia</i> , 2012, 687, 61-69.   | 1.0 | 6         |
| 2835 | Optimization of a SNP assay for genotyping <i>Theobroma cacao</i> under field conditions. <i>Molecular Breeding</i> , 2012, 30, 33-52.   | 1.0 | 22        |
| 2836 | Large-scale development of expressed sequence tag-derived simple sequence repeat markers and diversity analysis in <i>Arachis</i> spp.. <i>Molecular Breeding</i> , 2012, 30, 125-138.                                   | 1.0 | 75        |
| 2837 | Single nucleotide polymorphism discovery in common bean. <i>Molecular Breeding</i> , 2012, 30, 419-428.  | 1.0 | 16        |
| 2838 | QTL analysis for resistance to bacterial wilt ( <i>Burkholderia caryophylli</i> ) in carnation ( <i>Dianthus</i> ) Tj ETQq1 1 0.784314 <sub>18</sub> / Overlock 10 <sub>41</sub>   | 1.8 | 41        |
| 2839 | Transcriptional responses to drought stress in root and leaf of chickpea seedling. <i>Molecular Biology Reports</i> , 2012, 39, 8147-8158.   | 1.0 | 28        |
| 2840 | Differential gene expression of rice roots inoculated with the diazotroph <i>Herbaspirillum seropedicae</i> . <i>Plant and Soil</i> , 2012, 356, 113-125.  | 1.8 | 61        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2841 | Construction of cDNA library from intestine, mesentery and coelomocyte of <i>Apostichopus japonicus</i> Selenka infected with <i>Vibrio</i> sp. and a preliminary analysis of immunity-related genes. <i>Journal of Ocean University of China</i> , 2012, 11, 187-196.         | 0.6 | 3         |
| 2842 | The RIPK2 gene: a positional candidate for tick burden supported by genetic associations in cattle and immunological response of knockout mouse. <i>Immunogenetics</i> , 2012, 64, 379-388.  | 1.2 | 9         |
| 2843 | Ranano expression pattern during oogenesis and early embryonic development in <i>Rhynchosciara americana</i> . <i>Development Genes and Evolution</i> , 2012, 222, 153-164.  | 0.4 | 5         |
| 2844 | Comparative mapping, genomic structure, and expression analysis of eight pseudo-response regulator genes in <i>Brassica rapa</i> . <i>Molecular Genetics and Genomics</i> , 2012, 287, 373-388.  | 1.0 | 23        |
| 2845 | Expression of genes of cellulose and lignin synthesis in <i>Eucalyptus urophylla</i> and its relation to some economic traits. <i>Trees - Structure and Function</i> , 2012, 26, 893-901.  | 0.9 | 7         |
| 2846 | A Second Generation Integrated Map of the Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Genome: Analysis of Conserved Synteny with Model Fish Genomes. <i>Marine Biotechnology</i> , 2012, 14, 343-357.   | 1.1 | 45        |
| 2847 | Functional features of a single chromosome arm in wheat (1AL) determined from its structure. <i>Functional and Integrative Genomics</i> , 2012, 12, 173-182.   | 1.4 | 24        |
| 2848 | A novel blast resistance gene, Pi54rh cloned from wild species of rice, <i>Oryza rhizomatis</i> confers broad spectrum resistance to <i>Magnaporthe oryzae</i> . <i>Functional and Integrative Genomics</i> , 2012, 12, 215-228.   | 1.4 | 130       |
| 2849 | Characterization of alginate lyase gene using a metagenomic library constructed from the gut microflora of abalone. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 585-593.   | 1.4 | 26        |
| 2850 | The genome sequence of <i>Desulfatibacillum alkenivorans</i> : a blueprint for anaerobic alkane oxidation. <i>Environmental Microbiology</i> , 2012, 14, 101-113.  | 1.8 | 137       |
| 2851 | Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. <i>Environmental Microbiology</i> , 2012, 14, 254-267.   | 1.8 | 56        |
| 2852 | <i>Trypanosoma rangeli</i> expresses a $\beta$ -galactofuranosyl transferase. <i>Experimental Parasitology</i> , 2012, 130, 246-252.   | 0.5 | 8         |
| 2853 | CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus (Boophilus) microplus</i> . <i>International Journal for Parasitology</i> , 2012, 42, 161-169.   | 1.3 | 55        |
| 2854 | <i>Trichoderma harzianum</i> expressed sequence tags for identification of genes with putative roles in mycoparasitism against <i>Fusarium solani</i> . <i>Biological Control</i> , 2012, 61, 134-140.   | 1.4 | 38        |
| 2855 | Integrative taxonomy at work: DNA barcoding of taeniids harboured by wild and domestic cats. <i>Molecular Ecology Resources</i> , 2012, 12, 403-413.   | 2.2 | 30        |
| 2856 | CHARACTERISATION, IDENTIFICATION AND TECHNOLOGICAL PROPERTIES OF PSYCHOTROPIC LACTIC ACID BACTERIA ORIGINATING FROM TUNISIAN FRESH FISH. <i>Journal of Food Safety</i> , 2012, 32, 333-344.  | 1.1 | 15        |
| 2857 | Laboratory evolution of new lactate transporter genes in a <i>jen1<sup>Δ</sup></i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. <i>FEMS Yeast Research</i> , 2012, 12, 359-374. | 1.1 | 56        |
| 2858 | Characterization of a new Acidobacteria-derived moderately thermostable lipase from a Brazilian Atlantic Forest soil metagenome. <i>FEMS Microbiology Ecology</i> , 2012, 81, 386-394.   | 1.3 | 36        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2859 | Next-generation sequencing approaches for genetic mapping of complex diseases. <i>Journal of Neuroimmunology</i> , 2012, 248, 10-22.   | 1.1 | 19        |
| 2860 | Genes under positive selection in a model plant pathogenic fungus, <i>Botrytis</i> . <i>Infection, Genetics and Evolution</i> , 2012, 12, 987-996.   | 1.0 | 40        |
| 2861 | Structure of the genomic sequence comprising the immunoglobulin heavy constant (IGHC) genes from <i>Sus scrofa</i> . <i>Molecular Immunology</i> , 2012, 52, 97-107.   | 1.0 | 27        |
| 2862 | Coibanoles, a new class of meroterpenoids produced by <i>Pycnoporus sanguineus</i> . <i>Tetrahedron Letters</i> , 2012, 53, 919-922.   | 0.7 | 23        |
| 2863 | Expressed sequence tag based identification and expression analysis of some cold inducible elements in seabuckthorn ( <i>Hippophae rhamnoides</i> L.). <i>Plant Physiology and Biochemistry</i> , 2012, 51, 123-128.   | 2.8 | 25        |
| 2864 | Mitochondrial DNA differentiation between the antitropical blue whiting species <i>Micromesistius poutassou</i> and <i>Micromesistius australis</i> . <i>Journal of Fish Biology</i> , 2012, 81, 253-269.  | 0.7 | 3         |
| 2865 | DNA sequences corroborate <i>Soesiladeepakius</i> as a non-salticoid genus of jumping spiders: placement with lapsiines, phylogeny, and description of six new species (Araneae, Salticidae). <i>Zoological Journal of the Linnean Society</i> , 2012, 165, 274-295. | 1.0 | 5         |
| 2866 | Genetic structure of three fosmid fragments encoding 16S rRNA genes of the Miscellaneous Crenarchaeotic Group (MCG): implications for physiology and evolution of marine sedimentary archaea. <i>Environmental Microbiology</i> , 2012, 14, 467-479.                 | 1.8 | 19        |
| 2867 | Cyanobacterial construction of hot spring siliceous stromatolites in Yellowstone National Park. <i>Environmental Microbiology</i> , 2012, 14, 1182-1197.   | 1.8 | 75        |
| 2868 | <i>Acinetobacter</i> , <i>Aeromonas</i> and <i>Trichococcus</i> populations dominate the microbial community within urban sewer infrastructure. <i>Environmental Microbiology</i> , 2012, 14, 2538-2552.   | 1.8 | 153       |
| 2869 | The response of marine picoplankton to ocean acidification. <i>Environmental Microbiology</i> , 2012, 14, 2293-2307.   | 1.8 | 124       |
| 2870 | <i>Plasmodium vivax</i> populations revisited: mitochondrial genomes of temperate strains in Asia suggest ancient population expansion. <i>BMC Evolutionary Biology</i> , 2012, 12, 22.  | 3.2 | 19        |
| 2871 | Characterisation of full-length cDNA sequences provides insights into the <i>Eimeria tenella</i> transcriptome. <i>BMC Genomics</i> , 2012, 13, 21.  | 1.2 | 20        |
| 2872 | Validation of reference genes for expression analysis in the salivary gland and the intestine of <i>Rhodnius prolixus</i> (Hemiptera, Reduviidae) under different experimental conditions by quantitative real-time PCR. <i>BMC Research Notes</i> , 2012, 5, 128.   | 0.6 | 89        |
| 2873 | <i>WDR62</i> missense mutation in a consanguineous family with primary microcephaly. <i>American Journal of Medical Genetics, Part A</i> , 2012, 158A, 622-625.  | 0.7 | 12        |
| 2874 | The first draft of the pigeonpea genome sequence. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2012, 21, 98-112.   | 0.9 | 167       |
| 2875 | Polyphasic approach for the characterization of rhizobial symbionts effective in fixing N <sub>2</sub> with common bean ( <i>Phaseolus vulgaris</i> L.). <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 2035-2049.  | 1.7 | 31        |
| 2876 | Exploration for the salt stress tolerance genes from a salt-treated halophyte, <i>Suaeda asparagoides</i> . <i>Plant Cell Reports</i> , 2012, 31, 35-48.   | 2.8 | 32        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2877 | Identification and mapping of conserved ortholog set (COS) II sequences of cacao and their conversion to SNP markers for marker-assisted selection in <i>Theobroma cacao</i> and comparative genomics studies. <i>Tree Genetics and Genomes</i> , 2012, 8, 97-111. | 0.6 | 25        |
| 2878 | Characterizing the walnut genome through analyses of BAC end sequences. <i>Plant Molecular Biology</i> , 2012, 78, 95-107.   | 2.0 | 27        |
| 2879 | Construction and characterization of a normalized cDNA library from the river snail <i>Bellamya aeruginosa</i> after exposure to copper. <i>Ecotoxicology</i> , 2012, 21, 260-267.   | 1.1 | 10        |
| 2880 | Identification of biotic and abiotic stress up-regulated ESTs in <i>Gossypium arboreum</i> . <i>Molecular Biology Reports</i> , 2012, 39, 1011-1018.   | 1.0 | 23        |
| 2881 | The complete mitochondrial genome of two recently derived species of the fish genus <i>Nannoperca</i> (Perciformes, Percichthyidae). <i>Molecular Biology Reports</i> , 2012, 39, 2767-2772.   | 1.0 | 50        |
| 2882 | Large-scale sequencing of normalized full-length cDNA library of soybean seed at different developmental stages and analysis of the gene expression profiles based on ESTs. <i>Molecular Biology Reports</i> , 2012, 39, 2867-2874.                                | 1.0 | 11        |
| 2883 | Generation and analysis of expressed sequence tags from the bone marrow of Chinese Sika deer. <i>Molecular Biology Reports</i> , 2012, 39, 2981-2990.  | 1.0 | 4         |
| 2884 | Matita, a new retroelement from peanut: characterization and evolutionary context in the light of the <i>Arachis</i> "B genome divergence. <i>Molecular Genetics and Genomics</i> , 2012, 287, 21-38.  | 1.0 | 43        |
| 2885 | Genome-scale analyses of butanol tolerance in <i>Saccharomyces cerevisiae</i> reveal an essential role of protein degradation. <i>Biotechnology for Biofuels</i> , 2013, 6, 48.  | 6.2 | 68        |
| 2886 | Characterisation and identification of spoilage psychrotrophic Gram-negative bacteria originating from Tunisian fresh fish. <i>Annals of Microbiology</i> , 2013, 63, 733-744.   | 1.1 | 14        |
| 2887 | Phylogenetic analysis and reconfiguration of genera in the cestode order Diphyllidea. <i>International Journal for Parasitology</i> , 2013, 43, 621-639.   | 1.3 | 22        |
| 2888 | Development of simple sequence repeat markers and construction of a high-density linkage map of <i>Capsicum annuum</i> . <i>Molecular Breeding</i> , 2013, 31, 909-920.  | 1.0 | 41        |
| 2889 | Molecular Identification of Melanised Non-Sporulating Moulds: A Useful Tool for Studying the Epidemiology of Phaeoophomycosis. <i>Mycopathologia</i> , 2013, 175, 445-454.   | 1.3 | 37        |
| 2890 | Molecular Characterization of <i>Wolbachia</i> Strains Associated with the Invasive Asian Citrus Psyllid <i>Diaphorina citri</i> in Brazil. <i>Microbial Ecology</i> , 2013, 65, 475-486.  | 1.4 | 41        |
| 2891 | Diversity and symbiotic effectiveness of beta-rhizobia isolated from sub-tropical legumes of a Brazilian Araucaria Forest. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 2335-2342.   | 1.7 | 21        |
| 2892 | Genomics and Breeding for Climate-Resilient Crops. , 2013, , .   |     | 9         |
| 2893 | Next Generation Sequencing and Sequence Assembly. <i>SpringerBriefs in Systems Biology</i> , 2013, , .   | 0.1 | 15        |
| 2894 | Molecular phylogeny, divergence times and biogeography of spiders of the subfamily Euophryinae (Araneae: Salticidae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 81-92.  | 1.2 | 62        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2895 | Analysis of expressed sequence tags (ESTs) from avocado seed ( <i>Persea Americana</i> var. <i>drymifolia</i> ) reveals abundant expression of the gene encoding the antimicrobial peptide snakain. <i>Plant Physiology and Biochemistry</i> , 2013, 70, 318-324. | 2.8 | 18        |
| 2896 | Population origin and historical demography in hawksbill ( <i>Eretmochelys imbricata</i> ) feeding and nesting aggregates from Brazil. <i>Journal of Experimental Marine Biology and Ecology</i> , 2013, 446, 334-344.  | 0.7 | 33        |
| 2897 | Molecular phylogeny of <i>G</i> eopalaninae ( <i>P</i> latyhelminthes) challenges current classification: proposal of taxonomic actions. <i>Zoologica Scripta</i> , 2013, 42, 508-528.  | 0.7 | 59        |
| 2898 | Expressed Sequence Tags (ESTs) analysis of <i>Tenebrio molitor</i> larvae. <i>Entomological Research</i> , 2013, 43, 168-176.   | 0.6 | 5         |
| 2899 | Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. <i>Statistics in Biosciences</i> , 2013, 5, 3-25.  | 0.6 | 15        |
| 2900 | WEP: a high-performance analysis pipeline for whole-exome data. <i>BMC Bioinformatics</i> , 2013, 14, S11.  | 1.2 | 43        |
| 2901 | Joint genotype inference with germline and somatic mutations. <i>BMC Bioinformatics</i> , 2013, 14, S3.   | 1.2 | 4         |
| 2902 | Benchmarking short sequence mapping tools. <i>BMC Bioinformatics</i> , 2013, 14, 184.   | 1.2 | 170       |
| 2903 | Base calling for high-throughput short-read sequencing: dynamic programming solutions. <i>BMC Bioinformatics</i> , 2013, 14, 129.   | 1.2 | 10        |
| 2904 | KONAGAbase: a genomic and transcriptomic database for the diamondback moth, <i>Plutella xylostella</i> . <i>BMC Genomics</i> , 2013, 14, 464.   | 1.2 | 47        |
| 2905 | Genomics of sablefish ( <i>Anoplopoma fimbria</i> ): expressed genes, mitochondrial phylogeny, linkage map and identification of a putative sex gene. <i>BMC Genomics</i> , 2013, 14, 452.  | 1.2 | 99        |
| 2906 | Construction of a plant-transformation-competent BIBAC library and genome sequence analysis of polyploid Upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2013, 14, 208.  | 1.2 | 15        |
| 2907 | A combined strategy involving Sanger and 454 pyrosequencing increases genomic resources to aid in the management of reproduction, disease control and genetic selection in the turbot ( <i>Scophthalmus</i> ) Tj ETQq0 0 OrgBT /Overlock 10 Tf                    |     |           |
| 2908 | Identification of differentially expressed genes from <i>Trichoderma harzianum</i> during growth on cell wall of <i>Fusarium solania</i> a tool for biotechnological application. <i>BMC Genomics</i> , 2013, 14, 177.  | 1.2 | 68        |
| 2909 | Identification of stress-responsive genes in <i>Ammopiptanthus mongolicus</i> using ESTs generated from cold- and drought-stressed seedlings. <i>BMC Plant Biology</i> , 2013, 13, 88.  | 1.6 | 53        |
| 2910 | Transcriptome resources and functional characterization of monoterpene synthases for two host species of the mountain pine beetle, lodgepole pine ( <i>Pinus contorta</i> ) and jack pine ( <i>Pinus banksiana</i> ). <i>BMC Plant Biology</i> , 2013, 13, 80.    | 1.6 | 57        |
| 2911 | Analysis of HCV quasispecies dynamic under selective pressure of combined therapy. <i>BMC Infectious Diseases</i> , 2013, 13, 61.   | 1.3 | 16        |
| 2912 | An Avian Coronavirus in Quail with Respiratory and Reproductive Signs. <i>Avian Diseases</i> , 2013, 57, 295-299.   | 0.4 | 16        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2913 | Extensive inter- and intraspecific venom variation in closely related parasites targeting the same host: The case of <i>Leptopilina</i> parasitoids of <i>Drosophila</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 601-611.                       | 1.2 | 100       |
| 2914 | Deep sequencing of <i>Lotus corniculatus</i> L. reveals key enzymes and potential transcription factors related to the flavonoid biosynthesis pathway. <i>Molecular Genetics and Genomics</i> , 2013, 288, 131-139.  | 1.0 | 17        |
| 2915 | Cloning, annotation and expression analysis of mycoparasitism-related genes in <i>Trichoderma harzianum</i> 88. <i>Journal of Microbiology</i> , 2013, 51, 174-182.  | 1.3 | 9         |
| 2916 | AlienTrimmer: A tool to quickly and accurately trim off multiple short contaminant sequences from high-throughput sequencing reads. <i>Genomics</i> , 2013, 102, 500-506.  | 1.3 | 195       |
| 2917 | Gene Expression Analysis of the Brazilian Type of Hereditary Persistence of Fetal Hemoglobin: Identification of Genes that Could be Related to $\beta^3$ -Globin Activation. <i>Hemoglobin</i> , 2013, 37, 516-535.  | 0.4 | 4         |
| 2918 | Technical and implementation issues in using next-generation sequencing of cancers in clinical practice. <i>British Journal of Cancer</i> , 2013, 109, 827-835.  | 2.9 | 91        |
| 2919 | Characterization of MHC class II B polymorphism in bottlenecked New Zealand saddlebacks reveals low levels of genetic diversity. <i>Immunogenetics</i> , 2013, 65, 619-633.  | 1.2 | 21        |
| 2920 | Integration, stability and expression of the <i>E. coli</i> phytase transgene in the Cassie line of Yorkshire Enviropigã,ç. <i>Transgenic Research</i> , 2013, 22, 379-389.  | 1.3 | 31        |
| 2921 | Phylogenetic diversity of prokaryotes associated with the mandibulate nasute termite <i>Cornitermes cumulans</i> and its mound. <i>Biology and Fertility of Soils</i> , 2013, 49, 567-574.   | 2.3 | 13        |
| 2922 | Sequencing of Sitka spruce ( <i>Picea sitchensis</i> ) cDNA libraries constructed from autumn buds and foliage reveals autumn-specific spruce transcripts. <i>Tree Genetics and Genomes</i> , 2013, 9, 683-691.  | 0.6 | 6         |
| 2923 | Mitochondrial genome sequences of <i>Artemia tibetiana</i> and <i>Artemia urmiana</i> : assessing molecular changes for high plateau adaptation. <i>Science China Life Sciences</i> , 2013, 56, 440-452.   | 2.3 | 37        |
| 2924 | Functional profiling of the <i>Tritrichomonas foetus</i> transcriptome and proteome. <i>Molecular and Biochemical Parasitology</i> , 2013, 187, 60-71.   | 0.5 | 17        |
| 2925 | The prokaryotic community of a historically mining-impacted tropical stream sediment is as diverse as that from a pristine stream sediment. <i>Extremophiles</i> , 2013, 17, 301-309.  | 0.9 | 49        |
| 2926 | Sewage reflects the distribution of human faecal <i>Achnospiraceae</i> . <i>Environmental Microbiology</i> , 2013, 15, 2213-2227.  | 1.8 | 88        |
| 2927 | A Copy Number Variant at the <i>KITLG</i> Locus Likely Confers Risk for Canine Squamous Cell Carcinoma of the Digit. <i>PLoS Genetics</i> , 2013, 9, e1003409.   | 1.5 | 60        |
| 2928 | Microbial Corrosion in Linepipe Steel Under the Influence of a Sulfate-Reducing Consortium Isolated from an Oil Field. <i>Journal of Materials Engineering and Performance</i> , 2013, 22, 3517-3529.  | 1.2 | 52        |
| 2929 | Identification of a novel mutation in UDP-glucuronosyltransferase ( <i>UGT1A1</i> ) gene in a child with neonatal unconjugated hyperbilirubinemia. <i>Clinical Biochemistry</i> , 2013, 46, 170-172.   | 0.8 | 2         |
| 2930 | Transcriptome responses in the rectal gland of fed and fasted spiny dogfish shark ( <i>Squalus acanthias</i> ) determined by suppression subtractive hybridization. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 334-343. | 0.4 | 8         |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2931 | Stage 0 sporulation gene <i>σ<sup>A</sup></i> as a molecular marker to study diversity of endospore-forming Firmicutes. <i>Environmental Microbiology Reports</i> , 2013, 5, 911-924.   | 1.0 | 35        |
| 2932 | Molecular epidemiology of <i>Flavobacterium psychrophilum</i> from Swiss fish farms. <i>Diseases of Aquatic Organisms</i> , 2013, 105, 203-210.   | 0.5 | 31        |
| 2933 | Rare Variants in Hypermutable Genes Underlie Common Morphology and Growth Traits in Wild <i>Saccharomyces paradoxus</i> . <i>Genetics</i> , 2013, 195, 513-525.   | 1.2 | 16        |
| 2934 | Next generation sequencing for human papillomavirus genotyping. <i>Journal of Clinical Virology</i> , 2013, 58, 437-442.  | 1.6 | 46        |
| 2935 | <i>Consed</i> : a graphical editor for next-generation sequencing. <i>Bioinformatics</i> , 2013, 29, 2936-2937.   | 1.8 | 260       |
| 2936 | Diversity of human papillomaviruses in skin lesions. <i>Virology</i> , 2013, 447, 300-311.  | 1.1 | 32        |
| 2937 | Wide distribution of CC92 carbapenem-resistant and OXA-23-producing <i>Acinetobacter baumannii</i> in multiple provinces of China. <i>International Journal of Antimicrobial Agents</i> , 2013, 42, 322-328.  | 1.1 | 88        |
| 2938 | Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. <i>Pharmacogenomics Journal</i> , 2013, 13, 148-158.  | 0.9 | 29        |
| 2939 | Long-term performance and operational strategies of a poultry slaughterhouse waste stabilization pond system in a tropical climate. <i>Resources, Conservation and Recycling</i> , 2013, 71, 7-14.  | 5.3 | 24        |
| 2940 | The Assembly of Sequencing Data. <i>SpringerBriefs in Systems Biology</i> , 2013, , 41-54.  | 0.1 | 0         |
| 2941 | Assessment of drug resistance related genes as candidate markers for treatment outcome prediction of cutaneous leishmaniasis in Brazil. <i>Acta Tropica</i> , 2013, 126, 132-141.   | 0.9 | 18        |
| 2943 | Coupling Deep Transcriptome Analysis with Untargeted Metabolic Profiling in <i>Ophiorrhiza pumila</i> to Further the Understanding of the Biosynthesis of the Anti-Cancer Alkaloid Camptothecin and Anthraquinones. <i>Plant and Cell Physiology</i> , 2013, 54, 686-696. | 1.5 | 88        |
| 2944 | Multilocus analyses reveal little evidence for lineage-wide adaptive evolution within major clades of soft pines ( <i>Pinus</i> subgenus <i>Sectrobus</i> ). <i>Molecular Ecology</i> , 2013, 22, 5635-5650.  | 2.0 | 45        |
| 2945 | Pliocene intraspecific divergence and Pliocene range expansions within <i>Picea likiangensis</i> (Lijiang spruce), a dominant forest tree of the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2013, 22, 5237-5255.   | 2.0 | 112       |
| 2946 | afterParty: turning raw transcriptomes into permanent resources. <i>BMC Bioinformatics</i> , 2013, 14, 301.   | 1.2 | 8         |
| 2947 | Bacterial and archaeal communities in the acid pit lake sediments of a chalcopyrite mine. <i>Extremophiles</i> , 2013, 17, 941-951.   | 0.9 | 22        |
| 2948 | A quick and low-cost PCR-based assay for <i>Candida</i> spp. identification in positive blood culture bottles. <i>BMC Infectious Diseases</i> , 2013, 13, 467.  | 1.3 | 10        |
| 2949 | Next-generation sequencing-based mRNA and microRNA expression profiling analysis revealed pathways involved in the rapid growth of developing culms in Moso bamboo. <i>BMC Plant Biology</i> , 2013, 13, 119.   | 1.6 | 87        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 2950 | Small ruminant lentivirus genetic subgroups associate with sheep TMEM154 genotypes. <i>Veterinary Research</i> , 2013, 44, 64.  | 1.1 | 19        |
| 2951 | Nanochloropsis plastid and mitochondrial phylogenomes reveal organelle diversification mechanism and intragenus phylotyping strategy in microalgae. <i>BMC Genomics</i> , 2013, 14, 534.  | 1.2 | 55        |
| 2952 | The neuropeptide complement of the marine annelid <i>Platynereis dumerilii</i> . <i>BMC Genomics</i> , 2013, 14, 906.   | 1.2 | 139       |
| 2953 | A BAC based physical map and genome survey of the rice false smut fungus <i>Villosiclava virens</i> . <i>BMC Genomics</i> , 2013, 14, 883.  | 1.2 | 10        |
| 2954 | Analysis of hepatitis B virus genotyping and drug resistance gene mutations based on massively parallel sequencing. <i>Journal of Virological Methods</i> , 2013, 193, 341-347.   | 1.0 | 13        |
| 2955 | Culturable populations of <i>Acinetobacter</i> can promptly respond to contamination by alkanes in mangrove sediments. <i>Marine Pollution Bulletin</i> , 2013, 76, 214-219.  | 2.3 | 21        |
| 2956 | De novo assembly methods for next generation sequencing data. <i>Tsinghua Science and Technology</i> , 2013, 18, 500-514.   | 4.1 | 15        |
| 2957 | SHIFTING FITNESS LANDSCAPES IN RESPONSE TO ALTERED ENVIRONMENTS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3512-3522.  | 1.1 | 114       |
| 2958 | SEME: A Fast Mapper of Illumina Sequencing Reads with Statistical Evaluation. <i>Journal of Computational Biology</i> , 2013, 20, 847-860.  | 0.8 | 6         |
| 2959 | Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2013, , .   | 1.0 | 17        |
| 2960 | Genome duplication and mutations in <i>ACE2</i> cause multicellular, fast-sedimenting phenotypes in evolved <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4223-31. | 3.3 | 100       |
| 2961 | Immune gene discovery by expressed sequence tag (EST) analysis of hemocytes in the ridgetail white prawn <i>Exopalaemon carinicauda</i> . <i>Fish and Shellfish Immunology</i> , 2013, 34, 173-182.   | 1.6 | 27        |
| 2962 | Sex Differences in the Gut Microbiome Drive Hormone-Dependent Regulation of Autoimmunity. <i>Science</i> , 2013, 339, 1084-1088.  | 6.0 | 1,565     |
| 2963 | Conversion of Microsatellite Markers to Single Nucleotide Polymorphism (SNP) Markers for Genetic Fingerprinting of <i>Theobroma cacao</i> . <i>Journal of Crop Improvement</i> , 2013, 27, 215-241.   | 0.9 | 7         |
| 2964 | Transcriptome Analysis in the Saccharinae. , 2013, , 121-139.   |     | 2         |
| 2965 | Musket: a multistage <i>k</i> -mer spectrum-based error corrector for Illumina sequence data. <i>Bioinformatics</i> , 2013, 29, 308-315.  | 1.8 | 266       |
| 2966 | A study of the relationships of cultivated peanut ( <i>Arachis hypogaea</i> ) and its most closely related wild species using intron sequences and microsatellite markers. <i>Annals of Botany</i> , 2013, 111, 113-126.                                    | 1.4 | 166       |
| 2967 | Phylogeny and biogeography of highly diverged freshwater fish species (Leuciscinae, Cyprinidae.) <i>Tj ETQq1 1 0.784314 rgBT /Qverlock 1</i>  | 1.0 | 91        |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 2968 | Deep relationships of Rhizaria revealed by phylogenomics: A farewell to Haeckel's Radiolaria. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 53-59.  | 1.2  | 65        |
| 2969 | Evaluation of DNA from the Papanicolaou Test to Detect Ovarian and Endometrial Cancers. <i>Science Translational Medicine</i> , 2013, 5, 167ra4.   | 5.8  | 264       |
| 2970 | Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.   | 13.7 | 564       |
| 2971 | Intraspecific comparative genomics of <i>Candida albicans</i> mitochondria reveals non-coding regions under neutral evolution. <i>Infection, Genetics and Evolution</i> , 2013, 14, 302-312.   | 1.0  | 19        |
| 2972 | SRmapper: a fast and sensitive genome-hashing alignment tool. <i>Bioinformatics</i> , 2013, 29, 316-321.   | 1.8  | 29        |
| 2973 | Transcriptome de novo assembly from next-generation sequencing and comparative analyses in the hexaploid salt marsh species <i>Spartina maritima</i> and <i>Spartina alterniflora</i> (Poaceae). <i>Heredity</i> , 2013, 110, 181-193. | 1.2  | 50        |
| 2974 | Next-generation sequencing in the clinic: Promises and challenges. <i>Cancer Letters</i> , 2013, 340, 284-295.   | 3.2  | 272       |
| 2975 | A genome-wide BAC end-sequence survey of sugarcane elucidates genome composition, and identifies BACs covering much of the euchromatin. <i>Plant Molecular Biology</i> , 2013, 81, 139-147.  | 2.0  | 26        |
| 2976 | Sequencing of Virulence Genes Shows Limited Genetic Variability in <i>Yersinia pseudotuberculosis</i> . <i>Foodborne Pathogens and Disease</i> , 2013, 10, 21-27.  | 0.8  | 2         |
| 2977 | Interpretation and Relevance of Advanced Technique Results. , 2013, , 911-936.   |      | 1         |
| 2978 | Positional cloning of a candidate gene for resistance to the sunflower downy mildew, <i>Plasmopara halstedii</i> race 300. <i>Theoretical and Applied Genetics</i> , 2013, 126, 359-367.   | 1.8  | 15        |
| 2979 | Going Forward with Genetics. <i>American Journal of Pathology</i> , 2013, 182, 1462-1473.  | 1.9  | 57        |
| 2980 | Construction, expression, purification and antigenicity of recombinant <i>Campylobacter jejuni</i> flagellar proteins. <i>Microbiological Research</i> , 2013, 168, 192-198.   | 2.5  | 18        |
| 2981 | A new species of <i>Eualus</i> Thallwitz, 1892 and new record of <i>Lebbeus antarcticus</i> (Hale, 1941) (Crustacea: Tj ETQq1 1 0.784314 rgBT / 0.6 8<br><i>Oceanography</i> , 2013, 92, 145-156.                                      | 0.6  | 8         |
| 2982 | Active site characterization and molecular cloning of <i>Tenebrio molitor</i> midgut trehalase and comments on their insect homologs. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 768-780.                            | 1.2  | 20        |
| 2983 | Tumor Evolution and Intratumor Heterogeneity of an Oropharyngeal Squamous Cell Carcinoma Revealed by Whole-Genome Sequencing. <i>Neoplasia</i> , 2013, 15, 1371-IN7.   | 2.3  | 78        |
| 2984 | Lack of host specificity of <i>Colletotrichum</i> spp. isolates associated with anthracnose symptoms on mango in Brazil. <i>Plant Pathology</i> , 2013, 62, 1038-1047.   | 1.2  | 19        |
| 2985 | Genetic variability in <i>Mycosporium canis</i> isolated from cats, dogs and humans in Brazil. <i>Mycoses</i> , 2013, 56, 582-588.   | 1.8  | 16        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 2986 | Fine Mapping QTLs Affecting Milk Production Traits on BTA6 in Chinese Holstein with SNP Markers. <i>Journal of Integrative Agriculture</i> , 2013, 12, 110-117.  | 1.7 | 11        |
| 2987 | Identification and expression analysis of key enzymes of the terpenoids biosynthesis pathway of a liverwort <i>Plagiochasma appendiculatum</i> by EST analysis. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 107-118.  | 1.0 | 14        |
| 2988 | Genome Analysis Suggests that the Soil Oligotrophic Bacterium <i>Agromonas oligotrophica</i> ( <i>Bradyrhizobium oligotrophicum</i> ) Is a Nitrogen-Fixing Symbiont of <i>Aeschynomene indica</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 2542-2551.   | 1.4 | 49        |
| 2989 | Evolutionary history of bulldog bats (genus <i>Noctilio</i> ): recent diversification and the role of the Caribbean in Neotropical biogeography. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 210-224.  | 0.7 | 25        |
| 2990 | <i>Propionibacterium acnes</i> Strain Populations in the Human Skin Microbiome Associated with Acne. <i>Journal of Investigative Dermatology</i> , 2013, 133, 2152-2160.   | 0.3 | 557       |
| 2991 | Footprints of selection in wild populations of <i>Bicyclus anynana</i> along a latitudinal cline. <i>Molecular Ecology</i> , 2013, 22, 341-353.  | 2.0 | 13        |
| 2992 | Initial description of the phylogeography, population structure and genetic diversity of Atlantic spotted dolphins from Brazil and the Caribbean, inferred from analyses of mitochondrial and nuclear DNA. <i>Biochemical Systematics and Ecology</i> , 2013, 48, 263-270. | 0.6 | 23        |
| 2993 | Going where traditional markers have not gone before: utility of and promise for RAD sequencing in marine invertebrate phylogeography and population genomics. <i>Molecular Ecology</i> , 2013, 22, 2953-2970.   | 2.0 | 184       |
| 2994 | Molecular phylogeny of kinorhynchs. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 303-310.  | 1.2 | 43        |
| 2995 | Enhancing xylanases production by a new Amazon Forest strain of <i>Aspergillus oryzae</i> using solid-state fermentation under controlled operation conditions. <i>Industrial Crops and Products</i> , 2013, 45, 465-471.  | 2.5 | 50        |
| 2996 | Identification of Mutations in Evolved Bacterial Genomes. <i>Methods in Molecular Biology</i> , 2013, 985, 249-267.  | 0.4 | 4         |
| 2997 | A User-Friendly Computational Workflow for the Analysis of MicroRNA Deep Sequencing Data. <i>Methods in Molecular Biology</i> , 2013, 936, 35-45.  | 0.4 | 3         |
| 2998 | Experimentally induced habitat filtering in marine bacterial communities. <i>Marine Ecology - Progress Series</i> , 2013, 477, 77-86.  | 0.9 | 18        |
| 2999 | Cystic fibrosis testing in a referral laboratory: results and lessons from a six-year period. <i>Journal of Clinical Bioinformatics</i> , 2013, 3, 3.  | 1.2 | 2         |
| 3000 | Metagenomic sequencing of HPV-negative condylomas detects novel putative HPV types. <i>Virology</i> , 2013, 440, 1-7.  | 1.1 | 66        |
| 3001 | Phage mutations in response to CRISPR diversification in a bacterial population. <i>Environmental Microbiology</i> , 2013, 15, 463-470.  | 1.8 | 97        |
| 3002 | Rapid identification of bacterial isolates from wheat roots by high resolution whole cell MALDI-TOF MS analysis. <i>Journal of Biotechnology</i> , 2013, 165, 167-174.   | 1.9 | 36        |
| 3003 | Development of 24 new microsatellite markers in the Crested Serpent Eagle ( <i>Spilornis cheela hoyi</i> ). <i>Conservation Genetics Resources</i> , 2013, 5, 417-420.   | 0.4 | 2         |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 3004 | Influence of sulfate reducing bacterial biofilm on corrosion behavior of low-alloy, high-strength steel (API-5L X80). <i>International Biodeterioration and Biodegradation</i> , 2013, 78, 34-42.   | 1.9  | 191       |
| 3005 | Principles of transcriptome analysis and gene expression quantification: an <i>RNA-seq</i> tutorial. <i>Molecular Ecology Resources</i> , 2013, 13, 559-572.  | 2.2  | 167       |
| 3006 | Translating next generation sequencing to practice: Opportunities and necessary steps. <i>Molecular Oncology</i> , 2013, 7, 743-755.  | 2.1  | 34        |
| 3007 | Partial venom gland transcriptome of a <i>Drosophila</i> parasitoid wasp, <i>Leptopilina heterotoma</i> , reveals novel and shared bioactive profiles with stinging Hymenoptera. <i>Gene</i> , 2013, 526, 195-204.  | 1.0  | 54        |
| 3008 | Topographic diversity of fungal and bacterial communities in human skin. <i>Nature</i> , 2013, 498, 367-370.  | 13.7 | 950       |
| 3009 | Developing Genome and Exome Sequencing for Candidate Gene Identification in Inherited Disorders: An Integrated Technical and Bioinformatics Approach. <i>Archives of Pathology and Laboratory Medicine</i> , 2013, 137, 415-433.                            | 1.2  | 45        |
| 3010 | Sequencing of the sea lamprey ( <i>Petromyzon marinus</i> ) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013, 45, 415-421.   | 9.4  | 588       |
| 3011 | Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2013, 16, 38-53.   | 1.0  | 157       |
| 3012 | Systems Metabolic Engineering. <i>Methods in Molecular Biology</i> , 2013, , .  | 0.4  | 3         |
| 3013 | The characterization of the <i>Plebotomus papatasi</i> transcriptome. <i>Insect Molecular Biology</i> , 2013, 22, 211-232.  | 1.0  | 20        |
| 3014 | Identification of <i>KCNJ11</i> as a functional candidate gene for bovine meat tenderness. <i>Physiological Genomics</i> , 2013, 45, 1215-1221.   | 1.0  | 14        |
| 3015 | Secoemestrin D, a Cytotoxic Epitetrathiodioxopiperazine, and Emericellenes A-E, Five Sesterterpenoids from <i>Emericella</i> sp. AST0036, a Fungal Endophyte of <i>Astragalus lentiginosus</i> 1. <i>Journal of Natural Products</i> , 2013, 76, 2330-2336. | 1.5  | 48        |
| 3016 | Genomic Resources for Gene Discovery, Functional Genome Annotation, and Evolutionary Studies of Maize and Its Close Relatives. <i>Genetics</i> , 2013, 195, 723-737.  | 1.2  | 15        |
| 3017 | Genome-scale Sequencing to Identify Genes Involved in Mendelian Disorders. <i>Current Protocols in Human Genetics</i> , 2013, 79, Unit 6.13..   | 3.5  | 4         |
| 3018 | Functional Screening of a Metagenomic Library Reveals Operons Responsible for Enhanced Intestinal Colonization by Gut Commensal Microbes. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3829-3838.  | 1.4  | 23        |
| 3020 | Draft Genome Sequence of <i>Methylobacterium buryatense</i> Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. <i>Genome Announcements</i> , 2013, 1, .   | 0.8  | 36        |
| 3021 | Genome Sequence of a Freshwater Low-Nucleic-Acid-Content Bacterium, <i>Betaproteobacterium</i> Strain CB. <i>Genome Announcements</i> , 2013, 1, e0013513.  | 0.8  | 8         |
| 3022 | Genome Sequence of Non-O1 <i>Vibrio cholerae</i> PS15. <i>Genome Announcements</i> , 2013, 1, .   | 0.8  | 15        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3023 | Draft Genome Sequence of an Oscillatorian Cyanobacterium, Strain ESFC-1. Genome Announcements, 2013, 1, .  | 0.8 | 5         |
| 3024 | Complete Genome Sequence of a Thermophilic Hydrogenotrophic Methanogen, <i>Methanothermobacter</i> sp. Strain CaT2. Genome Announcements, 2013, 1, .   | 0.8 | 13        |
| 3025 | Draft Genome Sequence of Medium-Chain-Length Polyhydroxyalkanoate-Producing <i>Pseudomonas putida</i> Strain LS46. Genome Announcements, 2013, 1, e0015113.  | 0.8 | 6         |
| 3026 | Complete Genome Sequence of the Carbazole Degrader <i>Pseudomonas resinovorans</i> Strain CA10 (NBRC) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 67 Td (american)  | 0.8 | 12        |
| 3027 | Complete Genome Sequence of <i>Clostridium</i> sp. Strain DL-VIII, a Novel Solventogenic <i>Clostridium</i> Species Isolated from Anaerobic Sludge. Genome Announcements, 2013, 1, .   | 0.8 | 5         |
| 3028 | Complete Genome Sequence of <i>Bacillus thuringiensis</i> Serovar Israelensis Strain HD-789. Genome Announcements, 2013, 1, .  | 0.8 | 30        |
| 3029 | Genome Sequencing of the Plant Pathogen <i>Taphrina deformans</i> , the Causal Agent of Peach Leaf Curl. MBio, 2013, 4, e00055-13.   | 1.8 | 81        |
| 3030 | Complete Genome of <i>Serratia</i> sp. Strain FGI 94, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. Genome Announcements, 2013, 1, e0023912.  | 0.8 | 15        |
| 3031 | Clinical analysis of genome next-generation sequencing data using the Omicia platform. Expert Review of Molecular Diagnostics, 2013, 13, 529-540.  | 1.5 | 31        |
| 3032 | Complete Genome Sequence of the Hyperthermophilic Sulfate-Reducing Bacterium <i>Thermodesulfobacterium geofontis</i> OPF15 <sup>T</sup> . Genome Announcements, 2013, 1, e0016213.   | 0.8 | 4         |
| 3033 | <i>An-1</i> Encodes a Basic Helix-Loop-Helix Protein That Regulates Awn Development, Grain Size, and Grain Number in Rice. Plant Cell, 2013, 25, 3360-3376.  | 3.1 | 226       |
| 3034 | Computational analysis of bacterial RNA-Seq data. Nucleic Acids Research, 2013, 41, e140-e140.   | 6.5 | 573       |
| 3035 | Bacterial Community Response to Petroleum Hydrocarbon Amendments in Freshwater, Marine, and Hypersaline Water-Containing Microcosms. Applied and Environmental Microbiology, 2013, 79, 5927-5935.  | 1.4 | 90        |
| 3036 | Mobility of the Native <i>Bacillus subtilis</i> Conjugative Plasmid pLS20 Is Regulated by Intercellular Signaling. PLoS Genetics, 2013, 9, e1003892.   | 1.5 | 71        |
| 3037 | Tracing the Geographic Origins of Weedy <i>Ipomoea purpurea</i> in the Southeastern United States. Journal of Heredity, 2013, 104, 666-677.  | 1.0 | 12        |
| 3038 | Draft Genome Sequence and Description of <i>Janthinobacterium</i> sp. Strain CG3, a Psychrotolerant Antarctic Supraglacial Stream Bacterium. Genome Announcements, 2013, 1, .  | 0.8 | 10        |
| 3039 | Immune response of the Caribbean sea fan, <i>Gorgonia ventalina</i> , exposed to an Aplanochytrium parasite as revealed by transcriptome sequencing. Frontiers in Physiology, 2013, 4, 180.  | 1.3 | 58        |
| 3040 | Antibacterial Activity of Defensin PaDef from Avocado Fruit ( <i>Persea</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 67 Td (american) <i>coli</i> and <i>Staphylococcus aureus</i> . BioMed Research International, 2013, 2013, 1-9. | 0.9 | 43        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3041 | Development of a real-time polymerase chain reaction assay for single nucleotide polymorphism genotyping codons 136, 154, and 171 of the prnp gene and application to Brazilian sheep herds. <i>Journal of Veterinary Diagnostic Investigation</i> , 2013, 25, 120-124. | 0.5 | 7         |
| 3042 | Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. <i>International Journal of Molecular Sciences</i> , 2013, 14, 15423-15458.   | 1.8 | 22        |
| 3043 | Effects of Copper and Cadmium Exposure on mRNA Expression of Catalase, Glutamine Synthetase, Cytochrome P450 and Heat Shock Protein 70 in Tambaqui Fish ( <i>Colossoma Macropomum</i> ). <i>Gene Expression To Genetical Genomics</i> , 2013, , 1.                      | 1.0 | 7         |
| 3044 | Cloning, Characterization and Effect of TmPGRP-LE Gene Silencing on Survival of <i>Tenebrio Molitor</i> against <i>Listeria monocytogenes</i> Infection. <i>International Journal of Molecular Sciences</i> , 2013, 14, 22462-22482.                                    | 1.8 | 26        |
| 3045 | Barcoding Life's Matrix: Translating Biodiversity Genomics into High School Settings to Enhance Life Science Education. <i>PLoS Biology</i> , 2013, 11, e1001471.   | 2.6 | 21        |
| 3046 | Nearly finished genomes produced using gel microdroplet culturing reveal substantial intraspecies genomic diversity within the human microbiome. <i>Genome Research</i> , 2013, 23, 878-888.  | 2.4 | 53        |
| 3047 | Ancient Properties of Spider Silks Revealed by the Complete Gene Sequence of the Prey-Wrapping Silk Protein (AcSp1). <i>Molecular Biology and Evolution</i> , 2013, 30, 589-601.  | 3.5 | 76        |
| 3048 | Distribution of dehalogenation activity in subseafloor sediments of the Nankai Trough subduction zone. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120249.   | 1.8 | 35        |
| 3049 | Distribution of Long-Range Linkage Disequilibrium and Tajima's D Values in Scandinavian Populations of Norway Spruce ( <i>Picea abies</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 795-806.  | 0.8 | 26        |
| 3050 | Sequence verification of synthetic DNA by assembly of sequencing reads. <i>Nucleic Acids Research</i> , 2013, 41, e25-e25.  | 6.5 | 13        |
| 3051 | SOAPindel: Efficient identification of indels from short paired reads. <i>Genome Research</i> , 2013, 23, 195-200.  | 2.4 | 115       |
| 3052 | Transcriptome and Proteome Data Reveal Candidate Genes for Pollinator Attraction in Sexually Deceptive Orchids. <i>PLoS ONE</i> , 2013, 8, e64621.  | 1.1 | 46        |
| 3053 | Comparative Genomic Analysis of Phylogenetically Closely Related <i>Hydrogenobaculum</i> sp. Isolates from Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2932-2943.  | 1.4 | 39        |
| 3054 | Unraveling the Molecular Basis of Temperature-Dependent Genetic Regulation in <i>Penicillium marneffei</i> . <i>Eukaryotic Cell</i> , 2013, 12, 1214-1224.  | 3.4 | 32        |
| 3055 | Genomic Makeup of the Marine Flavobacterium <i>Nonlabens (Donghaeana) dokdonensis</i> and Identification of a Novel Class of Rhodopsins. <i>Genome Biology and Evolution</i> , 2013, 5, 187-199.  | 1.1 | 84        |
| 3056 | Genome Sequence of <i>Streptomyces viridosporus</i> Strain T7A ATCC 39115, a Lignin-Degrading Actinomycete. <i>Genome Announcements</i> , 2013, 1, .  | 0.8 | 20        |
| 3057 | Filtering duplicate reads from 454 pyrosequencing data. <i>Bioinformatics</i> , 2013, 29, 830-836.  | 1.8 | 18        |
| 3058 | Abundance and Distribution of Transposable Elements in Two <i>Drosophila</i> QTL Mapping Resources. <i>Molecular Biology and Evolution</i> , 2013, 30, 2311-2327.   | 3.5 | 118       |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 3059 | Complete Genome Sequence of Micromonospora Strain L5, a Potential Plant-Growth-Regulating Actinomycete, Originally Isolated from Casuarina equisetifolia Root Nodules. Genome Announcements, 2013, 1, .   | 0.8  | 19        |
| 3060 | Genome Reference and Sequence Variation in the Large Repetitive Central Exon of Human <i>MUC5AC</i> . American Journal of Respiratory Cell and Molecular Biology, 2014, 50, 223-232.  | 1.4  | 32        |
| 3061 | Candida mesorugosasp. nov., a novel yeast species similar to Candida rugosa, isolated from a tertiary hospital in Brazil. Medical Mycology, 2013, 51, 231-242.  | 0.3  | 19        |
| 3062 | Direct assessment of transcription fidelity by high-resolution RNA sequencing. Nucleic Acids Research, 2013, 41, 9090-9104.   | 6.5  | 79        |
| 3063 | Factors Influencing the Sensitivity and Specificity of Conventional Sequencing in Human Immunodeficiency Virus Type 1 Tropism Testing. Journal of Clinical Microbiology, 2013, 51, 444-451.   | 1.8  | 11        |
| 3064 | Multilocus Sequence Typing of Candida tropicalis Shows the Presence of Different Clonal Clusters and Fluconazole Susceptibility Profiles in Sequential Isolates from Candidemia Patients in São Paulo, Brazil. Journal of Clinical Microbiology, 2013, 51, 268-277. | 1.8  | 23        |
| 3065 | Complete Genome Sequences of Elephant Endotheliotropic Herpesviruses 1A and 1B Determined Directly from Fatal Cases. Journal of Virology, 2013, 87, 6700-6712.  | 1.5  | 52        |
| 3066 | A Large Pseudoautosomal Region on the Sex Chromosomes of the Frog Silurana tropicalis. Genome Biology and Evolution, 2013, 5, 1087-1098.  | 1.1  | 26        |
| 3067 | Novel bioresources for studies of <i>Borassia oleracea</i> : identification of a kale <i>MYB</i> transcription factor responsible for glucosinolate production. Plant Biotechnology Journal, 2013, 11, 1017-1027.   | 4.1  | 40        |
| 3068 | Colonization of freshwater biofilms by nitrifying bacteria from activated sludge. FEMS Microbiology Ecology, 2013, 85, 104-115.   | 1.3  | 41        |
| 3069 | Genomic resource development for shellfish of conservation concern. Molecular Ecology Resources, 2013, 13, 295-305.   | 2.2  | 13        |
| 3070 | Origin and demographic history of the endemic Taiwan spruce ( <i>Picea morrisonicola</i> ). Ecology and Evolution, 2013, 3, 3320-3333.  | 0.8  | 10        |
| 3071 | Decreased cortical muscarinic M1 receptors in schizophrenia are associated with changes in gene promoter methylation, mRNA and gene targeting microRNA. Translational Psychiatry, 2013, 3, e230-e230.   | 2.4  | 59        |
| 3072 | The Evolutionary Genetics of the Genes Underlying Phenotypic Associations for Loblolly Pine ( <i>Pinus taeda</i> , Pinaceae). Genetics, 2013, 195, 1353-1372.   | 1.2  | 41        |
| 3073 | Next-generation sequencing reveals cryptic mtDNA diversity of Plasmodium relictum in the Hawaiian Islands. Parasitology, 2013, 140, 1741-1750.  | 0.7  | 16        |
| 3074 | Molecular hyperdiversity defines populations of the nematode <i>Caenorhabditis brenneri</i> . Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11056-11060.  | 3.3  | 90        |
| 3075 | RNA-level unscrambling of fragmented genes in <i>Diplonema</i> mitochondria. RNA Biology, 2013, 10, 301-313.  | 1.5  | 33        |
| 3077 | The physical map of wheat chromosome 1BS provides insights into its gene space organization and evolution. Genome Biology, 2013, 14, R138.  | 13.9 | 40        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3078 | Generation, functional annotation and comparative analysis of black spruce ( <i>Picea mariana</i> ) ESTs: an important conifer genomic resource. <i>BMC Genomics</i> , 2013, 14, 702.   | 1.2 | 10        |
| 3079 | Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI943.. <i>Standards in Genomic Sciences</i> , 2013, 9, 232-242.   | 1.5 | 3         |
| 3080 | Genome sequence of the <i>Trifolium rueppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012.. <i>Standards in Genomic Sciences</i> , 2013, 9, 283-293.  | 1.5 | 3         |
| 3081 | <i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , 2013, 7, 449-468.                                  | 1.5 | 31        |
| 3082 | Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23T. <i>Standards in Genomic Sciences</i> , 2013, 8, 375-388.   | 1.5 | 44        |
| 3083 | Permanent draft genome sequences of the symbiotic nitrogen fixing <i>Ensifer meliloti</i> strains BO21CC and AK58. <i>Standards in Genomic Sciences</i> , 2013, 9, 352-333.   | 1.5 | 7         |
| 3084 | Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. <i>Standards in Genomic Sciences</i> , 2013, 9, 243-253.  | 1.5 | 10        |
| 3085 | Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. <i>Standards in Genomic Sciences</i> , 2013, 9, 254-263.  | 1.5 | 0         |
| 3086 | Genome sequence of <i>Ensifer arboris</i> strain LMG 14919T; a microsymbiont of the legume <i>Prosopis chilensis</i> growing in Kosti, Sudan. <i>Standards in Genomic Sciences</i> , 2013, 9, 473-483.                                | 1.5 | 6         |
| 3087 | Genome sequence of <i>Rhizobium leguminosarum</i> bv <i>trifolii</i> strain WSM1689, the microsymbiont of the one flowered clover <i>Trifolium uniflorum</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 527-539.               | 1.5 | 27        |
| 3088 | Permanent draft genome sequence of <i>Comamonas testosteroni</i> KF-1. <i>Standards in Genomic Sciences</i> , 2013, 8, 239-254.   | 1.5 | 14        |
| 3089 | Complete genome sequence of <i>Mesorhizobium australicum</i> type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013, 9, 410-419.   | 1.5 | 11        |
| 3090 | Cloning and Purification of IpaC Antigen from <i>Shigella flexneri</i> : Proposal of a New Methodology. <i>Protein and Peptide Letters</i> , 2013, 20, 133-139.   | 0.4 | 3         |
| 3091 | Complete genome sequence of <i>Enterobacter</i> sp. IIT-BT 08: A potential microbial strain for high rate hydrogen production. <i>Standards in Genomic Sciences</i> , 2013, 9, 359-369.   | 1.5 | 16        |
| 3092 | Error analysis of idealized nanopore sequencing. <i>Electrophoresis</i> , 2013, 34, 2137-2144.  | 1.3 | 30        |
| 3093 | Complete Genome of <i>Enterobacteriaceae</i> Bacterium Strain FGI 57, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <i>Genome Announcements</i> , 2013, 1, .   | 0.8 | 4         |
| 3094 | Genome Sequence of <i>Salmonella enterica</i> Serotype Tennessee Strain CDC07-0191, Implicated in the 2006-2007 Multistate Food-Borne Outbreak Linked to Peanut Butter in the United States. <i>Genome Announcements</i> , 2013, 1, . | 0.8 | 4         |
| 3095 | Pharmacogenetics in American Indian populations. <i>Pharmacogenetics and Genomics</i> , 2013, 23, 403-414.  | 0.7 | 54        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3096 | Sequencing and De Novo Analysis of the Hemocytes Transcriptome in <i>Litopenaeus vannamei</i> Response to White Spot Syndrome Virus Infection. <i>PLoS ONE</i> , 2013, 8, e76718.  | 1.1 | 79        |
| 3097 | Genomics and genetics of <i>Sulfolobus islandicus</i> LAL14/1, a model hyperthermophilic archaeon. <i>Open Biology</i> , 2013, 3, 130010.  | 1.5 | 55        |
| 3098 | Development of real-time reverse transcription polymerase chain reaction assays to quantify insulin-like growth factor receptor and insulin receptor expression in equine tissue. <i>Onderstepoort Journal of Veterinary Research</i> , 2013, 80, 402. | 0.6 | 1         |
| 3099 | Caracteriza o do gene <i>vip3A</i> e toxicidade da prote na Vip3Aa50   lagarta-do-cartucho e   lagarta-da-soja. <i>Pesquisa Agropecuaria Brasileira</i> , 2013, 48, 1220-1227.   | 0.9 | 9         |
| 3100 | Molecular identification based on coat protein sequences of the Barley yellow dwarf virus from Brazil. <i>Scientia Agricola</i> , 2013, 70, 428-434.   | 0.6 | 3         |
| 3101 | Identification and association of polymorphisms in <i>CAPN1</i> and <i>CAPN3</i> candidate genes related to performance and meat quality traits in chickens. <i>Genetics and Molecular Research</i> , 2013, 12, 472-482.                               | 0.3 | 23        |
| 3102 | Polymorphisms in <i>FGFBP1</i> and <i>FGFBP2</i> genes associated with carcass and meat quality traits in chickens. <i>Genetics and Molecular Research</i> , 2013, 12, 208-222.  | 0.3 | 11        |
| 3103 | Insights into the <i>Melipona scutellaris</i> (Hymenoptera, Apidae, Meliponini) fat body transcriptome. <i>Genetics and Molecular Biology</i> , 2013, 36, 292-297.   | 0.6 | 12        |
| 3104 | Canine distemper virus infection in a lesser grison ( <i>Galictis cuja</i> ): first report and virus phylogeny. <i>Pesquisa Veterinaria Brasileira</i> , 2013, 33, 247-250.  | 0.5 | 14        |
| 3105 | 10-Deoxy-10-hydroxyascoclorin, a New Cell Migration Inhibitor and Other Metabolites from <i>Acremonium</i> sp., a Fungal Endophyte in <i>Ephedra trifurca</i> . <i>Natural Product Communications</i> , 2013, 8, 1934578X1300800.                      | 0.2 | 2         |
| 3106 | Functional analysis of the acetic acid resistance ( <i>aar</i> ) gene cluster in <i>Acetobacter aceti</i> strain 1023. <i>Acetic Acid Bacteria</i> , 2013, 2, 3.   | 1.0 | 11        |
| 3107 | Comparative Chloroplast Genomes of <i>Camellia</i> Species. <i>PLoS ONE</i> , 2013, 8, e73053.   | 1.1 | 141       |
| 3108 | Bioactivity of Fungal Endophytes as a Function of Endophyte Taxonomy and the Taxonomy and Distribution of Their Host Plants. <i>PLoS ONE</i> , 2013, 8, e73192.  | 1.1 | 91        |
| 3109 | Base-Calling Algorithm with Vocabulary (BCV) Method for Analyzing Population Sequencing Chromatograms. <i>PLoS ONE</i> , 2013, 8, e54835.  | 1.1 | 11        |
| 3110 | An Integrated Transcriptome-Wide Analysis of Cave and Surface Dwelling <i>Astyanax mexicanus</i> . <i>PLoS ONE</i> , 2013, 8, e55659.  | 1.1 | 69        |
| 3111 | Compression of FASTQ and SAM Format Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e59190.  | 1.1 | 167       |
| 3112 | Genetic Diversity and Lack of Artemisinin Selection Signature on the <i>Plasmodium falciparum</i> ATP6 in the Greater Mekong Subregion. <i>PLoS ONE</i> , 2013, 8, e59192.   | 1.1 | 11        |
| 3113 | On Hepatitis C Virus Evolution: The Interaction between Virus and Host towards Treatment Outcome. <i>PLoS ONE</i> , 2013, 8, e62393.   | 1.1 | 10        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3114 | A Rapid Transcriptome Response Is Associated with Desiccation Resistance in Aerially-Exposed Killifish Embryos. PLoS ONE, 2013, 8, e64410.  | 1.1 | 17        |
| 3115 | Simplified Large-Scale Sanger Genome Sequencing for Influenza A/H3N2 Virus. PLoS ONE, 2013, 8, e64785.  | 1.1 | 24        |
| 3116 | SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. PLoS ONE, 2013, 8, e65632.   | 1.1 | 104       |
| 3117 | Unbiased Approach for Virus Detection in Skin Lesions. PLoS ONE, 2013, 8, e65953.   | 1.1 | 55        |
| 3118 | Performance Comparison of Bench-Top Next Generation Sequencers Using Microdroplet PCR-Based Enrichment for Targeted Sequencing in Patients with Autism Spectrum Disorder. PLoS ONE, 2013, 8, e74167.                  | 1.1 | 31        |
| 3119 | Development of Genomic Resources for a thraustochytrid Pathogen and Investigation of Temperature Influences on Gene Expression. PLoS ONE, 2013, 8, e74196.  | 1.1 | 20        |
| 3120 | NeSSM: A Next-Generation Sequencing Simulator for Metagenomics. PLoS ONE, 2013, 8, e75448.  | 1.1 | 57        |
| 3121 | Ectopic KIT Copy Number Variation Underlies Impaired Migration of Primordial Germ Cells Associated with Gonadal Hypoplasia in Cattle ( <i>Bos taurus</i> ). PLoS ONE, 2013, 8, e75659.                                | 1.1 | 29        |
| 3122 | Expressed Sequence Tags for Bovine Muscle Satellite Cells, Myotube Formed-Cells and Adipocyte-Like Cells. PLoS ONE, 2013, 8, e79780.  | 1.1 | 13        |
| 3123 | Can RNA-Seq Resolve the Rapid Radiation of Advanced Moths and Butterflies (Hexapoda: Lepidoptera:)? <i>Tj ETQq1 1 0.784314 rrgBT /Over</i>  | 1.1 | 89        |
| 3124 | Analysis of the Genome of a Korean Isolate of the <i>Pieris rapae</i> Granulovirus Enabled by Its Separation from Total Host Genomic DNA by Pulse-Field Electrophoresis. PLoS ONE, 2013, 8, e84183.                   | 1.1 | 3         |
| 3125 | An Extensive Evaluation of Read Trimming Effects on Illumina NGS Data Analysis. PLoS ONE, 2013, 8, e85024.  | 1.1 | 358       |
| 3126 | The Use of a Combination of <i>alkB</i> Primers to Better Characterize the Distribution of Alkane-Degrading Bacteria. PLoS ONE, 2013, 8, e66565.  | 1.1 | 52        |
| 3127 | <i>Vulcanolepas scotiaensis</i> sp. nov., a new deep-sea scalpelliform barnacle (Eolepadidae: Neolepadinae) from hydrothermal vents in the Scotia Sea, Antarctica. <i>Zootaxa</i> , 2013, 3745, 551.                  | 0.2 | 28        |
| 3128 | Biotechnology of polyketides: new breath of life for the novel antibiotic genetic pathways discovery through metagenomics. <i>Brazilian Journal of Microbiology</i> , 2013, 44, 1007-1034.                            | 0.8 | 67        |
| 3129 | Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. <i>Frontiers in Microbiology</i> , 2013, 4, 115.   | 1.5 | 53        |
| 3130 | The complete nucleotide sequence of the genome of Barley yellow dwarf virus-RMV reveals it to be a new Ploverivirus distantly related to other yellow dwarf viruses. <i>Frontiers in Microbiology</i> , 2013, 4, 205. | 1.5 | 52        |
| 3131 | Comparative genomics of freshwater Fe-oxidizing bacteria: implications for physiology, ecology, and systematics. <i>Frontiers in Microbiology</i> , 2013, 4, 254.   | 1.5 | 188       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3132 | Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. <i>Frontiers in Microbiology</i> , 2013, 4, 282.                                | 1.5 | 44        |
| 3133 | POP BAM: Tools for Evolutionary Analysis of Short Read Sequence Alignments. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S12751.   | 0.6 | 15        |
| 3134 | Novel ERBB Receptor Feedback Inhibitor 1 (ERRFI1)+ 808 T/G Polymorphism Confers Protective Effect on Diabetic Nephropathy in a Korean Population. <i>Disease Markers</i> , 2013, 34, 113-120.   | 0.6 | 4         |
| 3135 | Microsatellite marker discovery using single molecule real-time circular consensus sequencing on the Pacific Biosciences RS. <i>BioTechniques</i> , 2013, 55, 253-256.  | 0.8 | 24        |
| 3136 | Low-Penetrance Variants and Susceptibility to Sporadic Malignant Melanoma. , 2013, , .  |     | 0         |
| 3137 | Shallow-Water Northern Hemisphere Jaera (Crustacea, Isopoda, Janiridae) Found on Whale Bones in the Southern Ocean Deep Sea: Ecology and Description of <i>Jaera tyleri</i> sp. nov. <i>PLoS ONE</i> , 2014, 9, e93018.                       | 1.1 | 9         |
| 3138 | Comparative Transcriptome of Wild Type and Selected Strains of the Microalgae <i>Tisochrysis lutea</i> Provides Insights into the Genetic Basis, Lipid Metabolism and the Life Cycle. <i>PLoS ONE</i> , 2014, 9, e86889.                      | 1.1 | 52        |
| 3139 | Antimicrobial Susceptibility of <i>Vibrio vulnificus</i> and <i>Vibrio parahaemolyticus</i> Recovered from Recreational and Commercial Areas of Chesapeake Bay and Maryland Coastal Bays. <i>PLoS ONE</i> , 2014, 9, e89616.                  | 1.1 | 136       |
| 3140 | Patterns of Nucleotide Diversity at Photoperiod Related Genes in Norway Spruce [ <i>Picea abies</i> (L.) Karst.]. <i>PLoS ONE</i> , 2014, 9, e95306.  | 1.1 | 20        |
| 3141 | Identification of a Retroelement from the Resurrection Plant <i>Boea hygrometrica</i> That Confers Osmotic and Alkaline Tolerance in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2014, 9, e98098.   | 1.1 | 19        |
| 3142 | Recurrent Respiratory Papillomatosis: HPV Genotypes and Risk of High-Grade Laryngeal Neoplasia. <i>PLoS ONE</i> , 2014, 9, e99114.  | 1.1 | 75        |
| 3143 | IIS “ Integrated Interactome System: A Web-Based Platform for the Annotation, Analysis and Visualization of Protein-Metabolite-Gene-Drug Interactions by Integrating a Variety of Data Sources and Tools. <i>PLoS ONE</i> , 2014, 9, e100385. | 1.1 | 58        |
| 3144 | Patterns of MiRNA Expression in Arctic Charr Development. <i>PLoS ONE</i> , 2014, 9, e106084.   | 1.1 | 22        |
| 3145 | Specific Microbiome Changes in a Mouse Model of Parenteral Nutrition Associated Liver Injury and Intestinal Inflammation. <i>PLoS ONE</i> , 2014, 9, e110396.   | 1.1 | 64        |
| 3146 | Population Structure of <i>Geosmithia morbida</i> , the Causal Agent of Thousand Cankers Disease of Walnut Trees in the United States. <i>PLoS ONE</i> , 2014, 9, e112847.  | 1.1 | 38        |
| 3147 | Phages of non-dairy lactococci: isolation and characterization of $\phi$ L47, a phage infecting the grass isolate <i>Lactococcus lactis</i> ssp. <i>cremoris</i> DPC6860. <i>Frontiers in Microbiology</i> , 2014, 4, 417.                    | 1.5 | 10        |
| 3148 | In Phase HLA Genotyping by Next Generation Sequencing “ A Comparison Between Two Massively Parallel Sequencing Bench-Top Systems, the Roche GS Junior and Ion Torrent PGM. , 2014, , .  |     | 3         |
| 3149 | The expression sequence tag is an effective method for screening DNA segments that predict urinary bladder transitional cell carcinoma prognosis. <i>OncoTargets and Therapy</i> , 2014, 7, 1777.   | 1.0 | 0         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3150 | Performance of pineapple slips inoculated with diazotrophic phosphate-solubilizing bacteria and rock phosphate. <i>Revista Ceres</i> , 2014, 61, 414-423.   | 0.1 | 0         |
| 3151 | Four Generations of Sequencing- Is it Ready for the Clinic Yet?. <i>Journal of Next Generation Sequencing &amp; Applications</i> , 2014, 01, .  | 0.3 | 5         |
| 3152 | A Novel Complex Recombinant Form of Type 48-Related Human Adenovirus Species D Isolated in Japan. <i>Japanese Journal of Infectious Diseases</i> , 2014, 67, 282-287.   | 0.5 | 13        |
| 3153 | First Evaluation of an Outbreak of Bovine Babesiosis and Anaplasmosis in Southern Brazil Using Multiplex PCR. <i>Korean Journal of Parasitology</i> , 2014, 52, 507-511.  | 0.5 | 16        |
| 3154 | Identification of a novel de novo deletion in <i>RAF1</i> associated with biventricular hypertrophy in Noonan syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2014, 164, 2069-2073.   | 0.7 | 5         |
| 3155 | DNA Storage under High Temperature Conditions Does Not Affect Performance in Human Leukocyte Antigen Genotyping via Next-Generation Sequencing (DNA Integrity Maintained in Extreme Conditions). <i>Biopreservation and Biobanking</i> , 2014, 12, 402-408. | 0.5 | 5         |
| 3156 | Induction of Diabetes in the RIP-B7.1 Mouse Model Is Critically Dependent on TLR3 and MyD88 Pathways and Is Associated With Alterations in the Intestinal Microbiome. <i>Diabetes</i> , 2014, 63, 619-631.  | 0.3 | 44        |
| 3157 | Comparative genomics of planktonic Flavobacteriaceae from the Gulf of Maine using metagenomic data. <i>Microbiome</i> , 2014, 2, 34.  | 4.9 | 28        |
| 3158 | An integrated transcriptome and expressed variant analysis of sepsis survival and death. <i>Genome Medicine</i> , 2014, 6, 111.   | 3.6 | 70        |
| 3159 | SNPest: a probabilistic graphical model for estimating genotypes. <i>BMC Research Notes</i> , 2014, 7, 698.   | 0.6 | 6         |
| 3160 | A review of software for analyzing molecular sequences. <i>BMC Research Notes</i> , 2014, 7, 830.   | 0.6 | 63        |
| 3161 | Transcriptomic complexity in young maize primary roots in response to low water potentials. <i>BMC Genomics</i> , 2014, 15, 741.  | 1.2 | 69        |
| 3162 | Adaptive reference-free compression of sequence quality scores. <i>Bioinformatics</i> , 2014, 30, 24-30.  | 1.8 | 31        |
| 3163 | 16S rRNA Gene-Based Identification of Bacteria and Archaea using the EzTaxon Server. <i>Methods in Microbiology</i> , 2014, 41, 61-74.  | 0.4 | 64        |
| 3164 | TIPP: taxonomic identification and phylogenetic profiling. <i>Bioinformatics</i> , 2014, 30, 3548-3555.   | 1.8 | 93        |
| 3165 | Genome-wide profiling of DNA methylation and gene expression in <i>Crassostrea gigas</i> male gametes. <i>Frontiers in Physiology</i> , 2014, 5, 224.   | 1.3 | 92        |
| 3166 | Historical Perspective, Development and Applications of Next-Generation Sequencing in Plant Virology. <i>Viruses</i> , 2014, 6, 106-136.  | 1.5 | 225       |
| 3167 | Widespread occurrence of organelle genome-encoded 5S rRNAs including permuted molecules. <i>Nucleic Acids Research</i> , 2014, 42, 13764-13777.   | 6.5 | 129       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3168 | Target Capture and Massive Sequencing of Genes Transcribed in <i>Mytilus galloprovincialis</i> . <i>BioMed Research International</i> , 2014, 2014, 1-9.  | 0.9 | 9         |
| 3169 | Development of EST-SSR markers and construction of a linkage map in faba bean (&i>Vicia) Tj ETQq1 1 0.784314 rgBT /Overlock 11  | 0.9 | 30        |
| 3170 | Long Non-Coding RNA and Alternative Splicing Modulations in Parkinson's Leukocytes Identified by RNA Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003517.  | 1.5 | 167       |
| 3171 | Comparative Analysis of Salivary Gland Transcriptomes of <i>Phlebotomus orientalis</i> Sand Flies from Endemic and Non-endemic Foci of Visceral Leishmaniasis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2709.  | 1.3 | 53        |
| 3172 | Correcting for Sequencing Error in Maximum Likelihood Phylogeny Inference. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2545-2552.  | 0.8 | 10        |
| 3173 | <i>Wolbachia</i> is not all about sex: male-feminizing <i>Wolbachia</i> alters the leafhopper <i>Zyginidia pullula</i> transcriptome in a mainly sex-independent manner. <i>Frontiers in Microbiology</i> , 2014, 5, 430.   | 1.5 | 15        |
| 3174 | Capacity of Aromatic Compound Degradation by Bacteria from Amazon Dark Earth. <i>Diversity</i> , 2014, 6, 339-353.  | 0.7 | 20        |
| 3175 | Characterization of HPV DNA methylation of contiguous CpG sites by bisulfite treatment and massively parallel sequencing—the FRAGMENT approach. <i>Frontiers in Genetics</i> , 2014, 5, 150.  | 1.1 | 8         |
| 3176 | AlienTrimmer removes adapter oligonucleotides with high sensitivity in short-insert paired-end reads. Commentary on Turner (2014) Assessment of insert sizes and adapter content in FASTQ data from NexteraXT libraries. <i>Frontiers in Genetics</i> , 2014, 5, 130. | 1.1 | 36        |
| 3177 | Complete Genome Sequence of <i>Corynebacterium falsenii</i> DSM 44353 To Study the Evolution of <i>Corynebacterium</i> Cluster 3 Species. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 5         |
| 3178 | Draft Genome Assembly of <i>Acinetobacter baumannii</i> ATCC 19606. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 20        |
| 3179 | Finished Genome of <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> Strain CP4, an Applied Ethanol Producer. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 13        |
| 3180 | Draft Genome Assembly of <i>Bordetella bronchiseptica</i> ATCC 10580, a Historical Canine Clinical Isolate. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 1         |
| 3181 | Draft Genome Assembly of <i>Delftia acidovorans</i> Type Strain 2167. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 0         |
| 3182 | Whole-Genome Sequences of Nine <i>Francisella</i> Isolates. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 5         |
| 3183 | Draft Genome Assembly of <i>Neisseria lactamica</i> Type Strain A7515. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 1         |
| 3184 | Complete Genome Assembly of Reference Strain <i>Ochrobactrum anthropi</i> ATCC 49687. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 3         |
| 3185 | Genome Assembly of <i>Serratia marcescens</i> Type Strain ATCC 13880. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 18        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3186 | Complete Genome Assembly of <i>Enterococcus faecalis</i> 29212, a Laboratory Reference Strain. <i>Genome Announcements</i> , 2014, 2, .                                 | 0.8 | 13        |
| 3187 | Complete Genome Assembly of <i>Escherichia coli</i> ATCC 25922, a Serotype O6 Reference Strain. <i>Genome Announcements</i> , 2014, 2, .                                | 0.8 | 44        |
| 3188 | Whole-Genome Sequence of <i>Listeria monocytogenes</i> Type Strain 53 XXIII. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 0         |
| 3189 | Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Type Strain 810-2 (ATCC 13637). <i>Genome Announcements</i> , 2014, 2, .                                | 0.8 | 16        |
| 3190 | Complete Genome Assembly of <i>Streptococcus pyogenes</i> ATCC 19615, a Group A $\hat{A}$ -Hemolytic Reference Strain. <i>Genome Announcements</i> , 2014, 2, .         | 0.8 | 1         |
| 3191 | Genome Assembly of <i>Shigella flexneri</i> ATCC 12022, a Quality Control Reference Strain. <i>Genome Announcements</i> , 2014, 2, .                                    | 0.8 | 2         |
| 3192 | Whole-Genome <i>Yersinia</i> sp. Assemblies from 10 Diverse Strains. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 8         |
| 3193 | Complete Genome Assembly of <i>Staphylococcus epidermidis</i> AmMS 205. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 3         |
| 3194 | Draft Genome Sequence of <i>Syntrophorhabdus aromaticivorans</i> Strain UI, a Mesophilic Aromatic Compound-Degrading Syntroph. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 23        |
| 3195 | Complete Genome Assembly of <i>Corynebacterium</i> sp. Strain ATCC 6931. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 0         |
| 3196 | Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis Strain SEJ. <i>Genome Announcements</i> , 2014, 2, .                  | 0.8 | 1         |
| 3197 | Whole-Genome Assemblies of 56 <i>Burkholderia</i> Species. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 27        |
| 3198 | Anal microbiota profiles in HIV-positive and HIV-negative MSM. <i>Aids</i> , 2014, 28, 753-760.   | 1.0 | 63        |
| 3199 | Toward Efficient Variant Calling Inside Main-Memory Database Systems. , 2014, , .   |     | 2         |
| 3200 | Genome Sequence of <i>Serratia plymuthica</i> RVH1, Isolated from a Raw Vegetable-Processing Line. <i>Genome Announcements</i> , 2014, 2, .                             | 0.8 | 7         |
| 3201 | Draft Genome Sequence of the Multidrug-Resistant Clinical Isolate <i>Dermabacter hominis</i> 1368. <i>Genome Announcements</i> , 2014, 2, .                             | 0.8 | 2         |
| 3202 | Draft Genome Assembly of <i>Pseudomonas aeruginosa</i> Quality Control Reference Strain Boston 41501. <i>Genome Announcements</i> , 2014, 2, .                          | 0.8 | 2         |
| 3203 | Microbial population in an aerated thermophilic reactor that treats recycled cardboard plant wastewater. <i>Journal of Water Process Engineering</i> , 2014, 4, 74-81.  | 2.6 | 6         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3204 | Draft Genome Assemblies of <i>Proteus mirabilis</i> ATCC 7002 and <i>Proteus vulgaris</i> ATCC 49132. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 7         |
| 3205 | Full-Genome Assembly of Reference Strain <i>Providencia stuartii</i> ATCC 33672. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 12        |
| 3206 | Studying the organization of genes encoding plant cell wall degrading enzymes in <i>Chrysomela tremula</i> provides insights into a leaf beetle genome. <i>Insect Molecular Biology</i> , 2014, 23, 286-300.   | 1.0 | 14        |
| 3207 | <i>Halorhabdus tiamateae</i> proteogenomics and glycosidase activity measurements identify the first cultivated euryarchaeon from a deep-sea anoxic brine lake as potential polysaccharide degrader. <i>Environmental Microbiology</i> , 2014, 16, 2525-2537.  | 1.8 | 41        |
| 3208 | Novel polymorphisms in the promoter region of the perforin gene among distinct Brazilian populations and their functional impact. <i>International Journal of Immunogenetics</i> , 2014, 41, 198-205.  | 0.8 | 0         |
| 3210 | Clinal Variation at Phenology-Related Genes in Spruce: Parallel Evolution in <i>FTL2</i> and <i>Gigantea</i> ?. <i>Genetics</i> , 2014, 197, 1025-1038.  | 1.2 | 41        |
| 3211 | Integrated Sequence Analysis Pipeline Provides One-Stop Solution for Identifying Disease-Causing Mutations. <i>Human Mutation</i> , 2014, 35, 1427-1435.   | 1.1 | 31        |
| 3212 | Genomes correction and assembling: present methods and tools. <i>Proceedings of SPIE</i> , 2014, , .   | 0.8 | 6         |
| 3213 | Comparative and Evolutionary Analysis of Major Peanut Allergen Gene Families. <i>Genome Biology and Evolution</i> , 2014, 6, 2468-2488.  | 1.1 | 15        |
| 3214 | Construction of Full-Length cDNA Library and Development of EST-Derived Simple Sequence Repeat (EST-SSR) Markers in <i>Senecio scandens</i> . <i>Biochemical Genetics</i> , 2014, 52, 494-508.   | 0.8 | 5         |
| 3215 | European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. <i>Nature Communications</i> , 2014, 5, 5770.  | 5.8 | 382       |
| 3216 | Mitochondrial and nuclear phylogenetic analysis with Sanger and next-generation sequencing shows that, in Área de Conservación Guanacaste, northwestern Costa Rica, the skipper butterfly named <i>Urbanus belli</i> (family Hesperidae) comprises three morphologically cryptic species. <i>BMC Evolutionary Biology</i> , 2014, 14, 153. | 3.2 | 27        |
| 3217 | A novel <i>Bacillus pumilus</i> -related strain from tropical landfarm soil is capable of rapid dibenzothiophene degradation and biodesulfurization. <i>BMC Microbiology</i> , 2014, 14, 257.  | 1.3 | 11        |
| 3218 | Major haplotype divergence including multiple germin-like protein genes, at the wheat <i>Sr2</i> adult plant stem rust resistance locus. <i>BMC Plant Biology</i> , 2014, 14, 379.   | 1.6 | 36        |
| 3219 | Genome Assembly of Methicillin-Resistant Quality Control Strain <i>Staphylococcus aureus</i> CDC73-57501 (ATCC 29247). <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 1         |
| 3220 | A Bayesian MCMC Approach to Assess the Complete Distribution of Fitness Effects of New Mutations: Uncovering the Potential for Adaptive Walks in Challenging Environments. <i>Genetics</i> , 2014, 196, 841-852.   | 1.2 | 100       |
| 3221 | Comparison of Varicella-Zoster Virus RNA Sequences in Human Neurons and Fibroblasts. <i>Journal of Virology</i> , 2014, 88, 5877-5880.   | 1.5 | 62        |
| 3222 | Navigating the Rapids: The Development of Regulated Next-Generation Sequencing-Based Clinical Trial Assays and Companion Diagnostics. <i>Frontiers in Oncology</i> , 2014, 4, 78.  | 1.3 | 71        |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3223 | Single Nucleotide Polymorphisms (SNPs). , 2014, , 55-80.   |     | 2         |
| 3224 | Whole-Exome Sequencing Data “ Identifying Somatic Mutations. , 2014, , 419-427.  |     | 0         |
| 3225 | Adaptive response of <i>Amphibacillus xylanus</i> to normal aerobic and forced oxidative stress conditions. <i>Microbiology (United Kingdom)</i> , 2014, 160, 340-352.   | 0.7 | 3         |
| 3226 | Expressed Sequence Tag-Simple Sequence Repeat (EST-SSR) Marker Resources for Diversity Analysis of Mango ( <i>Mangifera indica</i> L.). <i>Diversity</i> , 2014, 6, 72-87.   | 0.7 | 30        |
| 3227 | Whole-Genome Sequences of 24 <i>Brucella</i> Strains. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 10        |
| 3228 | Transcriptome sequencing and analysis of the zoonotic parasite <i>Spirometra erinacei</i> spargana (plerocercoids). <i>Parasites and Vectors</i> , 2014, 7, 368.   | 1.0 | 15        |
| 3229 | Landscape of Standing Variation for Tandem Duplications in <i>Drosophila yakuba</i> and <i>Drosophila simulans</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 1750-1766.   | 3.5 | 89        |
| 3230 | Multi-perspective quality control of Illumina exome sequencing data using QC3. <i>Genomics</i> , 2014, 103, 323-328.   | 1.3 | 79        |
| 3231 | Insights into the transcriptome of the marine copepod <i>Calanus helgolandicus</i> feeding on the oxyllipin-producing diatom <i>Skeletonema marinoi</i> . <i>Harmful Algae</i> , 2014, 31, 153-162.  | 2.2 | 31        |
| 3232 | The evolution and functional divergence of the beta-carotene oxygenase gene family in teleost fish—Exemplified by Atlantic salmon. <i>Gene</i> , 2014, 543, 268-274.   | 1.0 | 14        |
| 3233 | A novel highly reactive Fab antibody for breast cancer tissue diagnostics and staging also discriminates a subset of good prognostic triple-negative breast cancers. <i>Cancer Letters</i> , 2014, 343, 275-285.   | 3.2 | 11        |
| 3234 | Diversification of 13S globulins, allergenic seed storage proteins, of common buckwheat. <i>Food Chemistry</i> , 2014, 155, 192-198.   | 4.2 | 16        |
| 3235 | Complete genome of a new <i>Firmicutes</i> species belonging to the dominant human colonic microbiota (“ <i>Uminococcus bicirculans</i> ”) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , 2014, 16, 2879-2890. | 1.8 | 62        |
| 3236 | An assay for quantitative virulence in <i>Rhynchosporium commune</i> reveals an association between effector genotype and virulence. <i>Plant Pathology</i> , 2014, 63, 405-414.   | 1.2 | 30        |
| 3237 | Biominerall Proteins from <i>Mytilus edulis</i> Mantle Tissue Transcriptome. <i>Marine Biotechnology</i> , 2014, 16, 34-45.  | 1.1 | 55        |
| 3238 | Identification, characterisation and molecular modelling of two <i>AP</i> endonucleases from base excision repair pathway in sugarcane provide insights on the early evolution of green plants. <i>Plant Biology</i> , 2014, 16, 622-631.                                      | 1.8 | 5         |
| 3239 | Improved reduced representation bisulfite sequencing for epigenomic profiling of clinical samples. <i>Biological Procedures Online</i> , 2014, 16, 1.  | 1.4 | 44        |
| 3240 | Fungal Endophytes of Aquatic Macrophytes: Diverse Host-Generalists Characterized by Tissue Preferences and Geographic Structure. <i>Microbial Ecology</i> , 2014, 67, 735-747.   | 1.4 | 57        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3241 | Analysis of expressed sequence tags from <i>Centella asiatica</i> (L.) Urban hairy roots elicited by methyl jasmonate to discover genes related to cytochrome P450s and glucosyltransferases. <i>Plant Biotechnology Reports</i> , 2014, 8, 211-220. | 0.9 | 19        |
| 3242 | High prevalence of hepatitis B virus subgenotypes A1 and D4 in Maranhão state, Northeast Brazil. <i>Infection, Genetics and Evolution</i> , 2014, 24, 68-75.   | 1.0 | 28        |
| 3243 | Isolation, growth and genome of the Rhodothermus RM378 thermophilic bacteriophage. <i>Extremophiles</i> , 2014, 18, 261-270.   | 0.9 | 18        |
| 3244 | Response of the Archaeal Community to Simulated Petroleum Hydrocarbon Contamination in Marine and Hypersaline Ecosystems. <i>Water, Air, and Soil Pollution</i> , 2014, 225, 1.  | 1.1 | 12        |
| 3245 | From cheek swabs to consensus sequences: an A to Z protocol for high-throughput DNA sequencing of complete human mitochondrial genomes. <i>BMC Genomics</i> , 2014, 15, 68.  | 1.2 | 27        |
| 3246 | QTrim: a novel tool for the quality trimming of sequence reads generated using the Roche/454 sequencing platform. <i>BMC Bioinformatics</i> , 2014, 15, 33.  | 1.2 | 28        |
| 3247 | Genetic data generated from virus-host complexes obtained by membrane co-immobilization are equivalent to data obtained from tangential filtrate virus concentrates and virus cultures. <i>Virus Genes</i> , 2014, 48, 160-167.                      | 0.7 | 2         |
| 3248 | Genome sequencing of high-penicillin producing industrial strain of <i>Penicillium chrysogenum</i> . <i>BMC Genomics</i> , 2014, 15, S11.  | 1.2 | 41        |
| 3249 | Genetic Origins of Lactase Persistence and the Spread of Pastoralism in Africa. <i>American Journal of Human Genetics</i> , 2014, 94, 496-510.   | 2.6 | 174       |
| 3250 | Monitoring of Calicivirus among day-care children: Evidence of asymptomatic viral excretion and first report of GI.7 norovirus and GI.3 sapovirus in Brazil. <i>Journal of Medical Virology</i> , 2014, 86, 1569-1575.                               | 2.5 | 23        |
| 3251 | Patterns of coding variation in the complete exomes of three Neandertals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6666-6671.   | 3.3 | 223       |
| 3252 | Evolutionary history of <i>Picea canadensis</i> (Mill.) B.S.P. in the Great Lakes region: homoploid hybrid origin and Pleistocene expansion. <i>Molecular Ecology</i> , 2014, 23, 343-359.   | 2.0 | 97        |
| 3253 | Natural variation of TaGAS7-A1 affects grain length in common wheat under multiple cultivation conditions. <i>Molecular Breeding</i> , 2014, 34, 937-947.  | 1.0 | 102       |
| 3254 | Phylogeny of harvestmen family Gonyleptidae inferred from a multilocus approach (Arachnida: Tardigrada). <i>Journal of Molecular Evolution</i> , 2014, 78, 1-13.   | 1.5 | 66        |
| 3255 | Molecular Testing in Cancer. , 2014, , .   |     | 2         |
| 3256 | Archaeal diversity and the extent of iron and manganese pyritization in sediments from a tropical mangrove creek (Cardoso Island, Brazil). <i>Estuarine, Coastal and Shelf Science</i> , 2014, 146, 1-13.  | 0.9 | 18        |
| 3257 | Characterization of EST-SSR markers in durum wheat EST library and functional analysis of SSR-containing EST fragments. <i>Molecular Genetics and Genomics</i> , 2014, 289, 625-640.   | 1.0 | 17        |
| 3258 | Three-stage quality control strategies for DNA re-sequencing data. <i>Briefings in Bioinformatics</i> , 2014, 15, 879-889.   | 3.2 | 141       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3259 | <sc>HLA</sc> typing by next-generation sequencing "Getting closer to reality. Tissue Antigens, 2014, 83, 65-75.  | 1.0 | 80        |
| 3260 | Major repeat components covering one-third of the ginseng (<i>Panax ginseng</i> C.A.) Tj ETQq1 1 0,784314,rgBT /O  | 2.8 | 66        |
| 3261 | A general framework for estimating the relative pathogenicity of human genetic variants. Nature Genetics, 2014, 46, 310-315.   | 9.4 | 5,167     |
| 3262 | The Ability of Bifidobacteria To Degrade Arabinoxylan Oligosaccharide Constituents and Derived Oligosaccharides Is Strain Dependent. Applied and Environmental Microbiology, 2014, 80, 204-217.              | 1.4 | 114       |
| 3264 | Molecular characterization of metalloproteases from Bothrops alternatus snake venom. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2014, 12, 74-83.                               | 0.4 | 6         |
| 3265 | tassel-less1 Encodes a Boron Channel Protein Required for Inflorescence Development in Maize. Plant and Cell Physiology, 2014, 55, 1044-1054.  | 1.5 | 46        |
| 3266 | Whole-genome haplotyping approaches and genomic medicine. Genome Medicine, 2014, 6, 73.  | 3.6 | 66        |
| 3267 | Towards a phylogenetic position for the morphologically-defined genus Pannus (Cyanobacteria). Nova Hedwigia, 2014, 99, 511-524.  | 0.2 | 12        |
| 3268 | Trigger of autoimmune diseases (SLE): Identification of LINE transposition based novel therapeutic molecular targets. Medical Hypotheses, 2014, 83, 825-831.   | 0.8 | 0         |
| 3269 | Tissue storage and primer selection influence pyrosequencing-based inferences of diversity and community composition of endolichenic and endophytic fungi. Molecular Ecology Resources, 2014, 14, 1032-1048. | 2.2 | 83        |
| 3270 | Complex Polymorphisms in the Plasmodium falciparum Multidrug Resistance Protein 2 Gene and Its Contribution to Antimalarial Response. Antimicrobial Agents and Chemotherapy, 2014, 58, 7390-7397.            | 1.4 | 25        |
| 3271 | Prospective study on Norovirus infection among allogeneic stem cell transplant recipients: Prolonged viral excretion and viral RNA in the blood. Journal of Clinical Virology, 2014, 61, 329-333.            | 1.6 | 29        |
| 3272 | Twenty Whole-Genome Bacillus sp. Assemblies. Genome Announcements, 2014, 2, .  | 0.8 | 6         |
| 3273 | Diet Alters Both the Structure and Taxonomy of the Ovine Gut Microbial Ecosystem. DNA Research, 2014, 21, 115-125.   | 1.5 | 37        |
| 3274 | The Online Diagnosis System for sanger sequencing based genetic testing. , 2014, , .   |     | 2         |
| 3275 | Online Diagnosis System: A webserver for analysis of Sanger sequencing-based genetic testing data. Methods, 2014, 69, 230-236.   | 1.9 | 1         |
| 3276 | Quorum-Dependent Mannopine-Inducible Conjugative Transfer of an Agrobacterium Opine-Catabolic Plasmid. Journal of Bacteriology, 2014, 196, 1031-1044.  | 1.0 | 15        |
| 3277 | The C-Score: A Bayesian Framework to Sharply Improve Proteoform Scoring in High-Throughput Top Down Proteomics. Journal of Proteome Research, 2014, 13, 3231-3240.   | 1.8 | 76        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3278 | Protease inhibitor resistance mutations in untreated Brazilian patients infected with HCV: Novel insights about targeted genotyping approaches. <i>Journal of Medical Virology</i> , 2014, 86, 1714-1721.   | 2.5 | 16        |
| 3279 | Characterization and antigenicity of recombinant <i>Campylobacter jejuni</i> flagellar capping protein FljD. <i>Journal of Medical Microbiology</i> , 2014, 63, 602-609.  | 0.7 | 28        |
| 3280 | The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.   | 9.4 | 225       |
| 3281 | Lossy compression of quality scores in genomic data. <i>Bioinformatics</i> , 2014, 30, 2130-2136.   | 1.8 | 58        |
| 3282 | A new genome of <i>Acidithiobacillus thiooxidans</i> provides insights into adaptation to a bioleaching environment. <i>Research in Microbiology</i> , 2014, 165, 743-752.  | 1.0 | 48        |
| 3283 | Chromosomal organizations of major repeat families on potato ( <i>Solanum tuberosum</i> ) and further exploring in its sequenced genome. <i>Molecular Genetics and Genomics</i> , 2014, 289, 1307-1319.   | 1.0 | 16        |
| 3284 | ShrimpGPAT: a gene and protein annotation tool for knowledge sharing and gene discovery in shrimp. <i>BMC Genomics</i> , 2014, 15, 506.   | 1.2 | 7         |
| 3285 | A nonsense mutation in PLD4 is associated with a zinc deficiency-like syndrome in Fleckvieh cattle. <i>BMC Genomics</i> , 2014, 15, 623.  | 1.2 | 31        |
| 3286 | Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. <i>Plant Methods</i> , 2014, 10, 21.   | 1.9 | 339       |
| 3287 | A novel cost effective and high-throughput isolation and identification method for marine microalgae. <i>Plant Methods</i> , 2014, 10, 26.  | 1.9 | 11        |
| 3288 | Validation of high throughput sequencing and microbial forensics applications. <i>Investigative Genetics</i> , 2014, 5, 9.  | 3.3 | 59        |
| 3289 | Joint assembly and genetic mapping of the Atlantic horseshoe crab genome reveals ancient whole genome duplication. <i>GigaScience</i> , 2014, 3, 9.   | 3.3 | 86        |
| 3290 | About Sequence Quality: Impact on Clinical Applications. <i>Genetic Testing and Molecular Biomarkers</i> , 2014, 18, 299-305.   | 0.3 | 2         |
| 3291 | Zooplankton community analysis in the Changjiang River estuary by single-gene-targeted metagenomics. <i>Chinese Journal of Oceanology and Limnology</i> , 2014, 32, 858-870.  | 0.7 | 5         |
| 3292 | Characterization and reactivity of broiler chicken sera to selected recombinant <i>Campylobacter jejuni</i> chemotactic proteins. <i>Archives of Microbiology</i> , 2014, 196, 375-383.   | 1.0 | 4         |
| 3293 | Bacterial Community Assemblages Associated with the Phyllosphere, Dermosphere, and Rhizosphere of Tree Species of the Atlantic Forest are Host Taxon Dependent. <i>Microbial Ecology</i> , 2014, 68, 567-574.   | 1.4 | 92        |
| 3294 | Integrated physical, genetic and genome map of chickpea ( <i>Cicer arietinum</i> L.). <i>Functional and Integrative Genomics</i> , 2014, 14, 59-73.   | 1.4 | 49        |
| 3295 | Leaf, panel- and latex-expressed sequenced tags from the rubber tree ( <i>Hevea brasiliensis</i> ) under cold-stressed and suboptimal growing conditions: the development of gene-targeted functional markers for stress response. <i>Molecular Breeding</i> , 2014, 34, 1035-1053. | 1.0 | 32        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3296 | Draft Genome Comparison of Representatives of the Three Dominant Genotype Groups of Dairy <i>Bacillus licheniformis</i> Strains. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3453-3462.               | 1.4 | 13        |
| 3297 | An improved dual-indexing approach for multiplexed 16S rRNA gene sequencing on the Illumina MiSeq platform. <i>Microbiome</i> , 2014, 2, 6.   | 4.9 | 1,454     |
| 3298 | Strategies to Design and Analyze Targeted Sequencing Data. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 335-343.  | 5.1 | 18        |
| 3299 | Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear ( <i>Pyrus pyrifolia</i> Nakai). <i>Tree Genetics and Genomes</i> , 2014, 10, 853-863.                               | 0.6 | 24        |
| 3300 | The Effect of PPI Use on Human Gut Microbiota and Weight Loss in Patients Undergoing Laparoscopic Roux-en-Y Gastric Bypass. <i>Obesity Surgery</i> , 2014, 24, 1567-1571.   | 1.1 | 41        |
| 3302 | Regional effects on chimera formation in 454 pyrosequenced amplicons from a mock community. <i>Journal of Microbiology</i> , 2014, 52, 566-573.   | 1.3 | 10        |
| 3303 | Identification and analysis of expressed sequence tags present in xylem tissues of kelampayan ( <i>Neolamarckia cadamba</i> (Roxb.) Bosser). <i>Physiology and Molecular Biology of Plants</i> , 2014, 20, 393-397. | 1.4 | 10        |
| 3304 | Adaptable probabilistic mapping of short reads using position specific scoring matrices. <i>BMC Bioinformatics</i> , 2014, 15, 100.   | 1.2 | 42        |
| 3305 | An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. <i>BMC Evolutionary Biology</i> , 2014, 14, 67.  | 3.2 | 21        |
| 3306 | Analysis of EST data of the marine protist <i>Oxyrrhis marina</i> , an emerging model for alveolate biology and evolution. <i>BMC Genomics</i> , 2014, 15, 122.   | 1.2 | 26        |
| 3307 | Genome variations account for different response to three mineral elements between <i>Medicago truncatula</i> ecotypes Jemalong A17 and R108. <i>BMC Plant Biology</i> , 2014, 14, 122.                             | 1.6 | 15        |
| 3308 | Construction of a high-coverage bacterial artificial chromosome library and comprehensive genetic linkage map of yellowtail <i>Seriola quinqueradiata</i> . <i>BMC Research Notes</i> , 2014, 7, 200.               | 0.6 | 11        |
| 3309 | Whole-genome sequence variation, population structure and demographic history of the Dutch population. <i>Nature Genetics</i> , 2014, 46, 818-825.  | 9.4 | 641       |
| 3310 | Pseudogenes. <i>Methods in Molecular Biology</i> , 2014, 1167, v.   | 0.4 | 5         |
| 3311 | Interannual variation and host affiliations of endophytic fungi associated with ferns at La Selva, Costa Rica. <i>Mycologia</i> , 2014, 106, 8-21.  | 0.8 | 42        |
| 3312 | Deconvolving tumor purity and ploidy by integrating copy number alterations and loss of heterozygosity. <i>Bioinformatics</i> , 2014, 30, 2121-2129.  | 1.8 | 37        |
| 3313 | Screening of mutations in <i>GNAL</i> in sporadic dystonia patients. <i>Movement Disorders</i> , 2014, 29, 1193-1196.   | 2.2 | 19        |
| 3314 | A General Sequence Processing and Analysis Program for Protein Engineering. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 3020-3032.  | 2.5 | 6         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3315 | Carbon Dioxide and Hydrogen Sulfide Associations with Regional Bacterial Diversity Patterns in Microbially Induced Concrete Corrosion. <i>Environmental Science &amp; Technology</i> , 2014, 48, 7357-7364.                                       | 4.6 | 33        |
| 3316 | Single Amino Acid Mutations in the Potato Immune Receptor R3a Expand Response to <i>Phytophthora</i> Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 624-637.  | 1.4 | 136       |
| 3317 | <i>Haplomyxa saranae</i> gen. nov. et sp. nov., a New Naked Freshwater Foraminifer. <i>Protist</i> , 2014, 165, 317-329.  | 0.6 | 11        |
| 3318 | Malignant catarrhal fever in American bison ( <i>Bison bison</i> ) experimentally infected with alcelaphine herpesvirus 2. <i>Veterinary Microbiology</i> , 2014, 172, 318-322.   | 0.8 | 10        |
| 3319 | High-throughput sequencing in mitochondrial DNA research. <i>Mitochondrion</i> , 2014, 17, 157-163.   | 1.6 | 71        |
| 3320 | High-quality and high-throughput massively parallel sequencing of the human mitochondrial genome using the Illumina MiSeq. <i>Forensic Science International: Genetics</i> , 2014, 12, 128-135.   | 1.6 | 155       |
| 3321 | Subtractive hybridization-mediated analysis of genes and <i>in silico</i> prediction of associated microRNAs under waterlogged conditions in sugarcane ( <i>Saccharum</i> spp.). <i>FEBS Open Bio</i> , 2014, 4, 533-541.                         | 1.0 | 16        |
| 3322 | Novel ovine polymorphisms and adaptive evolution in mammalian TLR2 suggest existence of multiple pathogen binding regions. <i>Gene</i> , 2014, 540, 217-225.  | 1.0 | 6         |
| 3323 | Application of Massively Parallel Sequencing in the Clinical Diagnostic Testing of Inherited Cardiac Conditions. <i>Medical Sciences (Basel, Switzerland)</i> , 2014, 2, 98-126.  | 1.3 | 2         |
| 3325 | Purifying the Impure: Sequencing Metagenomes and Metatranscriptomes from Complex Animal-associated Samples. <i>Journal of Visualized Experiments</i> , 2014, , .  | 0.2 | 21        |
| 3326 | Genome sequence of the <i>Lotus corniculatus</i> microsymbiont <i>Mesorhizobium loti</i> strain R88B. <i>Standards in Genomic Sciences</i> , 2014, 9, 3.  | 1.5 | 12        |
| 3327 | Genome sequence of the dark pink pigmented <i>Listia bainesii</i> microsymbiont <i>Methylobacterium</i> sp. WSM2598. <i>Standards in Genomic Sciences</i> , 2014, 9, 5.   | 1.5 | 3         |
| 3328 | Genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain NZP2037. <i>Standards in Genomic Sciences</i> , 2014, 9, 7.   | 1.5 | 5         |
| 3329 | Genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain R7A. <i>Standards in Genomic Sciences</i> , 2014, 9, 6.   | 1.5 | 22        |
| 3330 | Concise and Broadly Applicable Method for Determining the Genomic Sequences of North-American Type Porcine Reproductive and Respiratory Syndrome Viruses in Various Clusters. <i>Journal of Veterinary Medical Science</i> , 2014, 76, 1249-1255. | 0.3 | 3         |
| 3331 | The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S13759.  | 0.6 | 23        |
| 3332 | Draft Genome Assembly of <i>Klebsiella pneumoniae</i> Type Strain ATCC 13883. <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 6         |
| 3333 | Complete Genome Sequence of Type Strain <i>Pasteurella multocida</i> subsp. <i>multocida</i> ATCC 43137. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 4         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3334 | Draft Genome Assemblies of <i>Enterobacter aerogenes</i> CDC 6003-71, <i>Enterobacter cloacae</i> CDC 442-68, and <i>Pantoea agglomerans</i> UA 0804-01. <i>Genome Announcements</i> , 2014, 2, .                           | 0.8 | 3         |
| 3335 | Genome sequence and emended description of <i>Leisingera nanhaiensis</i> strain DSM 24252T isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014, 9, 585-601.  | 1.5 | 8         |
| 3336 | Sequencing and comparative genomics analysis in <i>Senecio scandens</i> Buch.-Ham. Ex D. Don, based on full-length cDNA library. <i>Biotechnology and Biotechnological Equipment</i> , 2014, 28, 805-812.                   | 0.5 | 1         |
| 3337 | Complete Genome sequence of <i>Burkholderia phymatum</i> STM815T, a broad host range and efficient nitrogen-fixing symbiont of <i>Mimosa</i> species. <i>Standards in Genomic Sciences</i> , 2014, 9, 763-774.              | 1.5 | 71        |
| 3338 | Genome sequence of <i>Microvirga lupini</i> strain LUT6T, a novel <i>Lupinus</i> alphaproteobacterial microsymbiont from Texas. <i>Standards in Genomic Sciences</i> , 2014, 9, 1159-1167.                                  | 1.5 | 6         |
| 3339 | CASPER: context-aware scheme for paired-end reads from high-throughput amplicon sequencing. <i>BMC Bioinformatics</i> , 2014, 15, S10.  | 1.2 | 56        |
| 3340 | Complete Genome Assembly of a Quality Control Reference Isolate, <i>Moraxella catarrhalis</i> Strain ATCC 25240. <i>Genome Announcements</i> , 2014, 2, .   | 0.8 | 4         |
| 3341 | Draft Genome Assembly of <i>Ralstonia pickettii</i> Type Strain K-288 (ATCC 27853). <i>Genome Announcements</i> , 2014, 2, .  | 0.8 | 9         |
| 3342 | The <i>V</i> locus encodes for a CC-NBS-LRR protein that confers resistance to <i>Aphis gossypii</i> infestation and <i>A. gossypii</i> -mediated virus resistance. <i>Plant Journal</i> , 2014, 80, 993-1004.              | 2.8 | 90        |
| 3343 | Variability of the caprine whey protein genes and their association with milk yield, composition and renneting properties in the Sarda breed: 2. The <i>BLG</i> gene. <i>Journal of Dairy Research</i> , 2015, 82, 442-448. | 0.7 | 8         |
| 3344 | Complete genome sequence of <i>Geobacillus thermoglucosidasius</i> C56-YS93, a novel biomass degrader isolated from obsidian hot spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2015, 10, 73.  | 1.5 | 21        |
| 3345 | Amplicon Resequencing Identified Parental Mosaicism for Approximately 10% of <i>de novo</i> <i>SCN1A</i> Mutations in Children with Dravet Syndrome. <i>Human Mutation</i> , 2015, 36, 861-872.                             | 1.1 | 111       |
| 3346 | Genomic confirmation of nutrient-dependent mutability of mutators in <i>Escherichia coli</i> . <i>Genes To Cells</i> , 2015, 20, 972-981.   | 0.5 | 12        |
| 3347 | <i>Burkholderia</i> of Plant-Beneficial Group are Symbiotically Associated with Bordered Plant Bugs (Heteroptera: Pyrrhocoroidea: Largidae). <i>Microbes and Environments</i> , 2015, 30, 321-329.                          | 0.7 | 35        |
| 3348 | Transcriptome analysis identifies genes involved in adventitious branches formation of <i>Gracilaria lichenoides</i> in vitro. <i>Scientific Reports</i> , 2015, 5, 17099.  | 1.6 | 24        |
| 3349 | Genetic control of morphometric diversity in the maize shoot apical meristem. <i>Nature Communications</i> , 2015, 6, 8974.   | 5.8 | 100       |
| 3350 | Comparative genomics and experimental evolution of <i>Escherichia coli</i> BL21(DE3) strains reveal the landscape of toxicity escape from membrane protein overproduction. <i>Scientific Reports</i> , 2015, 5, 16076.      | 1.6 | 73        |
| 3352 | Generation and Analysis of Microbial Metatranscriptomes. , 2015, , 2.4.5-1-2.4.5-19.  |     | 1         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3353 | Reference-free inference of tumor phylogenies from single-cell sequencing data. <i>BMC Genomics</i> , 2015, 16, S7.  | 1.2 | 10        |
| 3354 | The evolution of <i>Homo sapiens denisova</i> and <i>Homo sapiens neanderthalensis</i> miRNA targeting genes in the prenatal and postnatal brain. <i>BMC Genomics</i> , 2015, 16, S4.  | 1.2 | 3         |
| 3355 | Complete genome sequence of the chromate-reducing bacterium <i>Thermoanaerobacter thermohydrosulfuricus</i> strain BSB-33. <i>Standards in Genomic Sciences</i> , 2015, 10, 74.  | 1.5 | 15        |
| 3356 | Construction, complete sequence, and annotation of a BAC contig covering the silkworm chorion locus. <i>Scientific Data</i> , 2015, 2, 150062.   | 2.4 | 2         |
| 3357 | Re-alignment of the unmapped reads with base quality score. <i>BMC Bioinformatics</i> , 2015, 16, S8.  | 1.2 | 14        |
| 3358 | MixClone: a mixture model for inferring tumor subclonal populations. <i>BMC Genomics</i> , 2015, 16, S1.   | 1.2 | 10        |
| 3359 | Developing expressed sequence tag libraries and the discovery of simple sequence repeat markers for two species of raspberry ( <i>Rubus</i> L.). <i>BMC Plant Biology</i> , 2015, 15, 258.   | 1.6 | 13        |
| 3360 | High-quality permanent draft genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia</i> sp. strain WSM4176. <i>Standards in Genomic Sciences</i> , 2015, 10, 79.   | 1.5 | 5         |
| 3361 | Partial genome sequence of <i>Thioalkalivibrio thiocyanodenitrificans</i> ARhD 1T, a chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium capable of complete denitrification. <i>Standards in Genomic Sciences</i> , 2015, 10, 84. | 1.5 | 2         |
| 3362 | The players may change but the game remains: network analyses of ruminal microbiomes suggest taxonomic differences mask functional similarity. <i>Nucleic Acids Research</i> , 2015, 43, gkv973.   | 6.5 | 98        |
| 3363 | The Utility of Genome Skimming for Phylogenomic Analyses as Demonstrated for Glycerid Relationships (Annelida, Glyceridae). <i>Genome Biology and Evolution</i> , 2015, 7, 3443-3462.  | 1.1 | 55        |
| 3364 | The pan-genome of <i>Lactobacillus reuteri</i> strains originating from the pig gastrointestinal tract. <i>BMC Genomics</i> , 2015, 16, 1023.  | 1.2 | 64        |
| 3365 | Finished Genome Assembly of <i>Yersinia pestis</i> EV76D and KIM 10v. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 2         |
| 3366 | Genome Assemblies for 11 <i>Yersinia pestis</i> Strains Isolated in the Caucasus Region. <i>Genome Announcements</i> , 2015, 3, .  | 0.8 | 21        |
| 3367 | Genome sequence of the soil bacterium <i>Corynebacterium callunae</i> type strain DSM 20147T. <i>Standards in Genomic Sciences</i> , 2015, 10, 5.  | 1.5 | 8         |
| 3368 | Transcriptomics of diapause in an isogenic self-fertilizing vertebrate. <i>BMC Genomics</i> , 2015, 16, 989.   | 1.2 | 12        |
| 3369 | Visualizing translocation dynamics and nascent transcript errors in paused RNA polymerases in vivo. <i>Genome Biology</i> , 2015, 16, 98.  | 3.8 | 82        |
| 3370 | <i>Phlebotomus papatasi</i> SP15: mRNA expression variability and amino acid sequence polymorphisms of field populations. <i>Parasites and Vectors</i> , 2015, 8, 298.   | 1.0 | 17        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3371 | Microbial aerosol liberation from soiled textiles isolated during routine residuals handling in a modern health care setting. <i>Microbiome</i> , 2015, 3, 72.  | 4.9 | 33        |
| 3372 | Complete genome sequences of <i>Geobacillus</i> sp. Y412MC52, a xylan-degrading strain isolated from obsidian hot spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2015, 10, 81. | 1.5 | 12        |
| 3373 | Finished Genome Assembly of Warm Spring Isolate <i>Francisella novicida</i> DPG 3A-IS. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 3         |
| 3374 | Genome Sequence of <i>Porphyromonas gingivalis</i> Strain AJW4. <i>Genome Announcements</i> , 2015, 3, .  | 0.8 | 4         |
| 3375 | Dominant ectosymbiotic bacteria of cellulolytic protists in the termite gut also have the potential to digest lignocellulose. <i>Environmental Microbiology</i> , 2015, 17, 4942-4953.                      | 1.8 | 55        |
| 3376 | Variation in genes controlling warfarin disposition and response in American Indian and Alaska Native people. <i>Pharmacogenetics and Genomics</i> , 2015, 25, 343-353.                                     | 0.7 | 37        |
| 3377 | Genome Sequence of <i>Porphyromonas gingivalis</i> Strain A7436. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 14        |
| 3378 | Draft Genome Sequence of the Cellulolytic and Xylanolytic Thermophile <i>Clostridium clariflavum</i> Strain 4-2a. <i>Genome Announcements</i> , 2015, 3, .  | 0.8 | 4         |
| 3379 | Genomic Instability of the Sex-Determining Locus in Atlantic Salmon ( <i>Salmo salar</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2513-2522.   | 0.8 | 52        |
| 3380 | Comparative Analysis of Vaginal Bacterial Diversity in Northern-Chinese Women Associated With or Without Bacterial Vaginosis. , 2015, s5, .   |     | 0         |
| 3381 | Characterization of NF1 frameshift mutations in pediatric patients with neurofibromatosis type I. <i>Genetics and Molecular Research</i> , 2015, 14, 8326-8337.   | 0.3 | 1         |
| 3382 | Bacterial community in two subtropical fishponds in So Paulo, Brazil. <i>African Journal of Microbiology Research</i> , 2015, 9, 404-413.   | 0.4 | 1         |
| 3383 | Differentially expressed genes in the pituitary of the Amazonian fish <i>Arapaima gigas</i> . <i>International Journal of Fisheries and Aquaculture</i> , 2015, 7, 132-141.                                 | 1.1 | 5         |
| 3384 | Molecular phylogeny and biogeography of the South American genus <i>Metrodorea</i> (Rutaceae). <i>Turkish Journal of Botany</i> , 2015, 39, 825-834.  | 0.5 | 5         |
| 3385 | Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015, 6, 235.  | 1.1 | 160       |
| 3386 | Analysis of genes that are differentially expressed during the <i>Sclerotinia sclerotiorum</i> – <i>Phaseolus vulgaris</i> interaction. <i>Frontiers in Microbiology</i> , 2015, 6, 1162.                   | 1.5 | 42        |
| 3387 | CHOPER Filters Enable Rare Mutation Detection in Complex Mutagenesis Populations by Next-Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0116877.   | 1.1 | 1         |
| 3388 | Genome and Transcriptome of <i>Clostridium phytofermentans</i> , Catalyst for the Direct Conversion of Plant Feedstocks to Fuels. <i>PLoS ONE</i> , 2015, 10, e0118285.                                     | 1.1 | 28        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3389 | Mo-CBP3, an Antifungal Chitin-Binding Protein from <i>Moringa oleifera</i> Seeds, Is a Member of the 2S Albumin Family. <i>PLoS ONE</i> , 2015, 10, e0119871.  | 1.1 | 47        |
| 3390 | The Transcriptome of Equine Peripheral Blood Mononuclear Cells. <i>PLoS ONE</i> , 2015, 10, e0122011.  | 1.1 | 17        |
| 3391 | Incongruent Nuclear and Mitochondrial Genetic Structure of New World Screwworm Fly Populations Due to Positive Selection of Mutations Associated with Dimethyl- and Diethyl-Organophosphates Resistance. <i>PLoS ONE</i> , 2015, 10, e0128441. | 1.1 | 8         |
| 3392 | Novel and Stress Relevant EST Derived SSR Markers Developed and Validated in Peanut. <i>PLoS ONE</i> , 2015, 10, e0129127.   | 1.1 | 44        |
| 3393 | High-Throughput, Amplicon-Based Sequencing of the CREBBP Gene as a Tool to Develop a Universal Platform-Independent Assay. <i>PLoS ONE</i> , 2015, 10, e0129195.   | 1.1 | 7         |
| 3394 | Association of Apolipoprotein B and Adiponectin Receptor 1 Genes with Carcass, Bone Integrity and Performance Traits in a Paternal Broiler Line. <i>PLoS ONE</i> , 2015, 10, e0136824.   | 1.1 | 9         |
| 3395 | Cloning and functional validation of early inducible <i>Magnaporthe oryzae</i> responsive CYP76M7 promoter from rice. <i>Frontiers in Plant Science</i> , 2015, 6, 371.  | 1.7 | 15        |
| 3396 | Constructing a Genome-Wide LD Map of Wild <i>A. gambiae</i> Using Next-Generation Sequencing. <i>BioMed Research International</i> , 2015, 2015, 1-8.  | 0.9 | 2         |
| 3397 | Cytotoxic Cytochalasins and Other Metabolites from <i>Xylariaceae</i> sp. FL0390, a Fungal Endophyte of Spanish Moss. <i>Natural Product Communications</i> , 2015, 10, 1934578X1501001.   | 0.2 | 3         |
| 3398 | Relação entre toxicidade de proteínas Vip3Aa e sua capacidade de ligação a receptores intestinais de lepidópteros-praga. <i>Pesquisa Agropecuária Brasileira</i> , 2015, 50, 637-648.  | 0.9 | 4         |
| 3399 | Human Enhancers Are Fragile and Prone to Deactivating Mutations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2161-2180.   | 3.5 | 17        |
| 3400 | Determination of DPYD Enzyme Activity in Korean Population. <i>Therapeutic Drug Monitoring</i> , 2015, 37, 147-151.  | 1.0 | 3         |
| 3401 | Discovery of a glowing millipede in California and the gradual evolution of bioluminescence in Diplopoda. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6419-6424.                       | 3.3 | 21        |
| 3402 | Genetic subgroup of small ruminant lentiviruses that infects sheep homozygous for TMEM154 frameshift deletion mutation A41>53. <i>Veterinary Research</i> , 2015, 46, 22.  | 1.1 | 13        |
| 3403 | Molecular analysis of single room humidifier bacteriology. <i>Water Research</i> , 2015, 69, 318-327.  | 5.3 | 9         |
| 3404 | Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12462.  | 1.0 | 317       |
| 3405 | Cephalothrix gen. nov. (Cyanobacteria): towards an intraspecific phylogenetic evaluation by multilocus analyses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2993-3007.                               | 0.8 | 35        |
| 3407 | Report of outbreaks of classical scrapie in Dorper sheep and associated prion protein gene polymorphisms in affected flocks. <i>Tropical Animal Health and Production</i> , 2015, 47, 1203-1212.   | 0.5 | 6         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3408 | Construction of a Spinach Bacterial Artificial Chromosome (BAC) Library as a Resource for Gene Identification and Marker Development. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1996-2005.   | 1.0 | 15        |
| 3409 | Genetic variants in glucocorticoid and mineralocorticoid receptors are associated with concentrations of plasma cortisol, muscle glycogen content, and meat quality traits in male Nellore cattle. <i>Domestic Animal Endocrinology</i> , 2015, 51, 105-113. | 0.8 | 9         |
| 3410 | Government-funded universal newborn hearing screening and genetic analyses of deafness predisposing genes in Taiwan. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2015, 79, 584-590.  | 0.4 | 12        |
| 3411 | A comparison of 454 sequencing and clonal sequencing for the characterization of hepatitis C virus NS3 variants. <i>Journal of Virological Methods</i> , 2015, 219, 28-37.   | 1.0 | 6         |
| 3412 | The sheep growth hormone gene polymorphism and its effects on milk traits. <i>Journal of Dairy Research</i> , 2015, 82, 169-176.   | 0.7 | 14        |
| 3413 | Exogenous application of methyl jasmonate induces a defense response and resistance against <i>Sclerotinia sclerotiorum</i> in dry bean plants. <i>Journal of Plant Physiology</i> , 2015, 182, 13-22.   | 1.6 | 26        |
| 3414 | Development of a comparative genomic fingerprinting assay for rapid and high resolution genotyping of <i>Arcobacter butzleri</i> . <i>BMC Microbiology</i> , 2015, 15, 94.   | 1.3 | 48        |
| 3415 | Genetic structuring and fixed polymorphisms in the gene period among natural populations of <i>Lutzomyia longipalpis</i> in Brazil. <i>Parasites and Vectors</i> , 2015, 8, 193.   | 1.0 | 16        |
| 3416 | Genome of <i>Methanoregula boonei</i> 6A8 reveals adaptations to oligotrophic peatland environments. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1572-1581.  | 0.7 | 17        |
| 3417 | Complete Genome Sequence of <i>Streptococcus iniae</i> YSFST01-82, Isolated from Olive Flounder in Jeju, South Korea. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 9         |
| 3418 | Complete Genome Assemblies for Two Single-Chromosome <i>Vibrio cholerae</i> Isolates, Strains 1154-74 (Serogroup O49) and 10432-62 (Serogroup O27). <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 17        |
| 3419 | Draft Genomes of Gammaproteobacterial Methanotrophs Isolated from Terrestrial Ecosystems. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 41        |
| 3420 | Whole-Genome Sequences of 80 Environmental and Clinical Isolates of <i>Burkholderia pseudomallei</i> . <i>Genome Announcements</i> , 2015, 3, .  | 0.8 | 38        |
| 3421 | Draft Genome Sequence of <i>Methyloferula stellata</i> AR4, an Obligate Methanotroph Possessing Only a Soluble Methane Monooxygenase. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 28        |
| 3422 | Complete Genome Sequence of <i>Methanosphaerula palustris</i> E1-9C <sup>T</sup> , a Hydrogenotrophic Methanogen Isolated from a Minerotrophic Fen Peatland. <i>Genome Announcements</i> , 2015, 3, .  | 0.8 | 9         |
| 3423 | Association between ACTA1 candidate gene and performance, organs and carcass traits in broilers. <i>Poultry Science</i> , 2015, 94, 2863-2869.   | 1.5 | 9         |
| 3424 | Characterization of <i>Physa acuta</i> expressed sequence tags and transcript mining following cadmium exposure. <i>Genes and Genomics</i> , 2015, 37, 1017-1025.  | 0.5 | 1         |
| 3425 | Detecting genetic risk factors for Alzheimer's disease in whole genome sequence data via Lasso screening. , 2015, 2015, 985-989.   |     | 26        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3426 | Complete genome sequence of Thioalkalivibrio paradoxus type strain ARh 1T, an obligately chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium isolated from a Kenyan soda lake. Standards in Genomic Sciences, 2015, 10, 105. | 1.5 | 5         |
| 3427 | Expressed sequence tag analysis and annotation of genetic information from the freshwater clam, Pisidium (Neopisidium) coreanum endemic to Korea. Genes and Genomics, 2015, 37, 1041-1049.   | 0.5 | 2         |
| 3428 | Genome sequence of Bradyrhizobium sp. WSM1253; a microsymbiont of Ornithopus compressus from the Greek Island of Sifnos. Standards in Genomic Sciences, 2015, 10, 113.   | 1.5 | 3         |
| 3429 | Patterns of SNP distribution provide a molecular basis for high genetic diversity and genetic differentiation in Vitis species. Tree Genetics and Genomes, 2015, 11, 1.  | 0.6 | 1         |
| 3430 | Arachis batizocoi: a study of its relationship to cultivated peanut (A. hypogaea) and its potential for introgression of wild genes into the peanut crop using induced allotetraploids. Annals of Botany, 2015, 115, 237-249.              | 1.4 | 51        |
| 3431 | Effects of sequence alterations on results from genotypic tropism testing. Journal of Clinical Virology, 2015, 65, 68-73.  | 1.6 | 1         |
| 3432 | Complete Genome Sequence of Geobacillus strain Y4.1MC1, a Novel CO-Utilizing Geobacillus thermoglucosidasius Strain Isolated from Bath Hot Spring in Yellowstone National Park. Bioenergy Research, 2015, 8, 1039-1045.                    | 2.2 | 19        |
| 3433 | Ancient human genomics: the methodology behind reconstructing evolutionary pathways. Journal of Human Evolution, 2015, 79, 21-34.  | 1.3 | 22        |
| 3434 | Holocene southward expansion in seasonally dry tropical forests in South America: phylogeography of <i>Ficus bonijesulapensis</i> (Moraceae). Botanical Journal of the Linnean Society, 2015, 177, 189-201.                                | 0.8 | 24        |
| 3435 | Current status and prospects for the study of Nicotiana genomics, genetics, and nicotine biosynthesis genes. Molecular Genetics and Genomics, 2015, 290, 11-21.  | 1.0 | 49        |
| 3436 | Genome-wide analyses of LINE-mediated nonallelic homologous recombination. Nucleic Acids Research, 2015, 43, 2188-2198.  | 6.5 | 79        |
| 3437 | Deciphering the Genome Repertoire of Pseudomonas sp. M1 toward $\alpha$ -Myrcene Biotransformation. Genome Biology and Evolution, 2015, 7, 1-17.   | 1.1 | 10        |
| 3438 | Insect midgut carboxypeptidases with emphasis on <i>S</i> 10 hemipteran and <i>M</i> 14 lepidopteran carboxypeptidases. Insect Molecular Biology, 2015, 24, 222-239.   | 1.0 | 19        |
| 3439 | Exploring the dynamics of bacterial community composition in soil: the pan-bacteriome approach. Antonie Van Leeuwenhoek, 2015, 107, 785-797.   | 0.7 | 8         |
| 3440 | Accounting for uncertainty in DNA sequencing data. Trends in Genetics, 2015, 31, 61-66.  | 2.9 | 51        |
| 3441 | RNA Bioinformatics. Methods in Molecular Biology, 2015, , .  | 0.4 | 3         |
| 3442 | Single Nucleotide Variant Detection Using Next Generation Sequencing. , 2015, , 109-127.   |     | 10        |
| 3443 | A missense variant of the ATP1A2 gene is associated with a novel phenotype of progressive sensorineural hearing loss associated with migraine. European Journal of Human Genetics, 2015, 23, 639-645.                                      | 1.4 | 18        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3444 | Phenotypic expression of blast resistance gene Pi54 is not affected by its chromosomal position. <i>Plant Cell Reports</i> , 2015, 34, 63-70.  | 2.8 | 5         |
| 3445 | Analysis of German cockroach ( <i>Blattella germanica</i> ) expressed sequence tags. <i>Genes and Genomics</i> , 2015, 37, 271-280.  | 0.5 | 4         |
| 3446 | Bacterial and Archaeal Communities in Bleached Mottles of Tropical Podzols. <i>Microbial Ecology</i> , 2015, 69, 372-382.  | 1.4 | 5         |
| 3447 | A proposed adhesin AoMad1 helps nematode-trapping fungus <i>Arthrobotrys oligospora</i> recognizing host signals for life-style switching. <i>Fungal Genetics and Biology</i> , 2015, 81, 172-181.                       | 0.9 | 32        |
| 3448 | Fungal Endophytes in Aboveground Tissues of Desert Plants: Infrequent in Culture, but Highly Diverse and Distinctive Symbionts. <i>Microbial Ecology</i> , 2015, 70, 61-76.  | 1.4 | 84        |
| 3449 | Multiple origins of subsociality in crab spiders (Thomisidae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 82, 330-340.   | 1.2 | 7         |
| 3450 | <i>Trypanosoma rangeli</i> displays a clonal population structure, revealing a subdivision of KP1(â) strains and the ancestry of the Amazonian group. <i>International Journal for Parasitology</i> , 2015, 45, 225-235. | 1.3 | 11        |
| 3451 | Lynch Syndrome Associated with Two <i>MLH1</i> Promoter Variants and Allelic Imbalance of <i>MLH1</i> Expression. <i>Human Mutation</i> , 2015, 36, 622-630.   | 1.1 | 26        |
| 3452 | Toll-like receptor 1 variations influence susceptibility and immune response to <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2015, 95, 328-335.   | 0.8 | 44        |
| 3453 | Hierarchical Bayesian Model for Rare Variant Association Analysis Integrating Genotype Uncertainty in Human Sequence Data. <i>Genetic Epidemiology</i> , 2015, 39, 89-100.   | 0.6 | 9         |
| 3454 | Extensive sequence variation in rice blast resistance gene Pi54 makes it broad spectrum in nature. <i>Frontiers in Plant Science</i> , 2015, 6, 345.   | 1.7 | 38        |
| 3455 | Application of Next Generation Sequencing for personalized medicine for sudden cardiac death. <i>Frontiers in Genetics</i> , 2015, 6, 55.  | 1.1 | 17        |
| 3456 | Eighteen New Candidate Effectors of the Phytonematode <i>Heterodera glycines</i> Produced Specifically in the Secretory Esophageal Gland Cells During Parasitism. <i>Phytopathology</i> , 2015, 105, 1362-1372.          | 1.1 | 57        |
| 3457 | Diversion of HIV-1 vaccine-induced immunity by gp41-microbiota cross-reactive antibodies. <i>Science</i> , 2015, 349, aab1253.   | 6.0 | 191       |
| 3458 | RNA-seq for gene identification and transcript profiling in relation to root growth of bermudagrass ( <i>Cynodon dactylon</i> ) under salinity stress. <i>BMC Genomics</i> , 2015, 16, 575.                              | 1.2 | 67        |
| 3459 | Genome Sequencing of 18 <i>Francisella</i> Strains To Aid in Assay Development and Testing. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 16        |
| 3460 | Genetic relatedness of selected clinical and environmental non-O1/O139 <i>Vibrio cholerae</i> . <i>International Journal of Infectious Diseases</i> , 2015, 37, 152-158.   | 1.5 | 9         |
| 3461 | Correcting for Sample Contamination in Genotype Calling of DNA Sequence Data. <i>American Journal of Human Genetics</i> , 2015, 97, 284-290.   | 2.6 | 39        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3462 | A Combination of Molecular Markers and Clinical Features Improve the Classification of Pancreatic Cysts. <i>Gastroenterology</i> , 2015, 149, 1501-1510.  | 0.6 | 376       |
| 3463 | Thirty-Two Complete Genome Assemblies of Nine <i>Yersinia</i> Species, Including <i>Y. pestis</i> , <i>Y. pseudotuberculosis</i> , and <i>Y. enterocolitica</i> . <i>Genome Announcements</i> , 2015, 3, .            | 0.8 | 31        |
| 3464 | Employing genome-wide SNP discovery and genotyping strategy to extrapolate the natural allelic diversity and domestication patterns in chickpea. <i>Frontiers in Plant Science</i> , 2015, 6, 162.                    | 1.7 | 104       |
| 3465 | A Minimal Set of Glycolytic Genes Reveals Strong Redundancies in <i>Saccharomyces cerevisiae</i> Central Metabolism. <i>Eukaryotic Cell</i> , 2015, 14, 804-816.  | 3.4 | 42        |
| 3466 | Phylogenetic Diversity of Sponge-Associated Fungi from the Caribbean and the Pacific of Panama and Their In Vitro Effect on Angiotensin and Endothelin Receptors. <i>Marine Biotechnology</i> , 2015, 17, 533-564.    | 1.1 | 19        |
| 3467 | Development and validation of an rDNA operon based primer walking strategy applicable to de novo bacterial genome finishing. <i>Frontiers in Microbiology</i> , 2014, 5, 769.   | 1.5 | 5         |
| 3468 | Alterations in Intestinal Microbiota Correlate With Susceptibility to Type 1 Diabetes. <i>Diabetes</i> , 2015, 64, 3510-3520.   | 0.3 | 246       |
| 3469 | Bioinformatics Tools for Small Genomes, Such as Hepatitis B Virus. <i>Viruses</i> , 2015, 7, 781-797.   | 1.5 | 21        |
| 3470 | The histone methyltransferase SETDB1 represses endogenous and exogenous retroviruses in B lymphocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8367-8372. | 3.3 | 78        |
| 3471 | Rapid genomic DNA changes in allotetraploid fish hybrids. <i>Heredity</i> , 2015, 114, 601-609.   | 1.2 | 27        |
| 3472 | Characterization of the Genotypic Profile of Hepatitis Delta Virus: Isolation of HDV Genotype-1 in the Western Amazon Region of Brazil. <i>Intervirology</i> , 2015, 58, 166-171.                                     | 1.2 | 22        |
| 3473 | Complete Genome Sequences for 59 <i>Burkholderia</i> Isolates, Both Pathogenic and Near Neighbor. <i>Genome Announcements</i> , 2015, 3, .  | 0.8 | 82        |
| 3474 | Major Breeding Plumage Color Differences of Male Ruffs ( <i>Philomachus pugnax</i> ) Are Not Associated With Coding Sequence Variation in the MC1R Gene. <i>Journal of Heredity</i> , 2015, 106, 211-215.             | 1.0 | 3         |
| 3475 | Improved detection of artifactual viral minority variants in high-throughput sequencing data. <i>Frontiers in Microbiology</i> , 2015, 5, 804.  | 1.5 | 15        |
| 3476 | LFQC: a lossless compression algorithm for FASTQ files. <i>Bioinformatics</i> , 2015, 31, 3276-3281.  | 1.8 | 52        |
| 3477 | A Perilipin Gene from <i>Clonostachys rosea</i> f. <i>Catenulata</i> HL-1-1 Is Related to Sclerotial Parasitism. <i>International Journal of Molecular Sciences</i> , 2015, 16, 5347-5362.                            | 1.8 | 11        |
| 3478 | A kinetic model-based algorithm to classify NGS short reads by their allele origin. <i>Journal of Biomedical Informatics</i> , 2015, 53, 121-127.   | 2.5 | 0         |
| 3479 | Mutation analysis in patients with total sperm immotility. <i>Journal of Assisted Reproduction and Genetics</i> , 2015, 32, 893-902.  | 1.2 | 36        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3480 | Diversity and evolution of Rp1 rust resistance genes in four maize lines. <i>Theoretical and Applied Genetics</i> , 2015, 128, 985-998.   | 1.8 | 21        |
| 3481 | Genetic evidence for susceptibility and resistance against scrapie in Indian sheep. <i>Journal of Genetics</i> , 2015, 94, 129-133.   | 0.4 | 0         |
| 3482 | ViVaMBC: estimating viral sequence variation in complex populations from illumina deep-sequencing data using model-based clustering. <i>BMC Bioinformatics</i> , 2015, 16, 59.  | 1.2 | 12        |
| 3483 | Identification of three extra-chromosomal replicons in <i>Leptospira</i> pathogenic strain and development of new shuttle vectors. <i>BMC Genomics</i> , 2015, 16, 90.  | 1.2 | 17        |
| 3484 | Genetic diversity of medically important and emerging <i>Candida</i> species causing invasive infection. <i>BMC Infectious Diseases</i> , 2015, 15, 57.   | 1.3 | 75        |
| 3485 | Clustering of reads with alignment-free measures and quality values. <i>Algorithms for Molecular Biology</i> , 2015, 10, 4.   | 0.3 | 26        |
| 3486 | Gene discovery in the developing xylem tissue of a tropical timber tree species: <i>Neolamarckia cadamba</i> (Roxb.) Bosser (kelampayan). <i>Tree Genetics and Genomes</i> , 2015, 11, 1.   | 0.6 | 6         |
| 3487 | Performance assessment of the Illumina massively parallel sequencing platform for deep sequencing analysis of viral minority variants. <i>Journal of Virological Methods</i> , 2015, 221, 29-38.  | 1.0 | 26        |
| 3488 | Investigation, Expression, and Molecular Modeling of ORF2, a Metagenomic Lipolytic Enzyme. <i>Applied Biochemistry and Biotechnology</i> , 2015, 175, 3875-3887.  | 1.4 | 8         |
| 3489 | A novel sigma factor reveals a unique regulon controlling cell-specific recombination in <i>Mycoplasma genitalium</i> . <i>Nucleic Acids Research</i> , 2015, 43, 4923-4936.  | 6.5 | 30        |
| 3490 | Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2813-9.   | 3.3 | 63        |
| 3491 | <i>Drosophila</i> Muller F Elements Maintain a Distinct Set of Genomic Properties Over 40 Million Years of Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 719-740.   | 0.8 | 84        |
| 3492 | Finished Genome Sequence of <i>Bacillus cereus</i> Strain 03BB87, a Clinical Isolate with <i>B. anthracis</i> Virulence Genes. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 5         |
| 3493 | Microbial diversity and hydrocarbon depletion in low and high diesel-polluted soil samples from Keller Peninsula, South Shetland Islands. <i>Antarctic Science</i> , 2015, 27, 263-273.   | 0.5 | 28        |
| 3494 | High-Resolution Microbial Community Succession of Microbially Induced Concrete Corrosion in Working Sanitary Manholes. <i>PLoS ONE</i> , 2015, 10, e0116400.  | 1.1 | 30        |
| 3495 | Rapid diversification associated with ecological specialization in Neotropical <i>Adelpha</i> butterflies. <i>Molecular Ecology</i> , 2015, 24, 2392-2405.  | 2.0 | 73        |
| 3496 | Pattern of multiresistant to antimicrobials and heavy metal tolerance in bacteria isolated from sewage sludge samples from a composting process at a recycling plant in southern Brazil. <i>Environmental Monitoring and Assessment</i> , 2015, 187, 328. | 1.3 | 15        |
| 3497 | Influence of killing method on <i>Lepidoptera</i> DNA barcode recovery. <i>Molecular Ecology Resources</i> , 2015, 15, 613-618.   | 2.2 | 9         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3498 | Composition and activity of endophytic bacterial communities in field-grown maize plants inoculated with <i>Azospirillum brasilense</i> . <i>Annals of Microbiology</i> , 2015, 65, 2187-2200.   | 1.1 | 26        |
| 3499 | A CC-NBS-LRR type gene GHNTR1 confers resistance to southern root-knot nematode in <i>Nicotiana benthamiana</i> and <i>Nicotiana tabacum</i> . <i>European Journal of Plant Pathology</i> , 2015, 142, 715-729.  | 0.8 | 11        |
| 3500 | Cyanobacterial distributions along a physicochemical gradient in the Northeastern Pacific Ocean. <i>Environmental Microbiology</i> , 2015, 17, 3692-3707.  | 1.8 | 42        |
| 3501 | Taking the next step forward – Diagnosing inherited infantile cholestatic disorders with next generation sequencing. <i>Molecular and Cellular Probes</i> , 2015, 29, 291-298.   | 0.9 | 36        |
| 3502 | Molecular Cloning and Differential Expression of Cytosolic Class I Small Hsp Gene Family in <i>Pennisetum glaucum</i> (L.). <i>Applied Biochemistry and Biotechnology</i> , 2015, 176, 598-612.  | 1.4 | 8         |
| 3503 | High Species C Human Adenovirus Genome Copy Numbers in the Treated Water Supply of a Neotropical Area of the Central-West Region of Brazil. <i>Food and Environmental Virology</i> , 2015, 7, 286-294.   | 1.5 | 5         |
| 3504 | Does human papillomavirus-negative condylomata exist?. <i>Virology</i> , 2015, 485, 283-288.   | 1.1 | 36        |
| 3505 | Complete Genome Sequences for 35 Biothreat Assay-Relevant <i>Bacillus</i> Species. <i>Genome Announcements</i> , 2015, 3, .  | 0.8 | 52        |
| 3506 | UrQt: an efficient software for the Unsupervised Quality trimming of NGS data. <i>BMC Bioinformatics</i> , 2015, 16, 137.  | 1.2 | 56        |
| 3507 | Isolation and characterization of major histocompatibility complex class II B genes in cranes. <i>Immunogenetics</i> , 2015, 67, 705-710.  | 1.2 | 8         |
| 3508 | Microbially influenced corrosion communities associated with fuel-grade ethanol environments. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6945-6957.   | 1.7 | 24        |
| 3509 | Cell periphery-related proteins as major genomic targets behind the adaptive evolution of an industrial <i>Saccharomyces cerevisiae</i> strain to combined heat and hydrolysate stress. <i>BMC Genomics</i> , 2015, 16, 514.                                     | 1.2 | 36        |
| 3510 | Identification and characterization of long non-coding RNAs involved in osmotic and salt stress in <i>Medicago truncatula</i> using genome-wide high-throughput sequencing. <i>BMC Plant Biology</i> , 2015, 15, 131.  | 1.6 | 181       |
| 3511 | Crystal structure of an antifungal osmotin-like protein from <i>Calotropis procera</i> and its effects on <i>Fusarium solani</i> spores, as revealed by atomic force microscopy: Insights into the mechanism of action. <i>Phytochemistry</i> , 2015, 119, 5-18. | 1.4 | 35        |
| 3512 | Isolation of high quality RNA from pistachio ( <i>Pistacia vera</i> L.) and other woody plants high in secondary metabolites. <i>Physiology and Molecular Biology of Plants</i> , 2015, 21, 597-603.   | 1.4 | 20        |
| 3513 | Molecular characterization of the gene feminizer in the stingless bee <i>Melipona interrupta</i> (Hymenoptera: Apidae) reveals association to sex and caste development. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 66, 24-30.                     | 1.2 | 23        |
| 3514 | Buying in to bioinformatics: an introduction to commercial sequence analysis software. <i>Briefings in Bioinformatics</i> , 2015, 16, 700-709.   | 3.2 | 36        |
| 3515 | Collection media and delayed freezing effects on microbial composition of human stool. <i>Microbiome</i> , 2015, 3, 33.  | 4.9 | 103       |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3517 | Transcriptomics of plant responses to apical damage reveals no negative correlation between tolerance and defense. <i>Plant Ecology</i> , 2015, 216, 1177-1190.  | 0.7 | 4         |
| 3518 | Phylogenetics and phylogeography of a long-legged harvestman (Arachnida : Opiliones) in the Brazilian Atlantic Rain Forest reveals poor dispersal, low diversity and extensive mitochondrial introgression. <i>Invertebrate Systematics</i> , 2015, 29, 386. | 0.5 | 24        |
| 3519 | Sesquiterpenes and other constituents of <i>Xylaria</i> sp. NC1214, a fungal endophyte of the moss <i>Hypnum</i> sp.. <i>Phytochemistry</i> , 2015, 118, 102-108.  | 1.4 | 41        |
| 3520 | Generation of expressed sequence tags from a cDNA library of <i>Coleus forskohlii</i> for identification of genes involved in terpene biosynthesis. <i>Biologia Plantarum</i> , 2015, 59, 463-468.   | 1.9 | 5         |
| 3521 | Under-detection of endospore-forming Firmicutes in metagenomic data. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 299-306.  | 1.9 | 88        |
| 3522 | The Genome of a Tortoise Herpesvirus (Testudinid Herpesvirus 3) Has a Novel Structure and Contains a Large Region That Is Not Required for Replication <i>In Vitro</i> or Virulence <i>In Vivo</i> . <i>Journal of Virology</i> , 2015, 89, 11438-11456.     | 1.5 | 27        |
| 3523 | Practical guidelines for B-cell receptor repertoire sequencing analysis. <i>Genome Medicine</i> , 2015, 7, 121.  | 3.6 | 215       |
| 3524 | Anteaglonialides A and Palmarumycins CE <sub>1</sub> and CE <sub>3</sub> from <i>Anteaglonium</i> sp. FL0768, a Fungal Endophyte of the Spikemoss <i>Selaginella arenicola</i> . <i>Journal of Natural Products</i> , 2015, 78, 2738-2747.                   | 1.5 | 22        |
| 3525 | Pantanalinema gen. nov. and Alkalinema gen. nov.: novel pseudanabaenacean genera (Cyanobacteria) isolated from saline/alkaline lakes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 298-308.                          | 0.8 | 100       |
| 3526 | Analysis of expressed sequence tags (ESTs) from a normalized cDNA library and isolation of EST simple sequence repeats from the invasive cotton mealybug <i>Phenacoccus solenopsis</i> . <i>Insect Science</i> , 2015, 22, 761-767.                          | 1.5 | 5         |
| 3527 | Whole transcriptome RNA sequencing data from blood leukocytes derived from Parkinson's disease patients prior to and following deep brain stimulation treatment. <i>Genomics Data</i> , 2015, 3, 57-60.  | 1.3 | 35        |
| 3528 | Barcoding Neotropical birds: assessing the impact of nonmonophyly in a highly diverse group. <i>Molecular Ecology Resources</i> , 2015, 15, 921-931.   | 2.2 | 19        |
| 3529 | Halotia gen. nov., a phylogenetically and physiologically coherent cyanobacterial genus isolated from marine coastal environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 663-675.                             | 0.8 | 91        |
| 3530 | Human papillomavirus type 197 is commonly present in skin tumors. <i>International Journal of Cancer</i> , 2015, 136, 2546-2555.   | 2.3 | 50        |
| 3531 | The genome of <i>Syntrophorhabdus aromaticivorans</i> strain UI provides new insights for syntrophic aromatic compound metabolism and electron flow. <i>Environmental Microbiology</i> , 2015, 17, 4861-4872.  | 1.8 | 72        |
| 3532 | Performance evaluation of Warshall algorithm and dynamic programming for Markov chain in local sequence alignment. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, 7, 78-81.  | 2.2 | 4         |
| 3533 | Multigene phylogeny resolves deep branching of Amoebozoa. <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 293-304.  | 1.2 | 84        |
| 3534 | VirVarSeq: a low-frequency virus variant detection pipeline for Illumina sequencing using adaptive base-calling accuracy filtering. <i>Bioinformatics</i> , 2015, 31, 94-101.  | 1.8 | 47        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3536 | Integrated next-generation sequencing analysis of whole exome and 409 cancer-related genes. <i>Biomedical Research</i> , 2016, 37, 367-379.   | 0.3 | 26        |
| 3537 | Genome Sequence of the Historical Clinical Isolate <i>Burkholderia pseudomallei</i> PHLS 6. <i>Genome Announcements</i> , 2016, 4, .  | 0.8 | 0         |
| 3538 | Monitoring Error Rates In Illumina Sequencing. <i>Journal of Biomolecular Techniques</i> , 2016, 27, 125-128.   | 0.8 | 65        |
| 3539 | The histone genes cluster in <i>Rhynchosciara americana</i> and its transcription profile in salivary glands during larval development. <i>Genetics and Molecular Biology</i> , 2016, 39, 580-588.  | 0.6 | 0         |
| 3540 | Is Hybridization a Source of Adaptive Venom Variation in Rattlesnakes? A Test, Using a <i>Crotalus scutulatus</i> – <i>viridis</i> Hybrid Zone in Southwestern New Mexico. <i>Toxins</i> , 2016, 8, 188.  | 1.5 | 29        |
| 3541 | Changes in <i>Bacillus anthracis</i> CodY regulation under host-specific environmental factor deprived conditions. <i>BMC Genomics</i> , 2016, 17, 645.   | 1.2 | 9         |
| 3542 | Evaluation of 16S rRNA Gene Primer Pairs for Monitoring Microbial Community Structures Showed High Reproducibility within and Low Comparability between Datasets Generated with Multiple Archaeal and Bacterial Primer Pairs. <i>Frontiers in Microbiology</i> , 2016, 7, 1297. | 1.5 | 73        |
| 3543 | Next Generation Sequencing in Aquatic Models. , 0, , .  |     | 0         |
| 3544 | Viral type characterization and clinical aspects of canine parvovirus in naturally infected dogs in São Paulo State, Brazil. <i>Pesquisa Veterinaria Brasileira</i> , 2016, 36, 1181-1185.  | 0.5 | 3         |
| 3545 | Uso de filtros de carvão ativado granular associado a microrganismos para remoção de fármacos no tratamento de água de abastecimento. <i>Engenharia Sanitaria E Ambiental</i> , 2016, 21, 709-720.  | 0.1 | 15        |
| 3546 | Challenges of Identifying Clinically Actionable Genetic Variants for Precision Medicine. <i>Journal of Healthcare Engineering</i> , 2016, 2016, 1-14.   | 1.1 | 34        |
| 3547 | From Conventional to Next Generation Sequencing of Epstein-Barr Virus Genomes. <i>Viruses</i> , 2016, 8, 60.  | 1.5 | 17        |
| 3548 | Diversity, Specificity, and Phylogenetic Relationships of Endohyphal Bacteria in Fungi That Inhabit Tropical Seeds and Leaves. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .   | 1.1 | 41        |
| 3549 | The Complete Genome Sequence of Hyperthermophile <i>Dictyoglomus turgidum</i> DSM 6724, Reveals a Specialized Carbohydrate Fermentor. <i>Frontiers in Microbiology</i> , 2016, 7, 1979.   | 1.5 | 14        |
| 3550 | A Point Mutation in a lincRNA Upstream of GDNF Is Associated to a Canine Insensitivity to Pain: A Spontaneous Model for Human Sensory Neuropathies. <i>PLoS Genetics</i> , 2016, 12, e1006482.  | 1.5 | 31        |
| 3551 | Factors Influencing Bacterial Diversity and Community Composition in Municipal Drinking Waters in the Ohio River Basin, USA. <i>PLoS ONE</i> , 2016, 11, e0157966.  | 1.1 | 70        |
| 3552 | Genome Analysis and Characterisation of the Exopolysaccharide Produced by <i>Bifidobacterium longum</i> subsp. <i>longum</i> 35624. <i>PLoS ONE</i> , 2016, 11, e0162983.   | 1.1 | 76        |
| 3553 | Airway Microbiota in Bronchoalveolar Lavage Fluid from Clinically Well Infants with Cystic Fibrosis. <i>PLoS ONE</i> , 2016, 11, e0167649.  | 1.1 | 53        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3554 | New insights from molecular characterization of the tick <i>Rhipicephalus (Boophilus) microplus</i> in Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2016, 25, 317-326.   | 0.2 | 20        |
| 3555 | Effect of Vitamin E With Therapeutic Iron Supplementation on Iron Repletion and Gut Microbiome in US Iron Deficient Infants and Toddlers. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 63, 379-385.                             | 0.9 | 51        |
| 3556 | Chemical constituents and their antibacterial activity from the tropical endophytic fungus <i>Diaporthe</i> sp. F2934. <i>Journal of Applied Microbiology</i> , 2016, 120, 1501-1508.   | 1.4 | 20        |
| 3557 | Transcriptome profiling in oral cavity and esophagus tissues from (S)â€”nitrosonornicotineâ€”treated rats reveals candidate genes involved in human oral cavity and esophageal carcinogenesis. <i>Molecular Carcinogenesis</i> , 2016, 55, 2168-2182. | 1.3 | 8         |
| 3558 | Diversity patterns of <i>Rhizobiaceae</i> communities inhabiting soils, root surfaces and nodules reveal a strong selection of rhizobial partners by legumes. <i>Environmental Microbiology</i> , 2016, 18, 2375-2391.                                | 1.8 | 50        |
| 3559 | Current Research Topics in Plant Virology. , 2016, , .  |     | 28        |
| 3560 | A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. <i>Plant Physiology</i> , 2016, 171, pp.00124.2016.  | 2.3 | 41        |
| 3561 | Evaluation of bacterial transmission to the paranasal sinuses through sinus irrigation. <i>International Forum of Allergy and Rhinology</i> , 2016, 6, 800-806.   | 1.5 | 7         |
| 3562 | Genomewide single nucleotide polymorphism discovery in Atlantic salmon ( <i>Salmo salar</i> ): validation in wild and farmed American and European populations. <i>Molecular Ecology Resources</i> , 2016, 16, 1002-1011.                             | 2.2 | 134       |
| 3563 | An FPGA-based quality filter for de novo sequence assembly pipeline. , 2016, , .  |     | 0         |
| 3564 | Novel equine tissue miRNAs and breed-related miRNA expressed in serum. <i>BMC Genomics</i> , 2016, 17, 831.   | 1.2 | 28        |
| 3566 | Permanent draft genome of strain ESFC-1: ecological genomics of a newly discovered lineage of filamentous diazotrophic cyanobacteria. <i>Standards in Genomic Sciences</i> , 2016, 11, 53.  | 1.5 | 4         |
| 3567 | Metagenomic Analysis of Slovak Bryndza Cheese Using Next-Generation 16S rDNA Amplicon Sequencing. <i>Nova Biotechnologica Et Chimica</i> , 2016, 15, 23-34.   | 0.1 | 13        |
| 3568 | Misincorporation by RNA polymerase is a major source of transcription pausing in vivo. <i>Nucleic Acids Research</i> , 2016, 45, gkw969.  | 6.5 | 31        |
| 3569 | pBACode: a random-barcode-based high-throughput approach for BAC paired-end sequencing and physical clone mapping. <i>Nucleic Acids Research</i> , 2017, 45, gkw1261.   | 6.5 | 9         |
| 3570 | Streamlined analysis of duplex sequencing data with Du Novo. <i>Genome Biology</i> , 2016, 17, 180.   | 3.8 | 24        |
| 3571 | The genome of Rhizobiales bacteria in predatory ants reveals urease gene functions but no genes for nitrogen fixation. <i>Scientific Reports</i> , 2016, 6, 39197.  | 1.6 | 55        |
| 3572 | Transcriptome (ESTs) of native Mexican avocado fruit is dominated by stress and innate immunity genes. <i>Acta Horticulturae</i> , 2016, , 43-48.   | 0.1 | 4         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3573 | Gelsolin role in microapocrine secretion. <i>Insect Molecular Biology</i> , 2016, 25, 810-820.  | 1.0 | 5         |
| 3574 | Human enamel thickness and ENAM polymorphism. <i>International Journal of Oral Science</i> , 2016, 8, 93-97.  | 3.6 | 29        |
| 3575 | A novel role for pigment genes in the stress response in rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Scientific Reports</i> , 2016, 6, 28969.  | 1.6 | 19        |
| 3576 | The Next Generation Sequencing and Applications in Clinical Research. <i>Translational Bioinformatics</i> , 2016, , 83-113.   | 0.0 | 0         |
| 3577 | Berberine Antifungal Activity in Fluconazole-Resistant Pathogenic Yeasts: Action Mechanism Evaluated by Flow Cytometry and Biofilm Growth Inhibition in <i>Candida</i> spp. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3551-3557. | 1.4 | 97        |
| 3578 | Vmp1 and stamp genes variability of <i>Candidatus phytoplasma solani</i> ™ in Bosnian and Herzegovinian grapevine. <i>European Journal of Plant Pathology</i> , 2016, 145, 221-225.   | 0.8 | 13        |
| 3579 | Next-Generation Sequencing of the HLA locus: Methods and impacts on HLA typing, population genetics and disease association studies. <i>Human Immunology</i> , 2016, 77, 1016-1023.   | 1.2 | 66        |
| 3580 | Nonoverlapping Clinical and Mutational Patterns in Melanomas from the Female Genital Tract and Atypical Genital Nevi. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1858-1865.   | 0.3 | 27        |
| 3581 | How To Live with Phosphorus Scarcity in Soil and Sediment: Lessons from Bacteria. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4652-4662.  | 1.4 | 60        |
| 3582 | Molecular analysis of nestling diet in a long-distance Neotropical migrant, the Louisiana Waterthrush ( <i>Parkesia motacilla</i> ). <i>Auk</i> , 2016, 133, 415-428.   | 0.7 | 40        |
| 3583 | Design and computational analysis of single-cell RNA-sequencing experiments. <i>Genome Biology</i> , 2016, 17, 63.  | 3.8 | 413       |
| 3584 | miRNA profiling of high, low and non-producing CHO cells during biphasic fed-batch cultivation reveals process relevant targets for host cell engineering. <i>Journal of Biotechnology</i> , 2016, 225, 31-43.                                  | 1.9 | 19        |
| 3585 | Novel bioinformatic developments for exome sequencing. <i>Human Genetics</i> , 2016, 135, 603-614.  | 1.8 | 37        |
| 3586 | Claudin 1 Expression Levels Affect miRNA Dynamics in Human Basal-Like Breast Cancer Cells. <i>DNA and Cell Biology</i> , 2016, 35, 328-339.   | 0.9 | 13        |
| 3587 | The omic approach to parasitic trematode research—a review of techniques and developments within the past 50 years. <i>Parasitology Research</i> , 2016, 115, 2523-2543.  | 0.6 | 10        |
| 3588 | The Complete Mitochondrial Genome and Song Evolution of the Monotypic Genus <i>U. Tarbinsky</i> , 1932 (Orthoptera: Tettigoniidae). <i>Environmental Entomology</i> , 2016, 45, 737-746.  | 0.7 | 1         |
| 3589 | How to Identify Pathogenic Mutations among All Those Variations: Variant Annotation and Filtration in the Genome Sequencing Era. <i>Human Mutation</i> , 2016, 37, 1272-1282.   | 1.1 | 28        |
| 3590 | A Primer on Infectious Disease Bacterial Genomics. <i>Clinical Microbiology Reviews</i> , 2016, 29, 881-913.  | 5.7 | 42        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3591 | Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016, 17, 249-260.   | 2.9 | 21        |
| 3592 | Expression of a putative dioxygenase gene adjacent to an insertion mutation is involved in the short internodes of columnar apples ( <i>Malus A— domestica</i> ). <i>Journal of Plant Research</i> , 2016, 129, 1109-1126.                    | 1.2 | 33        |
| 3593 | Genetic diversity and population structure of <i>Corollospora maritima sensu lato</i> : new insights from population genetics. <i>Botanica Marina</i> , 2016, 59, 307-320.  | 0.6 | 8         |
| 3594 | Prevalence of the genus <i>Cladosporium</i> on the integument of leaf-cutting ants characterized by 454 pyrosequencing. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 1235-1243.  | 0.7 | 6         |
| 3595 | Impact of post-alignment processing in variant discovery from whole exome data. <i>BMC Bioinformatics</i> , 2016, 17, 403.  | 1.2 | 28        |
| 3596 | Functional evaluation of Heat Shock Proteins 70 (HSP70/HSC70) on <i>Rhodnius prolixus</i> (Hemiptera, Tj ETQq1 1 0.784314 rgBT /Overl Molecular Biology, 2016, 77, 10-20.   | 1.2 | 63        |
| 3597 | Genome-wide single nucleotide polymorphism (SNP) identification and characterization in a non-model organism, the African buffalo ( <i>Syncerus caffer</i> ), using next generation sequencing. <i>Mammalian Biology</i> , 2016, 81, 595-603. | 0.8 | 11        |
| 3598 | Identifying wrong assemblies in de novo short read primary sequence assembly contigs. <i>Journal of Biosciences</i> , 2016, 41, 455-474.  | 0.5 | 0         |
| 3599 | The hepatitis delta genotype 8 in Northeast Brazil: The North Atlantic slave trade as the potential route for infection. <i>Virus Research</i> , 2016, 224, 6-11.   | 1.1 | 12        |
| 3600 | Investigation of bacterial repopulation after sinus surgery and perioperative antibiotics. <i>International Forum of Allergy and Rhinology</i> , 2016, 6, 34-40.  | 1.5 | 47        |
| 3601 | Molecular and genealogical analyses reveal multiple sources of the mutation associated with dermatosparaxis in Brazilian White Dorper sheep. <i>Small Ruminant Research</i> , 2016, 140, 46-49.   | 0.6 | 2         |
| 3602 | High-throughput miRNA sequencing and identification of biomarkers for forensically relevant biological fluids. <i>Electrophoresis</i> , 2016, 37, 2780-2788.  | 1.3 | 65        |
| 3604 | A new laboratory evolution approach to select for constitutive acetic acid tolerance in <i>Saccharomyces cerevisiae</i> and identification of causal mutations. <i>Biotechnology for Biofuels</i> , 2016, 9, 173.                             | 6.2 | 109       |
| 3606 | Towards precision medicine. <i>Nature Reviews Genetics</i> , 2016, 17, 507-522.   | 7.7 | 651       |
| 3607 | CSAM: Compressed SAM format. <i>Bioinformatics</i> , 2016, 32, 3709-3716.   | 1.8 | 10        |
| 3608 | Assembly and Application to the Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , 139-158.  | 0.3 | 0         |
| 3609 | Groundwater—surface water mixing shifts ecological assembly processes and stimulates organic carbon turnover. <i>Nature Communications</i> , 2016, 7, 11237.  | 5.8 | 290       |
| 3610 | Microbial diversity in individuals and their household contacts following typical antibiotic courses. <i>Microbiome</i> , 2016, 4, 39.  | 4.9 | 135       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3611 | Diagnosis of Plant Viruses Using Next-Generation Sequencing and Metagenomic Analysis. , 2016, , 323-335.  |     | 30        |
| 3612 | Integrating multiple evidences in taxonomy: species diversity and phylogeny of mustached bats (Mormoopidae: Pteronotus). Molecular Phylogenetics and Evolution, 2016, 103, 184-198.   | 1.2 | 50        |
| 3613 | Bacterial selection by mycospheres of Atlantic Rainforest mushrooms. Antonie Van Leeuwenhoek, 2016, 109, 1353-1365.   | 0.7 | 28        |
| 3614 | An Alignment-Free "Metapeptide" Strategy for Metaproteomic Characterization of Microbiome Samples Using Shotgun Metagenomic Sequencing. Journal of Proteome Research, 2016, 15, 2697-2705.  | 1.8 | 67        |
| 3615 | Preserving the Sequence of a Biopolymer's Monomers as They Enter an Electrospray Mass Spectrometer. Physical Review Applied, 2016, 6, .   | 1.5 | 15        |
| 3616 | On the (un)predictability of a large intragenic fitness landscape. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14085-14090.   | 3.3 | 104       |
| 3617 | Isolation of dengue virus serotype 4 genotype II from a patient with high viral load and a mixed Th1/Th17 inflammatory cytokine profile in South Brazil. Virology Journal, 2016, 13, 93.  | 1.4 | 24        |
| 3618 | The Next State-of-the-Art Forensic Genetics Technology: Massively Parallel Sequencing. Security Science and Technology, 2016, , 249-291.  | 0.5 | 1         |
| 3619 | Genome and metagenome analyses reveal adaptive evolution of the host and interaction with the gut microbiota in the goose. Scientific Reports, 2016, 6, 32961.  | 1.6 | 36        |
| 3620 | Amino Acid Changes in the HIV-1 gp41 Membrane Proximal Region Control Virus Neutralization Sensitivity. EBioMedicine, 2016, 12, 196-207.  | 2.7 | 34        |
| 3621 | Complete genome sequence of the Antarctic Halorubrum lacusprofundi type strain ACAM 34. Standards in Genomic Sciences, 2016, 11, 70.  | 1.5 | 21        |
| 3622 | Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing $\beta$ -proteobacterium Thioalkalimicrobium cyclicum type strain ALM 1 (DSM 14477T). Standards in Genomic Sciences, 2016, 11, 38. | 1.5 | 6         |
| 3623 | ESAP plus: a web-based server for EST-SSR marker development. BMC Genomics, 2016, 17, 1035.   | 1.2 | 12        |
| 3624 | Complete genome sequence of the actinomycete Actinoalloteichus hymeniacidonis type strain HPA 177T isolated from a marine sponge. Standards in Genomic Sciences, 2016, 11, 91.  | 1.5 | 11        |
| 3625 | Fast comparison of genomic and meta-genomic reads with alignment-free measures based on quality values. BMC Medical Genomics, 2016, 9, 36.  | 0.7 | 6         |
| 3626 | Identification of Variants in Genes Associated with Single-gene Inflammatory Bowel Disease by Whole-exome Sequencing. Inflammatory Bowel Diseases, 2016, 22, 2317-2327.   | 0.9 | 39        |
| 3627 | Population genetic evidence for cold adaptation in European <i>Drosophila melanogaster</i> populations. Molecular Ecology, 2016, 25, 1175-1191.   | 2.0 | 25        |
| 3628 | Trimming of sequence reads alters RNA-Seq gene expression estimates. BMC Bioinformatics, 2016, 17, 103.   | 1.2 | 154       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3629 | The complete genome sequence and analysis of a plasmid-bearing myxobacterial strain <i>Myxococcus fulvus</i> 124B02 (M 206081). <i>Standards in Genomic Sciences</i> , 2016, 11, 1.                                      | 1.5 | 83        |
| 3630 | Replacement of the initial steps of ethanol metabolism in <i>Saccharomyces cerevisiae</i> by ATP-independent acetylating acetaldehyde dehydrogenase. <i>FEMS Yeast Research</i> , 2016, 16, fow006.                      | 1.1 | 13        |
| 3631 | Toward reliable biomarker signatures in the age of liquid biopsies - how to standardize the small RNA-Seq workflow. <i>Nucleic Acids Research</i> , 2016, 44, 5995-6018.   | 6.5 | 97        |
| 3632 | Mode of Delivery Determines Neonatal Pharyngeal Bacterial Composition and Early Intestinal Colonization. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 63, 320-328.                                 | 0.9 | 43        |
| 3633 | Single nucleotide polymorphism in sugar pathway and disease resistance genes in sugarcane. <i>Plant Cell Reports</i> , 2016, 35, 1629-1653.  | 2.8 | 5         |
| 3634 | A comparison of tools for the simulation of genomic next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2016, 17, 459-469.   | 7.7 | 163       |
| 3635 | Improvement in detection of minor alleles in next generation sequencing by base quality recalibration. <i>BMC Genomics</i> , 2016, 17, 139.  | 1.2 | 8         |
| 3636 | ChlamyNET: a <i>Chlamydomonas</i> gene co-expression network reveals global properties of the transcriptome and the early setup of key co-expression patterns in the green lineage. <i>BMC Genomics</i> , 2016, 17, 227. | 1.2 | 45        |
| 3637 | The expansion of heterochromatin blocks in rye reflects the co-amplification of tandem repeats and adjacent transposable elements. <i>BMC Genomics</i> , 2016, 17, 337.  | 1.2 | 32        |
| 3638 | Red Sea Atlantis II brine pool nitrilase with unique thermostability profile and heavy metal tolerance. <i>BMC Biotechnology</i> , 2016, 16, 14.   | 1.7 | 19        |
| 3639 | Complete genome sequence of <i>Methanospirillum hungatei</i> type strain JF1. <i>Standards in Genomic Sciences</i> , 2016, 11, 2.  | 1.5 | 33        |
| 3640 | Novel Hydrogenosomes in the Microaerophilic Jakobid <i>Stygiella incarcerata</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2318-2336.   | 3.5 | 52        |
| 3641 | Complete genome sequences of <i>Geobacillus</i> sp. WCH70, a thermophilic strain isolated from wood compost. <i>Standards in Genomic Sciences</i> , 2016, 11, 33.  | 1.5 | 11        |
| 3642 | Evaluation of methanol preservation for molecular and morphological studies in cyanobacteria using <i>Planktothrix agardhii</i> . <i>Journal of Applied Phycology</i> , 2016, 28, 1713-1723.                             | 1.5 | 2         |
| 3643 | Draft Genomes for Eight <i>Burkholderia mallei</i> Isolates from Turkey. <i>Genome Announcements</i> , 2016, 4, .  | 0.8 | 4         |
| 3644 | A history of DNA sequence assembly. <i>IT - Information Technology</i> , 2016, 58, 126-132.  | 0.6 | 23        |
| 3645 | An introduction to plant phylogenomics with a focus on palms. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 234-255.  | 0.8 | 42        |
| 3646 | Genome-wide survey of artificial mutations induced by ethyl methanesulfonate and gamma rays in tomato. <i>Plant Biotechnology Journal</i> , 2016, 14, 51-60.   | 4.1 | 155       |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3647 | <i>Pararhinebothroides</i>”Neither the Sister-Taxon of<i>Rhinebothroides</i>Nor a Valid Genus. Journal of Parasitology, 2016, 102, 249-259.  | 0.3 | 20        |
| 3648 | Oxaspirol B with p97 Inhibitory Activity and Other Oxaspirols from <i>Lecythophora</i> sp. FL1375 and FL1031, Endolichenic Fungi Inhabiting <i>Parmotrema tinctorum</i> and <i>Cladonia evansii</i>. Journal of Natural Products, 2016, 79, 340-352.   | 1.5 | 29        |
| 3649 | A FASTQ compressor based on integer-mapped k-mer indexing for biologist. Gene, 2016, 579, 75-81.   | 1.0 | 18        |
| 3650 | Isolation of Endohyphal Bacteria from Foliar Ascomycota and <i>In Vitro</i> Establishment of Their Symbiotic Associations. Applied and Environmental Microbiology, 2016, 82, 2943-2949.  | 1.4 | 61        |
| 3651 | Next generation sequencing for whole genome analysis and surveillance of influenza A viruses. Journal of Clinical Virology, 2016, 79, 44-50.   | 1.6 | 63        |
| 3652 | Pleurochrysome: A Web Database ofPleurochrysisTranscripts and Orthologs Among Heterogeneous Algae. Plant and Cell Physiology, 2016, 57, e6-e6.   | 1.5 | 4         |
| 3653 | Does phylogeny control <math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" overflow="scroll"><mrow><msubsup><mrow><mi>U</mi></mrow></mrow></math> sensitivity? Implications for lacustrine alkenone paleothermometry. Geochimica Et Cosmochimica Acta, 2016, 175, 168-180. | 1.6 | 374       |
| 3654 | Overview of Sequence Data Formats. Methods in Molecular Biology, 2016, 1418, 3-17.   | 0.4 | 30        |
| 3655 | Variant Calling From Next Generation Sequence Data. Methods in Molecular Biology, 2016, 1418, 209-224.   | 0.4 | 11        |
| 3656 | Changes in rhizosphere bacterial gene expression following glyphosate treatment. Science of the Total Environment, 2016, 553, 32-41.   | 3.9 | 90        |
| 3657 | Feature based quality assessment of DNA sequencing chromatograms. Applied Soft Computing Journal, 2016, 41, 420-427.   | 4.1 | 5         |
| 3658 | Intraspecific Variation in Mitogenomes of Five Crassostrea Species Provides Insight into Oyster Diversification and Speciation. Marine Biotechnology, 2016, 18, 242-254.   | 1.1 | 30        |
| 3659 | Genomic characterization of Pasteurella multocida HB01, a serotype A bovine isolate from China. Gene, 2016, 581, 85-93.  | 1.0 | 36        |
| 3660 | microRNA in native and processed cow's milk and its implication for the farm milk effect on asthma. Journal of Allergy and Clinical Immunology, 2016, 137, 1893-1895.e13.  | 1.5 | 69        |
| 3661 | Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). Molecular Phylogenetics and Evolution, 2016, 98, 210-232.   | 1.2 | 110       |
| 3662 | Next-Generation Sequencing: Principles for Clinical Application. , 2016, , 889-909.  |     | 0         |
| 3663 | A computer program for fast and easy typing of a partial endoglucanase gene sequence into genospecies and sequevars 1&2 of the Ralstonia solanacearum species complex. Journal of Microbiological Methods, 2016, 123, 101-107.   | 0.7 | 11        |
| 3664 | Association of the IGF1 gene with fasting insulin levels. European Journal of Human Genetics, 2016, 24, 1337-1343.   | 1.4 | 5         |



| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 3665 | Decoding DNA, RNA and peptides with quantum tunnelling. <i>Nature Nanotechnology</i> , 2016, 11, 117-126.  | 15.6 | 183       |
| 3666 | Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.  | 6.0  | 30        |
| 3667 | fqtools: an efficient software suite for modern FASTQ file manipulation. <i>Bioinformatics</i> , 2016, 32, 1883-1884.  | 1.8  | 26        |
| 3668 | Complete genome sequence of a deeply branched marine Bacteroidia bacterium <i>Draconibacterium orientale</i> type strain FH5T. <i>Marine Genomics</i> , 2016, 26, 13-16.                                   | 0.4  | 6         |
| 3669 | De novo transcriptome analysis of carotenoid and polyunsaturated fatty acid metabolism in <i>Rhodomonas</i> sp.. <i>Journal of Applied Phycology</i> , 2016, 28, 1649-1656.                                | 1.5  | 10        |
| 3670 | Pervasive Effects of Wildfire on Foliar Endophyte Communities in Montane Forest Trees. <i>Microbial Ecology</i> , 2016, 71, 452-468.   | 1.4  | 37        |
| 3671 | MSuPDA: A Memory Efficient Algorithm for Sequence Alignment. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 84-94.  | 2.2  | 3         |
| 3672 | Variation in ectomycorrhizal fungal communities associated with <i>Oreomunnea mexicana</i> (Juglandaceae) in a Neotropical montane forest. <i>Mycorrhiza</i> , 2016, 26, 1-17.                             | 1.3  | 72        |
| 3673 | Faba bean drought responsive gene identification and validation. <i>Saudi Journal of Biological Sciences</i> , 2017, 24, 80-89.  | 1.8  | 16        |
| 3674 | Montagnophilones Aâ€“G, Azaphilones from <i>Montagnulaceae</i> sp. DM0194, a Fungal Endophyte of Submerged Roots of <i>Persicaria amphibia</i> . <i>Journal of Natural Products</i> , 2017, 80, 76-81.     | 1.5  | 10        |
| 3675 | Genome Sequence of <i>Porphyromonas gingivalis</i> Strain 381. <i>Genome Announcements</i> , 2017, 5, .  | 0.8  | 18        |
| 3676 | JACUSA: site-specific identification of RNA editing events from replicate sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 7.  | 1.2  | 76        |
| 3677 | Modeling Human Population Separation History Using Physically Phased Genomes. <i>Genetics</i> , 2017, 205, 385-395.  | 1.2  | 46        |
| 3678 | Chlorinated Dehydrocurvularins and Alterperyleneoxide A from <i>Alternaria</i> sp. AST0039, a Fungal Endophyte of <i>Astragalus lentiginosus</i> . <i>Journal of Natural Products</i> , 2017, 80, 427-433. | 1.5  | 23        |
| 3679 | High-throughput sequencing of the T-cell receptor repertoire: pitfalls and opportunities. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw138.   | 3.2  | 88        |
| 3680 | DNA damage is a pervasive cause of sequencing errors, directly confounding variant identification. <i>Science</i> , 2017, 355, 752-756.  | 6.0  | 196       |
| 3681 | Statistical modelling of Ion PGM HID STR 10-plex MPS data. <i>Forensic Science International: Genetics</i> , 2017, 28, 82-89.  | 1.6  | 14        |
| 3682 | De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease. <i>Genome Medicine</i> , 2017, 9, 8.  | 3.6  | 27        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3683 | Antigenic and genotypic characterization of rabies virus isolated from bats (Mammalia: Chiroptera) from municipalities in São Paulo State, Southeastern Brazil. <i>Archives of Virology</i> , 2017, 162, 1201-1209.                         | 0.9 | 10        |
| 3684 | Complete mitochondrial genome from South American catfish <i>Pseudoplatystoma reticulatum</i> (Eigenmann & Eigenmann) and its impact in Siluriformes phylogenetic tree. <i>Genetica</i> , 2017, 145, 51-66.                                 | 0.5 | 9         |
| 3685 | Draft Genome Sequence of Sorghum Grain Mold Fungus <i>Epicoccum sorghinum</i> , a Producer of Tenuazonic Acid. <i>Genome Announcements</i> , 2017, 5, .   | 0.8 | 19        |
| 3686 | Simple discovery of bacterial biocatalysts from environmental samples through functional metaproteomics. <i>Microbiome</i> , 2017, 5, 28.   | 4.9 | 20        |
| 3687 | Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. <i>Nature Genetics</i> , 2017, 49, 643-650.  | 9.4 | 600       |
| 3688 | Investigation of intra-herd spread of <i>Mycobacterium caprae</i> in cattle by generation and use of a whole-genome sequence. <i>Veterinary Research Communications</i> , 2017, 41, 113-128.  | 0.6 | 19        |
| 3689 | An Overview of Next-Generation Sequencing (NGS) Technologies to Study the Molecular Diversity of Genome. , 2017, , 295-317.   |     | 1         |
| 3690 | In vitro anti-Candida activity of selective serotonin reuptake inhibitors against fluconazole-resistant strains and their activity against biofilm-forming isolates. <i>Microbial Pathogenesis</i> , 2017, 107, 341-348.                    | 1.3 | 42        |
| 3691 | Assessment of a quantitative 5' nuclease real-time polymerase chain reaction using groEL gene for Ehrlichia and Anaplasma species in rodents in Brazil. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 646-656.                            | 1.1 | 22        |
| 3692 | Delivering Clinical Grade Sequencing and Genetic Test Interpretation for Cardiovascular Medicine. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .   | 5.1 | 11        |
| 3693 | cDNA cloning, molecular modeling and docking calculations of L-type lectins from <i>Swartzia simplex</i> var. <i>grandiflora</i> (Leguminosae, Papilionoideae), a member of the tribe Swartzieae. <i>Phytochemistry</i> , 2017, 139, 60-71. | 1.4 | 6         |
| 3694 | Evidence and molecular characterization of <i>Bartonella</i> spp. and hemoplasmas in neotropical bats in Brazil. <i>Epidemiology and Infection</i> , 2017, 145, 2038-2052.  | 1.0 | 46        |
| 3695 | Similarities between Reproductive and Immune Pistil Transcriptomes of <i>Arabidopsis</i> Species. <i>Plant Physiology</i> , 2017, 174, 1559-1575.   | 2.3 | 20        |
| 3696 | Comparative authentication of <i>Hypericum perforatum</i> herbal products using DNA metabarcoding, TLC and HPLC-MS. <i>Scientific Reports</i> , 2017, 7, 1291.  | 1.6 | 100       |
| 3697 | An assessment of the molecular mechanisms contributing to tolerance to apical damage in natural populations of <i>Arabidopsis thaliana</i> . <i>Plant Ecology</i> , 2017, 218, 265-276.   | 0.7 | 6         |
| 3698 | Distribution of Anaerobic Hydrocarbon-Degrading Bacteria in Soils from King George Island, Maritime Antarctica. <i>Microbial Ecology</i> , 2017, 74, 810-820.   | 1.4 | 27        |
| 3699 | High-throughput sequencing of African chikanda cake highlights conservation challenges in orchids. <i>Biodiversity and Conservation</i> , 2017, 26, 2029-2046.  | 1.2 | 26        |
| 3700 | High precision genome sequencing of engineered <i>Gluconobacter oxydans</i> 621H by combining long nanopore and short accurate Illumina reads. <i>Journal of Biotechnology</i> , 2017, 258, 197-205.  | 1.9 | 17        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3701 | Complete Genome Sequence of <i>Flavobacterium psychrophilum</i> Strain OSU THCO2-90, Used for Functional Genetic Analysis. <i>Genome Announcements</i> , 2017, 5, .   | 0.8 | 11        |
| 3702 | Genome Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1525, 3-33.  | 0.4 | 33        |
| 3703 | Infrared laser ablation sample transfer of tissue DNA for genomic analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 4119-4126.   | 1.9 | 10        |
| 3704 | Prevalence of naturally occurring protease inhibitor resistance-associated variants in hemodialysis and renal transplant patients with hepatitis C virus infection. <i>European Journal of Gastroenterology and Hepatology</i> , 2017, 29, 754-758. | 0.8 | 0         |
| 3705 | Description of a tropical new species of <i>Wilmottia</i> (Oscillatoriales, Cyanobacteria) and considerations about the monophyly of <i>W. murrayi</i> . <i>Phytotaxa</i> , 2017, 307, 43.  | 0.1 | 14        |
| 3706 | Microbiota Analysis Using an Illumina MiSeq Platform to Sequence 16S rRNA Genes. <i>Current Protocols in Mouse Biology</i> , 2017, 7, 100-129.  | 1.2 | 37        |
| 3707 | Improving the DNA specificity and applicability of base editing through protein engineering and protein delivery. <i>Nature Communications</i> , 2017, 8, 15790.  | 5.8 | 343       |
| 3708 | Seasonal and regional occurrence of heat-resistant spore-forming bacteria in the course of ultra-high temperature milk production in Tunisia. <i>Journal of Dairy Science</i> , 2017, 100, 6090-6099.   | 1.4 | 16        |
| 3709 | Genotyping <i>Toxoplasma gondii</i> with the <i>B1</i> Gene in Naturally Infected Sheep from an Endemic Region in the Pacific Coast of Mexico. <i>Vector-Borne and Zoonotic Diseases</i> , 2017, 17, 495-502.                                       | 0.6 | 9         |
| 3710 | Diversity of aromatic hydroxylating dioxygenase genes in mangrove microbiome and their biogeographic patterns across global sites. <i>MicrobiologyOpen</i> , 2017, 6, e00490.   | 1.2 | 11        |
| 3711 | Phylogenomics. , 2017, , .  |     | 47        |
| 3712 | PhredEM: a phred-score-informed genotype-calling approach for next-generation sequencing studies. <i>Genetic Epidemiology</i> , 2017, 41, 375-387.  | 0.6 | 21        |
| 3713 | Diet shifts provoke complex and variable changes in the metabolic networks of the ruminal microbiome. <i>Microbiome</i> , 2017, 5, 60.  | 4.9 | 38        |
| 3714 | Phylogenetic analysis of G1P[8] and G12P[8] rotavirus A samples obtained in the pre- and post-vaccine periods, and molecular modeling of VP4 and VP7 proteins. <i>Acta Tropica</i> , 2017, 173, 153-159.  | 0.9 | 6         |
| 3715 | Occurrence and molecular characterization of hemoplasmas in domestic dogs and wild mammals in a Brazilian wetland. <i>Acta Tropica</i> , 2017, 171, 172-181.  | 0.9 | 36        |
| 3716 | A Survey of Bioinformatics-Based Tools in RNA-Sequencing (RNA-Seq) Data Analysis. <i>Translational Medicine Research</i> , 2017, , 223-248.   | 0.0 | 3         |
| 3717 | Analysis of <i>Shigella flexneri</i> Resistance, Biofilm Formation, and Transcriptional Profile in Response to Bile Salts. <i>Infection and Immunity</i> , 2017, 85, .  | 1.0 | 65        |
| 3719 | epiC: statistical inference and profiling of DNA methylation from whole-genome bisulfite sequencing data. <i>Genome Biology</i> , 2017, 18, 38.   | 3.8 | 6         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3721 | Longitudinal and Source-to-Tap New Orleans, LA, U.S.A. Drinking Water Microbiology. Environmental Science & Technology, 2017, 51, 4220-4229.   | 4.6 | 48        |
| 3722 | Canu: scalable and accurate long-read assembly via adaptive <i>k</i> -mer weighting and repeat separation. Genome Research, 2017, 27, 722-736.   | 2.4 | 5,620     |
| 3723 | Complete genome sequence of <i>Pseudomonas stutzeri</i> strain RCH2 isolated from a Hexavalent Chromium [Cr(VI)] contaminated site. Standards in Genomic Sciences, 2017, 12, 23.                                     | 1.5 | 12        |
| 3724 | <i>Botryococcus braunii</i> strains compared for biomass productivity, hydrocarbon and carbohydrate content. Journal of Biotechnology, 2017, 248, 77-86.   | 1.9 | 50        |
| 3725 | Using cytochrome b to identify nests and museum specimens of cryptic songbirds. Conservation Genetics Resources, 2017, 9, 451-458.   | 0.4 | 6         |
| 3726 | Validating sonication as a DNA extraction method for use with carrion flies. Forensic Science International, 2017, 275, 171-177.   | 1.3 | 6         |
| 3727 | Community structure of fern-affiliated endophytes in three neotropical forests. Journal of Tropical Ecology, 2017, 33, 60-73.  | 0.5 | 18        |
| 3728 | Screening and functional identification of lncRNAs under $\beta$ -diketone antibiotic exposure to zebrafish ( <i>Danio rerio</i> ). <i>Journal of Experimental Biology</i> , 2017, 210, 1784-1794.                   | 1.9 | 14        |
| 3729 | Novel mutations involving $\beta$ -tubulin I, $\beta$ -tubulin II, or $\beta$ -tubulin III isotypes with functional resemblance to $\beta$ -tubulin III in breast cancer. <i>Protoplasma</i> , 2017, 254, 1163-1173. | 1.0 | 22        |
| 3730 | Experimental pathogenicity and complete genome characterization of a pig origin <i>Pasteurella multocida</i> serogroup F isolate HN07. <i>Veterinary Microbiology</i> , 2017, 198, 23-33.                            | 0.8 | 30        |
| 3731 | Identification of genome variations in patients with lung adenocarcinoma using whole genome re-sequencing. <i>Molecular Medicine Reports</i> , 2017, 16, 9464-9472.  | 1.1 | 6         |
| 3732 | <i>Actinoalloteichus fjordicus</i> sp. nov. isolated from marine sponges: phenotypic, chemotaxonomic and genomic characterisation. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1705-1717.                            | 0.7 | 7         |
| 3733 | Clinical and environmental isolates of <i>Burkholderia pseudomallei</i> from Brazil: Genotyping and detection of virulence gene. <i>Asian Pacific Journal of Tropical Medicine</i> , 2017, 10, 945-951.              | 0.4 | 6         |
| 3734 | Algorithms for Next-Generation Sequencing Data. , 2017, , .  |     | 2         |
| 3735 | Preprocessing and Quality Control for Whole-Genome Sequences from the Illumina HiSeq X Platform. <i>Methods in Molecular Biology</i> , 2017, 1666, 629-647.  | 0.4 | 10        |
| 3736 | Sequence Accuracy in Primary Databases: A Case Study on HIV-1B. , 2017, , 779-822.   |     | 0         |
| 3737 | Genotype-by-sequencing of three geographically distinct populations of Olympia oysters, <i>Ostrea lurida</i> . <i>Scientific Data</i> , 2017, 4, 170130.   | 2.4 | 5         |
| 3738 | Draft Genome Sequence of <i>Magnetospirillum</i> sp. Strain 15-1, a Denitrifying Toluene Degradator Isolated from a Planted Fixed-Bed Reactor. <i>Genome Announcements</i> , 2017, 5, .                              | 0.8 | 5         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3739 | tGBS <sup>®</sup> genotyping-by-sequencing enables reliable genotyping of heterozygous loci. <i>Nucleic Acids Research</i> , 2017, 45, e178-e178.   | 6.5 | 115       |
| 3740 | Viruses in cancers among the immunosuppressed. <i>International Journal of Cancer</i> , 2017, 141, 2498-2504.   | 2.3 | 20        |
| 3741 | Piecing together the puzzle: nanopore technology in detection and quantification of cancer biomarkers. <i>RSC Advances</i> , 2017, 7, 42653-42666.  | 1.7 | 13        |
| 3742 | Transcriptome sequencing and estimation of DNA methylation level in the subsocial wood-feeding cockroach <i>Cryptocercus punctulatus</i> (Blattodea: Cryptoceridae). <i>Applied Entomology and Zoology</i> , 2017, 52, 643-651. | 0.6 | 9         |
| 3743 | Discovery of Variants Underlying Host Susceptibility to Virus Infection Using Whole-Exome Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1656, 209-227.  | 0.4 | 0         |
| 3744 | DNA metabarcoding of orchid-derived products reveals widespread illegal orchid trade. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171182.   | 1.2 | 53        |
| 3745 | An Efficient Approach to Merging Paired-End Reads and Incorporation of Uncertainties. , 2017, , 299-325.  |     | 0         |
| 3746 | CUSHAW Suite: Parallel and Efficient Algorithms for NGS Read Alignment. , 2017, , 203-233.  |     | 0         |
| 3747 | Differentiating Botulinum Neurotoxin-Producing Clostridia with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , 2017, 83, .   | 1.4 | 18        |
| 3748 | 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.   | 2.3 | 9         |
| 3749 | Construction and characterization of a bacterial artificial chromosome library for <i>Camellia sinensis</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.   | 0.6 | 6         |
| 3750 | Diplosporous development in <i>Boehmeria tricuspidis</i> : Insights from de novo transcriptome assembly and comprehensive expression profiling. <i>Scientific Reports</i> , 2017, 7, 46043.                                     | 1.6 | 13        |
| 3751 | Divergent evolution and niche differentiation within the common peatmoss <i>Sphagnum magellanicum</i> . <i>American Journal of Botany</i> , 2017, 104, 1060-1072.   | 0.8 | 28        |
| 3752 | Metabolic and evolutionary patterns in the extremely acidophilic archaeon <i>Ferroplasma acidiphilum</i> YT. <i>Scientific Reports</i> , 2017, 7, 3682.   | 1.6 | 21        |
| 3753 | Bottom-up effects on herbivore-induced plant defences: a case study based on compositional patterns of rhizosphere microbial communities. <i>Scientific Reports</i> , 2017, 7, 6251.  | 1.6 | 15        |
| 3754 | A widespread cyanobacterium supported by polyphasic approach: proposition of <i>Koinonema pervagatum</i> gen. & sp. nov. (Oscillatoriales). <i>Journal of Phycology</i> , 2017, 53, 1097-1105.                                  | 1.0 | 7         |
| 3755 | Morphology, phylogeny, growth rate and nodularin production of <i>Nodularia spumigena</i> from Brazil. <i>Marine Biology Research</i> , 2017, 13, 1095-1107.  | 0.3 | 8         |
| 3757 | Use of Swabs for Sampling Epithelial Cells for Molecular Genetics Analyses in <i>Enteroctopus</i> . <i>American Malacological Bulletin</i> , 2017, 35, 145-157.   | 0.2 | 7         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3758 | Plant Bioinformatics: Next Generation Sequencing Approaches. , 2017, , 1-106.   |     | 1         |
| 3759 | Mutation accumulation under UV radiation in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2017, 7, 14531.   | 1.6 | 55        |
| 3760 | Anaplasmataceae agents among wild mammals and ectoparasites in Brazil. <i>Epidemiology and Infection</i> , 2017, 145, 3424-3437.  | 1.0 | 39        |
| 3761 | Phylogenetic relationships of Brazilian <i>Mikania</i> species (Asteraceae, Eupatorieae) based on multilocus DNA markers. <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 326-346.   | 0.8 | 10        |
| 3762 | Bacterial Biofilms in Jones Tubes. <i>Ophthalmic Plastic and Reconstructive Surgery</i> , 2017, 33, 279-284.  | 0.4 | 0         |
| 3763 | Genomic exaptation enables <i>Lasius niger</i> adaptation to urban environments. <i>BMC Evolutionary Biology</i> , 2017, 17, 39.  | 3.2 | 28        |
| 3764 | Comparative analyses of glycerotoxin expression unveil a novel structural organization of the bloodworm venom system. <i>BMC Evolutionary Biology</i> , 2017, 17, 64.   | 3.2 | 17        |
| 3765 | High-quality permanent draft genome sequence of the <i>Bradyrhizobium elkanii</i> type strain USDA 76T, isolated from <i>Glycine max</i> (L.) Merr. <i>Standards in Genomic Sciences</i> , 2017, 12, 26.  | 1.5 | 11        |
| 3766 | Sequencing and de novo assembly of visceral mass transcriptome of the critically endangered land snail <i>Satsuma myomphala</i> : Annotation and SSR discovery. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 21, 77-89.                             | 0.4 | 10        |
| 3767 | Human Oral Buccal Microbiomes Are Associated with Farmworker Status and Azinphos-Methyl Agricultural Pesticide Exposure. <i>Applied and Environmental Microbiology</i> , 2017, 83, .  | 1.4 | 33        |
| 3768 | From next-generation resequencing reads to a high-quality variant data set. <i>Heredity</i> , 2017, 118, 111-124.   | 1.2 | 68        |
| 3769 | A six-gene phylogeny provides new insights into choanoflagellate evolution. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 166-178.  | 1.2 | 59        |
| 3770 | Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.   | 2.8 | 199       |
| 3771 | Pig lacks functional NLRC4 and NAIP genes. <i>Immunogenetics</i> , 2017, 69, 125-130.   | 1.2 | 9         |
| 3772 | Mutation in the S gene <i>a</i> determinant of the hepatitis B virus associated with concomitant HBsAg and anti-HBs in a population in Northeastern Brazil. <i>Journal of Medical Virology</i> , 2017, 89, 458-462.   | 2.5 | 7         |
| 3773 | Identification of regulatory motifs in the CHO genome for stable monoclonal antibody production. <i>Cytotechnology</i> , 2017, 69, 451-460.   | 0.7 | 10        |
| 3774 | Integration of next-generation sequencing in clinical diagnostic molecular pathology laboratories for analysis of solid tumours; an expert opinion on behalf of IQN Path ASBL. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2017, 470, 5-20. | 1.4 | 82        |
| 3775 | Evidence of bottleneck effect on hepatitis C virus transmission between a couple under interferon based therapy. <i>Infection, Genetics and Evolution</i> , 2017, 47, 87-93.  | 1.0 | 2         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3776 | Specific populations of the yeast <i>Geotrichum candidum</i> revealed by molecular typing. <i>Yeast</i> , 2017, 34, 165-178.   | 0.8 | 31        |
| 3777 | Investigation of sinonasal microbiome spatial organization in chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2017, 7, 16-23.  | 1.5 | 43        |
| 3778 | ABI Base Recall: Automatic Correction and Ends Trimming of DNA Sequences. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 682-686.  | 2.2 | 2         |
| 3779 | Novel phosphate deficiency-responsive long non-coding RNAs in the legume model plant <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 5937-5948.   | 2.4 | 77        |
| 3780 | Single-Molecule Analysis Methods Using Nanogap Electrodes and Their Application to DNA Sequencing Technologies. <i>Bulletin of the Chemical Society of Japan</i> , 2017, 90, 1189-1210.  | 2.0 | 18        |
| 3781 | Paternal phylogeographic structure of the brown bear ( <i>Ursus arctos</i> ) in northeastern Asia and the effect of male-mediated gene flow to insular populations. <i>Zoological Letters</i> , 2017, 3, 21.   | 0.7 | 42        |
| 3782 | ALL-CQS: Adaptive locality-based lossy compression of quality scores. , 2017, , .  |     | 2         |
| 3783 | Transcriptome Sequencing for Precise and Accurate Measurement of Transcripts and Accessibility of TCGA for Cancer Datasets and Analysis. , 0, , .  |     | 0         |
| 3784 | MEEPTOOLS: a maximum expected error based FASTQ read filtering and trimming toolkit. <i>International Journal of Computational Biology and Drug Design</i> , 2017, 10, 237.  | 0.3 | 7         |
| 3785 | Fine Mapping of a Clubroot Resistance Gene in Chinese Cabbage Using SNP Markers Identified from Bulked Segregant RNA Sequencing. <i>Frontiers in Plant Science</i> , 2017, 8, 1448.  | 1.7 | 82        |
| 3786 | Comparative Genomics of <i>Ralstonia solanacearum</i> Identifies Candidate Genes Associated with Cool Virulence. <i>Frontiers in Plant Science</i> , 2017, 8, 1565.  | 1.7 | 25        |
| 3787 | Reliable Detection of Herpes Simplex Virus Sequence Variation by High-Throughput Resequencing. <i>Viruses</i> , 2017, 9, 226.  | 1.5 | 9         |
| 3788 | Patterns of genetic divergence in the <i>Ilyodromus amplicolis</i> lineage (Crustacea, Ostracoda), with descriptions of three new species. <i>Zootaxa</i> , 2017, 4318, .  | 0.2 | 4         |
| 3789 | Purification and characterization of a thermostable alkaline cellulase produced by <i>Bacillus licheniformis</i> 380 isolated from compost. <i>Anais Da Academia Brasileira De Ciencias</i> , 2017, 89, 2359-2370.   | 0.3 | 23        |
| 3790 | Iron in Micronutrient Powder Promotes an Unfavorable Gut Microbiota in Kenyan Infants. <i>Nutrients</i> , 2017, 9, 776.  | 1.7 | 65        |
| 3791 | Comparison of Direct Sequencing, Real-Time PCR-High Resolution Melt (PCR-HRM) and PCR-Restriction Fragment Length Polymorphism (PCR-RFLP) Analysis for Genotyping of Common Thiopurine Intolerant Variant Alleles NUDT15 c.415C>T and TPMT c.719A>G (TPMT*3C). <i>Diagnostics</i> , 2017, 7, 27. | 1.3 | 16        |
| 3792 | Genome-Wide Epigenetic Studies in Chicken: A Review. <i>Epigenomes</i> , 2017, 1, 20.  | 0.8 | 11        |
| 3793 | Next-Generation Sequencing in the Clinical Laboratory. , 2017, , 25-33.  |     | 1         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3794 | The Dynamics of microRNA Transcriptome in Bovine Corpus Luteum during Its Formation, Function, and Regression. <i>Frontiers in Genetics</i> , 2017, 8, 213.  | 1.1 | 30        |
| 3795 | <i>Bacillus</i> spp. Isolated from Puba as a Source of Biosurfactants and Antimicrobial Lipopeptides. <i>Frontiers in Microbiology</i> , 2017, 8, 61.  | 1.5 | 75        |
| 3796 | Plant Growth Promoting Bacteria Associated with <i>Langsdorffia hypogaea</i> -Rhizosphere-Host Biological Interface: A Neglected Model of Bacterial Prospection. <i>Frontiers in Microbiology</i> , 2017, 8, 172.    | 1.5 | 32        |
| 3797 | Genomic Analysis of <i>Caldithrix abyssi</i> , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum <i>Calditrichaeota</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 195.                          | 1.5 | 66        |
| 3798 | An Endohyphal Bacterium (Chitinophaga, Bacteroidetes) Alters Carbon Source Use by <i>Fusarium keratoplasticum</i> ( <i>F. solani</i> Species Complex, Nectriaceae). <i>Frontiers in Microbiology</i> , 2017, 8, 350. | 1.5 | 69        |
| 3799 | The Genomic Architecture of Novel <i>Simulium damnosum</i> <i>Wolbachia</i> Prophage Sequence Elements and Implications for Onchocerciasis Epidemiology. <i>Frontiers in Microbiology</i> , 2017, 8, 852.            | 1.5 | 7         |
| 3800 | Systematics and diversification of <i>Anindobothrium</i> Marques, Brooks & Lasso, 2001 (Eucestoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf   | 1.1 | 18        |
| 3801 | An Efficient Approach in Analysis of DNA Base Calling Using Neural Fuzzy Model. <i>Advances in Bioinformatics</i> , 2017, 2017, 1-7.   | 5.7 | 0         |
| 3802 | Preparing and Analyzing Expressed Sequence Tags (ESTs) Library for the Mammary Tissue of Local Turkish Kivircik Sheep. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.                                  | 0.8 | 0         |
| 3803 | Clarifying the Cryptic Host Specificity of <i>Blastocystis</i> spp. Isolates from <i>Alouatta palliata</i> and <i>A. pigra</i> Howler Monkeys. <i>PLoS ONE</i> , 2017, 12, e0169637.                                 | 1.1 | 24        |
| 3804 | Viruses in case series of tumors: Consistent presence in different cancers in the same subject. <i>PLoS ONE</i> , 2017, 12, e0172308.  | 1.1 | 6         |
| 3805 | A highly specific and sensitive massive parallel sequencer-based test for somatic mutations in non-small cell lung cancer. <i>PLoS ONE</i> , 2017, 12, e0176525.   | 1.1 | 11        |
| 3806 | Investigation of horizontal gene transfer of pathogenicity islands in <i>Escherichia coli</i> using next-generation sequencing. <i>PLoS ONE</i> , 2017, 12, e0179880.  | 1.1 | 35        |
| 3807 | A novel association between relaxin receptor polymorphism and hematopoietic stem cell yield after mobilization. <i>PLoS ONE</i> , 2017, 12, e0179986.  | 1.1 | 5         |
| 3808 | RNA-sequencing-based transcriptome and biochemical analyses of steroidal saponin pathway in a complete set of <i>Allium fistulosum</i> "A. cepa monosomic addition lines. <i>PLoS ONE</i> , 2017, 12, e0181784.      | 1.1 | 67        |
| 3809 | Maternal treatment with short-chain fatty acids modulates the intestinal microbiota and immunity and ameliorates type 1 diabetes in the offspring. <i>PLoS ONE</i> , 2017, 12, e0183786.                             | 1.1 | 46        |
| 3810 | A putative <i>Vibrio cholerae</i> two-component system controls a conserved periplasmic protein in response to the antimicrobial peptide polymyxin B. <i>PLoS ONE</i> , 2017, 12, e0186199.                          | 1.1 | 26        |
| 3811 | Analysis of large versus small dogs reveals three genes on the canine X chromosome associated with body weight, muscling and back fat thickness. <i>PLoS Genetics</i> , 2017, 13, e1006661.                          | 1.5 | 51        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3812 | Estimating Phred scores of Illumina base calls by logistic regression and sparse modeling. <i>BMC Bioinformatics</i> , 2017, 18, 335.   | 1.2 | 5         |
| 3813 | Diversification of defensins and NLRs in <i>Arabidopsis</i> species by different evolutionary mechanisms. <i>BMC Evolutionary Biology</i> , 2017, 17, 255.  | 3.2 | 32        |
| 3814 | Estimation of linkage disequilibrium and effective population size in New Zealand sheep using three different methods to create genetic maps. <i>BMC Genetics</i> , 2017, 18, 68.   | 2.7 | 43        |
| 3815 | Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in <i>Volvox carteri</i> . <i>BMC Biology</i> , 2017, 15, 111.   | 1.7 | 19        |
| 3816 | <i>Dirofilaria immitis</i> JYD-34 isolate: whole genome analysis. <i>Parasites and Vectors</i> , 2017, 10, 494.   | 1.0 | 9         |
| 3817 | fastQ_brew: module for analysis, preprocessing, and reformatting of FASTQ sequence data. <i>BMC Research Notes</i> , 2017, 10, 275.   | 0.6 | 6         |
| 3818 | High-quality genome sequence of the radioresistant bacterium <i>Deinococcus ficus</i> KS 0460. <i>Standards in Genomic Sciences</i> , 2017, 12, 46.   | 1.5 | 10        |
| 3819 | Detection of <i>Anaplasma</i> sp. phylogenetically related to <i>A. phagocytophilum</i> in a free-living bird in Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2017, 26, 505-510.   | 0.2 | 4         |
| 3820 | Transcriptome (ESTs) of Avocado "Native" Mexicano Early Seed Development Shows Abundance of Regulatory, Antioxidant and Defense Genes. , 0, , .   |     | 0         |
| 3821 | Detection of differentially methylated regions of irradiated fig tree selections. <i>Scientia Agricola</i> , 2017, 74, 285-293.   | 0.6 | 2         |
| 3822 | Population structure and genetic diversity of the giant anteater ( <i>Myrmecophaga tridactyla</i> ): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 T   | 0.6 | 13        |
| 3823 | Phylogeographic history of South American populations of the silky anteater <i>Cyclopes didactylus</i> (Pilosa: Cyclopedidae). <i>Genetics and Molecular Biology</i> , 2017, 40, 40-49.   | 0.6 | 15        |
| 3824 | Genome Sequence of <i>Porphyromonas gingivalis</i> Strain A7A1-28. <i>Genome Announcements</i> , 2017, 5, .   | 0.8 | 4         |
| 3825 | Computational Errors and Biases in Short Read Next Generation Sequencing. <i>Journal of Proteomics and Bioinformatics</i> , 2017, 10, .   | 0.4 | 26        |
| 3826 | Petroleum biodegrading and co-resistance to antibiotics by <i>Serratia marcescens</i> strain isolated in Coari, Amazonas. <i>Acta Scientiarum - Biological Sciences</i> , 2017, 39, 489.  | 0.3 | 2         |
| 3827 | Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrothrix</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018, 20, 2686-2708. | 1.8 | 32        |
| 3828 | Regulation of Hydrolytic Enzyme Activity in Aquatic Microbial Communities Hosted by Carnivorous Pitcher Plants. <i>Microbial Ecology</i> , 2018, 76, 885-898.   | 1.4 | 10        |
| 3829 | SNP-based pool genotyping and haplotype analysis accelerate fine-mapping of the wheat genomic region containing stripe rust resistance gene Yr26. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1481-1496.   | 1.8 | 61        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3830 | Exploring the loblolly pine ( <i>Pinus taeda</i> L.) genome by BAC sequencing and Cot analysis. <i>Gene</i> , 2018, 663, 165-177.  | 1.0 | 13        |
| 3831 | Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. <i>Nature Protocols</i> , 2018, 13, 946-986.   | 5.5 | 70        |
| 3832 | Contrasting patterns of the bacterial and archaeal communities in a high-elevation river in northwestern China. <i>Journal of Microbiology</i> , 2018, 56, 104-112.  | 1.3 | 7         |
| 3833 | Management of the American cockroach's oothecae: The potential of entomopathogenic fungi control. <i>Journal of Invertebrate Pathology</i> , 2018, 153, 30-34.   | 1.5 | 5         |
| 3834 | Zinc Deficiency-Like Syndrome in Fleckvieh Calves: Clinical and Pathological Findings and Differentiation from Bovine Hereditary Zinc Deficiency. <i>Journal of Veterinary Internal Medicine</i> , 2018, 32, 853-859.                                  | 0.6 | 4         |
| 3835 | Cytotoxic and Noncytotoxic Metabolites from <i>Teratosphaeria</i> sp. FL2137, a Fungus Associated with <i>Pinus clausa</i> . <i>Journal of Natural Products</i> , 2018, 81, 616-624.   | 1.5 | 11        |
| 3836 | Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. <i>GigaScience</i> , 2018, 7, 1-8.  | 3.3 | 168       |
| 3837 | Highly sensitive detection of mutations in CHO cell recombinant DNA using multi-parallel single molecule real-time DNA sequencing. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1485-1498.   | 1.7 | 12        |
| 3838 | Influences of organic carbon speciation on hyporheic corridor biogeochemistry and microbial ecology. <i>Nature Communications</i> , 2018, 9, 585.  | 5.8 | 110       |
| 3839 | Molecular detection of hemogregarines and haemosporidians in Brazilian free-living testudines. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2018, 7, 75-84.   | 0.6 | 9         |
| 3840 | CALQ: compression of quality values of aligned sequencing data. <i>Bioinformatics</i> , 2018, 34, 1650-1658.   | 1.8 | 16        |
| 3841 | Molecular characterization and potential sources of aqueous humor bacterial contamination during phacoemulsification with intraocular lens implantation in dogs. <i>Veterinary Microbiology</i> , 2018, 213, 95-101.                                   | 0.8 | 3         |
| 3842 | Mobile genetic elements and antibiotic resistance in mine soil amended with organic wastes. <i>Science of the Total Environment</i> , 2018, 621, 725-733.  | 3.9 | 27        |
| 3843 | Genomic insights into the <i>Acidobacteria</i> reveal strategies for their success in terrestrial environments. <i>Environmental Microbiology</i> , 2018, 20, 1041-1063.   | 1.8 | 228       |
| 3844 | Organellar genome assembly methods and comparative analysis of horticultural plants. <i>Horticulture Research</i> , 2018, 5, 3.  | 2.9 | 53        |
| 3845 | Genetic Diversity of <i>Bartonella</i> spp. in Wild Mammals and Ectoparasites in Brazilian Pantanal. <i>Microbial Ecology</i> , 2018, 76, 544-554.   | 1.4 | 26        |
| 3846 | Taxonomic review of the genus <i>Cyclopes</i> Gray, 1821 ( <i>Xenarthra: Pilosa</i> ), with the revalidation and description of new species. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 687-721.                                    | 1.0 | 35        |
| 3847 | RNA Sequencing, <i>De novo</i> assembly, functional annotation and SSR analysis of the endangered diving beetle <i>Cybister chinensis</i> (= <i>Cybister japonicus</i> ) using the Illumina platform. <i>Entomological Research</i> , 2018, 48, 60-72. | 0.6 | 3         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3848 | Setup, Validation, and Quality Control of a Centralized Whole-Genome-Sequencing Laboratory: Lessons Learned. <i>Journal of Clinical Microbiology</i> , 2018, 56, .   | 1.8 | 11        |
| 3849 | Enhancing the accuracy of next-generation sequencing for detecting rare and subclonal mutations. <i>Nature Reviews Genetics</i> , 2018, 19, 269-285.   | 7.7 | 374       |
| 3850 | Machine Learned Replacement of N-Labels for Basecalled Sequences in DNA Barcoding. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 191-204.   | 1.9 | 2         |
| 3851 | Optimal Block-Based Trimming for Next Generation Sequencing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 364-376.   | 1.9 | 0         |
| 3852 | Association of low race performance with mtDNA haplogroup L3b of Australian thoroughbred horses. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 323-330.   | 0.7 | 6         |
| 3853 | Base-Calling Using a Random Effects Mixture Model on Next-Generation Sequencing Data. <i>Statistics in Biosciences</i> , 2018, 10, 3-19.   | 0.6 | 1         |
| 3854 | Whole exome sequencing: a state-of-the-art approach for defining (and exploring!) genetic landscapes in pediatric nephrology. <i>Pediatric Nephrology</i> , 2018, 33, 745-761.   | 0.9 | 8         |
| 3855 | The transcriptome, extracellular proteome and active secretome of agroinfiltrated <i>Nicotiana benthamiana</i> uncover a large, diverse protease repertoire. <i>Plant Biotechnology Journal</i> , 2018, 16, 1068-1084.   | 4.1 | 54        |
| 3856 | Molecular characterization of hepatitis C virus in end-stage renal disease patients under hemodialysis. <i>Journal of Medical Virology</i> , 2018, 90, 537-544.  | 2.5 | 4         |
| 3857 | Diversity of piroplasmids among wild and domestic mammals and ectoparasites in Pantanal wetland, Brazil. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 245-253.  | 1.1 | 50        |
| 3858 | Structural characterization of two isolectins from the marine red alga <i>Solieria filiformis</i> (Rhodophyta) P.W. Gabrielson and their anticancer effect on MCF-7 breast cancer cells. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 1320-1329. | 3.6 | 45        |
| 3859 | Transcriptome mining for phylogenetic markers in a recently radiated genus of tropical plants ( <i>Renealmia</i> L.f., Zingiberaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 13-24.  | 1.2 | 13        |
| 3860 | Mutational Events in Lung Cancer. , 2018, , 95-103.e2.   |     | 5         |
| 3861 | Molecular identification of Tomato spotted wilt virus on pepper and tobacco in Republic of Srpska (Bosnia and Herzegovina). <i>European Journal of Plant Pathology</i> , 2018, 150, 785-789.   | 0.8 | 5         |
| 3862 | Sphaerocavum: a coccoid morphogenus identical to Microcystis in terms of 16S rDNA and ITS sequence phylogenies. <i>Hydrobiologia</i> , 2018, 811, 35-48.   | 1.0 | 11        |
| 3863 | Rickettsia spp. among wild mammals and their respective ectoparasites in Pantanal wetland, Brazil. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 10-17.  | 1.1 | 23        |
| 3864 | Elucidating the Cronbergia (cyanobacteria) dilemma with the description of Cronbergia amazonensis sp. nov. isolated from Solimões river (Amazonia, Brazil). <i>Algal Research</i> , 2018, 29, 233-241.   | 2.4 | 7         |
| 3865 | The Aboveground Vegetation Type and Underground Soil Property Mediate the Divergence of Soil Microbiomes and the Biological Interactions. <i>Microbial Ecology</i> , 2018, 75, 434-446.  | 1.4 | 30        |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 3866 | Vector-borne viruses and their detection by viral metagenomics. <i>Infection Ecology and Epidemiology</i> , 2018, 8, 1553465.  | 0.5  | 3         |
| 3867 | High Prevalence of Hepatitis B Subgenotype D4 in Northeast Brazil: an Ancient Relic from African Continent?. <i>Annals of Hepatology</i> , 2018, 17, 54-63.  | 0.6  | 8         |
| 3868 | Proteogenomic Analysis of Epibacterium Mobile BBCC367, a Relevant Marine Bacterium Isolated From the South Pacific Ocean. <i>Frontiers in Microbiology</i> , 2018, 9, 3125.  | 1.5  | 4         |
| 3869 | Transcriptome-wide responses of adult melon thrips ( <i>Thrips palmi</i> ) associated with capsicum chlorosis virus infection. <i>PLoS ONE</i> , 2018, 13, e0208538.   | 1.1  | 20        |
| 3870 | NGmerge: merging paired-end reads via novel empirically-derived models of sequencing errors. <i>BMC Bioinformatics</i> , 2018, 19, 536.  | 1.2  | 142       |
| 3871 | Phylogenetic Analysis: Basic Concepts and Its Use as a Tool for Virology and Molecular Epidemiology. <i>Acta Scientiae Veterinariae</i> , 2018, 44, 20.  | 0.2  | 0         |
| 3872 | Identification of single nucleotide polymorphisms in the prion protein gene in Santa Ines and Dorset sheep. <i>Pesquisa Veterinaria Brasileira</i> , 2018, 38, 624-628.  | 0.5  | 3         |
| 3873 | Molecular detection of vector borne pathogens in anemic and thrombocytopenic dogs in southern Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2018, 27, 505-513.   | 0.2  | 5         |
| 3874 | Hemotropic mycoplasmas in naturally infected cats in Northeastern Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2018, 27, 446-454.   | 0.2  | 4         |
| 3875 | Prevalence of resistance-associated substitutions to direct-acting antiviral agents in hemodialysis and renal transplant patients infected with hepatitis C virus. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1993-2000.                      | 1.1  | 12        |
| 3876 | Human Leukocyte Antigen Typing by Next-Generation Sequencing. <i>Clinics in Laboratory Medicine</i> , 2018, 38, 565-578.   | 0.7  | 25        |
| 3877 | Sensitive tumour detection and classification using plasma cell-free DNA methylomes. <i>Nature</i> , 2018, 563, 579-583.   | 13.7 | 624       |
| 3878 | Genomes and Variants. , 2018, , 17-33.   |      | 0         |
| 3879 | Polymorphism analysis of the <i>apxIA</i> gene of <i>Actinobacillus pleuropneumoniae</i> serovar 5 isolated in swine herds from Brazil. <i>PLoS ONE</i> , 2018, 13, e0208789.  | 1.1  | 1         |
| 3880 | The first complete mitochondrial genome of the Mariana Trench <i>Freyastera benthophila</i> (Asteroidea: Brisingida: Brisingidae) allows insights into the deep-sea adaptive evolution of Brisingida. <i>Ecology and Evolution</i> , 2018, 8, 10673-10686. | 0.8  | 19        |
| 3881 | Analysis of the transcriptome data in <i>Litopenaeus vannamei</i> reveals the immune basis and predicts the hub regulation-genes in response to high-pH stress. <i>PLoS ONE</i> , 2018, 13, e0207771.  | 1.1  | 20        |
| 3882 | Bioinformatics and Computational Biology in Toxicology: Gateways for Precision Medicine. , 2018, , 720-728.  |      | 1         |
| 3883 | The Bermuda Triangle: The Pragmatics, Policies, and Principles for Data Sharing in the History of the Human Genome Project. <i>Journal of the History of Biology</i> , 2018, 51, 693-805.  | 0.2  | 42        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 3884 | Complete mitochondrial genome of Benthodytes marianensis (Holothuroidea: Elasipodida: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 To  | 1.1 | 31        |
| 3885 | Comprehensive simulation of metagenomic sequencing data with non-uniform sampling distribution. Quantitative Biology, 2018, 6, 175-185.  | 0.3 | 2         |
| 3886 | Gene floR e a resistÃancia ao florfenicol em isolados de Aeromonas spp. autÃctones de organismos aquÃticos. Pesquisa Veterinaria Brasileira, 2018, 38, 357-366.  | 0.5 | 0         |
| 3887 | Genetic Diversity, Population Structure, and Botanical Variety of 320 Global Peanut Accessions Revealed Through Tunable Genotyping-by-Sequencing. Scientific Reports, 2018, 8, 14500.                                      | 1.6 | 33        |
| 3888 | Genomic characterization reveals significant divergence within Chlorella sorokiniana (Chlorellales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 To   | 2.4 | 27        |
| 3889 | Island biogeography and ecological modeling of the amblypygid <i>Phrynus marginemaculatus</i> in the Florida Keys archipelago. Ecology and Evolution, 2018, 8, 9139-9151.  | 0.8 | 3         |
| 3890 | RNA-Seq-Based Analysis Reveals Heterogeneity in Mature 16S rRNA 3â€² Termini and Extended Anti-Shine-Dalgarno Motifs in Bacterial Species. G3: Genes, Genomes, Genetics, 2018, 8, 3973-3979.                               | 0.8 | 4         |
| 3891 | Genome and Transcriptome Sequencing. Computational Biology, 2018, , 293-306.   | 0.1 | 0         |
| 3892 | Comparative study on mitogenomes of green tide algae. Genetica, 2018, 146, 529-540.  | 0.5 | 12        |
| 3893 | Challenges in the Structuralâ€“Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. Methods in Enzymology, 2018, 611, 607-675. | 0.4 | 7         |
| 3894 | FUT2 Variants Confer Susceptibility to Familial Otitis Media. American Journal of Human Genetics, 2018, 103, 679-690.  | 2.6 | 40        |
| 3895 | Lavender Decline in France Is Associated with Chronic Infection by Lavender-Specific Strains of â€œCandidatus Phytoplasma solaniâ€“. Applied and Environmental Microbiology, 2018, 84, .                                   | 1.4 | 17        |
| 3896 | Prey Range and Genome Evolution of Halobacteriovorax marinus Predatory Bacteria from an Estuary. MSphere, 2018, 3, .   | 1.3 | 10        |
| 3897 | Protocol: a versatile, inexpensive, high-throughput plant genomic DNA extraction method suitable for genotyping-by-sequencing. Plant Methods, 2018, 14, 75.  | 1.9 | 50        |
| 3898 | The effect of water source and soil supplementation on parasite contamination in organic vegetable gardens. Brazilian Journal of Veterinary Parasitology, 2018, 27, 327-337.   | 0.2 | 27        |
| 3899 | Transcriptomic responses to extreme low salinity among locally adapted populations of Olympia oyster (<i>Ostrea lurida</i>). Molecular Ecology, 2018, 27, 4225-4240.   | 2.0 | 41        |
| 3900 | Characterization of avian pathogenic Escherichia coli isolated from free-range helmeted guineafowl. Brazilian Journal of Microbiology, 2018, 49, 107-112.  | 0.8 | 20        |
| 3901 | Gene Expression Analysis. Methods in Molecular Biology, 2018, , .  | 0.4 | 3         |

| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 3902 | Viremia preceding multiple sclerosis: Two nested case-control studies. <i>Virology</i> , 2018, 520, 21-29.   | 1.1  | 3         |
| 3903 | Underutilised and Neglected Crops: Next Generation Sequencing Approaches for Crop Improvement and Better Food Security. , 2018, , 287-380.   |      | 3         |
| 3904 | High Throughput Sequencing-Based Approaches for Gene Expression Analysis. <i>Methods in Molecular Biology</i> , 2018, 1783, 299-323.   | 0.4  | 8         |
| 3905 | Distributions of ectomycorrhizal and foliar endophytic fungal communities associated with <i>Pinus ponderosa</i> along a spatially constrained elevation gradient. <i>American Journal of Botany</i> , 2018, 105, 687-699.       | 0.8  | 26        |
| 3906 | A Multi-Omics Database for Parasitic Nematodes and Trematodes. <i>Methods in Molecular Biology</i> , 2018, 1757, 371-397.  | 0.4  | 10        |
| 3907 | Molecular detection of <i>Bartonella</i> spp. and <i>Rickettsia</i> spp. in bat ectoparasites in Brazil. <i>PLoS ONE</i> , 2018, 13, e0198629.   | 1.1  | 26        |
| 3908 | Early stage NSCLC " challenges to implementing ctDNA-based screening and MRD detection. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 577-586.   | 12.5 | 281       |
| 3909 | Integrative analysis of genome-wide lncRNA and mRNA expression in newly synthesized <i>Brassica</i> hexaploids. <i>Ecology and Evolution</i> , 2018, 8, 6034-6052.   | 0.8  | 20        |
| 3911 | Evolutionary relationships of <i>Bresadolia</i> (Basidiomycota, Polyporales) based on molecular and morphological evidence. <i>Mycological Progress</i> , 2018, 17, 1031-1048.   | 0.5  | 3         |
| 3912 | snpAD: an ancient DNA genotype caller. <i>Bioinformatics</i> , 2018, 34, 4165-4171.  | 1.8  | 52        |
| 3913 | RNAseq analysis of $\pm$ -proteobacterium <i>Gluconobacter oxydans</i> 621H. <i>BMC Genomics</i> , 2018, 19, 24.   | 1.2  | 16        |
| 3914 | A new Aura virus isolate in Brazil shows segment duplication in the variable region of the nsP3 gene. <i>Parasites and Vectors</i> , 2018, 11, 321.  | 1.0  | 3         |
| 3915 | Candidate DNA Barcode Tags Combined With High Resolution Melting (Bar-HRM) Curve Analysis for Authentication of <i>Senna alexandrina</i> Mill. With Validation in Crude Drugs. <i>Frontiers in Plant Science</i> , 2018, 9, 283. | 1.7  | 18        |
| 3916 | Exploiting the Genomic Diversity of Rice ( <i>Oryza sativa</i> L.): SNP-Typing in 11 Early-Backcross Introgression-Breeding Populations. <i>Frontiers in Plant Science</i> , 2018, 9, 849.                                       | 1.7  | 28        |
| 3917 | Integration of Genetic and Cytogenetic Maps and Identification of Sex Chromosome in Garden Asparagus ( <i>Asparagus officinalis</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1068.                                      | 1.7  | 18        |
| 3918 | Genetic and Historical Colonization Analyses of an Endemic Savanna Tree, <i>Qualea grandiflora</i> , Reveal Ancient Connections Between Amazonian Savannas and Cerrado Core. <i>Frontiers in Plant Science</i> , 2018, 9, 981.   | 1.7  | 31        |
| 3919 | Cross-Contamination Explains "Inter and Intraspecific Horizontal Genetic Transfers" between Asexual Bdelloid Rotifers. <i>Current Biology</i> , 2018, 28, 2436-2444.e14.   | 1.8  | 30        |
| 3920 | Comprehensive analysis of hippocampal miRNomes in humans and mice. <i>Epigenomics</i> , 2018, 10, 813-828.   | 1.0  | 0         |

| #    | ARTICLE   | IF   | CITATIONS |
|------|---|------|-----------|
| 3921 | Succession of toxicity and microbiota in hydraulic fracturing flowback and produced water in the Denverâ€“Julesburg Basin. <i>Science of the Total Environment</i> , 2018, 644, 183-192.  | 3.9  | 35        |
| 3922 | Global Transcriptome Analysis of Brown Adipose Tissue of Diet-Induced Obese Mice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1095.  | 1.8  | 17        |
| 3923 | Genetic diversity of <i>Pneumocystis jirovecii</i> from a cluster of cases of pneumonia in renal transplant patients: Cross-sectional study. <i>Mycoses</i> , 2018, 61, 845-852.  | 1.8  | 9         |
| 3924 | Generating <i>scp</i> DNA sequence data with limited resources for molecular biology: Lessons from a barcoding project in Indonesia. <i>Applications in Plant Sciences</i> , 2018, 6, e01167.                                       | 0.8  | 6         |
| 3925 | Identification of novel miRNAs and their target genes in <i>Eucalyptus grandis</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.  | 0.6  | 10        |
| 3926 | Functional intraepithelial lymphocyte changes in inflammatory bowel disease and spondyloarthritis have disease specific correlations with intestinal microbiota. <i>Arthritis Research and Therapy</i> , 2018, 20, 149.             | 1.6  | 39        |
| 3927 | Integrative taxonomy unravels the species diversity of <i>Parachristianella</i> (Cestoda : Trypanorhyncha) from both sides of the Panamanian isthmus. <i>Invertebrate Systematics</i> , 2018, 32, 278.                              | 0.5  | 3         |
| 3928 | Metagenomic investigation of vestimentiferan tubeworm endosymbionts from Mid-Cayman Rise reveals new insights into metabolism and diversity. <i>Microbiome</i> , 2018, 6, 19.   | 4.9  | 32        |
| 3929 | The 'Peripatos' in Eurogondwana? Lack of evidence that southeast Asian onychophorans walked through Europe. <i>Invertebrate Systematics</i> , 2018, 32, 842.  | 0.5  | 26        |
| 3930 | DNA barcoding Brooklyn (New York): A first assessment of biodiversity in Marine Park by citizen scientists. <i>PLoS ONE</i> , 2018, 13, e0199015.   | 1.1  | 11        |
| 3931 | A Two-Level Scheme for Quality Score Compression. <i>Journal of Computational Biology</i> , 2018, 25, 1141-1151.  | 0.8  | 1         |
| 3932 | Genetic characterization of inbred lines from Shaan A and B groups for identifying loci associated with maize grain yield. <i>BMC Genetics</i> , 2018, 19, 63.  | 2.7  | 28        |
| 3933 | Probiotic supplements prevented oxonic acid-induced hyperuricemia and renal damage. <i>PLoS ONE</i> , 2018, 13, e0202901.   | 1.1  | 57        |
| 3934 | Characterization of leaf transcriptome, development and utilization of unigenes-derived microsatellite markers in sugarcane ( <i>Saccharum sp. hybrid</i> ). <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 665-682. | 1.4  | 2         |
| 3935 | Nutrient Dependent Cross-Kingdom Interactions: Fungi and Bacteria From an Oligotrophic Desert Oasis. <i>Frontiers in Microbiology</i> , 2018, 9, 1755.  | 1.5  | 33        |
| 3936 | HSF1 and HSPA6 as functional candidate genes associated with heat tolerance in Angus cattle. <i>Revista Brasileira De Zootecnia</i> , 2018, 47, .   | 0.3  | 17        |
| 3937 | Molecular detection of Anaplasmataceae agents in <i>Dasyprocta azarae</i> in northeastern Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2018, 27, 98-104.   | 0.2  | 2         |
| 3938 | Environment and host as large-scale controls of ectomycorrhizal fungi. <i>Nature</i> , 2018, 558, 243-248.  | 13.7 | 282       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3939 | Quantitative analysis of DNA with single-molecule sequencing. <i>Scientific Reports</i> , 2018, 8, 8517.  | 1.6 | 31        |
| 3940 | Using collections data to infer biogeographic, environmental, and host structure in communities of endophytic fungi. <i>Mycologia</i> , 2018, 110, 47-62.   | 0.8 | 19        |
| 3941 | New insights into the genetic diversity of Leishmania RNA Virus 1 and its species-specific relationship with Leishmania parasites. <i>PLoS ONE</i> , 2018, 13, e0198727.  | 1.1 | 21        |
| 3942 | Phylogeography of <i>Plectostylus</i> Beck, 1837 (Gastropoda: Stylommatophora: Orthalicoidea): Origin and isolation of the Fray Jorge forest relicts in northern Chile. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 57-66. | 0.6 | 2         |
| 3943 | “Endless forms most beautiful”: taxonomic revision of the planarian <i>Geoplana vaginuloides</i> (Darwin, 1845). <i>Linnean Society</i> , 2019, 185, 1-65.  | 1.0 | 8         |
| 3944 | Genome-Wide Scanning of Gene Expression. , 2019, , 452-462.   |     | 0         |
| 3945 | Diversity, natural infection and blood meal sources of phlebotomine sandflies (Diptera, Phlebotomidae) in the western Brazilian Amazon. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e190170.   | 0.8 | 25        |
| 3946 | Phylogeography of msp4 genotypes of <i>Anaplasma marginale</i> in beef cattle from the Brazilian Pantanal. <i>Brazilian Journal of Veterinary Parasitology</i> , 2019, 28, 451-457.   | 0.2 | 10        |
| 3947 | Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.   | 3.8 | 21        |
| 3948 | Transcriptomic analysis of immune response to bacterial lipopolysaccharide in zebra finch ( <i>Taeniopygia guttata</i> ). <i>BMC Genomics</i> , 2019, 20, 647.  | 1.2 | 17        |
| 3949 | Heterogeneity spacers in 16S rDNA primers improve analysis of mouse gut microbiomes via greater nucleotide diversity. <i>BioTechniques</i> , 2019, 67, 55-62.   | 0.8 | 14        |
| 3950 | Acidobacteria Subgroups and Their Metabolic Potential for Carbon Degradation in Sugarcane Soil Amended With Vinasse and Nitrogen Fertilizers. <i>Frontiers in Microbiology</i> , 2019, 10, 1680.  | 1.5 | 61        |
| 3951 | Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.  | 5.9 | 184       |
| 3952 | Differential expression of immune-related genes in head kidney and spleen of cobia ( <i>Rachycentron</i> ). <i>Journal of Fish Diseases</i> , 2019, 42, 842-850.  | 1.6 | 17        |
| 3953 | Genetic diversity of Hepatozoon spp. in rodents from Brazil. <i>Scientific Reports</i> , 2019, 9, 10122.  | 1.6 | 15        |
| 3954 | Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. <i>GigaScience</i> , 2019, 8, .   | 3.3 | 132       |
| 3955 | Gene expression profiles of the small intestine of village chickens from an <i>Ascaridia galli</i> infested environment. <i>Veterinary Parasitology</i> , 2019, 276, 100012.  | 2.7 | 4         |
| 3956 | Whole-genome sequencing based on formalin-fixed paraffin-embedded endomyocardial biopsies for genetic studies on outcomes after heart transplantation. <i>PLoS ONE</i> , 2019, 14, e0217747.  | 1.1 | 2         |



| #    | ARTICLE  | IF   | CITATIONS |
|------|--|------|-----------|
| 3958 | HoBi-like pestivirus infection in an outbreak of bovine respiratory disease. <i>Research in Veterinary Science</i> , 2019, 126, 184-191.   | 0.9  | 13        |
| 3959 | Sample descriptors linked to metagenomic sequencing data from human and animal enteric samples from Vietnam. <i>Scientific Data</i> , 2019, 6, 202.  | 2.4  | 2         |
| 3960 | Unique Shinealgarno Sequences in Cyanobacteria and Chloroplasts Reveal Evolutionary Differences in Their Translation Initiation. <i>Genome Biology and Evolution</i> , 2019, 11, 3194-3206.  | 1.1  | 10        |
| 3961 | Exploration of genetic diversity of <i>Bacillus</i> spp. from industrial shrimp ponds in Vietnam by multi-locus sequence typing. <i>Fisheries and Aquatic Sciences</i> , 2019, 22, .   | 0.3  | 3         |
| 3962 | Omics Approaches to Understanding Muscle Biology. , 2019, , .  |      | 3         |
| 3963 | Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019, 10, 5029.  | 5.8  | 1,007     |
| 3964 | Deep sequencing of B cell receptor repertoire. <i>BMB Reports</i> , 2019, 52, 540-547.   | 1.1  | 17        |
| 3965 | Transcriptome analysis to understand the effects of the toxoflavin and tropolone produced by phytopathogenic <i>Burkholderia</i> on <i>Escherichia coli</i> . <i>Journal of Microbiology</i> , 2019, 57, 781-794.                    | 1.3  | 8         |
| 3966 | Accurate estimation of microbial sequence diversity with Distanced. <i>Bioinformatics</i> , 2020, 36, 728-734.   | 1.8  | 5         |
| 3967 | PASA: IDENTIFYING MORE CREDIBLE STRUCTURAL VARIANTS OF HEDOU12. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.  | 1.9  | 1         |
| 3968 | Feline coronavirus isolates from a part of Brazil: insights into molecular epidemiology and phylogeny inferred from the 7b gene. <i>Journal of Veterinary Medical Science</i> , 2019, 81, 1455-1460.                                 | 0.3  | 11        |
| 3969 | Different Gut Microbial Profiles in Sub-Saharan African and South Asian Women of Childbearing Age Are Primarily Associated With Dietary Intakes. <i>Frontiers in Microbiology</i> , 2019, 10, 1848.                                  | 1.5  | 16        |
| 3970 | Hepatozoon sp. gamonts as an accidental finding in synovial liquid from an injured maned wolf ( <i>Chrysocyon brachyurus</i> ) in southeastern Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2019, 28, 779-785.      | 0.2  | 8         |
| 3971 | HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. <i>Cell Host and Microbe</i> , 2019, 26, 347-358.e7.  | 5.1  | 117       |
| 3972 | Cognitive characterization of SCAR10 caused by a homozygous c.132dupA mutation in the ANO10 gene. <i>Neurocase</i> , 2019, 25, 195-201.  | 0.2  | 7         |
| 3973 | Multilocus approach reveals a complex evolutionary history of the invasive mile-a-minute plant, <i>Mikania micrantha</i> (Asteraceae), in its natural habitat. <i>Botanical Journal of the Linnean Society</i> , 2019, 191, 188-215. | 0.8  | 1         |
| 3974 | DNA Sequencing Technologies. <i>ACM Computing Surveys</i> , 2020, 52, 1-30.  | 16.1 | 8         |
| 3975 | Polyphasic taxonomic analysis of <i>Paracoccus ravus</i> sp. nov., an alphaproteobacterium isolated from marine sediment. <i>FEMS Microbiology Letters</i> , 2019, 366, .  | 0.7  | 3         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3976 | Proto-dolomite formation in microbial consortia dominated by Halomonas strains. <i>Extremophiles</i> , 2019, 23, 765-781.   | 0.9 | 9         |
| 3977 | Immediate Effects of Ammonia Shock on Transcription and Composition of a Biogas Reactor Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 2064.  | 1.5 | 18        |
| 3978 | De novo transcriptome sequencing of <i>Monodopsis subterranea</i> CCALA 830 and identification of genes involved in the biosynthesis of eicosapentanoic acid and triacylglycerol. <i>Vegetos</i> , 2019, 32, 600-608.                       | 0.8 | 2         |
| 3979 | Acylated Ghrelin Supports the Ovarian Transcriptome and Follicles in the Mouse: Implications for Fertility. <i>Frontiers in Endocrinology</i> , 2018, 9, 815.   | 1.5 | 15        |
| 3980 | Multi-locus DNA metabarcoding of zooplankton communities and scat reveal trophic interactions of a generalist predator. <i>Scientific Reports</i> , 2019, 9, 281.   | 1.6 | 42        |
| 3981 | EST (Expressed Sequence Tag): A Technique for Identification of Plant Secondary Metabolite Genes. , 2019, , 207-225.  |     | 1         |
| 3982 | Comparison of splenocyte microRNA expression profiles of pigs during acute and chronic toxoplasmosis. <i>BMC Genomics</i> , 2019, 20, 97.   | 1.2 | 36        |
| 3983 | Bioinformatics Basics for High-Throughput Hybridization-Based Targeted DNA Sequencing from FFPE-Derived Tumor Specimens: From Reads to Variants. <i>Methods in Molecular Biology</i> , 2019, 1908, 37-48.                                   | 0.4 | 0         |
| 3984 | Eutherian third-party data gene collections. <i>Gene Reports</i> , 2019, 16, 100414.  | 0.4 | 4         |
| 3985 | <i>Neospora caninum</i> DNA in feces of crab-eating fox ( <i>Cerdocyon thous</i> â€“ Linnaeus, 1776) from northeastern Brazil. <i>Acta Tropica</i> , 2019, 197, 105068.   | 0.9 | 7         |
| 3986 | Abundance of HPV L1 Intra-Genotype Variants With Capsid Epitopic Modifications Found Within Low- and High-Grade Pap Smears With Potential Implications for Vaccinology. <i>Frontiers in Genetics</i> , 2019, 10, 489.                       | 1.1 | 6         |
| 3987 | Transcriptome Analysis of Gene Families Involved in Chemosensory Function in <i>Spodoptera littoralis</i> (Lepidoptera: Noctuidae). <i>BMC Genomics</i> , 2019, 20, 428.  | 1.2 | 69        |
| 3988 | Analysis of the bacterial communities and endosymbionts of natural populations of <i>Bemisia tabaci</i> in several crop fields from Mexico semi-arid zone. <i>Annals of Microbiology</i> , 2019, 69, 909-922.                               | 1.1 | 8         |
| 3989 | Evaluating the Effect of QIIME Balanced Default Parameters on Metataxonomic Analysis Workflows With a Mock Community. <i>Frontiers in Microbiology</i> , 2019, 10, 1084.  | 1.5 | 8         |
| 3990 | Draft Genome Sequences of Two <i>Staphylococcus warneri</i> Clinical Isolates, Strains SMA0023-04 (UGA3) and SMA0670-05 (UGA28), from Siaya County Referral Hospital, Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.3 | 0         |
| 3991 | Comparison of mitochondrial DNA enrichment and sequencing methods from fish tissue. <i>Food Chemistry</i> , 2019, 294, 333-338.   | 4.2 | 14        |
| 3992 | Ancient habitat shifts and organismal diversification are decoupled in the African viper genus <i>Bitis</i> (Serpentes: Viperidae). <i>Journal of Biogeography</i> , 2019, 46, 1234-1248.   | 1.4 | 26        |
| 3993 | Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. <i>Plant Cell</i> , 2019, 31, 1466-1487.   | 3.1 | 89        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 3994 | Genome Sequence of <i>Staphylococcus pettenkoferi</i> Strain SMA0010-04 (UGA20), a Clinical Isolate from Siaya County Referral Hospital in Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .                            | 0.3 | 2         |
| 3995 | Genome Sequence of a <i>Staphylococcus xylosus</i> Clinical Isolate, Strain SMA0341-04 (UGA5), from Siaya County Referral Hospital in Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .                                 | 0.3 | 2         |
| 3996 | scruff: an R/Bioconductor package for preprocessing single-cell RNA-sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 222.   | 1.2 | 19        |
| 3997 | Identification of candidate genes responsible for the susceptibility of apple ( <i>Malus Ñ— domestica</i> ) Tj ETQq1 1 0.784314 rgBT /Overloc   | 1.6 | 14        |
| 3998 | Systematic analysis of the effects of different nitrogen source and ICDH knockout on glycolate synthesis in <i>Escherichia coli</i> . <i>Journal of Biological Engineering</i> , 2019, 13, 30.  | 2.0 | 9         |
| 3999 | Genome Sequences of a <i>Staphylococcus aureus</i> Clinical Isolate, Strain SMA0034-04 (UGA22), from Siaya County Referral Hospital in Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .                                | 0.3 | 1         |
| 4000 | A genome-wide association analysis identifies 16 novel susceptibility loci for carpal tunnel syndrome. <i>Nature Communications</i> , 2019, 10, 1030.   | 5.8 | 57        |
| 4001 | A Phylogenetic and Functional Perspective on Volatile Organic Compound Production by <i>Actinobacteria</i> . <i>MSystems</i> , 2019, 4, .   | 1.7 | 35        |
| 4002 | Diversity of <i>Anaplasma</i> species in cattle in Mozambique. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 651-664.  | 1.1 | 21        |
| 4003 | Genetic diversity of <i>Anaplasma marginale</i> in beef cattle in the Brazilian Pantanal. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 805-814.   | 1.1 | 15        |
| 4004 | Genetic and morphological variation in the circumpolar distribution range of <i>Sphagnum warnstorffii</i> : indications of vicariant divergence in a common peatmoss. <i>Botanical Journal of the Linnean Society</i> , 2019, 189, 408-423. | 0.8 | 8         |
| 4005 | Apoptotic tumor cell-derived microRNA-375 uses CD36 to alter the tumor-associated macrophage phenotype. <i>Nature Communications</i> , 2019, 10, 1135.  | 5.8 | 108       |
| 4006 | Characterization and genome analysis of the temperate bacteriophage $\Phi$ SAJS1 from <i>Streptomyces avermitilis</i> . <i>Virus Research</i> , 2019, 265, 34-42.   | 1.1 | 8         |
| 4007 | Understanding the Loss of Maternal Care in Avian Brood Parasites Using Preoptic Area Transcriptome Comparisons in Brood Parasitic and Non-parasitic Blackbirds. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1075-1084.                   | 0.8 | 5         |
| 4008 | Discovery and genetic characterization of diverse smacoviruses in Zambian non-human primates. <i>Scientific Reports</i> , 2019, 9, 5045.  | 1.6 | 8         |
| 4009 | A Guide to Next Generation Sequence Analysis of <i>Leishmania</i> Genomes. <i>Methods in Molecular Biology</i> , 2019, 1971, 69-94.   | 0.4 | 7         |
| 4010 | Pathogen Detection and Microbiome Analysis of Infected Wheat Using a Portable DNA Sequencer. <i>Phytobiomes Journal</i> , 2019, 3, 92-101.  | 1.4 | 33        |
| 4011 | Biochemical Characterization of Heat-Tolerant Recombinant l-Arabinose Isomerase from <i>Enterococcus faecium</i> DBFIQ E36 Strain with Feasible Applications in d-Tagatose Production. <i>Molecular Biotechnology</i> , 2019, 61, 385-399.  | 1.3 | 12        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4012 | Whole genome sequencing of canids reveals genomic regions under selection and variants influencing morphology. <i>Nature Communications</i> , 2019, 10, 1489.  | 5.8 | 220       |
| 4013 | High frequency and molecular characterization of porcine hemotrophic mycoplasmas in Brazil. <i>Veterinary Microbiology</i> , 2019, 231, 33-39.   | 0.8 | 15        |
| 4014 | Barcoding the Neotropical freshwater fish fauna using a new pair of universal COI primers with a discussion of primer dimers and M13 primer tails. <i>Genome</i> , 2019, 62, 77-83.  | 0.9 | 20        |
| 4015 | Predicting the origin of stains from whole miRNome massively parallel sequencing data. <i>Forensic Science International: Genetics</i> , 2019, 40, 131-139.  | 1.6 | 25        |
| 4016 | Cave Drip Water-Related Samples as a Natural Environment for Aromatic Hydrocarbon-Degrading Bacteria. <i>Microorganisms</i> , 2019, 7, 33.   | 1.6 | 25        |
| 4017 | Classification of Hepatitis Viruses from Sequencing Chromatograms Using Multiscale Permutation Entropy and Support Vector Machines. <i>Entropy</i> , 2019, 21, 1149.   | 1.1 | 2         |
| 4018 | The Many Faces of Gene Regulation in Cancer: A Computational Oncogenomics Outlook. <i>Genes</i> , 2019, 10, 865.   | 1.0 | 34        |
| 4019 | Tripartite Symbiosis of an Anaerobic Scuticociliate with Two Hydrogenosome-Associated Endosymbionts, a <i>Holospira</i> -Related Alphaproteobacterium and a Methanogenic Archaeon. <i>Applied and Environmental Microbiology</i> , 2019, 85, . | 1.4 | 26        |
| 4020 | Maximize Resolution or Minimize Error? Using Genotyping-By-Sequencing to Investigate the Recent Diversification of <i>Helianthemum</i> (Cistaceae). <i>Frontiers in Plant Science</i> , 2019, 10, 1416.  | 1.7 | 15        |
| 4021 | Analysis of TCR $\hat{I}^2$ CDR3 sequencing data for tracking anti-tumor immunity. <i>Methods in Enzymology</i> , 2019, 629, 443-464.  | 0.4 | 4         |
| 4022 | Children with vesico-ureteric reflux have joint hypermobility and occasional TNXB sequence variants. <i>Canadian Urological Association Journal</i> , 2019, 14, E128-E136.   | 0.3 | 1         |
| 4023 | RNASeqR: An R Package for Automated Two-Group RNA-Seq Analysis Workflow. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2023-2031.   | 1.9 | 6         |
| 4024 | Association between single-nucleotide polymorphisms within candidate genes and fertility in Landrace and Duroc pigs. <i>Acta Veterinaria Scandinavica</i> , 2019, 61, 58.  | 0.5 | 2         |
| 4025 | Clinal variation in growth cessation and FTL2 expression in Siberian spruce. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.   | 0.6 | 4         |
| 4026 | Influence of the HIV GWG variant in the HIV infection progression in mono and HCV coinfecting patients. <i>Medicine (United States)</i> , 2019, 98, e16376.  | 0.4 | 1         |
| 4027 | Global Screening of Genomic and Transcriptomic Factors Associated with Phenotype Differences between Multidrug-Resistant and -Susceptible <i>Candida haemulonii</i> Strains. <i>MSystems</i> , 2019, 4, .                                      | 1.7 | 9         |
| 4028 | Comparative Transcriptome Profiling of Resistant and Susceptible Sugarcane Cultivars in Response to Infection by <i>Xanthomonas albilineans</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 6138.                         | 1.8 | 26        |
| 4029 | Bryozoan genera <i>Fenestrulina</i> and <i>Microporella</i> no longer confamilial; multi-gene phylogeny supports separation. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 190-199.  | 1.0 | 13        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4030 | The Acute Influence of Acid Suppression with Esomeprazole on Gastrointestinal Microbiota and Brain Gene Expression Profiles in a Murine Model of Restraint Stress. <i>Neuroscience</i> , 2019, 398, 206-217.                    | 1.1 | 11        |
| 4031 | CADD: predicting the deleteriousness of variants throughout the human genome. <i>Nucleic Acids Research</i> , 2019, 47, D886-D894.  | 6.5 | 2,360     |
| 4032 | Next-Generation Sequencing Technologies. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a036798.   | 2.9 | 143       |
| 4033 | Optimised isolation method for RNA extraction suitable for RNA sequencing from feline teeth collected in a clinical setting and at post mortem. <i>Veterinary Research Communications</i> , 2019, 43, 17-27.                    | 0.6 | 4         |
| 4034 | Changes in long chain alkenone distributions and Isochrysidales groups along the Baltic Sea salinity gradient. <i>Organic Geochemistry</i> , 2019, 127, 92-103.   | 0.9 | 31        |
| 4035 | Structural and enzymatic characterization of Peruvianin, the first germin-like protein with proteolytic activity. <i>International Journal of Biological Macromolecules</i> , 2019, 126, 1167-1176.                             | 3.6 | 7         |
| 4036 | Illumina midi-barcodes: quality proof and applications. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 490-499.   | 0.7 | 10        |
| 4037 | Bioinformatics tools to assess metagenomic data for applied microbiology. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 69-82.   | 1.7 | 43        |
| 4038 | Long-term investigation of microbial community composition and transcription patterns in a biogas plant undergoing ammonia crisis. <i>Microbial Biotechnology</i> , 2019, 12, 305-323.  | 2.0 | 25        |
| 4039 | Polyphasic approach using multilocus analyses supports the establishment of the new aerophytic cyanobacterial genus <i>Pycnacronema</i> (Coleofasciculaceae, Oscillatoriales). <i>Journal of Phycology</i> , 2019, 55, 146-159. | 1.0 | 20        |
| 4040 | Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .   | 1.8 | 221       |
| 4041 | Transcriptomic analysis of MicroRNA expression in enamel-producing cells. <i>Gene</i> , 2019, 688, 193-203.   | 1.0 | 3         |
| 4042 | Bioinformatics Tools in Clinical Genomics. , 2019, , 163-182.   |     | 0         |
| 4043 | Phylogenetic connection among close genera of Aphanizomenonaceae (Cyanobacteria): Amphiheterocytum gen. nov., Cylindrospermopsis and Sphaerospermopsis. <i>Algal Research</i> , 2019, 37, 205-214.                              | 2.4 | 8         |
| 4044 | In-depth comparative analysis of Illumina MiSeq run metrics: Development of a wet-lab quality assessment tool. <i>Molecular Ecology Resources</i> , 2019, 19, 377-387.  | 2.2 | 7         |
| 4045 | Nanopore sequencing: An enrichment-free alternative to mitochondrial DNA sequencing. <i>Electrophoresis</i> , 2019, 40, 272-280.  | 1.3 | 34        |
| 4046 | Introduction to Non-coding RNAs and High Throughput Sequencing. , 2019, , 3-31.   |     | 1         |
| 4049 | Mitochondrial haplotypes are not associated with mice selectively bred for high voluntary wheel running. <i>Mitochondrion</i> , 2019, 46, 134-139.  | 1.6 | 4         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4050 | A rapid protocol for generating arthropod DNA barcodes suitable for use with undergraduate students. <i>Journal of Biological Education</i> , 2020, 54, 521-529.   | 0.8 | 0         |
| 4051 | Alphacoronavirus Detection in Lungs, Liver, and Intestines of Bats from Brazil. <i>Microbial Ecology</i> , 2020, 79, 203-212.  | 1.4 | 16        |
| 4053 | Cultivable fungi from deep-sea oil reserves in the Gulf of Mexico: Genetic signatures in response to hydrocarbons. <i>Marine Environmental Research</i> , 2020, 153, 104816.   | 1.1 | 23        |
| 4054 | The evolution of polymorphism in the warning coloration of the Amazonian poison frog <i>Adelphobates galactonotus</i> . <i>Heredity</i> , 2020, 124, 439-456.  | 1.2 | 11        |
| 4055 | Evaluation of <i>Brassica oleracea</i> accessions for resistance to <i>Plasmodiophora brassicae</i> and identification of genomic regions associated with resistance. <i>Genome</i> , 2020, 63, 91-101.  | 0.9 | 24        |
| 4056 | Changes in Airway Microbiome and Inflammation with Ivacaftor Treatment in Patients with Cystic Fibrosis and the G551D Mutation. <i>Annals of the American Thoracic Society</i> , 2020, 17, 212-220.  | 1.5 | 113       |
| 4057 | Exploring the impact of morphology, multiple sequence alignment and choice of optimality criteria in phylogenetic inference: a case study with the Neotropical orb-weaving spider genus <i>Wagneriana</i> (Araneae: Araneidae). <i>Zoological Journal of the Linnean Society</i> , 2020, 188, 976-1151.                      | 1.0 | 14        |
| 4058 | Dereplication of Natural Products with Antimicrobial and Anticancer Activity from Brazilian Cyanobacteria. <i>Toxins</i> , 2020, 12, 12.   | 1.5 | 27        |
| 4059 | Construction of High-Density Genetic Map and Mapping of Sex-Related Loci in the Yellow Catfish ( <i>Pelteobagrus fulvidraco</i> ). <i>Marine Biotechnology</i> , 2020, 22, 31-40.  | 1.1 | 8         |
| 4060 | <i>Paenibacillus</i> infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. <i>Science Translational Medicine</i> , 2020, 12, .   | 5.8 | 39        |
| 4061 | Genome-Wide Identification and Characterization of <i>Fusarium graminearum</i> -Responsive lncRNAs in <i>Triticum aestivum</i> . <i>Genes</i> , 2020, 11, 1135.  | 1.0 | 4         |
| 4062 | Transgenerational accumulation of methylome changes discovered in commercially reared honey bee ( <i>Apis mellifera</i> ) queens. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103476.  | 1.2 | 4         |
| 4063 | From Sequence Data to Patient Result: A Solution for HIV Drug Resistance Genotyping With Exatype, End to End Software for Pol-HIV-1 Sanger Based Sequence Analysis and Patient HIV Drug Resistance Result Generation. <i>Journal of the International Association of Providers of AIDS Care</i> , 2020, 19, 232595822096268. | 0.6 | 5         |
| 4064 | How do genes flow? Identifying potential dispersal mode for the semi-aquatic lichen <i>Dermatocarpon luridum</i> using spatial modelling and photobiont markers. <i>BMC Ecology</i> , 2020, 20, 56.  | 3.0 | 2         |
| 4065 | An epigenetic modifier induces production of 3-(4-oxopyrano)-chromen-2-ones in <i>Aspergillus</i> sp. AST0006, an endophytic fungus of <i>Astragalus lentiginosus</i> . <i>Tetrahedron</i> , 2020, 76, 131525.   | 1.0 | 8         |
| 4066 | NGS_SNPAnalyzer: a desktop software supporting genome projects by identifying and visualizing sequence variations from next-generation sequencing data. <i>Genes and Genomics</i> , 2020, 42, 1311-1317.   | 0.5 | 2         |
| 4067 | Warming, but Not Acidification, Restructures Epibacterial Communities of the Baltic Macroalga <i>Fucus vesiculosus</i> With Seasonal Variability. <i>Frontiers in Microbiology</i> , 2020, 11, 1471.   | 1.5 | 9         |
| 4068 | Performance evaluation of lossy quality compression algorithms for RNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 321.  | 1.2 | 1         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4069 | Assembly of the threespine stickleback Y chromosome reveals convergent signatures of sex chromosome evolution. <i>Genome Biology</i> , 2020, 21, 177.   | 3.8 | 79        |
| 4070 | DNA Barcoding for Delimitation of Putative Mexican Marine Nematodes Species. <i>Diversity</i> , 2020, 12, 107.  | 0.7 | 14        |
| 4071 | Using molecular and crowd-sourcing methods to assess breeding ground diet of a migratory brood parasite of conservation concern. <i>Journal of Avian Biology</i> , 2020, 51, .  | 0.6 | 8         |
| 4072 | Data Processing for RNA/DNA Sequencing. , 2020, , 507-514.  |     | 0         |
| 4073 | CONY: A Bayesian procedure for detecting copy number variations from sequencing read depths. <i>Scientific Reports</i> , 2020, 10, 10493.   | 1.6 | 6         |
| 4074 | Regulation of $\hat{1}^3$ -Aminobutyrate (GABA) Utilization in <i>Corynebacterium glutamicum</i> by the PucR-Type Transcriptional Regulator GabR and by Alternative Nitrogen and Carbon Sources. <i>Frontiers in Microbiology</i> , 2020, 11, 544045. | 1.5 | 10        |
| 4075 | Intra- and Inter-Host Assessment of Bartonella Diversity with Focus on Non-Hematophagous Bats and Associated Ectoparasites from Brazil. <i>Microorganisms</i> , 2020, 8, 1822.  | 1.6 | 16        |
| 4076 | &lt;p&gt;&lt;strong&gt;Biological soil crusts: new genera and species of Cyanobacteria from Brazilian semi-arid regions&lt;/strong&gt;&lt;/p&gt;. <i>Phytotaxa</i> , 2020, 470, 263-281.  | 0.1 | 9         |
| 4077 | Insights on Zika virus envelope gene conservation in American outbreaks. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 1601-1605.  | 0.8 | 1         |
| 4078 | Assessing the Impact of Data Preprocessing on Analyzing Next Generation Sequencing Data. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 817.   | 2.0 | 22        |
| 4079 | The co-infection with Ehrlichia minasensis, Anaplasma marginale and Anaplasma platys is not associated with anemia in beef cattle in the Brazilian Pantanal. <i>Veterinary Parasitology: Regional Studies and Reports</i> , 2020, 21, 100437.         | 0.3 | 3         |
| 4080 | Molecular epidemiology and glycomics of swine influenza viruses circulating in commercial swine farms in the southeastern and midwest United States. <i>Veterinary Microbiology</i> , 2020, 251, 108914.  | 0.8 | 6         |
| 4081 | Deep whole-genome sequencing of multiple proband tissues and parental blood reveals the complex genetic etiology of congenital diaphragmatic hernias. <i>Human Genetics and Genomics Advances</i> , 2020, 1, 100008.                                  | 1.0 | 5         |
| 4082 | Effect of Host, Environment and Fungal Growth on Fungal Leaf Endophyte Communities in Taiwan. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 244.  | 1.5 | 7         |
| 4083 | Construction of a dense genetic map of the Malus fusca fire blight resistant accession MAL0045 using tunable genotyping-by-sequencing SNPs and microsatellites. <i>Scientific Reports</i> , 2020, 10, 16358.  | 1.6 | 17        |
| 4084 | Proteomic and Transcriptomic Analyses Indicate Metabolic Changes and Reduced Defense Responses in Mycorrhizal Roots of Oeceoclades maculata (Orchidaceae) Collected in Nature. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 148.           | 1.5 | 13        |
| 4086 | Nanopore sequencing at Mars, Europa, and microgravity conditions. <i>Npj Microgravity</i> , 2020, 6, 24.  | 1.9 | 17        |
| 4087 | Molecular detection of Apicomplexan hemoparasites in anurans from Brazil. <i>Parasitology Research</i> , 2020, 119, 3469-3479.  | 0.6 | 3         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4088 | Ocrepeira klatmt sp. n. (Araneae: Araneidae), a novel spider species from an Andean páramo in Colombia. PLoS ONE, 2020, 15, e0237499.  | 1.1 | 1         |
| 4089 | Transcriptomic, Morphological, and Developmental Comparison of Adult Honey Bee Queens (<i>Apis) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 5<br>2020, 113, 2581-2587.  | 0.8 | 6         |
| 4090 | Rapid, robust plasmid verification by de novo assembly of short sequencing reads. Nucleic Acids Research, 2020, 48, e106-e106.   | 6.5 | 12        |
| 4091 | Performance and Application of 16S rRNA Gene Cycle Sequencing for Routine Identification of Bacteria in the Clinical Microbiology Laboratory. Clinical Microbiology Reviews, 2020, 33, .                             | 5.7 | 116       |
| 4092 | Differential Expression and PAH Degradation: What <i>Burkholderia vietnamiensis</i> G4 Can Tell Us?. International Journal of Microbiology, 2020, 2020, 1-9.   | 0.9 | 8         |
| 4093 | HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. Genome Research, 2020, 30, 1291-1305.   | 2.4 | 440       |
| 4094 | Ehrlichia spp. and Anaplasma spp. in Xenarthra mammals from Brazil, with evidence of novel ã€Candidatus Anaplasma spp.ã€™. Scientific Reports, 2020, 10, 12615.  | 1.6 | 21        |
| 4095 | Vertical stratification of sand fly diversity in relation to natural infections of Leishmania sp. and blood-meal sources in Jamari National Forest, RondÃ nia State, Brazil. Parasites and Vectors, 2020, 13, 422.   | 1.0 | 10        |
| 4096 | Assessing the Diversity and Population Substructure of Sarda Breed Bucks by Using Mtdna and Y-Chromosome Markers. Animals, 2020, 10, 2194.   | 1.0 | 0         |
| 4097 | UMI-Gen: A UMI-based read simulator for variant calling evaluation in paired-end sequencing NGS libraries. Computational and Structural Biotechnology Journal, 2020, 18, 2270-2280.                                  | 1.9 | 6         |
| 4098 | Occurrence of Methicillin-Resistant Staphylococcus spp. on Brazilian Dairy Farms that Produce Unpasteurized Cheese. Toxins, 2020, 12, 779.   | 1.5 | 5         |
| 4099 | Mapping of the Waxy Bloom Gene in ã€Black Jewelã€™ in a Parental Linkage Map of ã€Black Jewelã€™ Ã— ã€Glen Ampleã€™ (Rubus) Interspecific Population. Agronomy, 2020, 10, 1579.                                      | 1.3 | 5         |
| 4100 | Porcine hemotrophic mycoplasmas infection associated with productive impact in intensive pig production. Porcine Health Management, 2020, 6, 33.   | 0.9 | 5         |
| 4101 | Teratopyrones Aã€C, Dimeric Naphtho-Î³-Pyrones and Other Metabolites from Teratosphaeria sp. AK1128, a Fungal Endophyte of Equisetum arvense. Molecules, 2020, 25, 5058.   | 1.7 | 1         |
| 4102 | Wildlife Population Genomics: Applications and Approaches. Population Genomics, 2020, , 3-59.  | 0.2 | 7         |
| 4103 | Phylogenomics of the Andean Tetraploid Clade of the American Amaryllidaceae (Subfamily) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 5<br>Frontiers in Plant Science, 2020, 11, 582422.                                  | 1.7 | 9         |
| 4104 | Relationships between Foliar Fungal Endophyte Communities and Ecophysiological Traits of CAM and C3 Epiphytic Bromeliads in a Neotropical Rainforest. Diversity, 2020, 12, 378.                                      | 0.7 | 7         |
| 4105 | Comprehensive analysis of miRNAs, lncRNAs, and mRNAs reveals potential players of sexually dimorphic and left-right asymmetry in chicken gonad during gonadal differentiation. Poultry Science, 2020, 99, 2696-2707. | 1.5 | 12        |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4106 | Performance of the Alethia CMV Assay for Detection of Cytomegalovirus by Use of Neonatal Saliva Swabs. <i>Journal of Clinical Microbiology</i> , 2020, 58, .  | 1.8 | 16        |
| 4107 | Muc5ac Expression Protects the Colonic Barrier in Experimental Colitis. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 1353-1367.   | 0.9 | 30        |
| 4108 | Deep sequencing of non-enzymatic RNA primer extension. <i>Nucleic Acids Research</i> , 2020, 48, e70-e70.   | 6.5 | 25        |
| 4109 | Fecal Viral Community Responses to High-Fat Diet in Mice. <i>MSphere</i> , 2020, 5, .   | 1.3 | 33        |
| 4110 | Transcriptomics in Toxicogenomics, Part II: Preprocessing and Differential Expression Analysis for High Quality Data. <i>Nanomaterials</i> , 2020, 10, 903.   | 1.9 | 31        |
| 4111 | &lt;p&gt;Adamantinomatous Craniopharyngioma in an Adult: A Case Report with NGS Analysis&lt;/p&gt;. <i>International Medical Case Reports Journal</i> , 2020, Volume 13, 123-137.                             | 0.3 | 11        |
| 4112 | Leaf tissue specific transcriptome sequence and de novo assembly datasets of Asiatic mangrove <i>Rhizophora mucronata</i> Lam.. <i>Data in Brief</i> , 2020, 31, 105747.                                      | 0.5 | 4         |
| 4113 | Effects of High-Dose Ionizing Radiation in Human Gene Expression: A Meta-Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1938.   | 1.8 | 8         |
| 4114 | Multi-locus sequencing reveals a novel <i>Bartonella</i> in mammals from the Superorder Xenarthra. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2020.   | 1.3 | 16        |
| 4115 | Identification of tissue-specific and cold-responsive lncRNAs in <i>Medicago truncatula</i> by high-throughput RNA sequencing. <i>BMC Plant Biology</i> , 2020, 20, 99.                                       | 1.6 | 29        |
| 4117 | Introgression of Eastern Chinese and Southern Chinese haplotypes contributes to the improvement of fertility and immunity in European modern pigs. <i>GigaScience</i> , 2020, 9, .                            | 3.3 | 31        |
| 4118 | Global microRNA profiling in human urinary exosomes reveals novel disease biomarkers and cellular pathways for autosomal dominant polycystic kidney disease. <i>Kidney International</i> , 2020, 98, 420-435. | 2.6 | 40        |
| 4119 | Molecular Diagnostics of Non-Hodgkin Lymphoma. <i>Cancer Journal (Sudbury, Mass )</i> , 2020, 26, 186-194.  | 1.0 | 3         |
| 4120 | Multiplex profiling of serum proteins in solution using barcoded antibody fragments and next generation sequencing. <i>Communications Biology</i> , 2020, 3, 339.   | 2.0 | 2         |
| 4121 | <i>Plasmodium vivax</i> AMA1: Implications of distinct haplotypes for immune response. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008471.  | 1.3 | 10        |
| 4122 | Phylogeny and biogeography of <i>Astraea</i> with new insights into the evolutionary history of <i>Crotoneae</i> ( <i>Euphorbiaceae</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106738.  | 1.2 | 9         |
| 4123 | Symposium review: Advances in sequencing technology herald a new frontier in cattle genomics and genome-enabled selection. <i>Journal of Dairy Science</i> , 2020, 103, 5278-5290.                            | 1.4 | 15        |
| 4124 | Novel somatic alterations underlie Chinese papillary thyroid carcinoma. <i>Cancer Biomarkers</i> , 2020, 27, 445-460.   | 0.8 | 16        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4125 | Estrogen receptor alpha (ER $\alpha$ )-mediated coregulator binding and gene expression discriminates the toxic ER $\alpha$ agonist diethylstilbestrol (DES) from the endogenous ER $\alpha$ agonist 17 $\beta$ -estradiol (E2). <i>Cell Biology and Toxicology</i> , 2020, 36, 417-435. | 2.4 | 10        |
| 4126 | Bile acid sequestration reverses liver injury and prevents progression of nonalcoholic steatohepatitis in Western diet-fed mice. <i>Journal of Biological Chemistry</i> , 2020, 295, 4733-4747.  | 1.6 | 37        |
| 4127 | De novo genome assembly of <i>Candida glabrata</i> reveals cell wall protein complement and structure of dispersed tandem repeat arrays. <i>Molecular Microbiology</i> , 2020, 113, 1209-1224.   | 1.2 | 25        |
| 4128 | Decimated little brown bats show potential for adaptive change. <i>Scientific Reports</i> , 2020, 10, 3023.  | 1.6 | 28        |
| 4129 | Enabling Precision Oncology Through Precision Diagnostics. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2020, 15, 97-121.  | 9.6 | 50        |
| 4130 | Live-cell PCR and one-step purification streamline DNA engineering. <i>FASEB Journal</i> , 2020, 34, 3448-3460.  | 0.2 | 3         |
| 4131 | Tissue memory CD4 <sup>+</sup> T cells expressing IL-7 receptor-alpha (CD127) preferentially support latent HIV-1 infection. <i>PLoS Pathogens</i> , 2020, 16, e1008450.   | 2.1 | 34        |
| 4132 | Application of Viral Metagenomics for Study of Emerging and Reemerging Tick-Borne Viruses. <i>Vector-Borne and Zoonotic Diseases</i> , 2020, 20, 557-565.  | 0.6 | 8         |
| 4133 | Thousands of missing variants in the UK Biobank are recoverable by genome realignment. <i>Annals of Human Genetics</i> , 2020, 84, 214-220.  | 0.3 | 20        |
| 4134 | Long-Read Nanopore Sequencing Validated for Human Leukocyte Antigen Class I Typing in Routine Diagnostics. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 912-919.  | 1.2 | 16        |
| 4135 | Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. <i>Plant Cell</i> , 2020, 32, 833-852.  | 3.1 | 60        |
| 4136 | Supervised machine learning is superior to indicator value inference in monitoring the environmental impacts of salmon aquaculture using eDNA metabarcodes. <i>Molecular Ecology</i> , 2021, 30, 2988-3006.  | 2.0 | 47        |
| 4137 | Identification and validation of mutation points associated with waxy phenotype in cassava. <i>BMC Plant Biology</i> , 2020, 20, 164.  | 1.6 | 4         |
| 4138 | Clopidogrel, a CYP2C8 inhibitor, causes a clinically relevant increase in the systemic exposure to the active metabolite of selexipag in healthy subjects. <i>British Journal of Clinical Pharmacology</i> , 2021, 87, 119-128.  | 1.1 | 9         |
| 4139 | Segmental Ipsilateral Odontognathic Dysplasia (Mandibular Involvement in Segmental) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (O Gingival Tissue. <i>Head and Neck Pathology</i> , 2021, 15, 368-373.  | 1.3 | 5         |
| 4140 | Effects of commercial queen rearing methods on queen fecundity and genome methylation. <i>Apidologie</i> , 2021, 52, 282-291.  | 0.9 | 3         |
| 4141 | Robustness, sensitivity and reproducibility of eDNA metabarcoding as an environmental biomonitoring tool in coastal salmon aquaculture - An inter-laboratory study. <i>Ecological Indicators</i> , 2021, 121, 107049.  | 2.6 | 24        |
| 4142 | Morphological and molecular phylogeny of <i>Epiperipatus</i> (Onychophora: Peripatidae): a combined approach. <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 763-793.   | 1.0 | 4         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4143 | AmpliCI: a high-resolution model-based approach for denoising Illumina amplicon data. <i>Bioinformatics</i> , 2021, 36, 5151-5158.   | 1.8 | 15        |
| 4144 | Temporal airway microbiome changes related to ventilator-associated pneumonia in children. <i>European Respiratory Journal</i> , 2021, 57, 2001829.  | 3.1 | 16        |
| 4145 | First molecular detection of piroplasmids in non-hematophagous bats from Brazil, with evidence of putative novel species. <i>Parasitology Research</i> , 2021, 120, 301-310.   | 0.6 | 14        |
| 4146 | Long-term souring treatment using nitrate and biocides in high-temperature oil reservoirs. <i>Fuel</i> , 2021, 288, 119731.  | 3.4 | 15        |
| 4147 | Detection of <i>Leishmania</i> species (Kinetoplastida, Trypanosomatidae) in phlebotomine sand flies (Diptera, Psychodidae) from Porto Velho, Northern Brazil. <i>Acta Tropica</i> , 2021, 213, 105757.  | 0.9 | 11        |
| 4148 | Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology</i> 2000, 2021, 85, 12-27.  | 6.3 | 16        |
| 4149 | Fire and local factors shape ectomycorrhizal fungal communities associated with <i>Pinus ponderosa</i> in mountains of the Madrean Sky Island Archipelago. <i>Fungal Ecology</i> , 2021, 49, 101013.   | 0.7 | 4         |
| 4150 | High Genetic Diversity in <i>Flavobacterium psychrophilum</i> Isolates from Healthy Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Farmed in the Same Watershed, Revealed by Two Typing Methods. <i>Applied and Environmental Microbiology</i> , 2021, 87, .             | 1.4 | 6         |
| 4151 | Correlation of <i>Trichosporon asahii</i> Genotypes with Anatomical Sites and Antifungal Susceptibility Profiles: Data Analyses from 284 Isolates Collected in the Last 22 Years across 24 Medical Centers. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, . | 1.4 | 13        |
| 4152 | Assessment of littoral algal diversity from the northern Gulf of Mexico using environmental DNA metabarcoding. <i>Journal of Phycology</i> , 2021, 57, 269-278.  | 1.0 | 4         |
| 4153 | A Single Amino Acid Change to Taq DNA Polymerase Enables Faster PCR, Reverse Transcription and Strand-Displacement. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 553474.  | 2.0 | 7         |
| 4154 | SeqErr: measuring and suppressing sequencer errors in next-generation sequencing data. <i>Genome Biology</i> , 2021, 22, 37.   | 3.8 | 15        |
| 4155 | Population genetic structure of the highly endangered butterfly <i>Coenonympha oedippus</i> (Nymphalidae: Satyrinae) at its southern edge of distribution. <i>Genetica</i> , 2021, 149, 21-36.   | 0.5 | 0         |
| 4156 | Fine-scale temporal variation of intertidal marine fungal community structure: insights from an impacted Baja California sandy beach in Mexico. <i>Marine Biodiversity</i> , 2021, 51, 1.  | 0.3 | 7         |
| 4157 | Methodological Approaches Frame Insights into Endophyte Richness and Community Composition. <i>Microbial Ecology</i> , 2021, 82, 21-34.  | 1.4 | 13        |
| 4158 | RNA Sequencing Analyses for Deciphering Potato Molecular Responses. <i>Methods in Molecular Biology</i> , 2021, 2354, 57-94.   | 0.4 | 2         |
| 4159 | Dealing with Pseudogenes in Molecular Diagnostics in the Next Generation Sequencing Era. <i>Methods in Molecular Biology</i> , 2021, 2324, 363-381.  | 0.4 | 1         |
| 4160 | Large CRISPR-Cas-induced deletions in the oxamniquine resistance locus of the human parasite <i>Schistosoma mansoni</i> . <i>Wellcome Open Research</i> , 2020, 5, 178.  | 0.9 | 19        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4161 | Functional Metagenomics for Identification of Antibiotic Resistance Genes (ARGs). <i>Methods in Molecular Biology</i> , 2021, 2242, 173-183.  | 0.4 | 2         |
| 4162 | Integrating Evolutionary Genetics to Medical Genomics: Evolutionary Approaches to Investigate Disease-Causing Variants. , 0, , .  |     | 0         |
| 4163 | Development of Single-Molecule Science. <i>Molecular Science</i> , 2021, 15, A0120.   | 0.2 | 0         |
| 4164 | sangeranalyseR: Simple and Interactive Processing of Sanger Sequencing Data in R. <i>Genome Biology and Evolution</i> , 2021, 13, .   | 1.1 | 17        |
| 4166 | Comparative genomic and phenotypic characterization of invasive non-typhoidal Salmonella isolates from Siaya, Kenya. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0008991.  | 1.3 | 3         |
| 4167 | Convergent evolution: A new subfamily for bipaliinâ€like Chilean land planarians (platyhelminthes). <i>Zoologica Scripta</i> , 2021, 50, 500-508.   | 0.7 | 9         |
| 4168 | Genotyping by Sequencing Reveals Genetic Relatedness of Southwestern U.S. Blue Maize Landraces. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3436.  | 1.8 | 4         |
| 4169 | Cell wall protein variation, breakâ€induced replication, and subtelomere dynamics in <i>Candida glabrata</i> . <i>Molecular Microbiology</i> , 2021, 116, 260-276.  | 1.2 | 16        |
| 4170 | Polymorphisms at Myostatin Gene (MSTN) and the Associations with Sport Performances in Anglo-Arabian Racehorses. <i>Animals</i> , 2021, 11, 964.  | 1.0 | 6         |
| 4171 | <i>De novo</i> assembly and SSR loci analysis in <i>Gasterophilus nasalis</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 0,6 4  |     |           |
| 4172 | A single donor is sufficient to produce a highly functional in vitro antibody library. <i>Communications Biology</i> , 2021, 4, 350.  | 2.0 | 12        |
| 4173 | Resequencing of Microbial Isolates: A Lab Module to Introduce Novices to Command-Line Bioinformatics. <i>Frontiers in Microbiology</i> , 2021, 12, 578859.  | 1.5 | 0         |
| 4174 | Transcriptome from opaque cornea of Fanconi anemia patient uncovers fibrosis and two connected players. <i>Molecular Genetics and Metabolism Reports</i> , 2021, 26, 100712.  | 0.4 | 0         |
| 4175 | Robust, flexible, and scalable tests for Hardyâ€Weinberg equilibrium across diverse ancestries. <i>Genetics</i> , 2021, 218, .  | 1.2 | 6         |
| 4176 | Diversity of Culturable Bacteria Isolated From the Feces of Wild <i>Anopheles darlingi</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 0,9 9 10 Tf 5  |     |           |
| 4177 | A bioinformatics approach to microRNA-sequencing analysis. <i>Osteoarthritis and Cartilage Open</i> , 2021, 3, 100131.  | 0.9 | 34        |
| 4179 | Modified PCR protocol to increase sensitivity for determination of bacterial community composition. <i>Microbiome</i> , 2021, 9, 90.  | 4.9 | 2         |
| 4180 | Transcriptome analysis of immune- and iron-related genes after <i>Francisella noatunensis</i> subsp. <i>orientalis</i> infection in Nile tilapia ( <i>Oreochromis niloticus</i> ). <i>Fish and Shellfish Immunology</i> , 2021, 111, 36-48. | 1.6 | 13        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4181 | ngsComposer: an automated pipeline for empirically based NGS data quality filtering. <i>Briefings in Bioinformatics</i> , 2021, 22, .  | 3.2 | 9         |
| 4182 | Occurrence and diversity of Sarcocystidae protozoa in muscle and brain tissues of bats from São Paulo state, Brazil. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 14, 91-96.  | 0.6 | 6         |
| 4183 | Challenges in the application of NGS in the clinical laboratory. <i>Human Immunology</i> , 2021, 82, 812-819.  | 1.2 | 16        |
| 4184 | Characterisation of turnip mosaic virus isolates reveals high genetic variability and occurrence of pathotype 1 in Brazil. <i>European Journal of Plant Pathology</i> , 2021, 160, 883-900.  | 0.8 | 3         |
| 4185 | Global Trends of Benthic Bacterial Diversity and Community Composition Along Organic Enrichment Gradients of Salmon Farms. <i>Frontiers in Microbiology</i> , 2021, 12, 637811.  | 1.5 | 14        |
| 4186 | IL-7 coupled with IL-12 increases intratumoral T cell clonality, leading to complete regression of non-immunogenic tumors. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 3557-3571.  | 2.0 | 11        |
| 4187 | An Introduction to Next Generation Sequencing Bioinformatic Analysis in Gut Microbiome Studies. <i>Biomolecules</i> , 2021, 11, 530.   | 1.8 | 62        |
| 4188 | Phenotypic, molecular and pathogenic characterization of <i>Colletotrichum scovillei</i> infecting <i>Capsicum</i> species in Rio de Janeiro, Brazil. <i>PeerJ</i> , 2021, 9, e10782.  | 0.9 | 8         |
| 4189 | Remoção de herbicida atrazina por meio de filtros de carvão ativado granular associados com microrganismos no tratamento de água para abastecimento. <i>Engenharia Sanitaria E Ambiental</i> , 2021, 26, 263-272.  | 0.1 | 1         |
| 4190 | Multi-USV Adaptive Exploration Using Kernel Information and Residual Variance. <i>Frontiers in Robotics and AI</i> , 2021, 8, 572243.  | 2.0 | 2         |
| 4191 | Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. <i>Genes</i> , 2021, 12, 847.  | 1.0 | 19        |
| 4193 | Porcine Circovirus 3a Field Strains in Free-Living Wild Boars in Paraná State, Brazil. <i>Animals</i> , 2021, 11, 1634.  | 1.0 | 7         |
| 4194 | CollectSeq: In silico discovery of antibodies targeting integral membrane proteins combining in situ selections and next-generation sequencing. <i>Communications Biology</i> , 2021, 4, 561.  | 2.0 | 8         |
| 4195 | Amazonocrinis nigriterrae gen. nov., sp. nov., Atlanticothrix silvestris gen. nov., sp. nov. and Dendronalium phyllosphericum gen. nov., sp. nov., nostocacean cyanobacteria from Brazilian environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, . | 0.8 | 30        |
| 4196 | Screening and verification of extranuclear genetic markers in green tide algae from the Yellow Sea. <i>PLoS ONE</i> , 2021, 16, e0250968.  | 1.1 | 11        |
| 4197 | Gut Microbiota Perturbation in IgA Deficiency Is Influenced by IgA-Autoantibody Status. <i>Gastroenterology</i> , 2021, 160, 2423-2434.e5.   | 0.6 | 34        |
| 4198 | Extra-Heavy Crude Oil Degradation by <i>Alternaria</i> sp. Isolated from Deep-Sea Sediments of the Gulf of Mexico. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 6090.   | 1.3 | 10        |
| 4199 | An in vitro model of tumor heterogeneity resolves genetic, epigenetic, and stochastic sources of cell state variability. <i>PLoS Biology</i> , 2021, 19, e3000797.   | 2.6 | 21        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4200 | Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .   | 4.7 | 53        |
| 4201 | The Usability Testing of SSAAT, a Bioinformatic Web Application for DNA Analysis at a Nucleotide Level. <i>Engineering, Technology &amp; Applied Science Research</i> , 2021, 11, 7075-7078.                                   | 0.8 | 1         |
| 4202 | Systematics and phylogeography of the Brazilian Atlantic Forest endemic harvestmen <i>Neosadocus Mello-Leitão</i> , 1926 (Arachnida: Opiliones: Gonyleptidae). <i>PLoS ONE</i> , 2021, 16, e0249746.                           | 1.1 | 3         |
| 4203 | Molecular Survey and Genetic Diversity of <i>Bartonella</i> spp. in Small Indian Mongooses ( <i>Urva</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj  | 1.6 | 5         |
| 4204 | Identifying Circulating MicroRNA in Kawasaki Disease by Next-Generation Sequencing Approach. <i>Current Issues in Molecular Biology</i> , 2021, 43, 485-500.   | 1.0 | 5         |
| 4205 | A Molecular Signature Response Classifier to Predict Inadequate Response to Tumor Necrosis Factor- $\alpha$ Inhibitors: The NETWORK-004 Prospective Observational Study. <i>Rheumatology and Therapy</i> , 2021, 8, 1159-1176. | 1.1 | 16        |
| 4206 | DNA-based blood meal analysis of <i>Culicoides</i> (Diptera: Ceratopogonidae) species from Jamari National Forest, Southwestern Amazon, Brazil. <i>Acta Tropica</i> , 2021, 221, 106025.                                       | 0.9 | 4         |
| 4207 | Genomic selection to introgress exotic maize germplasm into elite maize in China to improve kernel dehydration rate. <i>Euphytica</i> , 2021, 217, 1.  | 0.6 | 1         |
| 4208 | Integration of Complete Plasmids Containing Bont Genes into Chromosomes of <i>Clostridium parbotulinum</i> , <i>Clostridium sporogenes</i> , and <i>Clostridium argentinense</i> . <i>Toxins</i> , 2021, 13, 473.              | 1.5 | 11        |
| 4209 | A Large-Scale and Serverless Computational Approach for Improving Quality of NGS Data Supporting Big Multi-Omics Data Analyses. <i>Frontiers in Genetics</i> , 2021, 12, 699280.   | 1.1 | 3         |
| 4210 | Molecular phylogeny for the Neotropical freshwater stingrays (Myliobatiformes: Potamotrygoninae) reveals limitations of traditional taxonomy. <i>Biological Journal of the Linnean Society</i> , 2021, 134, 381-401.           | 0.7 | 14        |
| 4212 | Hearing Impairment with Monoallelic GJB2 Variants. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 1279-1291.  | 1.2 | 10        |
| 4213 | Human Papillomavirus Detection by Whole-Genome Next-Generation Sequencing: Importance of Validation and Quality Assurance Procedures. <i>Viruses</i> , 2021, 13, 1323.   | 1.5 | 11        |
| 4214 | Endomembrane-Targeting <i>Plasmodiophora brassicae</i> Effectors Modulate PAMP Triggered Immune Responses in Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 651279.  | 1.5 | 19        |
| 4216 | Transcriptome of rat subcortical white matter and spinal cord after spinal injury and cortical stimulation. <i>Scientific Data</i> , 2021, 8, 175.   | 2.4 | 1         |
| 4217 | Genome assembly of <i>Vitis rotundifolia</i> Michx. using third-generation sequencing (Oxford Nanopore) Tj ETQq1 1 0.784314 rgBT /Overlock 0,1   | 0.1 | 0         |
| 4218 | Species delimitation in <i>Noccaea densiflora</i> species complex (Brassicaceae) based on morphological and molecular data. <i>Botany</i> , 2021, 99, 389-402.   | 0.5 | 0         |
| 4219 | Mapping of flowering time, seed quality and clubroot resistance in rutabaga $\tilde{\text{—}}$ spring canola populations and their association. <i>Euphytica</i> , 2021, 217, 1.   | 0.6 | 2         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4220 | Single-cell RNA sequencing of freshly isolated bovine milk cells and cultured primary mammary epithelial cells. <i>Scientific Data</i> , 2021, 8, 177.  | 2.4 | 7         |
| 4221 | Paraphyly and evolutionary independent lineages in <i>Gymnotus pantherinus</i> (Gymnotiformes: Tj ETQq1 1 0.784314 rgBT /Overlock 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 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1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 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| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4239 | Strobiloscyphones Aâ€“F, 6-Isopentylsphaeropsidones and Other Metabolites from <i>Strobiloscypha</i> sp. AZ0266, a Leaf-Associated Fungus of Douglas Fir. <i>Journal of Natural Products</i> , 2021, 84, 2575-2586. | 1.5 | 2         |
| 4240 | A novel variant in DYNC1H1 could contribute to human amyotrophic lateral sclerosis-frontotemporal dementia spectrum.. <i>Journal of Physical Education and Sports Management</i> , 2021, , mcs.a006096.             | 0.5 | 8         |
| 4241 | Genetic diversity and Multilocus Sequence Typing Analysis of <i>Bartonella henselae</i> in domestic cats from Southeastern Brazil. <i>Acta Tropica</i> , 2021, 222, 106037.   | 0.9 | 21        |
| 4242 | Context-dependent regulation of immunoglobulin mutagenesis by p53. <i>Molecular Immunology</i> , 2021, 138, 128-136.  | 1.0 | 1         |
| 4243 | Differential expression and activity of arginine kinase between the American trypanosomatids <i>Trypanosoma rangeli</i> and <i>Trypanosoma cruzi</i> . <i>Experimental Parasitology</i> , 2021, 230, 108159.        | 0.5 | 0         |
| 4244 | Identifying daily changes in circRNAs and circRNA-associated-ceRNA networks in the rat pineal gland. <i>International Journal of Medical Sciences</i> , 2021, 18, 1225-1239.  | 1.1 | 6         |
| 4245 | Identification of Genetic Variants and de novo Mutations Based on NGS. <i>Learning Materials in Biosciences</i> , 2021, , 123-142.  | 0.2 | 0         |
| 4246 | Sex determination through Xâ€“Y heterogamety in <i>Salix nigra</i> . <i>Heredity</i> , 2021, 126, 630-639.  | 1.2 | 26        |
| 4247 | Physical Characterization of Genomes Through BAC End Sequencing. , 0, , 261-274.  |     | 2         |
| 4248 | Sequencing Gene Rich Regions of <i>Medicago truncatula</i> , a Model Legume. , 2004, , 333-344.   |     | 9         |
| 4249 | The <i>Gossypium</i> Transcriptome. , 2009, , 157-185.  |     | 4         |
| 4250 | Genomics of Banana and Plantain ( <i>Musa</i> spp.), Major Staple Crops in the Tropics. , 2008, , 83-111.   |     | 28        |
| 4251 | Analysis of RNA Sequencing Data Using CLC Genomics Workbench. <i>Methods in Molecular Biology</i> , 2020, 2102, 61-113.   | 0.4 | 50        |
| 4252 | Quality Control of RNA-Seq Experiments. <i>Methods in Molecular Biology</i> , 2015, 1269, 137-146.  | 0.4 | 51        |
| 4253 | Haplotype Structure of the Mouse Genome. , 2005, , 71-83.   |     | 6         |
| 4254 | How to Make a Defined Near-Saturation Mutant Library. Case 1: <i>Pseudomonas aeruginosa</i> PAO1. <i>Methods in Molecular Biology</i> , 2008, 416, 133-152.   | 0.4 | 2         |
| 4255 | Duplicate Ditag Analysis in LongSAGE. <i>Methods in Molecular Biology</i> , 2008, 387, 143-149.   | 0.4 | 1         |
| 4256 | Extraction and Annotation of SAGE Tags Using Sequence Quality Values. <i>Methods in Molecular Biology</i> , 2008, 387, 123-132.   | 0.4 | 1         |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4257 | GenColors. Methods in Molecular Biology, 2007, , 75-96.   | 0.4 | 8         |
| 4258 | novoSNP3. Methods in Molecular Biology, 2007, 396, 331-344.   | 0.4 | 8         |
| 4259 | Obtaining Accurate Translations from Expressed Sequence Tags. Methods in Molecular Biology, 2009, 533, 221-239.                                     | 0.4 | 5         |
| 4260 | EST Processing: From Trace to Sequence. Methods in Molecular Biology, 2009, 533, 189-220.   | 0.4 | 3         |
| 4261 | Isolation Independent Methods of Characterizing Phage Communities 2: Characterizing a Metagenome. Methods in Molecular Biology, 2009, 502, 279-289. | 0.4 | 11        |
| 4262 | Genome Sequencing and Assembly. Methods in Molecular Biology, 2011, 722, 1-9.   | 0.4 | 7         |
| 4263 | Comparative View of In Silico DNA Sequencing Analysis Tools. Methods in Molecular Biology, 2011, 760, 207-221.                                      | 0.4 | 2         |
| 4264 | Assembly and Data Quality. , 2017, , 81-103.  |     | 2         |
| 4265 | New EST Trimming Procedure Applied to SUCEST Sequences. , 2007, , 57-68.  |     | 2         |
| 4266 | SeqTrim " A Validation and Trimming Tool for All Purpose Sequence Reads. Advances in Intelligent and Soft Computing, 2007, , 353-360.               | 0.2 | 5         |
| 4267 | naiveBayesCall: An Efficient Model-Based Base-Calling Algorithm for High-Throughput Sequencing. Lecture Notes in Computer Science, 2010, , 233-247. | 1.0 | 5         |
| 4268 | Seed Design Framework for Mapping SOLiD Reads. Lecture Notes in Computer Science, 2010, , 384-396.  | 1.0 | 1         |
| 4269 | Fast Mapping and Precise Alignment of ABÂSOLiD Color Reads to Reference DNA. Lecture Notes in Computer Science, 2010, , 176-188.                    | 1.0 | 7         |
| 4270 | SEME: A Fast Mapper of Illumina Sequencing Reads with Statistical Evaluation. Lecture Notes in Computer Science, 2013, , 14-29.                     | 1.0 | 1         |
| 4271 | Genomics for Fungi. , 2001, , 267-297.  |     | 15        |
| 4272 | QCluster: Extending Alignment-Free Measures with Quality Values for Reads Clustering. Lecture Notes in Computer Science, 2014, , 1-13.              | 1.0 | 3         |
| 4273 | Functional Analysis of the Synechococcus elongatus PCC 7942 Genome. Advances in Photosynthesis and Respiration, 2012, , 119-137.                    | 1.0 | 14        |
| 4274 | Functional genomics and cell wall biosynthesis in loblolly pine. , 2001, , 275-291.   |     | 44        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4275 | Characterization of Microbial Communities from Coastal Waters Using Microarrays. , 2003, , 327-336.   |     | 9         |
| 4276 | Assigning forensic body fluids to donors in mixed body fluids by targeted RNA/DNA deep sequencing of coding region SNPs. International Journal of Legal Medicine, 2020, 134, 473-485.                                     | 1.2 | 22        |
| 4277 | Mussels ( <i>Mytilus</i> spp.) products authentication: A case study on the Italian market confirms issues in species identification and arises concern on commercial names attribution. Food Control, 2020, 118, 107379. | 2.8 | 10        |
| 4278 | Biosynthesis of microcystin hepatotoxins in the cyanobacterial genus <i>Fischerella</i> . Toxicon, 2018, 141, 43-50.  | 0.8 | 15        |
| 4279 | Molecular detection of Hepatozoon spp. in non-hematophagous bats in Brazil. Ticks and Tick-borne Diseases, 2020, 11, 101401.  | 1.1 | 5         |
| 4280 | Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . Nature Plants, 2017, 3, 715-723.   | 4.7 | 98        |
| 4281 | The genomic organisation of the metabotropic glutamate receptor subtype 5 gene, and its association with schizophrenia. , 0, .  |     | 1         |
| 4282 | Experimental infection with H1N1 European swine influenza virus protects pigs from an infection with the 2009 pandemic H1N1 human influenza virus. Veterinary Research, 2010, 41, 74.                                     | 1.1 | 71        |
| 4283 | GeneCodeq: quality score compression and improved genotyping using a Bayesian framework. Bioinformatics, 2016, 32, 3124-3132.   | 1.8 | 20        |
| 4284 | The <i>Neurospora crassa</i> Genome: Cosmid Libraries Sorted by Chromosome. Genetics, 2001, 157, 979-990.   | 1.2 | 51        |
| 4285 | Comparative Sequencing in the Genus <i>Lycopersicon</i> : Implications for the Evolution of Fruit Size in the Domestication of Cultivated Tomatoes. Genetics, 2002, 162, 365-379.   | 1.2 | 187       |
| 4286 | The Regulatory Regions Required for <i>B1</i> Paramutation and Expression Are Located Far Upstream of the Maize <i>b1</i> Transcribed Sequences. Genetics, 2002, 162, 917-930.  | 1.2 | 116       |
| 4287 | Molecular Population Genetics of the Arabidopsis <i>CLAVATA2</i> Region: The Genomic Scale of Variation and Selection in a Selfing Species. Genetics, 2003, 163, 1083-1095.   | 1.2 | 44        |
| 4288 | Mapping by Sequencing the Pneumocystis Genome Using the Ordering DNA Sequences V3 Tool. Genetics, 2003, 163, 1299-1313.   | 1.2 | 10        |
| 4289 | A Bacterial Artificial Chromosome Contig Spanning the Major Domestication Locus <i>Q</i> in Wheat and Identification of a Candidate Gene. Genetics, 2003, 164, 311-321.   | 1.2 | 182       |
| 4290 | Comparison of Global Brain Gene Expression Profiles Between Inbred Long-Sleep and Inbred Short-Sleep Mice by High-Density Gene Array Hybridization. Alcoholism: Clinical and Experimental Research, 2001, 25, 810-818.    | 1.4 | 1         |
| 4291 | Influence of Acid Blockade on the Aerodigestive Tract Microbiome in Children With Cystic Fibrosis. Journal of Pediatric Gastroenterology and Nutrition, 2021, 72, 520-527.  | 0.9 | 3         |
| 4292 | 16S rDNA sequence analysis of environmental <i>Bdellovibrio</i> -and-like organisms (BALO) reveals extensive diversity.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 2089-2094.          | 0.8 | 39        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4293 | The sequence of camelpox virus shows it is most closely related to variola virus, the cause of smallpox. <i>Journal of General Virology</i> , 2002, 83, 855-872.  | 1.3 | 143       |
| 4294 | Molecular evolution of the GDP-mannose pathway genes ( <i>manB</i> and <i>manC</i> ) in <i>Salmonella enterica</i> The GenBank accession numbers for the sequences reported in this paper are AY012160 and AY012201.. <i>Microbiology (United Kingdom)</i> , 2001, 147, 599-610.        | 0.7 | 34        |
| 4295 | Genome plasticity in <i>Yersinia pestis</i> The GenBank accession numbers for the sequences reported in this paper can be found in Table 1 T1 ; the GenBank accession number for DFR4 is AF426171.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 1687-1698.                        | 0.7 | 67        |
| 4296 | Functional and genomic diversity of methylotrophic Rhodocyclaceae: description of <i>Methyloversatilis discipulorum</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2227-2233.   | 0.8 | 71        |
| 4297 | <i>Phyllonema aviceniicola</i> gen. nov., sp. nov. and <i>Foliisarcina bertioensis</i> gen. nov., sp. nov., epiphyllic cyanobacteria associated with <i>Avicennia schaueriana</i> leaves. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 689-700. | 0.8 | 43        |
| 4298 | Proposal of <i>Ancylothrix</i> gen. nov., a new genus of Phormidiaceae (Cyanobacteria, Oscillatoriales) based on a polyphasic approach. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2396-2405.   | 0.8 | 24        |
| 4299 | <i>Aliterella atlantica</i> gen. nov., sp. nov., and <i>Aliterella antarctica</i> sp. nov., novel members of coccoid Cyanobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2853-2861.   | 0.8 | 36        |
| 4300 | <i>Potamolinea</i> gen. nov. (Oscillatoriales, Cyanobacteria): a phylogenetically and ecologically coherent cyanobacterial genus. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3632-3641.   | 0.8 | 23        |
| 4301 | <i>Kryptousia macronema</i> gen. nov., sp. nov. and <i>Kryptousia microlepis</i> sp. nov., nostocalean cyanobacteria isolated from phyllospheres. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3301-3309.                                       | 0.8 | 31        |
| 4302 | <i>Amazoninema</i> gen. nov., (Synechococcales, Pseudanabaenaceae) a novel cyanobacteria genus from Brazilian Amazonian rivers. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2249-2257.   | 0.8 | 24        |
| 4303 | Variation in genome content and predatory phenotypes between <i>Bdellovibrio</i> sp. NC01 isolated from soil and <i>B. bacteriovorus</i> type strain HD100. <i>Microbiology (United Kingdom)</i> , 2019, 165, 1315-1330.  | 0.7 | 11        |
| 4304 | DC-SIGN (CD209) gene promoter polymorphisms in a Brazilian population and their association with human T-cell lymphotropic virus type 1 infection. <i>Journal of General Virology</i> , 2009, 90, 927-934.  | 1.3 | 25        |
| 4305 | Sequences of complete human cytomegalovirus genomes from infected cell cultures and clinical specimens. <i>Journal of General Virology</i> , 2010, 91, 605-615.   | 1.3 | 108       |
| 4306 | Homology between the human cytomegalovirus RL11 gene family and human adenovirus E3 genes. <i>Journal of General Virology</i> , 2003, 84, 657-663.  | 1.3 | 79        |
| 4332 | Gene Discovery Using Computational and Microarray Analysis of Transcription in the <i>Drosophila melanogaster</i> Testis. <i>Genome Research</i> , 2000, 10, 2030-2043.   | 2.4 | 178       |
| 4333 | <i>Tropheryma whipplei</i> Twist: A Human Pathogenic Actinobacteria With a Reduced Genome. <i>Genome Research</i> , 2003, 13, 1800-1809.  | 2.4 | 161       |
| 4334 | A Cattle-Human Comparative Map Built with Cattle BAC-Ends and Human Genome Sequence. <i>Genome Research</i> , 2003, 13, 1966-1972.  | 2.4 | 126       |
| 4335 | Sequence Variation Within the Fragile X Locus. <i>Genome Research</i> , 2001, 11, 1382-1391.  | 2.4 | 12        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4336 | Single Nucleotide Polymorphism Markers for Genetic Mapping in <i>Drosophila melanogaster</i> . Genome Research, 2001, 11, 1100-1113.   | 2.4 | 44        |
| 4337 | Mining SNPs From EST Databases. Genome Research, 1999, 9, 167-174.   | 2.4 | 252       |
| 4338 | Assembly, Annotation, and Integration of UNIGENE Clusters into the Human Genome Draft. Genome Research, 2001, 11, 904-918.   | 2.4 | 52        |
| 4339 | The Finished Genome Sequence of Homo sapiens. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 1-12.   | 2.0 | 10        |
| 4340 | Gene Expression Profiling of Cells, Tissues, and Developmental Stages of the Nematode <i>C. elegans</i> . Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 159-170.  | 2.0 | 273       |
| 4341 | DNA Sequence Assembly and Multiple Sequence Alignment by an Eulerian Path Approach. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 205-212.  | 2.0 | 5         |
| 4342 | Assessing the Quality of Finished Genomic Sequence. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 31-38.  | 2.0 | 2         |
| 4343 | Development of an Online Tool for European Working Group for <i>Legionella</i> Infections Sequence-Based Typing, Including Automatic Quality Assessment and Data Submission. , 0, , 163-166.   |     | 3         |
| 4344 | The <i>Legionella pneumophila</i> Sequencing Project. , 0, , 97-104.   |     | 2         |
| 4345 | The 102-Kilobase <i>pgm</i> Locus of <i>Yersinia pestis</i> : Sequence Analysis and Comparison of Selected Regions among Different <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> Strains. Infection and Immunity, 1999, 67, 4851-4861. | 1.0 | 128       |
| 4346 | The Genome of <i>Melanoplus sanguinipes</i> Entomopoxvirus. Journal of Virology, 1999, 73, 533-552.  | 1.5 | 189       |
| 4347 | Haplotype reconstruction from SNP alignment. , 2003, , .   |     | 6         |
| 4350 | Cystin, a novel cilia-associated protein, is disrupted in the cpk mouse model of polycystic kidney disease. Journal of Clinical Investigation, 2002, 109, 533-540.   | 3.9 | 131       |
| 4351 | Discovery of common human genetic variants of GTP cyclohydrolase 1 (GCH1) governing nitric oxide, autonomic activity, and cardiovascular risk. Journal of Clinical Investigation, 2007, 117, 2658-2671.  | 3.9 | 87        |
| 4353 | Using Workflow to Build an Information Management System for a Geographically Distributed Genome Sequencing Initiative. , 2003, , .  |     | 9         |
| 4354 | Expressed Sequence Tag Analysis in <i>Cycas</i> . , 2011, , 21-35.   |     | 1         |
| 4355 | A large-scale analysis of mRNAs expressed by primary mesenchyme cells of the sea urchin embryo. Development (Cambridge), 2001, 128, 2615-2627.   | 1.2 | 104       |
| 4356 | A PAK-like protein kinase is required for maturation of young hyphae and septation in the filamentous ascomycete <i>Ashbya gossypii</i> . Journal of Cell Science, 2000, 113, 4563-4575.   | 1.2 | 72        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4357 | bcbioRNASeq: R package for bcbio RNA-seq analysis. F1000Research, 0, 6, 1976.   | 0.8 | 6         |
| 4358 | bcbioRNASeq: R package for bcbio RNA-seq analysis. F1000Research, 0, 6, 1976.   | 0.8 | 21        |
| 4359 | A bovine CD18 signal peptide variant with increased binding activity to Mannheimia hemolytica leukotoxin. F1000Research, 2018, 7, 1985.   | 0.8 | 4         |
| 4360 | MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. F1000Research, 2013, 2, 217.  | 0.8 | 42        |
| 4361 | MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. F1000Research, 2013, 2, 217.  | 0.8 | 30        |
| 4362 | CoverView: a sequence quality evaluation tool for next generation sequencing data. Wellcome Open Research, 2018, 3, 36.   | 0.9 | 7         |
| 4363 | The Quality Sequencing Minimum (QSM): providing comprehensive, consistent, transparent next generation sequencing data quality assurance. Wellcome Open Research, 2018, 3, 37.  | 0.9 | 6         |
| 4364 | End Sequencing and Chromosomal <i>in silico</i> Mapping of BAC Clones Derived from an <i>indica</i> Rice Cultivar, Kasalath. Breeding Science, 2004, 54, 273-279.   | 0.9 | 29        |
| 4365 | Genomic Scanning Using Inverted Repeats of Microsatellites (GAG) <sub>6</sub> C, (AG) <sub>9</sub> C. Biogeosystem Technique, 2015, 4, 138-152.   | 0.5 | 2         |
| 4366 | Analysis of ESTs and gene expression patterns of the posterior silkgland in the fifth instar larvae of silkworm, Bombyx mori L.. Science in China Series C: Life Sciences, 2005, 48, 25.                              | 1.3 | 14        |
| 4367 | Comparison of C. elegans and C. briggsae Genome Sequences Reveals Extensive Conservation of Chromosome Organization and Synteny. PLoS Biology, 2007, 5, e167.   | 2.6 | 159       |
| 4368 | Widespread Genomic Signatures of Natural Selection in Hominid Evolution. PLoS Genetics, 2009, 5, e1000471.  | 1.5 | 398       |
| 4369 | Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen Pseudocercospora fijiensis (Synonym Mycosphaerella fijiensis) Genomes Reveal Clues for Disease Control. PLoS Genetics, 2016, 12, e1005876. | 1.5 | 77        |
| 4370 | Distribution of Plasmids in Distinct Leptospira Pathogenic Species. PLoS Neglected Tropical Diseases, 2015, 9, e0004220.  | 1.3 | 16        |
| 4371 | Genome Sequencing Shows that European Isolates of Francisella tularensis Subspecies tularensis Are Almost Identical to US Laboratory Strain Schu S4. PLoS ONE, 2007, 2, e352.   | 1.1 | 51        |
| 4372 | Transcriptome of Pneumocystis carinii during Fulminate Infection: Carbohydrate Metabolism and the Concept of a Compatible Parasite. PLoS ONE, 2007, 2, e423.  | 1.1 | 58        |
| 4373 | Complete Mitochondrial Genome Sequence of Three Tetrahymena Species Reveals Mutation Hot Spots and Accelerated Nonsynonymous Substitutions in Ymf Genes. PLoS ONE, 2007, 2, e650.                                     | 1.1 | 30        |
| 4374 | Genome Sequence of Fusobacterium nucleatum Subspecies Polymorphum "a Genetically Tractable Fusobacterium. PLoS ONE, 2007, 2, e659.  | 1.1 | 56        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4375 | Complete Genomic Characterization of a Pathogenic A.II Strain of <i>Francisella tularensis</i> Subspecies <i>tularensis</i> . PLoS ONE, 2007, 2, e947.                         | 1.1 | 46        |
| 4376 | <i>Deinococcus geothermalis</i> : The Pool of Extreme Radiation Resistance Genes Shrinks. PLoS ONE, 2007, 2, e955.   | 1.1 | 212       |
| 4377 | The Origins of Novel Protein Interactions during Animal Opsin Evolution. PLoS ONE, 2007, 2, e1054.   | 1.1 | 99        |
| 4378 | Group II Introns Break New Boundaries: Presence in a Bilaterian's Genome. PLoS ONE, 2008, 3, e1488.  | 1.1 | 78        |
| 4379 | Improving Phrap-Based Assembly of the Rat Using "Reliable" Overlaps. PLoS ONE, 2008, 3, e1836.   | 1.1 | 4         |
| 4380 | Hepatitis C Virus Diversity and Evolution in the Full Open-Reading Frame during Antiviral Therapy. PLoS ONE, 2008, 3, e2123.   | 1.1 | 45        |
| 4381 | Genotyping of <i>Bacillus cereus</i> Strains by Microarray-Based Resequencing. PLoS ONE, 2008, 3, e2513.   | 1.1 | 20        |
| 4382 | Targeted Development of Registries of Biological Parts. PLoS ONE, 2008, 3, e2671.  | 1.1 | 63        |
| 4383 | The Silkworm ( <i>Bombyx mori</i> ) microRNAs and Their Expressions in Multiple Developmental Stages. PLoS ONE, 2008, 3, e2997.  | 1.1 | 130       |
| 4384 | High-Resolution Analysis of the 5' End Transcriptome Using a Next Generation DNA Sequencer. PLoS ONE, 2009, 4, e4108.  | 1.1 | 42        |
| 4385 | Integron Gene Cassettes and Degradation of Compounds Associated with Industrial Waste: The Case of the Sydney Tar Ponds. PLoS ONE, 2009, 4, e5276.                             | 1.1 | 46        |
| 4386 | Assembling the Marine Metagenome, One Cell at a Time. PLoS ONE, 2009, 4, e5299.  | 1.1 | 320       |
| 4387 | Genomic Characterization of Methanomicrobiales Reveals Three Classes of Methanogens. PLoS ONE, 2009, 4, e5797.   | 1.1 | 103       |
| 4388 | Diversity and Strain Specificity of Plant Cell Wall Degrading Enzymes Revealed by the Draft Genome of <i>Ruminococcus flavefaciens</i> FD-1. PLoS ONE, 2009, 4, e6650.         | 1.1 | 124       |
| 4389 | Culture-Independent Microbiological Analysis of Foley Urinary Catheter Biofilms. PLoS ONE, 2009, 4, e7811.   | 1.1 | 76        |
| 4390 | Comparative Sequence Analysis of the Non-Protein-Coding Mitochondrial DNA of Inbred Rat Strains. PLoS ONE, 2009, 4, e8148.   | 1.1 | 11        |
| 4391 | Unbiased Transcriptional Comparisons of Generalist and Specialist Herbivores Feeding on Progressively Defenseless <i>Nicotiana attenuata</i> Plants. PLoS ONE, 2010, 5, e8735. | 1.1 | 95        |
| 4392 | Metagenomic Sequencing of an In Vitro-Simulated Microbial Community. PLoS ONE, 2010, 5, e10209.  | 1.1 | 200       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4393 | 18S rDNA Sequences from Microeukaryotes Reveal Oil Indicators in Mangrove Sediment. PLoS ONE, 2010, 5, e12437.  | 1.1 | 47        |
| 4394 | Reference-Free Validation of Short Read Data. PLoS ONE, 2010, 5, e12681.  | 1.1 | 23        |
| 4395 | The Complete Chloroplast Genome Sequence of Date Palm ( <i>Phoenix dactylifera</i> L.). PLoS ONE, 2010, 5, e12762.  | 1.1 | 255       |
| 4396 | Characteristic Male Urine Microbiomes Associate with Asymptomatic Sexually Transmitted Infection. PLoS ONE, 2010, 5, e14116.  | 1.1 | 234       |
| 4397 | Evolution of Disease Response Genes in Loblolly Pine: Insights from Candidate Genes. PLoS ONE, 2010, 5, e14234.   | 1.1 | 23        |
| 4398 | Monitoring the Long-Term Molecular Epidemiology of the Pneumococcus and Detection of Potential "Vaccine Escape"™ Strains. PLoS ONE, 2011, 6, e15950.                                      | 1.1 | 7         |
| 4399 | The Genome of <i>Akkermansia muciniphila</i> , a Dedicated Intestinal Mucin Degradator, and Its Use in Exploring Intestinal Metagenomes. PLoS ONE, 2011, 6, e16876.                       | 1.1 | 328       |
| 4400 | Allele-Specific, Age-Dependent and BMI-Associated DNA Methylation of Human MCHR1. PLoS ONE, 2011, 6, e17711.  | 1.1 | 43        |
| 4401 | Host Specific Diversity in <i>Lactobacillus johnsonii</i> as Evidenced by a Major Chromosomal Inversion and Phage Resistance Mechanisms. PLoS ONE, 2011, 6, e18740.                       | 1.1 | 41        |
| 4402 | The Complete Genome Sequence of <i>Fibrobacter succinogenes</i> S85 Reveals a Cellulolytic and Metabolic Specialist. PLoS ONE, 2011, 6, e18814.   | 1.1 | 199       |
| 4403 | The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. PLoS ONE, 2011, 6, e19838.                                       | 1.1 | 55        |
| 4404 | Cryptic Speciation in Brazilian <i>Epiperipatus</i> (Onychophora: Peripatidae) Reveals an Underestimated Diversity among the Peripatid Velvet Worms. PLoS ONE, 2011, 6, e19973.           | 1.1 | 34        |
| 4405 | Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095.   | 1.1 | 59        |
| 4406 | The Gut as Reservoir of Antibiotic Resistance: Microbial Diversity of Tetracycline Resistance in Mother and Infant. PLoS ONE, 2011, 6, e21644.  | 1.1 | 111       |
| 4407 | Adaptative Potential of the <i>Lactococcus Lactis</i> IL594 Strain Encoded in Its 7 Plasmids. PLoS ONE, 2011, 6, e22238.  | 1.1 | 56        |
| 4408 | Diversification and Species Boundaries of <i>Rhinebothrium</i> (Cestoda; Rhinebothriidea) in South American Freshwater Stingrays (Batoidea; Potamotrygonidae). PLoS ONE, 2011, 6, e22604. | 1.1 | 27        |
| 4409 | Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. PLoS ONE, 2011, 6, e25531.   | 1.1 | 40        |
| 4410 | RNA-Seq Reveals an Integrated Immune Response in Nucleated Erythrocytes. PLoS ONE, 2011, 6, e26998.   | 1.1 | 130       |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4411 | Interkingdom Gene Transfer of a Hybrid NPS/PKS from Bacteria to Filamentous Ascomycota. PLoS ONE, 2011, 6, e28231.  | 1.1 | 52        |
| 4412 | Development of Genomic Resources for Pacific Herring through Targeted Transcriptome Pyrosequencing. PLoS ONE, 2012, 7, e30908.  | 1.1 | 22        |
| 4413 | Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. PLoS ONE, 2012, 7, e31386.  | 1.1 | 214       |
| 4414 | Transposable Elements Are a Major Cause of Somatic Polymorphism in <i>Vitis vinifera</i> L.. PLoS ONE, 2012, 7, e32973.   | 1.1 | 109       |
| 4415 | Evolution of <i>Burkholderia pseudomallei</i> in Recurrent Melioidosis. PLoS ONE, 2012, 7, e36507.  | 1.1 | 96        |
| 4416 | The Development of a Genome Wide SNP Set for the Barnacle Goose <i>Branta leucopsis</i> . PLoS ONE, 2012, 7, e38412.  | 1.1 | 22        |
| 4417 | A Mitogenomic Re-Evaluation of the Bdelloid Phylogeny and Relationships among the Syndermata. PLoS ONE, 2012, 7, e43554.  | 1.1 | 17        |
| 4418 | The Social Brain: Transcriptome Assembly and Characterization of the Hippocampus from a Social Subterranean Rodent, the Colonial Tuco-Tuco ( <i>Ctenomys sociabilis</i> ). PLoS ONE, 2012, 7, e45524. | 1.1 | 21        |
| 4419 | Sequencing and Analysis of Full-Length cDNAs, 5â€™-ESTs and 3â€™-ESTs from a Cartilaginous Fish, the Elephant Shark ( <i>Callorhynchus milii</i> ). PLoS ONE, 2012, 7, e47174.                        | 1.1 | 10        |
| 4420 | Exploring the Diversity and Distribution of Neotropical Avian Malaria Parasites â€“ A Molecular Survey from Southeast Brazil. PLoS ONE, 2013, 8, e57770.  | 1.1 | 89        |
| 4421 | Generation and Analysis of the Expressed Sequence Tags from the Mycelium of <i>Ganoderma lucidum</i> . PLoS ONE, 2013, 8, e61127.   | 1.1 | 19        |
| 4422 | <i>Clostridium botulinum</i> Strain Af84 Contains Three Neurotoxin Gene Clusters: Bont/A2, bont/F4 and bont/F5. PLoS ONE, 2013, 8, e61205.  | 1.1 | 44        |
| 4423 | Comparative Transcriptional Profiling of the Axolotl Limb Identifies a Tripartite Regeneration-Specific Gene Program. PLoS ONE, 2013, 8, e61352.  | 1.1 | 107       |
| 4424 | Developmental Gene Discovery in a Hemimetabolous Insect: De Novo Assembly and Annotation of a Transcriptome for the Cricket <i>Gryllus bimaculatus</i> . PLoS ONE, 2013, 8, e61479.                   | 1.1 | 41        |
| 4425 | Sequencing of Candidate Chromosome Instability Genes in Endometrial Cancers Reveals Somatic Mutations in ESCO1, CHTF18, and MRE11A. PLoS ONE, 2013, 8, e63313.  | 1.1 | 27        |
| 4426 | A Filtering Method to Generate High Quality Short Reads Using Illumina Paired-End Technology. PLoS ONE, 2013, 8, e66643.  | 1.1 | 282       |
| 4427 | Genome Analysis and Physiological Comparison of <i>Alicyclophilus denitrificans</i> Strains BC and K601T. PLoS ONE, 2013, 8, e66971.  | 1.1 | 32        |
| 4428 | SNP Discovery in European Anchovy ( <i>Engraulis encrasicolus</i> , L) by High-Throughput Transcriptome and Genome Sequencing. PLoS ONE, 2013, 8, e70051.   | 1.1 | 38        |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4429 | Generation and Analysis of a Large-Scale Expressed Sequence Tag Database from a Full-Length Enriched cDNA Library of Developing Leaves of <i>Gossypium hirsutum</i> L. <i>PLoS ONE</i> , 2013, 8, e76443.  | 1.1 | 10        |
| 4430 | Effective Population Size, Genetic Variation, and Their Relevance for Conservation: The Bighorn Sheep in Tiburon Island and Comparisons with Managed Artiodactyls. <i>PLoS ONE</i> , 2013, 8, e78120.  | 1.1 | 26        |
| 4431 | Sloth Hair as a Novel Source of Fungi with Potent Anti-Parasitic, Anti-Cancer and Anti-Bacterial Bioactivity. <i>PLoS ONE</i> , 2014, 9, e84549.   | 1.1 | 24        |
| 4432 | What Does the Talking?: Quorum Sensing Signalling Genes Discovered in a Bacteriophage Genome. <i>PLoS ONE</i> , 2014, 9, e85131.   | 1.1 | 123       |
| 4433 | Lampreys Have a Single Gene Cluster for the Fast Skeletal Myosin Heavy Chain Gene Family. <i>PLoS ONE</i> , 2013, 8, e85500.   | 1.1 | 3         |
| 4434 | CUSHAW3: Sensitive and Accurate Base-Space and Color-Space Short-Read Alignment with Hybrid Seeding. <i>PLoS ONE</i> , 2014, 9, e86869.  | 1.1 | 45        |
| 4435 | Composition of Microbial Oral Biofilms during Maturation in Young Healthy Adults. <i>PLoS ONE</i> , 2014, 9, e87449.   | 1.1 | 29        |
| 4436 | Mutation Profiling of the Hepatitis B Virus Strains Circulating in North Indian Population. <i>PLoS ONE</i> , 2014, 9, e91150.   | 1.1 | 21        |
| 4437 | Genetic Profiling of the Isoprenoid and Sterol Biosynthesis Pathway Genes of <i>Trypanosoma cruzi</i> . <i>PLoS ONE</i> , 2014, 9, e96762.   | 1.1 | 19        |
| 4438 | Beyond the Chromosome: The Prevalence of Unique Extra-Chromosomal Bacteriophages with Integrated Virulence Genes in Pathogenic <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2014, 9, e100502.  | 1.1 | 48        |
| 4439 | Detection of Genome Donor Species of Neglected Tetraploid Crop <i>Vigna reflexo-pilosa</i> (CrÃ©ole Bean), and Genetic Structure of Diploid Species Based on Newly Developed EST-SSR Markers from Azuki Bean ( <i>Vigna angularis</i> ). <i>PLoS ONE</i> , 2014, 9, e104990. | 1.1 | 44        |
| 4440 | Optimization of Extraction of Circulating RNAs from Plasma â€œ Enabling Small RNA Sequencing. <i>PLoS ONE</i> , 2014, 9, e107259.  | 1.1 | 49        |
| 4441 | Intestinal Lesions Are Associated with Altered Intestinal Microbiome and Are More Frequent in Children and Young Adults with Cystic Fibrosis and Cirrhosis. <i>PLoS ONE</i> , 2015, 10, e0116967.  | 1.1 | 78        |
| 4442 | The Evolutionary Origins of the Southern Ocean Philobryid Bivalves: Hidden Biodiversity, Ancient Persistence. <i>PLoS ONE</i> , 2015, 10, e0121198.  | 1.1 | 7         |
| 4443 | Variation in the Ovine Abomasal Lymph Node Transcriptome between Breeds Known to Differ in Resistance to the Gastrointestinal Nematode. <i>PLoS ONE</i> , 2015, 10, e0124823.  | 1.1 | 16        |
| 4444 | Altered Interactions between the Gut Microbiome and Colonic Mucosa Precede Polyposis in APCMin/+ Mice. <i>PLoS ONE</i> , 2015, 10, e0127985.   | 1.1 | 48        |
| 4445 | Est16, a New Esterase Isolated from a Metagenomic Library of a Microbial Consortium Specializing in Diesel Oil Degradation. <i>PLoS ONE</i> , 2015, 10, e0133723.  | 1.1 | 26        |
| 4446 | Inbreeding Ratio and Genetic Relationships among Strains of the Western Clawed Frog, <i>Xenopus tropicalis</i> . <i>PLoS ONE</i> , 2015, 10, e0133963.   | 1.1 | 20        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4447 | Joint MiRNA/mRNA Expression Profiling Reveals Changes Consistent with Development of Dysfunctional Corpus Luteum after Weight Gain. <i>PLoS ONE</i> , 2015, 10, e0135163.                                   | 1.1 | 42        |
| 4448 | An Efficient Genotyping Method in Chicken Based on Genome Reducing and Sequencing. <i>PLoS ONE</i> , 2015, 10, e0137010.  | 1.1 | 8         |
| 4449 | AmpliconDuo: A Split-Sample Filtering Protocol for High-Throughput Amplicon Sequencing of Microbial Communities. <i>PLoS ONE</i> , 2015, 10, e0141590.  | 1.1 | 53        |
| 4450 | Genome Sequence of African Swine Fever Virus BA71, the Virulent Parental Strain of the Nonpathogenic and Tissue-Culture Adapted BA71V. <i>PLoS ONE</i> , 2015, 10, e0142889.                                | 1.1 | 69        |
| 4451 | Molecular Identification of <i>Staphylococcus aureus</i> in Airway Samples from Children with Cystic Fibrosis. <i>PLoS ONE</i> , 2016, 11, e0147643.  | 1.1 | 15        |
| 4452 | The Intestinal Eukaryotic Virome in Healthy and Diarrhoeic Neonatal Piglets. <i>PLoS ONE</i> , 2016, 11, e0151481.  | 1.1 | 28        |
| 4453 | Identification of Multiple Stress Responsive Genes by Sequencing a Normalized cDNA Library from Sea-Land Cotton ( <i>Gossypium barbadense</i> L.). <i>PLoS ONE</i> , 2016, 11, e0152927.                    | 1.1 | 33        |
| 4454 | Patterns of Transcript Abundance of Eukaryotic Biogeochemically-Relevant Genes in the Amazon River Plume. <i>PLoS ONE</i> , 2016, 11, e0160929.   | 1.1 | 17        |
| 4455 | Airway Microbial Community Turnover Differs by BPD Severity in Ventilated Preterm Infants. <i>PLoS ONE</i> , 2017, 12, e0170120.  | 1.1 | 62        |
| 4456 | Shared features of cryptic plasmids from environmental and pathogenic <i>Francisella</i> species. <i>PLoS ONE</i> , 2017, 12, e0183554.   | 1.1 | 16        |
| 4457 | Clonality and distribution of clinical <i>Ureaplasma</i> isolates recovered from male patients and infertile couples in China. <i>PLoS ONE</i> , 2017, 12, e0183947.  | 1.1 | 11        |
| 4458 | Evaluation of bloodstream infections, <i>Clostridium difficile</i> infections, and gut microbiota in pediatric oncology patients. <i>PLoS ONE</i> , 2018, 13, e0191232.                                     | 1.1 | 22        |
| 4459 | Annotation and validation of genes involved in photosynthesis and starch synthesis from a <i>Manihot</i> full-length cDNA library. <i>Frontiers of Agricultural Science and Engineering</i> , 2016, 3, 308. | 0.9 | 1         |
| 4460 | Single nucleotide polymorphisms at 15 codons of the prion protein gene from a scrapie-affected herd of Suffolk sheep in Brazil. <i>Pesquisa Veterinaria Brasileira</i> , 2011, 31, 893-898.                 | 0.5 | 8         |
| 4461 | Biodegradação da hepatotoxina(D-Leu1)-microcistina-LR por bactérias presentes em filtros biológicos de carvão. <i>Engenharia Sanitaria E Ambiental</i> , 2013, 18, 205-214.                                 | 0.1 | 5         |
| 4462 | Biosurfactants production by yeasts using soybean oil and glycerol as low cost substrate. <i>Brazilian Journal of Microbiology</i> , 2012, 43, 116-125.   | 0.8 | 45        |
| 4463 | Aortic valve endocarditis due to <i>Bartonella clarridgeiae</i> in a dog in Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2019, 28, 661-670.  | 0.2 | 10        |
| 4465 | RNA-Seq-based analysis of differential gene expression associated with hepatitis C virus infection in cell culture. <i>Acta Biochimica Polonica</i> , 2017, 63, 789-798.                                    | 0.3 | 5         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4466 | Inducible knock-out of BCL6 in lymphoma cells results in tumor stasis. <i>Oncotarget</i> , 2020, 11, 875-890.  | 0.8 | 22        |
| 4467 | MHC genetic diversity and avian malaria prevalence in Mokoia Island saddlebacks. , 2016, 40, 351-360.  |     | 5         |
| 4469 | Characterization of Three Osmotin-Like Proteins from <i>Plumeria rubra</i> and Prospection for Adiponectin Peptidomimetics. <i>Protein and Peptide Letters</i> , 2020, 27, 593-603.              | 0.4 | 3         |
| 4470 | Gene expression profiling and expression analysis of freshwater shrimp ( <i>Neocaridina denticulata</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock<br>Environmental Biology, 2018, 39, 51-57.          | 0.2 | 11        |
| 4471 | Linkage and Association With Type 1 Diabetes on Chromosome 1q42. <i>Diabetes</i> , 2002, 51, 3318-3325.  | 0.3 | 15        |
| 4472 | Induction, structural characterization, and genome sequence of Lv1, a prophage from a human vaginal <i>Lactobacillus jensenii</i> strain. <i>International Microbiology</i> , 2010, 13, 113-21.  | 1.1 | 21        |
| 4473 | MicrosatDesign is a pipeline for transforming sequencer trace files into DNA markers. <i>CGB Technical Report</i> , 2005, 2005, .  | 1.5 | 2         |
| 4474 | Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , 2004, 10, 2192-2195.   | 2.0 | 182       |
| 4475 | Novel ERBB receptor feedback inhibitor 1 (ERRF1) + 808 T/G polymorphism confers protective effect on diabetic nephropathy in a Korean population. <i>Disease Markers</i> , 2013, 34, 113-24.     | 0.6 | 6         |
| 4476 | Expressed Sequence Tags of <i>Trichinella spiralis</i> Muscle Stage Larvae. <i>Korean Journal of Parasitology</i> , 2008, 46, 59.  | 0.5 | 4         |
| 4477 | No two reefs are created equal: fine-scale population structure in the threatened coral species <i>Acropora palmata</i> and <i>A. cervicornis</i> . <i>Aquatic Biology</i> , 2010, 10, 69-83.    | 0.5 | 10        |
| 4478 | Phylogeny of cultivable heterotrophic bacteria derived from mixed colonies. <i>Aquatic Microbial Ecology</i> , 2012, 66, 95-106.   | 0.9 | 2         |
| 4479 | Epidemiology of skin ulceration disease in wild sea cucumber <i>Holothuria arguinensis</i> , a new aquaculture target species. <i>Diseases of Aquatic Organisms</i> , 2019, 135, 77-88.          | 0.5 | 7         |
| 4480 | Nitrogen fixation in the western English Channel (NE Atlantic Ocean). <i>Marine Ecology - Progress Series</i> , 2009, 374, 7-12.   | 0.9 | 85        |
| 4481 | Penetration of Pacific zooplankton into the western Arctic Ocean tracked with molecular population genetics. <i>Marine Ecology - Progress Series</i> , 2009, 381, 129-138.                       | 0.9 | 98        |
| 4482 | Next-Generation Sequencing Approaches in Cancer: Where Have They Brought Us and Where Will They Take Us?. <i>Cancers</i> , 2015, 7, 1925-1958.   | 1.7 | 51        |
| 4483 | Characterization of hepatitis B virus X gene quasispecies complexity in mono-infection and hepatitis delta virus superinfection. <i>World Journal of Gastroenterology</i> , 2019, 25, 1566-1579. | 1.4 | 7         |
| 4484 | A novel de novo variant of LAMA2 contributes to merosin deficient congenital muscular dystrophy type 1A: Case report. <i>Biomedical Reports</i> , 2020, 12, 46-50.                               | 0.9 | 5         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4485 | Characterization of SNPs of Bovine Prolcatin Gene of Holstein Cattle. <i>Biotechnology</i> , 2008, 7, 118-123.   | 0.5 | 4         |
| 4486 | Optimization of the Sample Preparation Method for DNA Sequencing. <i>Journal of Biological Sciences</i> , 2006, 7, 194-199.  | 0.1 | 2         |
| 4487 | Complete genome sequence of <i>Nitrosomonas</i> sp. Is79, an ammonia oxidizing bacterium adapted to low ammonium concentrations. <i>Standards in Genomic Sciences</i> , 2013, 7, 469-482.  | 1.5 | 43        |
| 4488 | Bioinformatics for Viral Metagenomics. <i>Journal of Data Mining in Genomics &amp; Proteomics</i> , 2013, 04, .  | 0.5 | 14        |
| 4489 | Phylogeny of Bacteria from Steelmaking Wastes and Their Acidic Enrichment Cultures. <i>Advances in Microbiology</i> , 2014, 04, 816-828.   | 0.3 | 1         |
| 4490 | Molecular characterization of an opossum <i>Didelphis albiventris</i> (Marsupialia: Didelphidae) population in an urban fragment of the Brazilian Atlantic Rainforest and support to species barcode identification. <i>Genetics and Molecular Research</i> , 2012, 11, 2487-2496. | 0.3 | 6         |
| 4491 | Molecular characterization of a mariner-like element in the <i>Atta sexdens rubropilosa</i> genome. <i>Genetics and Molecular Research</i> , 2012, 11, 1475-1485.  | 0.3 | 4         |
| 4492 | Identification of genes encoding hypothetical proteins in open-reading frame expressed sequence tags from mammalian stages of <i>Trypanosoma cruzi</i> . <i>Genetics and Molecular Research</i> , 2011, 10, 1589-1630.   | 0.3 | 4         |
| 4493 | Development and use of single nucleotide polymorphism markers for candidate resistance genes in wild peanuts ( <i>Arachis</i> spp). <i>Genetics and Molecular Research</i> , 2008, 7, 631-642.   | 0.3 | 21        |
| 4494 | ChromaPipe: a pipeline for analysis, quality control and management for a DNA sequencing facility. <i>Genetics and Molecular Research</i> , 2008, 7, 861-871.  | 0.3 | 112       |
| 4495 | Avian TAP genes: detection of nucleotide polymorphisms and comparative analysis across species. <i>Genetics and Molecular Research</i> , 2008, 7, 1267-1281.   | 0.3 | 5         |
| 4496 | Genetic variability in <i>Melipona quinquefasciata</i> (Hymenoptera, Apidae, Meliponini) from northeastern Brazil determined using the first internal transcribed spacer (ITS1). <i>Genetics and Molecular Research</i> , 2009, 8, 641-648.  | 0.3 | 4         |
| 4497 | Understanding bamboo flowering based on large-scale analysis of expressed sequence tags. <i>Genetics and Molecular Research</i> , 2010, 9, 1085-1093.  | 0.3 | 57        |
| 4499 | Phylogeography of the <i>Lessonia variegata</i> species complex (Phaeophyceae, Laminariales) in New Zealand. <i>Algae</i> , 2016, 31, 91-103.  | 0.9 | 10        |
| 4500 | New insights on <i>Bjerkandera</i> (Phanerochaetaceae, Polyporales) in the Neotropics with description of <i>Bjerkandera albocinerea</i> based on morphological and molecular evidence. <i>Plant Ecology and Evolution</i> , 2020, 153, 229-245.                                   | 0.3 | 8         |
| 4501 | Tomato genome sequencing: deciphering the euchromatin region of the chromosome 8. <i>Plant Biotechnology</i> , 2007, 24, 5-9.  | 0.5 | 9         |
| 4502 | Chromosomal Localization of Korean Cattle (Hanwoo) BAC Clones via BAC end Sequence Analysis. <i>Asian-Australasian Journal of Animal Sciences</i> , 2007, 20, 316-327.   | 2.4 | 9         |
| 4503 | Deep Sequencing Data Analysis: Challenges and Solutions. , 0, , .  |     | 4         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4504 | Isolation and Identification of Defense Responsive Genes in Wheat During Incompatible Interaction with <i>Bipolaris sorokiniana</i> (Cochliobolus sativus) using SSH Technique. <i>Vegetos</i> , 2014, 27, 11. | 0.8 | 1         |
| 4505 | ESMP: A high-throughput computational pipeline for mining SSR markers from ESTs. <i>Bioinformatics</i> , 2012, 8, 206-208.   | 0.2 | 7         |
| 4506 | Microorganismos asociados a la rizosfera de jitomate en un agroecosistema del valle de Guasave, Sinaloa, México. <i>Revista Mexicana De Biodiversidad</i> , 2012, 83, .  | 0.4 | 7         |
| 4507 | Pervasive epigenetic effects of <i>Drosophila</i> euchromatic transposable elements impact their evolution. <i>ELife</i> , 2017, 6, .  | 2.8 | 102       |
| 4508 | Metatranscriptomic analysis of a high-sulfide aquatic spring reveals insights into sulfur cycling and unexpected aerobic metabolism. <i>PeerJ</i> , 2015, 3, e1259.  | 0.9 | 17        |
| 4509 | Microfungal oasis in an oligotrophic desert: diversity patterns and community structure in three freshwater systems of Cuatro Ciénegas, Mexico. <i>PeerJ</i> , 2016, 4, e2064.                                 | 0.9 | 19        |
| 4510 | Agricultural land-use change in a Mexican oligotrophic desert depletes ecosystem stability. <i>PeerJ</i> , 2016, 4, e2365.   | 0.9 | 13        |
| 4511 | Diversity, taxonomic composition, and functional aspects of fungal communities in living, senesced, and fallen leaves at five sites across North America. <i>PeerJ</i> , 2016, 4, e2768.                       | 0.9 | 48        |
| 4512 | Impact of enzymatic digestion on bacterial community composition in CF airway samples. <i>PeerJ</i> , 2017, 5, e3362.  | 0.9 | 6         |
| 4513 | Taxonomic and chemical assessment of exceptionally abundant rock mine biofilm. <i>PeerJ</i> , 2017, 5, e3635.  | 0.9 | 5         |
| 4514 | Does haemosporidian infection affect hematological and biochemical profiles of the endangered Black-fronted piping-guan ( <i>Aburria jacutinga</i> )?. <i>PeerJ</i> , 2013, 1, e45.                            | 0.9 | 20        |
| 4515 | Experimental and molecular approximation to microbial niche: trophic interactions between oribatid mites and microfungi in an oligotrophic freshwater system. <i>PeerJ</i> , 2018, 6, e5200.                   | 0.9 | 3         |
| 4516 | Contrasting gene flow at different spatial scales revealed by genotyping-by-sequencing in <i>Isocladus armatus</i> , a massively colour polymorphic New Zealand marine isopod. <i>PeerJ</i> , 2018, 6, e5462.  | 0.9 | 17        |
| 4517 | The effects of afforestation on soil bacterial communities in temperate grassland are modulated by soil chemical properties. <i>PeerJ</i> , 2019, 7, e6147.  | 0.9 | 14        |
| 4518 | Transcriptome profiling reveals the role of ZBTB38 knock-down in human neuroblastoma. <i>PeerJ</i> , 2019, 7, e6352.   | 0.9 | 7         |
| 4519 | Nucleotide variation and balancing selection at the <i>Ckma</i> gene in Atlantic cod: analysis with multiple merger coalescent models. <i>PeerJ</i> , 2015, 3, e786.   | 0.9 | 45        |
| 4520 | Highly diverse root endophyte bacterial community is driven by growth substrate and is plant genotype-independent in common bean ( <i>Phaseolus vulgaris</i> L.). <i>PeerJ</i> , 2020, 8, e9423.               | 0.9 | 10        |
| 4521 | Trans-species polymorphism at antimicrobial innate immunity cathelicidin genes of Atlantic cod and related species. <i>PeerJ</i> , 2015, 3, e976.  | 0.9 | 22        |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4522 | Expressed sequence tag analysis of <i>Meretrix lusoria</i> (Veneridae) in Korea. <i>Korean Journal of Malacology</i> , 2012, 28, 377-384.   | 0.1 | 1         |
| 4523 | Classification and Phylogenetic Studies of Cephalopods from four countries of South-East Asia. <i>Korean Journal of Malacology</i> , 2016, 32, 55-62.   | 0.1 | 2         |
| 4524 | Characterization of Expressed Genes Under Ozone Stress in Soybean. <i>Plant Breeding and Biotechnology</i> , 2013, 1, 270-276.  | 0.3 | 1         |
| 4525 | Screening, Gene Sequencing and Biosurfactant Production from <i>Pichia Fermentans</i> Isolated From Dairy Effluents. <i>IOSR Journal of Environmental Science, Toxicology and Food Technology</i> , 2013, 6, 04-13. | 0.1 | 1         |
| 4526 | Molecular Systematics of Tribe Physarieae (Brassicaceae) Based on Nuclear ITS, LUMINIDEPENDENS, and Chloroplast ndhF. <i>Systematic Botany</i> , 2021, 46, 611-627.   | 0.2 | 3         |
| 4527 | Characterization of microbial communities from rumen and large intestine of lactating creole goats grazing in arid plant communities. <i>Microbiology (United Kingdom)</i> , 2021, 167, .                           | 0.7 | 0         |
| 4528 | Direct genome-wide identification of G-quadruplex structures by whole-genome resequencing. <i>Nature Communications</i> , 2021, 12, 6014.   | 5.8 | 24        |
| 4529 | Comparative Transcriptome Sequencing of Taro Corm Development With a Focus on the Starch and Sucrose Metabolism Pathway. <i>Frontiers in Genetics</i> , 2021, 12, 771081.   | 1.1 | 5         |
| 4530 | Building Natural Product Libraries Using Quantitative Clade-Based and Chemical Clustering Strategies. <i>MSystems</i> , 2021, 6, e0064421.  | 1.7 | 3         |
| 4531 | Genomic Landscapes and Strategies for Sequencing the Human Genome. <i>Stadler Genetics Symposia Series</i> , 2000, , 1-17.  | 0.0 | 0         |
| 4533 | The Use of Sequence Analysis for Homozygote and Heterozygote Base Variation Discovery. <i>Principles and Practice</i> , 2002, , 183-210.  | 0.3 | 1         |
| 4534 | Gene Coding Variant in Cas1 Between the C57BL/6J and DBA/2J Inbred Mouse Strains: Linkage to a QTL for Ethanol-Induced Locomotor Activation. <i>Alcoholism: Clinical and Experimental Research</i> , 2002, 26, 1-7. | 1.4 | 1         |
| 4535 | Identification of genomic organisation, sequence variants and analysis of the role of the human dishevelled 1 gene in late onset Alzheimer's disease. <i>Molecular Psychiatry</i> , 2002, 7, 104-109.               | 4.1 | 9         |
| 4536 | SNP ANALYSIS AND PRESENTATION IN THE PHARMACOGENETICS OF MEMBRANE TRANSPORTERS PROJECT. , 2002, , .   |     | 2         |
| 4537 | Datenanalyse von Biochips: Von der Sequenz zum System. , 2003, , 360-387.   |     | 0         |
| 4538 | Designing meaningful measures of read length for data produced by DNA sequencers. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 2003, , 295-306.                                   | 1.0 | 1         |
| 4539 | Bioinformatik. <i>Springer-Lehrbuch</i> , 2003, , 143-212.  | 0.1 | 1         |
| 4540 | Bioinformatics, Genomics, and Antimicrobial Drug Discovery. , 2003, , 27-42.  |     | 0         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4541 | Methods and Utility of EST and Whole Genome Sequencing. , 0, , .   |     | 0         |
| 4542 | Nucleic Acid Analysis of Viral Vectors: A Contract Research Organization's Perspective. BioProcessing: Advances and Trends in Biological Product Development, 2004, 3, 47-51.  | 0.1 | 0         |
| 4543 | EMASGRID: An NBBnet Grid Initiative for a Bioinformatics and Computational Biology ServicesInfrastructure in Malaysia. Lecture Notes in Computer Science, 2005, , 117-124.   | 1.0 | 0         |
| 4544 | Computer-Aided DNA Base Calling from Forward and Reverse Electropherograms. Lecture Notes in Computer Science, 2005, , 1-13.   | 1.0 | 1         |
| 4545 | The GATO gene annotation tool for research laboratories. Brazilian Journal of Medical and Biological Research, 2005, 38, 1571-1574.  | 0.7 | 2         |
| 4546 | Localization of 5,105 Hanwoo (Korean Cattle) BAC Clones on Bovine Chromosomes by the Analysis of BAC End Sequences (BESs) Involving 21,024 Clones. Asian-Australasian Journal of Animal Sciences, 2007, 20, 1636-1650. | 2.4 | 0         |
| 4547 | Classification and characterization of human full-length cDNA clones that are difficult to sequence. Chem-Bio Informatics Journal, 2008, 8, 1-13.  | 0.1 | 0         |
| 4548 | Amniote Phylogenomics: Testing Evolutionary Hypotheses with BAC Library Scanning and Targeted Clone Analysis of Large-Scale DNA Sequences from Reptiles. Methods in Molecular Biology, 2008, 422, 91-117.              | 0.4 | 8         |
| 4549 | Gene/Protein Sequence Analysis. Springer Protocols, 2008, , 323-347.   | 0.1 | 0         |
| 4550 | Effect of Porcine Reproductive and Respiratory Syndrome Virus on Porcine Alveolar Macrophage Function as Determined Using Serial Analysis of Gene Expression (SAGE). Developments in Biologicals, 2008, 132, 169-174.  | 0.4 | 7         |
| 4553 | Combinatorial Algorithms for Structural Variation Detection in High Throughput Sequenced Genomes. Lecture Notes in Computer Science, 2009, , 218-219.  | 1.0 | 3         |
| 4554 | Fuzzy Genome Sequence Assembly for Single and Environmental Genomes. Studies in Fuzziness and Soft Computing, 2009, , 19-44.   | 0.6 | 0         |
| 4555 | Doomsday Book, Vol. II. The Open Systems Biology Journal, 2009, 2, 8-17.   | 0.7 | 0         |
| 4556 | Identification of 1,531 cSNPs from Full-length Enriched cDNA Libraries of the Korean Native Pig Using in Silico Analysis. Genomics and Informatics, 2009, 7, 65-84.  | 0.4 | 2         |
| 4557 | Filogenia de lulo, tomate de Ñrjol y sus parientes silvestres. Ciencia Tecnologia Agropecuaria, 2014, 10, 180-190.   | 0.3 | 3         |
| 4558 | PMSG: A FAST DNA FRAGMENT ASSEMBLER. , 2010, , .   |     | 0         |
| 4559 | Whole Genome Sequencing. , 2010, , 120-174.  |     | 1         |
| 4560 | ESTs and their Role in Functional Genomics. , 2010, , 104-119.   |     | 0         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4561 | Identification of Causal and/or Rare Genetic Variants for Complex Traits by Targeted Resequencing in Population-based Cohorts. <i>Genomics and Informatics</i> , 2010, 8, 131-137.   | 0.4 | 1         |
| 4563 | Methodology Adaptation of a low-cost medium-throughput genotyping system for ovine prion protein gene polymorphisms associated with scrapie. <i>Genetics and Molecular Research</i> , 2011, 10, 3180-3185.   | 0.3 | 0         |
| 4564 | The complete mitochondrial genome of the verongid sponge <i>Aplysina cauliformis</i> : implications for DNA barcoding in demosponges. , 2011, , 61-69.   |     | 1         |
| 4565 | EST Analysis Pipeline: Use of Distributed Computing Resources. <i>Methods in Molecular Biology</i> , 2011, 722, 103-120.   | 0.4 | 0         |
| 4566 | Accuracy Assessment of Consensus Sequence from Shotgun Sequencing. , 2011, , 3-30.   |     | 0         |
| 4567 | Gene expression profiles in adenosine-treated human mast cells. <i>African Journal of Biotechnology</i> , 2011, 10, .  | 0.3 | 1         |
| 4568 | Molecular Phylogenetic study of <i>Acila divaricata vigila</i> based on the Partial Sequence of 16S rRNA Gene. <i>Korean Journal of Malacology</i> , 2011, 27, 395-400.  | 0.1 | 0         |
| 4569 | Whole Genome Sequencing in the Clinical Laboratory. , 2012, , 67-78.   |     | 0         |
| 4570 | Nested-PCR for the detection of <i>Mycoplasma hyopneumoniae</i> in bronchial alveolar swabs, frozen tissues and formalin-fixed paraffin-embedded swine lung samples: comparative evaluation with immunohistochemical findings and histological features. <i>Pesquisa Veterinaria Brasileira</i> , 2012, 32, 715-720. | 0.5 | 3         |
| 4571 | Emerging Concepts and Strategies for Genomics and Breeding. , 2013, , 241-283.   |     | 0         |
| 4572 | Genome analysis platform for Cephalopod studies and its prospects. <i>Hikaku Seiri Seikagaku(Comparative Physiology and Biochemistry)</i> , 2013, 30, 3-10.  | 0.0 | 0         |
| 4573 | Genome-wide SNP discovery in associating with human diseases phenotypes. <i>Sri Lanka Journal of Biomedical Information</i> , 2013, 3, 25.   | 0.1 | 2         |
| 4574 | Identification of Genes Expressed during Conidial Germination of the Pepper Anthracnose Pathogen, <i>Colletotrichum acutatum</i> . <i>Journal of Life Science</i> , 2013, 23, 8-14.  | 0.2 | 2         |
| 4576 | Molecular Data for the Sea Turtle Population in Brazil. <i>Dataset Papers in Science</i> , 2013, 2013, 1-7.  | 1.0 | 3         |
| 4578 | Identification, sequence characterization and expression analysis of the arginine kinase gene in response to laminarin challenge from the Oriental land snail, <i>Nesiohelix samarangae</i> . <i>Korean Journal of Malacology</i> , 2013, 29, 171-179.   | 0.1 | 2         |
| 4579 | A novel <i>Bacillus pumilus</i> -related strain from tropical landfarm soil is capable of rapid dibenzothiophene degradation and biodesulfurization. <i>BMC Microbiology</i> , 2014, 14, 257.  | 1.3 | 15        |
| 4580 | Cloning and expression of a novel cry gene that is potentially active against nematodes. <i>African Journal of Microbiology Research</i> , 2014, 8, 1017-1025.   | 0.4 | 1         |
| 4581 | <i>Campylobacter</i> Pathogenomics: Genomes and Beyond. , 0, , 160-195.  |     | 0         |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4584 | The Analyses of Global Gene Expression and Transcription Factor Regulation. <i>Translational Bioinformatics</i> , 2016, , 1-35.  | 0.0 | 2         |
| 4585 | Learning the Sequences Quality Control of Bioinformatics Analysis Method. , 2016, , .  |     | 0         |
| 4586 | Learning the Trimming Method of Sequence for Removing the Barcodes or Noise. , 0, , .  |     | 0         |
| 4587 | Learning the Quality Filter Method of Sequence by Quality Cut-off Value and Base Percent. , 0, , .   |     | 0         |
| 4588 | Learning the Sequence Reads Information of Bioinformatics Analysis Method. , 0, , .  |     | 0         |
| 4589 | Learning the Masking and Reverse Complement Method of the Sequence Reads. , 0, , .   |     | 0         |
| 4590 | Learning the Base Sequence Quality and Content of Bioinformatics Analysis Method. , 2016, , .  |     | 0         |
| 4591 | Learning the Comparing and Converting Method of Sequence Phred Quality Score. , 2016, , .  |     | 1         |
| 4594 | DNA Sequencing for Clinical and Public Health Virology: Some Assembly Required. , 0, , 173-199.  |     | 0         |
| 4596 | A Mitochondrial Cytochrome Oxidase I gene based identification of <i>Corbicula</i> ssp. commercially available in South Korea. <i>Korean Journal of Malacology</i> , 2016, 32, 127-131.                | 0.1 | 1         |
| 4599 | Use of MicroRNAs to Screen for Colon Cancer. , 2017, 1, 045-074.   |     | 1         |
| 4600 | Molecular analysis of endotracheal tube biofilms and tracheal aspirates in the pediatric intensive care unit. <i>Advances in Pediatric Research</i> , 2017, 4, .                                       | 2.0 | 1         |
| 4601 | Approaches to in silico analysis of microbiome biodiversity metrics of radionuclide contaminated soils. <i>Bioresursi Prirodokoristuvannâ</i> , 2017, 9, 10-16.  | 0.1 | 0         |
| 4603 | A new species of <i>Eisothistos</i> (Isopoda, Cymothoidea) and first molecular data on six species of Anthuroidea from the Peninsular Malaysia. <i>Zoosystematics and Evolution</i> , 2018, 94, 73-81. | 0.4 | 4         |
| 4604 | PASA: Identifying More Credible Structural Variants of Hedou12. <i>Lecture Notes in Computer Science</i> , 2018, , 553-558.  | 1.0 | 0         |
| 4605 | Big Data Analysis Techniques for Visualization of Genomics in Medicinal Plants. <i>Advances in Data Mining and Database Management Book Series</i> , 2018, , 749-781.                                  | 0.4 | 0         |
| 4611 | Big Data Analysis Techniques for Visualization of Genomics in Medicinal Plants. , 2019, , 804-837.   |     | 0         |
| 4612 | Guidelines for Bioinformatics and the Statistical Analysis of Omic Data. , 2019, , 45-75.  |     | 0         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4613 | Complete Genome Sequence of White Spot Syndrome Virus Isolated from Indian White Prawn ( <i>Penaeus monodon</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 7  | 0.3 | 2         |
| 4616 | Molecular study on <i>Senecio fontanicola</i> ( <i>S. doria</i> group, <i>Asteraceae</i> ) and its conservation status. Hacquetia, 2019, 18, 87-95.  | 0.2 | 1         |
| 4620 | First DNA barcode for the enigmatic <i>Leiobunum</i> sp. A (Opiliones). , 2019, 18, 94.  |     | 2         |
| 4621 | Role of Bioinformatics in Molecular Medicine. , 2020, , 55-68.   |     | 0         |
| 4622 | Quantitative Trait Locus Analysis in Avocado: The Challenge of a Slow-maturing Horticultural Tree Crop. Journal of the American Society for Horticultural Science, 2019, 144, 352-362.   | 0.5 | 4         |
| 4623 | Next-Generation Sequencing. , 2020, , 25-40.   |     | 0         |
| 4627 | FIVE DIATOM SPECIES IDENTIFIED BY USING POTENTIAL APPLICATION OF NEXT GENERATION DNA SEQUENCING. Bulletin of the Iraq Natural History Museum, 2020, 16, 39-61.   | 0.1 | 1         |
| 4632 | Bioinformatics Pre-Processing of Microbiome Data with An Application to Metagenomic Forensics. Frontiers in Probability and the Statistical Sciences, 2021, , 45-78.   | 0.1 | 1         |
| 4633 | Denoising Methods for Inferring Microbiome Community Content and Abundance. Frontiers in Probability and the Statistical Sciences, 2021, , 3-25.   | 0.1 | 1         |
| 4634 | Sequencing the Rice Genome: Gateway to Agricultural Development. , 2020, , 109-157.  |     | 1         |
| 4638 | Root growth in tomato seedlings in response to bacterial inoculation <i>Serratia</i> sp.. Research, Society and Development, 2020, 9, e89973634.   | 0.0 | 2         |
| 4639 | Discovery of Missing Proteins from an Aneuploidy Cell Line Using a Proteogenomic Approach. Journal of Proteome Research, 2021, 20, 5329-5339.  | 1.8 | 2         |
| 4640 | Analytical and clinical validation of an RNA sequencing-based assay for quantitative, accurate evaluation of a molecular signature response classifier in rheumatoid arthritis. Expert Review of Molecular Diagnostics, 2021, 21, 1235-1243. | 1.5 | 4         |
| 4641 | Physicochemical and Biotic Changes and the Phylogenetic Evenness of Microbial Community in Soil Subjected to Phytoreclamation. Microbial Ecology, 2022, 84, 1182-1194.   | 1.4 | 4         |
| 4642 | The transcriptome of <i>Balamuthia mandrillaris</i> trophozoites for structure-guided drug design. Scientific Reports, 2021, 11, 21664.  | 1.6 | 7         |
| 4643 | An Essay on Individual Sequence Variation in Expressed Sequence Tags(ESTs). , 2002, , 83-94.   |     | 0         |
| 4645 | Whole Genome Sequencing: Methodology and Progress in Cereals. , 2004, , 385-423.   |     | 0         |
| 4647 | Sequencing the Human Genome: A Historical Perspective on Challenges for Systems Integration. , 2006, , 365-399.  |     | 0         |



| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4671 | Molecular Detection of Tick-Borne Agents in Cats from Southeastern and Northern Brazil. <i>Pathogens</i> , 2022, 11, 106.  | 1.2 | 3         |
| 4672 | Transcriptomic Profile of Canine DH82 Macrophages Infected by <i>Leishmania infantum</i> Promastigotes with Different Virulence Behavior. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1466.   | 1.8 | 4         |
| 4673 | ImmunoDataAnalyzer: a bioinformatics pipeline for processing barcoded and UMI tagged immunological NGS data. <i>BMC Bioinformatics</i> , 2022, 23, 21.   | 1.2 | 0         |
| 4675 | Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.  | 6.0 | 132       |
| 4676 | Antigenicity and adhesiveness of a <i>Plasmodium vivax</i> VIR-E protein from Brazilian isolates. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2022, 116, e210227.  | 0.8 | 5         |
| 4677 | Effect of Antimicrobial Prophylaxis on <i>Corynebacterium bovis</i> Infection and the Skin Microbiome of Immunodeficient Mice. <i>Comparative Medicine</i> , 2022, 72, 78-89.  | 0.4 | 7         |
| 4679 | Analysis of Novel Variants Associated with Three Human Ovarian Cancer Cell Lines. <i>Current Bioinformatics</i> , 2022, 17, 380-392.   | 0.7 | 1         |
| 4680 | Meta-Analysis of Common and Differential Transcriptomic Responses to Biotic and Abiotic Stresses in <i>Arabidopsis thaliana</i> . <i>Plants</i> , 2022, 11, 502.   | 1.6 | 8         |
| 4681 | Differential Selection on Caste-Associated Genes in a Subterranean Termite. <i>Insects</i> , 2022, 13, 224.  | 1.0 | 2         |
| 4682 | Chromosome-scale assembly of the highly heterozygous genome of red clover ( <i>Trifolium pratense</i> L.), an allogamous forage crop species. <i>GigaByte</i> , 0, 2022, 1-13.   | 0.0 | 6         |
| 4683 | Mapping Quantitative Trait Loci for Lettuce Resistance to <i>Verticillium dahliae</i> Race 3, Plant Development, and Leaf Color Using an Ultra-High-Density Bin Map Constructed from F <sub>2</sub> Progeny. <i>PhytoFrontiers</i> , 2022, 2, 257-267. | 0.8 | 3         |
| 4684 | Molecular investigation of haemotropic mycoplasmas and <i>Coxiella burnetii</i> in free-living <i>Xenarthra</i> mammals from Brazil, with evidence of new haemoplasma species. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .                | 1.3 | 8         |
| 4685 | Transcriptome Analysis Revealed the Molecular Response Mechanism of Non-heading Chinese Cabbage to Iron Deficiency Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 848424.   | 1.7 | 5         |
| 4686 | Identification of microRNAs associated with human fragile X syndrome using next-generation sequencing. <i>Scientific Reports</i> , 2022, 12, 5011.   | 1.6 | 3         |
| 4687 | Filarids (Spirurida: Onchocercidae) in wild carnivores and domestic dogs from the Brazilian Atlantic forest. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010213.   | 1.3 | 4         |
| 4690 | An ancient, Antarctic-specific species complex: large divergences between multiple Antarctic lineages of the tardigrade genus <i>Mesobiotus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 170, 107429.                                    | 1.2 | 13        |
| 4692 | Quality Control Metrics at Different Stages of Genomic Assembly in the Parallel Sequencing Using the NanoFor SPS. , 2021, , .  |     | 0         |
| 4693 | A Novel <i>PAX3</i> Variant in a Chinese Pedigree with Nonsyndromic Cleft Lip With or Without Palate. <i>Genetic Testing and Molecular Biomarkers</i> , 2021, 25, 749-756.   | 0.3 | 3         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4694 | Determination of the Maximum Length of DNA in a Polymer Based on Linear Poly(N,N-Dimethylacrylamide) Decoded with an Accuracy of 99% by Capillary Gel Electrophoresis with Laser-Induced Fluorescence. <i>Journal of Analytical Chemistry</i> , 2021, 76, 1408-1413. | 0.4 | 0         |
| 4696 | Development of a targeted gene panel for the diagnosis of Gorlin syndrome. <i>International Journal of Oral and Maxillofacial Surgery</i> , 2022, 51, 1431-1444.   | 0.7 | 4         |
| 4697 | Impact of SARS-CoV-2 Gamma lineage introduction and COVID-19 vaccination on the epidemiological landscape of a Brazilian city. <i>Communications Medicine</i> , 2022, 2, .   | 1.9 | 32        |
| 4698 | Microbiota Associated With Cholesteatoma Tissue in Chronic Suppurative Otitis Media. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 746428.   | 1.8 | 3         |
| 4699 | Genomics and the Use of Genomic Tools to Study Pathogenic Bacteria. , 0, , 78-114.   |     | 0         |
| 4796 | Sequencing the Genome. , 0, , 475-488.   |     | 2         |
| 4797 | Antiviral Strategies Against SARS-CoV-2: A Systems Biology Approach. <i>Methods in Molecular Biology</i> , 2022, 2452, 317-351.  | 0.4 | 1         |
| 4798 | Identification of Yeast and Mould Isolated from murcha in Nepal for Rice Wine Production. <i>Brazilian Archives of Biology and Technology</i> , 0, 65, .   | 0.5 | 3         |
| 4799 | Novel MicroRNA-Regulated Transcript Networks Are Associated with Chemotherapy Response in Ovarian Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4875.   | 1.8 | 2         |
| 4800 | Mitochondrial DNA Consensus Calling and Quality Filtering for Constructing Ancient Human Mitogenomes: Comparison of Two Widely Applied Methods. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4651.   | 1.8 | 0         |
| 4801 | Identification of differential hypothalamic DNA methylation and gene expression associated with sexual partner preferences in rams. <i>PLoS ONE</i> , 2022, 17, e0263319.  | 1.1 | 3         |
| 4802 | A mutation increases the specificity to plant compounds in an insect chemosensory protein. <i>Journal of Molecular Graphics and Modelling</i> , 2022, 114, 108191.   | 1.3 | 0         |
| 4803 | A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, .  |     | 4         |
| 4805 | Obtaining DNA Samples from Sensitive and Endangered Bird Species: A Comparison of Saliva and Blood Samples. <i>Ardeola</i> , 2022, 69, .   | 0.4 | 2         |
| 4806 | Positive Selection and Biochemical Changes Contribute to Adaptive Evolution of Gstd1 Protein in Cactophilic <i>Drosophila</i> Species. <i>SSRN Electronic Journal</i> , 0, , .   | 0.4 | 0         |
| 4807 | <i>mebipred</i>: identifying metal-binding potential in protein sequence. <i>Bioinformatics</i> , 2022, 38, 3532-3540.   | 1.8 | 15        |
| 4808 | Different DNA Sequencing Using DNA Graphs: A Study. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 5414.  | 1.3 | 3         |
| 4812 | MycoSNP: A Portable Workflow for Performing Whole-Genome Sequencing Analysis of <i>Candida auris</i> . <i>Methods in Molecular Biology</i> , 2022, , 215-228.  | 0.4 | 13        |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4813 | Sequences to Differences in Gene Expression: Analysis of RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2022, , 279-318.  | 0.4 | 2         |
| 4814 | Molecular detection of vector-borne agents in wild boars ( <i>Sus scrofa</i> ) and associated ticks from Brazil, with evidence of putative new genotypes of <i>Ehrlichia</i> , <i>Anaplasma</i> , and haemoplasmas. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .       | 1.3 | 6         |
| 4815 | Genetic subtyping and phylogenetic analysis of HA and NA from avian influenza virus in wild birds from Peru reveals unique features among circulating strains in America. <i>PLoS ONE</i> , 2022, 17, e0268957.  | 1.1 | 3         |
| 4816 | Combined Oral Contraceptive Treatment Does Not Alter the Gut Microbiome but Affects Amino Acid Metabolism in Sera of Obese Girls With Polycystic Ovary Syndrome. <i>Frontiers in Physiology</i> , 0, 13, .   | 1.3 | 2         |
| 4817 | Shepherd: accurate clustering for correcting DNA barcode errors. <i>Bioinformatics</i> , 2022, 38, 3710-3716.  | 1.8 | 2         |
| 4819 | Sub-5 nm nanogap electrodes towards single-molecular biosensing. <i>Biosensors and Bioelectronics</i> , 2022, 213, 114486.   | 5.3 | 8         |
| 4820 | Integrative taxonomy increases biodiversity knowledge of Gusana (Platyhelminthes, Tricladida,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50   | 0.5 | 2         |
| 4822 | Different Swine Production Systems Can Shape Slurry Resistome at Mechanism and Class Levels Based on Swine Manure Evaluation. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .   | 1.8 | 0         |
| 4823 | Complete Chloroplast Genome of an Endangered Species <i>Quercus litseoides</i> , and Its Comparative, Evolutionary, and Phylogenetic Study with Other <i>Quercus</i> Section <i>Cyclobalanopsis</i> Species. <i>Genes</i> , 2022, 13, 1184.  | 1.0 | 11        |
| 4824 | Traits along the leaf economics spectrum are associated with communities of foliar endophytic symbionts. <i>Frontiers in Microbiology</i> , 0, 13, .   | 1.5 | 5         |
| 4828 | Species-specific chromatin landscape determines how transposable elements shape genome evolution. <i>ELife</i> , 0, 11, .  | 2.8 | 9         |
| 4829 | Systematic revision and total evidence phylogenetic analysis of the Andean family <i>Metasarcidae</i> Kury, 1994 (Opiliones: Laniatores), with description of two new genera and twenty new species. <i>Arthropod Systematics and Phylogeny</i> , 0, 80, 309-388.                  | 5.5 | 0         |
| 4830 | First Report of <i>Bartonella</i> spp. in Marsupials from Brazil, with a Description of <i>Bartonella harrusi</i> sp. nov. and a New Proposal for the Taxonomic Reclassification of Species of the Genus <i>Bartonella</i> . <i>Microorganisms</i> , 2022, 10, 1609.               | 1.6 | 12        |
| 4831 | Complex Evolutionary History of the South American Fox Genus <i>Lycalopex</i> (Mammalia, Carnivora,) Tj ETQq1 1 0.784314 rgBT /Overlock 0.7 5  | 0.7 | 5         |
| 4832 | Detection of <i>Fur</i> , <i>AmoA</i> and <i>pvcAB</i> genes in <i>Aeromonas hydrophila</i> isolated from aquatic organisms and impact on bacterial growth under different iron concentrations. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2022, 74, 671-676. | 0.1 | 1         |
| 4833 | Molecular evidence for stimulation of methane oxidation in Amazonian floodplains by ammonia-oxidizing communities. <i>Frontiers in Microbiology</i> , 0, 13, .   | 1.5 | 1         |
| 4834 | Longitudinal Reduction in Diversity of Maternal Gut Microbiota During Pregnancy Is Observed in Multiple Low-Resource Settings: Results From the Women First Trial. <i>Frontiers in Microbiology</i> , 0, 13, .   | 1.5 | 4         |
| 4835 | Transcriptome Meta-Analysis Identifies Candidate Hub Genes and Pathways of Pathogen Stress Responses in <i>Arabidopsis thaliana</i> . <i>Biology</i> , 2022, 11, 1155.   | 1.3 | 3         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4836 | Novel Ehrlichia and Hepatozoon genotypes in white-eared opossums ( <i>Didelphis albiventris</i> ) and associated ticks from Brazil. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 102022.   | 1.1 | 5         |
| 4838 | Changes in gut microbiome correlate with intestinal barrier dysfunction and inflammation following a 3-day ethanol exposure in aged mice. <i>Alcohol</i> , 2023, 107, 136-143.   | 0.8 | 3         |
| 4839 | Effects of 4-n-nonylphenol in liver of male and female viviparous fish ( <i>Poecilia vivipara</i> ). <i>Chemosphere</i> , 2022, 308, 136565.   | 4.2 | 0         |
| 4840 | Translation of DNA Sequence to Chemical Structure in DNA-Encoded Libraries. <i>Methods in Molecular Biology</i> , 2022, , 187-194.   | 0.4 | 0         |
| 4841 | Construction of a massive genetic resource by transcriptome sequencing and genetic characterization of <i>Megasyllis nipponica</i> (Annelida: Syllidae). <i>Genes and Genetic Systems</i> , 2022, 97, 153-166.                               | 0.2 | 1         |
| 4842 | Reusing a prepaid health plan's fecal immunochemical tests for microbiome associations with colorectal adenoma. <i>Scientific Reports</i> , 2022, 12, .  | 1.6 | 0         |
| 4843 | Evolution of the Gut Microbiome in HIV-Exposed Uninfected and Unexposed Infants during the First Year of Life. <i>MBio</i> , 2022, 13, .   | 1.8 | 9         |
| 4844 | Sensitive and reproducible cell-free methylome quantification with synthetic spike-in controls. <i>Cell Reports Methods</i> , 2022, 2, 100294.   | 1.4 | 2         |
| 4845 | Comparative Transcriptome Analysis and Genetic Methods Revealed the Biocontrol Mechanism of <i>Paenibacillus polymyxa</i> NSY50 against Tomato Fusarium Wilt. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10907.          | 1.8 | 5         |
| 4846 | Purifying selection enduringly acts on the sequence evolution of highly expressed proteins in <i>Escherichia coli</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .  | 0.8 | 1         |
| 4847 | Two novel mutations in <i>ALDH18A1</i> and <i>SPG11</i> gene found by whole-exome sequencing in spastic paraplegia disease patients in Iran. <i>Genomics and Informatics</i> , 2022, 20, e30.  | 0.4 | 0         |
| 4848 | Construction of a trio-based structural variation panel utilizing activated T lymphocytes and long-read sequencing technology. <i>Communications Biology</i> , 2022, 5, .  | 2.0 | 4         |
| 4849 | The role of FXR and TGR5 in reversing and preventing progression of Western diet-induced hepatic steatosis, inflammation, and fibrosis in mice. <i>Journal of Biological Chemistry</i> , 2022, 298, 102530.                                  | 1.6 | 12        |
| 4850 | Environmental DNA-based profiling of benthic bacterial and eukaryote communities along a crude oil spill gradient in a coral reef in the Persian Gulf. <i>Marine Pollution Bulletin</i> , 2022, 184, 114143.                                 | 2.3 | 4         |
| 4851 | Identification of Gut Microbiota Affecting Fiber Digestibility in Pigs. <i>Current Issues in Molecular Biology</i> , 2022, 44, 4557-4569.  | 1.0 | 6         |
| 4852 | Phylogenetic relationships, hybridization events, and drivers of diversification of East Asian wild grapes as revealed by phylogenomic analyses. <i>Journal of Systematics and Evolution</i> , 2023, 61, 273-283.                            | 1.6 | 6         |
| 4854 | <i>Acrogenospora terricola</i> sp. nov., a fungal species associated with seeds of pioneer trees in the soil seed bank of a lowland forest in Panama. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, . | 0.8 | 1         |
| 4855 | High-Quality Draft Genome Sequence of <i>Fischerella thermalis</i> JSC-11, a Siderophilic Cyanobacterium with Bioremediation Potential. <i>Microbiology Resource Announcements</i> , 0, , .  | 0.3 | 0         |

| #    | ARTICLE  | IF  | CITATIONS |
|------|--|-----|-----------|
| 4856 | De Novo Transcriptome Dataset Generation of the Swamp Buffalo Brain and Non-Brain Tissues. <i>BioMed Research International</i> , 2022, 2022, 1-15.  | 0.9 | 1         |
| 4857 | <i>Phlebiodontia rajchenbergii</i> gen. et sp. nov. (Polyporales, Meruliaceae) from Brazilian Atlantic Forest based on morphological and molecular evidence. <i>Lilloa</i> , 0, , 305-330.   | 0.1 | 0         |
| 4858 | Complete Genome Sequence of <i>Lacticaseibacillus rhamnosus</i> DM065, Isolated from the Human Oral Cavity. <i>Microbiology Resource Announcements</i> , 0, , .  | 0.3 | 0         |
| 4859 | Multi-locus Sequencing Typing of <i>Bartonella henselae</i> isolates reveals coinfection with different variants in domestic cats from Midwestern Brazil. <i>Acta Tropica</i> , 2023, 237, 106742.   | 0.9 | 8         |
| 4860 | Complete Genome Sequence of Hydrogen Peroxide-Producing <i>Limosilactobacillus fermentum</i> DM072 Isolated from the Human Oral Cavity. <i>Microbiology Resource Announcements</i> , 2022, 11, .   | 0.3 | 1         |
| 4861 | The fifth family of the true crickets (Insecta: Orthoptera: Ensifera: Grylloidea), Oecanthidae defin. nov.: phylogenetic relationships and divergence times. <i>Zoological Journal of the Linnean Society</i> , 2023, 197, 1034-1077.        | 1.0 | 3         |
| 4862 | Biogeographical events, not cospeciation, might be the main drivers in the historical association between <i>Noctiliostrebla</i> species (Streblidae) and their bulldog bat hosts. <i>Biological Journal of the Linnean Society</i> , 0, , . | 0.7 | 0         |
| 4863 | Emergence of sulphonamide resistance in azithromycin-resistant pediatric strains of <i>Salmonella</i> Typhi and Paratyphi A: A genomics insight. <i>Gene</i> , 2023, 851, 146995.  | 1.0 | 5         |
| 4864 | CAPG: comprehensive allopolyploid genotyper. <i>Bioinformatics</i> , 2023, 39, .   | 1.8 | 2         |
| 4865 | Polymorphisms in Pattern Recognition Receptor Genes Are Associated with Respiratory Disease Severity in Pig Farms. <i>Animals</i> , 2022, 12, 3163.  | 1.0 | 1         |
| 4866 | Plasmids Harboring a Tandem Duplicate of <i>bla</i> <sub>VIM-24</sub> in Carbapenem-Resistant ST1816 <i>Pseudomonas aeruginosa</i> in Japan. <i>Microbial Drug Resistance</i> , 0, , .   | 0.9 | 0         |
| 4867 | The discovery of new Chilean taxa revolutionizes the systematics of Geoplaninae Neotropical land planarians (Platyhelminthes: Tricladida). <i>Zoological Journal of the Linnean Society</i> , 2023, 197, 837-898.                            | 1.0 | 2         |
| 4868 | ddRADseq-mediated detection of genetic variants in sugarcane. <i>Plant Molecular Biology</i> , 0, , .  | 2.0 | 2         |
| 4869 | Defining <i>Paenibacillus azoreducens</i> (P8) and <i>Acetobacter pasteurianus</i> (UMCC 2951) strains performances in producing acetic acid. <i>Frontiers in Microbiology</i> , 0, 13, .  | 1.5 | 1         |
| 4870 | Metagenome-assembled genome extraction and analysis from microbiomes using KBase. <i>Nature Protocols</i> , 2023, 18, 208-238.   | 5.5 | 7         |
| 4871 | Interrogating the Human Diplome: Computational Methods, Emerging Applications, and Challenges. <i>Methods in Molecular Biology</i> , 2023, , 1-30.   | 0.4 | 1         |
| 4872 | A Computational Pipeline for Predicting Cancer Neoepitopes. <i>Methods in Molecular Biology</i> , 2023, , 475-488.   | 0.4 | 1         |
| 4873 | Study of an RNA-Focused DNA-Encoded Library Informs Design of a Degradable r(CUG) Repeat Expansion. <i>Journal of the American Chemical Society</i> , 2022, 144, 21972-21979.  | 6.6 | 9         |



| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4874 | Temporal progress of gene expression analysis with RNA-Seq data: A review on the relationship between computational methods. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 86-98.   | 1.9 | 8         |
| 4875 | Alteration of oral microbiome composition in children living with pesticide-exposed farm workers. <i>International Journal of Hygiene and Environmental Health</i> , 2023, 248, 114090.   | 2.1 | 0         |
| 4876 | Comparative transcriptomic assessment of the chemosensory receptor repertoire of <i>Drosophila suzukii</i> adult and larval olfactory organs. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101049.  | 0.4 | 6         |
| 4877 | Multi-Locus Sequencing Reveals Putative Novel Anaplasmataceae Agents, <i>Candidatus Ehrlichia dumleri</i> ™ and <i>Anaplasma</i> sp., in Ring-Tailed Coatis ( <i>Carnivora: Nasua nasua</i> ) from Urban Forested Fragments at Midwestern Brazil. <i>Microorganisms</i> , 2022, 10, 2379. | 1.6 | 5         |
| 4878 | Identifying high-confidence variants in human cytomegalovirus genomes sequenced from clinical samples. <i>Virus Evolution</i> , 0, , .  | 2.2 | 0         |
| 4879 | The complete mitochondrial genome of <i>Aoria nigripes</i> (Coleoptera, Eumolpidae, Eumolpinae) and its phylogenetic status. <i>Biodiversity Data Journal</i> , 0, 10, .  | 0.4 | 0         |
| 4880 | Communities of endophytic fungi in a Puerto Rican rainforest vary along a gradient of disturbance due to Hurricane Maria. <i>Ecology and Evolution</i> , 2022, 12, .  | 0.8 | 1         |
| 4881 | Genomic Characterization of hox Genes in Senegalese Sole ( <i>Solea senegalensis</i> , Kaup 1858): Clues to Evolutionary Path in Pleuronectiformes. <i>Animals</i> , 2022, 12, 3586.  | 1.0 | 0         |
| 4882 | Mucosal Microbiota Associated With Eosinophilic Esophagitis and Eosinophilic Gastritis. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2023, 76, 347-354.   | 0.9 | 3         |
| 4883 | Vaccination induces HIV broadly neutralizing antibody precursors in humans. <i>Science</i> , 2022, 378, .   | 6.0 | 71        |
| 4884 | UGDR: a generic pipeline to detect recombined regions in polyploid and complex hybrid yeast genomes. <i>BMC Bioinformatics</i> , 2022, 23, .  | 1.2 | 0         |
| 4885 | Population structure and genetic diversity characterization of soybean for seed longevity. <i>PLoS ONE</i> , 2022, 17, e0278631.  | 1.1 | 2         |
| 4886 | Three distinctive <i>Preussia</i> (Sporormiaceae) from photosynthetic stems of <i>Ephedra trifurca</i> (Ephedraceae, Gnetophyta) in southeastern Arizona, USA. <i>Plant and Fungal Systematics</i> , 2022, 67, 63-74.   | 0.7 | 0         |
| 4887 | Investigating geological records of tsunamis in Western Thailand with environmental DNA. <i>Marine Geology</i> , 2023, , 106989.  | 0.9 | 1         |
| 4888 | Accurate estimation of molecular counts from amplicon sequence data with unique molecular identifiers. <i>Bioinformatics</i> , 2023, 39, .  | 1.8 | 3         |
| 4890 | Antagonism of volatile organic compounds of the <i>Bacillus</i> sp. against <i>Fusarium kalimantanense</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2023, 39, .   | 1.7 | 8         |
| 4891 | LMAS: evaluating metagenomic short <i>de novo</i> assembly methods through defined communities. <i>GigaScience</i> , 2022, 12, .  | 3.3 | 3         |
| 4892 | Application of DNA Metabarcoding for Identifying the Diet of Asian Clam ( <i>Corbicula fluminea</i> , Müller.) <i>TJ ETQq1 1.0.784314 rgBT /Ove</i>   | 1.6 | 1         |

| #    | ARTICLE  | IF    | CITATIONS |
|------|--|-------|-----------|
| 4893 | Different gut microbiota in U.S. formula-fed infants consuming a meat vs. dairy-based complementary foods: A randomized controlled trial. <i>Frontiers in Nutrition</i> , 0, 9, .  | 1.6   | 1         |
| 4895 | Identification of a forkhead box protein transcriptional network induced in human neutrophils in response to inflammatory stimuli. <i>Frontiers in Immunology</i> , 0, 14, .   | 2.2   | 0         |
| 4896 | Epidemiology and Integrative Taxonomy of Helminths of Invasive Wild Boars, Brazil. <i>Pathogens</i> , 2023, 12, 175.   | 1.2   | 2         |
| 4897 | Development and validation of e-probes with MiFi <sup>®</sup> system for detection of <i>Ralstonia solanacearum</i> species complex in blueberries. <i>PhytoFrontiers</i> , 0, , .   | 0.8   | 1         |
| 4898 | Wild deer (Pudu puda) from Chile harbor a novel ecotype of <i>Anaplasma phagocytophilum</i> . <i>Parasites and Vectors</i> , 2023, 16, .   | 1.0   | 3         |
| 4899 | VLF: An R package for the analysis of very low frequency variants in DNA sequences. <i>Biodiversity Data Journal</i> , 0, 11, .  | 0.4   | 1         |
| 4900 | &lt;i>FLOWERING LOCUS T (FT) gene regulates short-day flowering in low latitude Xishuangbanna cucumber (<i>Cucumis sativus var. Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4972 d (<i>xishua   | 497.2 | 4972      |
| 4902 | Taxonomic insights and evolutionary history in East Asian terrestrial slugs of the genus <i>Meghimatium</i> . <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107730.  | 1.2   | 1         |
| 4903 | Turfgrass-dependent mycotrophic change enhances soil deterioration in dry, cold and high-alkali environments. <i>Journal of Applied Microbiology</i> , 2023, 134, .  | 1.4   | 0         |
| 4904 | Detection and identification of fungi in the lower airway of children with and without cystic fibrosis. <i>Frontiers in Microbiology</i> , 0, 14, .  | 1.5   | 2         |
| 4905 | Differential Expression Genes of the Head Kidney and Spleen in <i>Streptococcus iniae</i> -Infected East Asian Fourfinger Threadfin Fish ( <i>Eleutheronema tetradactylum</i> ). <i>International Journal of Molecular Sciences</i> , 2023, 24, 3832.                | 1.8   | 4         |
| 4906 | Telomere-to-telomere assembly of diploid chromosomes with Verkko. <i>Nature Biotechnology</i> , 2023, 41, 1474-1482.   | 9.4   | 76        |
| 4907 | Highly accurate genome assembly of an improved high-yielding silkworm strain, Nichi01. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .   | 0.8   | 2         |
| 4910 | An Efficient Method to Prepare Barcoded cDNA Libraries from Plant Callus for Long-Read Sequencing. <i>Methods and Protocols</i> , 2023, 6, 31.   | 0.9   | 0         |
| 4912 | Complete sequence verification of plasmid DNA using the Oxford Nanopore Technologies <sup>™</sup> MinION device. <i>BMC Bioinformatics</i> , 2023, 24, .   | 1.2   | 8         |
| 4913 | Deciphering the Mechanism of Tolerance to Apple Replant Disease Using a Genetic Mapping Approach in a Malling 9 Å— M. Å— robusta 5 Population Identifies SNP Markers Linked to Candidate Genes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6307. | 1.8   | 1         |
| 4915 | Improving and Going Beyond Reference Genomes. , 2023, , 255-326.   |       | 0         |
| 4916 | Sequencing of the Pituitary Transcriptome after GnRH Treatment Uncovers the Involvement of lncRNA-m23b/miR-23b-3p/CAMK2D in FSH Synthesis and Secretion. <i>Genes</i> , 2023, 14, 846.   | 1.0   | 0         |

| #    | ARTICLE   | IF  | CITATIONS |
|------|---|-----|-----------|
| 4917 | Hierarchical DNN with Heterogeneous Computing Enabled High-Performance DNA Sequencing. , 2022, , .  |     | 0         |
| 4919 | Amplicon Sequencing Minimal Information (AsqMI): Quality and Reporting Guidelines for Actionable Calls in Biodefense Applications. Journal of AOAC INTERNATIONAL, 0, , .  | 0.7 | 0         |
| 4920 | Effects of Extended Cage Component Sanitation Interval on the Microenvironment, Health, and Gastrointestinal Microbiome of Rats (<i>Rattus norvegicus</i>). Journal of the American Association for Laboratory Animal Science, 2023, 62, 212-221. | 0.6 | 1         |
| 4921 | Extracellular enzyme activity in the coastal upwelling system off Peru: a mesocosm experiment. Biogeosciences, 2023, 20, 1605-1619.   | 1.3 | 1         |
| 4922 | Monitoring of biofilm development and physico-chemical changes of floating microplastics at the air-water interface. Environmental Pollution, 2023, 322, 121157.  | 3.7 | 15        |
| 4924 | DNA and RNA Sequencing. , 2022, , 324-349.  |     | 0         |
| 4935 | Basic Data Processing in QIIME 2. , 2023, , 65-94.  |     | 0         |
| 4981 | Transcriptomic profilingâ€‘based identification of biomarkers of stem cells. , 2024, , 203-214.   |     | 0         |
| 4988 | PyroTRF-ID: A Bioinformatics Methodology for Profiling Microbiomes with T-RLFP and Amplicon Sequencing Data. Springer Theses, 2024, , 189-270.  | 0.0 | 0         |
| 4991 | MICROBIAL GENOMICS- the Changing Technological Landscape of Microbiology via NGS. , 2024, , 307-330.  |     | 0         |