

Song-Nian Hu

List of Publications by Year in descending order

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267
papers

18,932
citations

19636

61
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15249

126
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273
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docs citations

273
times ranked

25339
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. indica). <i>Science</i> , 2002, 296, 79-92. | 6.0 | 3,146 |
| 2 | The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38. | 2.6 | 808 |
| 3 | A Brief Review on the Mechanisms of miRNA Regulation. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 147-154. | 3.0 | 711 |
| 4 | Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. <i>Nucleic Acids Research</i> , 2016, 44, W236-W241. | 6.5 | 610 |
| 5 | The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63. | 13.7 | 603 |
| 6 | Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. <i>Nucleic Acids Research</i> , 2019, 47, W270-W275. | 6.5 | 564 |
| 7 | EvoView, an online tool for visualizing, annotating and managing phylogenetic trees. <i>Nucleic Acids Research</i> , 2012, 40, W569-W572. | 6.5 | 400 |
| 8 | A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722. | 13.7 | 391 |
| 9 | Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <i>Salsola miltiorrhiza</i> and tanshinone biosynthesis. <i>Plant Journal</i> , 2015, 82, 951-961. | 2.8 | 337 |
| 10 | The rubber tree genome reveals new insights into rubber production and species adaptation. <i>Nature Plants</i> , 2016, 2, 16073. | 4.7 | 324 |
| 11 | On the nature of human housekeeping genes. <i>Trends in Genetics</i> , 2008, 24, 481-484. | 2.9 | 249 |
| 12 | Genome sequence of the date palm <i>Phoenix dactylifera</i> L. <i>Nature Communications</i> , 2013, 4, 2274. | 5.8 | 248 |
| 13 | Long Non-coding RNAs and Their Biological Roles in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 137-147. | 3.0 | 231 |
| 14 | Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110. | 5.8 | 230 |
| 15 | Analysis of gut microbiota diversity and auxiliary diagnosis as a biomarker in patients with schizophrenia: A cross-sectional study. <i>Schizophrenia Research</i> , 2018, 197, 470-477. | 1.1 | 222 |
| 16 | Oral Microbiota Community Dynamics Associated With Oral Squamous Cell Carcinoma Staging. <i>Frontiers in Microbiology</i> , 2018, 9, 862. | 1.5 | 211 |
| 17 | A Complete Sequence of the <i>T. tengcongensis</i> Genome. <i>Genome Research</i> , 2002, 12, 689-700. | 2.4 | 209 |
| 18 | Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1375-1386. | 1.4 | 206 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | Comparative transcriptome analysis of transporters, phytohormone and lipid metabolism pathways in response to arsenic stress in rice (<i>Oryza sativa</i>). <i>New Phytologist</i> , 2012, 195, 97-112. | 3.5 | 193 |
| 21 | A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. <i>Genomics</i> , 2010, 96, 259-265. | 1.3 | 184 |
| 22 | Arginine methylation mediated by the <i>Arabidopsis</i> homolog of PRMT5 is essential for proper pre-mRNA splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19114-19119. | 3.3 | 174 |
| 23 | Plasmid-mediated quinolone resistance determinants qnr and aac(6')-Ib-cr in extended-spectrum β -lactamase-producing <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 61, 1003-1006. | 1.3 | 169 |
| 24 | Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002869. | 1.5 | 167 |
| 25 | A Comparison of Rice Chloroplast Genomes. <i>Plant Physiology</i> , 2004, 135, 412-420. | 2.3 | 142 |
| 26 | Evolution and pathogenesis of <i>Staphylococcus aureus</i> : lessons learned from genotyping and comparative genomics. <i>FEMS Microbiology Reviews</i> , 2008, 32, 23-37. | 3.9 | 133 |
| 27 | Genetic Alterations in Esophageal Tissues From Squamous Dysplasia to Carcinoma. <i>Gastroenterology</i> , 2017, 153, 166-177. | 0.6 | 130 |
| 28 | The Silkworm (<i>Bombyx mori</i>) microRNAs and Their Expressions in Multiple Developmental Stages. <i>PLoS ONE</i> , 2008, 3, e2997. | 1.1 | 130 |
| 29 | Transcriptome-wide N ⁶ -methyladenosine profiling of rice callus and leaf reveals the presence of tissue-specific competitors involved in selective mRNA modification. <i>RNA Biology</i> , 2014, 11, 1180-1188. | 1.5 | 126 |
| 30 | Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6026-E6035. | 3.3 | 126 |
| 31 | 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 |
| 32 | On the molecular mechanism of GC content variation among eubacterial genomes. <i>Biology Direct</i> , 2012, 7, 2. | 1.9 | 121 |
| 33 | The apricot (<i>Prunus armeniaca</i> L.) genome elucidates Rosaceae evolution and beta-carotenoid synthesis. <i>Horticulture Research</i> , 2019, 6, 128. | 2.9 | 119 |
| 34 | Rapid growth of a hepatocellular carcinoma and the driving mutations revealed by cell-population genetic analysis of whole-genome data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12042-12047. | 3.3 | 117 |
| 35 | Genomic Analysis of the Multidrug-Resistant <i>Acinetobacter baumannii</i> Strain MDR-ZJ06 Widely Spread in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4506-4512. | 1.4 | 116 |
| 36 | Rice Expression Database (RED): An integrated RNA-Seq-derived gene expression database for rice. <i>Journal of Genetics and Genomics</i> , 2017, 44, 235-241. | 1.7 | 114 |

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|----|--|-----|-----------|
| 37 | A Complete Sequence and Transcriptomic Analyses of Date Palm (<i>Phoenix dactylifera</i> L.) Mitochondrial Genome. PLoS ONE, 2012, 7, e37164. | 1.1 | 106 |
| 38 | Energy efficiency trade-offs drive nucleotide usage in transcribed regions. Nature Communications, 2016, 7, 11334. | 5.8 | 104 |
| 39 | The genome evolution and domestication of tropical fruit mango. Genome Biology, 2020, 21, 60. | 3.8 | 104 |
| 40 | The Rice Mitochondrial Genomes and Their Variations. Plant Physiology, 2006, 140, 401-410. | 2.3 | 103 |
| 41 | A Novel OxyR Sensor and Regulator of Hydrogen Peroxide Stress with One Cysteine Residue in <i>Deinococcus radiodurans</i> . PLoS ONE, 2008, 3, e1602. | 1.1 | 98 |
| 42 | Metagenomic Insights into the Fibrolytic Microbiome in Yak Rumen. PLoS ONE, 2012, 7, e40430. | 1.1 | 98 |
| 43 | A novel antisense long noncoding RNA, <i>TWISTED LEAF</i> , maintains leaf blade flattening by regulating its associated sense MYB gene in rice. New Phytologist, 2018, 218, 774-788. | 3.5 | 96 |
| 44 | A Genome-wide Microsatellite Polymorphism Database for the Indica and Japonica Rice. DNA Research, 2007, 14, 37-45. | 1.5 | 94 |
| 45 | <i>Salmonella paratyphi</i> C: Genetic Divergence from <i>Salmonella choleraesuis</i> and Pathogenic Convergence with <i>Salmonella typhi</i> . PLoS ONE, 2009, 4, e4510. | 1.1 | 94 |
| 46 | Comparative genome analysis of programmed DNA elimination in nematodes. Genome Research, 2017, 27, 2001-2014. | 2.4 | 94 |
| 47 | PacBio full-length cDNA sequencing integrated with RNA-seq reads drastically improves the discovery of splicing transcripts in rice. Plant Journal, 2019, 97, 296-305. | 2.8 | 90 |
| 48 | De Novo Characterization of the Spleen Transcriptome of the Large Yellow Croaker (<i>Pseudosciaena</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 PLoS ONE, 2014, 9, e97471. | 1.1 | 89 |
| 49 | Marine Sediment Bacteria Harbor Antibiotic Resistance Genes Highly Similar to Those Found in Human Pathogens. Microbial Ecology, 2013, 65, 975-981. | 1.4 | 86 |
| 50 | Genome structure and evolution of <i>Antirrhinum majus</i> L. Nature Plants, 2019, 5, 174-183. | 4.7 | 85 |
| 51 | Complete Genome Sequence of <i>Lactobacillus casei</i> Zhang, a New Probiotic Strain Isolated from Traditional Homemade Koumiss in Inner Mongolia, China. Journal of Bacteriology, 2010, 192, 5268-5269. | 1.0 | 84 |
| 52 | Identification of differentially expressed genes in human lung squamous cell carcinoma using suppression subtractive hybridization. Cancer Letters, 2004, 212, 83-93. | 3.2 | 83 |
| 53 | Transcriptome comparison between honey bee queen- and worker-destined larvae. Insect Biochemistry and Molecular Biology, 2012, 42, 665-673. | 1.2 | 82 |
| 54 | Conserved Intramolecular Interactions Maintain Myosin Interacting-Heads Motifs Explaining Tarantula Muscle Super-Relaxed State Structural Basis. Journal of Molecular Biology, 2016, 428, 1142-1164. | 2.0 | 82 |

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|----|--|------|-----------|
| 55 | MVP: a microbe-phage interaction database. <i>Nucleic Acids Research</i> , 2018, 46, D700-D707. | 6.5 | 82 |
| 56 | The Complete Chloroplast and Mitochondrial Genome Sequences of <i>Boea hygrometrica</i> : Insights into the Evolution of Plant Organellar Genomes. <i>PLoS ONE</i> , 2012, 7, e30531. | 1.1 | 79 |
| 57 | Complete Genome Sequence of the Metabolically Versatile Halophilic Archaeon <i>Haloferax mediterranei</i> , a Poly(3-Hydroxybutyrate-3-Hydroxyvalerate) Producer. <i>Journal of Bacteriology</i> , 2012, 194, 4463-4464. | 1.0 | 75 |
| 58 | 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 |
| 59 | Ascarosides coordinate the dispersal of a plant-parasitic nematode with the metamorphosis of its vector beetle. <i>Nature Communications</i> , 2016, 7, 12341. | 5.8 | 69 |
| 60 | 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 |
| 61 | Pyrosequencing the <i>Bemisia tabaci</i> Transcriptome Reveals a Highly Diverse Bacterial Community and a Robust System for Insecticide Resistance. <i>PLoS ONE</i> , 2012, 7, e35181. | 1.1 | 67 |
| 62 | Fine-Tuning of MiR528 Accumulation Modulates Flowering Time in Rice. <i>Molecular Plant</i> , 2019, 12, 1103-1113. | 3.9 | 67 |
| 63 | Identification of microRNA in the protist <i>Trichomonas vaginalis</i> . <i>Genomics</i> , 2009, 93, 487-493. | 1.3 | 61 |
| 64 | A Critical Role for CLSP2 in the Modulation of Antifungal Immune Response in Mosquitoes. <i>PLoS Pathogens</i> , 2015, 11, e1004931. | 2.1 | 61 |
| 65 | The Complete Mitochondrial Genome of <i>Gossypium hirsutum</i> and Evolutionary Analysis of Higher Plant Mitochondrial Genomes. <i>PLoS ONE</i> , 2013, 8, e69476. | 1.1 | 58 |
| 66 | An efficient procedure for plant organellar genome assembly, based on whole genome data from the 454 GS FLX sequencing platform. <i>Plant Methods</i> , 2011, 7, 38. | 1.9 | 56 |
| 67 | Biomonitoring for traditional herbal medicinal products using DNA metabarcoding and single molecule, real-time sequencing. <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 488-497. | 5.7 | 55 |
| 68 | Comparative Transcriptome Analysis of the Accessory Sex Gland and Testis from the Chinese Mitten Crab (<i>Eriocheir sinensis</i>). <i>PLoS ONE</i> , 2013, 8, e53915. | 1.1 | 54 |
| 69 | The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198. | 13.7 | 53 |
| 70 | Discovery of immune-related genes in Chinese mitten crab (<i>Eriocheir sinensis</i>) by expressed sequence tag analysis of haemocytes. <i>Aquaculture</i> , 2009, 287, 297-303. | 1.7 | 53 |
| 71 | Transcriptomic profiling reveals MEP pathway contributing to ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>BMC Genomics</i> , 2019, 20, 383. | 1.2 | 52 |
| 72 | wapRNA: a web-based application for the processing of RNA sequences. <i>Bioinformatics</i> , 2011, 27, 3076-3077. | 1.8 | 51 |

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|----|--|-----|-----------|
| 73 | ICG: a wiki-driven knowledgebase of internal control genes for RT-qPCR normalization. <i>Nucleic Acids Research</i> , 2018, 46, D121-D126. | 6.5 | 49 |
| 74 | Proteomic profiling of rice embryos from a hybrid rice cultivar and its parental lines. <i>Proteomics</i> , 2008, 8, 4808-4821. | 1.3 | 48 |
| 75 | De novo transcriptome analysis of <i>Medicago falcata</i> reveals novel insights about the mechanisms underlying abiotic stress-responsive pathway. <i>BMC Genomics</i> , 2015, 16, 818. | 1.2 | 48 |
| 76 | De Novo Sequencing and Transcriptome Analysis of <i>Pleurotus eryngii</i> subsp. <i>tuoliensis</i> (Bailinggu) Mycelia in Response to Cold Stimulation. <i>Molecules</i> , 2016, 21, 560. | 1.7 | 48 |
| 77 | 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 |
| 78 | 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 |
| 79 | Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 397-404. | 3.0 | 46 |
| 80 | Analysis of immune-relevant genes expressed in red sea bream (<i>Chrysophrys major</i>) spleen. <i>Aquaculture</i> , 2004, 240, 115-130. | 1.7 | 45 |
| 81 | The genome and transcriptome of a newly described psychrophilic archaeon, <i>Methanohalobium psychrophilum</i> , reveal its cold adaptive characteristics. <i>Environmental Microbiology Reports</i> , 2012, 4, 633-641. | 1.0 | 45 |
| 82 | Tung Tree (<i>Vernicia fordii</i> , Hemsl.) Genome and Transcriptome Sequencing Reveals Co-Ordinate Up-Regulation of Fatty Acid β -Oxidation and Triacylglycerol Biosynthesis Pathways During Eleostearic Acid Accumulation in Seeds. <i>Plant and Cell Physiology</i> , 2018, 59, 1990-2003. | 1.5 | 45 |
| 83 | Transcriptomic insight into the immune defenses in the ghost moth, <i>Hepialus xiaojinensis</i> , during an <i>Ophiocordyceps sinensis</i> fungal infection. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 64, 1-15. | 1.2 | 44 |
| 84 | Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. <i>Nature Communications</i> , 2016, 7, 12845. | 5.8 | 43 |
| 85 | 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 |
| 86 | How Do Variable Substitution Rates Influence K_a and K_s Calculations?. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 116-127. | 3.0 | 42 |
| 87 | Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <i>Science China Life Sciences</i> , 2013, 56, 1-12. | 2.3 | 42 |
| 88 | Seasonally variable intestinal metagenomes of the red palm weevil (<i>Rhinocorymbus hynchophorus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 1.8 | 42 |
| 89 | Differential gene expression in an elite hybrid rice cultivar (<i>Oryza sativa</i> , L) and its parental lines based on SAGE data. <i>BMC Plant Biology</i> , 2007, 7, 49. | 1.6 | 41 |
| 90 | 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 |

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|-----|---|-----|-----------|
| 91 | DNA motifs determining the accuracy of repeat duplication during CRISPR adaptation in <i>Haloarcula hispanica</i> . <i>Nucleic Acids Research</i> , 2016, 44, 4266-4277. | 6.5 | 41 |
| 92 | Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180. | 6.5 | 41 |
| 93 | The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. <i>Molecular Plant</i> , 2019, 12, 402-409. | 3.9 | 41 |
| 94 | De novo Transcriptome Analysis Reveals Distinct Defense Mechanisms by Young and Mature Leaves of <i>Hevea brasiliensis</i> (Para Rubber Tree). <i>Scientific Reports</i> , 2016, 6, 33151. | 1.6 | 40 |
| 95 | The calcium-dependent protein kinase (CDPK) and CDPK-related kinase gene families in <i>Hevea brasiliensis</i> comparison with five other plant species in structure, evolution, and expression. <i>FEBS Open Bio</i> , 2017, 7, 4-24. | 1.0 | 40 |
| 96 | High-throughput sequencing-based gene profiling on multi-staged fruit development of date palm (<i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012, 78, 617-626. | 2.0 | 39 |
| 97 | Transcriptome and Expression Profiling Analysis of the Hemocytes Reveals a Large Number of Immune-Related Genes in Mud Crab <i>Scylla paramamosain</i> during <i>Vibrio parahaemolyticus</i> Infection. <i>PLoS ONE</i> , 2014, 9, e114500. | 1.1 | 39 |
| 98 | Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. <i>BMC Genomics</i> , 2015, 16, 851. | 1.2 | 39 |
| 99 | 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 |
| 100 | The small RNA profile in latex from <i>Hevea brasiliensis</i> trees is affected by tapping panel dryness. <i>Tree Physiology</i> , 2013, 33, 1084-1098. | 1.4 | 38 |
| 101 | Ribogenomics: the Science and Knowledge of RNA. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 57-63. | 3.0 | 38 |
| 102 | Plant editosome database: a curated database of RNA editosome in plants. <i>Nucleic Acids Research</i> , 2019, 47, D170-D174. | 6.5 | 38 |
| 103 | Novel microRNAs in silkworm (<i>Bombyx mori</i>). <i>Functional and Integrative Genomics</i> , 2010, 10, 405-415. | 1.4 | 37 |
| 104 | Evolution of genes on the <i>Salmonella</i> Virulence plasmid phylogeny revealed from sequencing of the virulence plasmids of <i>S. enterica</i> serotype Dublin and comparative analysis. <i>Genomics</i> , 2008, 92, 339-343. | 1.3 | 36 |
| 105 | Analysis of CYP3A4 genetic polymorphisms in Han Chinese. <i>Journal of Human Genetics</i> , 2011, 56, 415-422. | 1.1 | 36 |
| 106 | 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 |
| 107 | Complete Genome Sequence of <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> Strain ATCC 35246. <i>Journal of Bacteriology</i> , 2011, 193, 5583-5584. | 1.0 | 34 |
| 108 | A novel DNA sequence periodicity decodes nucleosome positioning. <i>Nucleic Acids Research</i> , 2008, 36, 6228-6236. | 6.5 | 33 |

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|-----|--|-----|-----------|
| 109 | Involvement of the GP63 protease in infection of <i>Trichomonas vaginalis</i> . <i>Parasitology Research</i> , 2011, 109, 71-79. | 0.6 | 33 |
| 110 | Complete Sequence and Analysis of Coconut Palm (<i>Cocos nucifera</i>) Mitochondrial Genome. <i>PLoS ONE</i> , 2016, 11, e0163990. | 1.1 | 33 |
| 111 | A discovery of novel microRNAs in the silkworm (<i>Bombyx mori</i>) genome. <i>Genomics</i> , 2009, 94, 438-444. | 1.3 | 32 |
| 112 | Complete Genome Analysis of <i>Sulfobacillus acidophilus</i> Strain TPY, Isolated from a Hydrothermal Vent in the Pacific Ocean. <i>Journal of Bacteriology</i> , 2011, 193, 5555-5556. | 1.0 | 32 |
| 113 | Dynamic transcriptomes of human myeloid leukemia cells. <i>Genomics</i> , 2013, 102, 250-256. | 1.3 | 32 |
| 114 | Special fasciculiform cataract caused by a mutation in the gammaD-crystallin gene. <i>Molecular Vision</i> , 2004, 10, 233-9. | 1.1 | 32 |
| 115 | The <i>Bryopsis hypnoides</i> Plastid Genome: Multimeric Forms and Complete Nucleotide Sequence. <i>PLoS ONE</i> , 2011, 6, e14663. | 1.1 | 31 |
| 116 | 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 |
| 117 | Distinct Contributions of Replication and Transcription to Mutation Rate Variation of Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 4-10. | 3.0 | 31 |
| 118 | Profiling microRNA expression during multi-staged date palm (<i>Phoenix dactylifera</i> L.) fruit development. <i>Genomics</i> , 2015, 105, 242-251. | 1.3 | 31 |
| 119 | A chymotrypsin-like serine protease cDNA involved in food protein digestion in the common cutworm, <i>Spodoptera litura</i> : Cloning, characterization, developmental and induced expression patterns, and localization. <i>Journal of Insect Physiology</i> , 2010, 56, 788-799. | 0.9 | 30 |
| 120 | Discovery, Identification and Comparative Analysis of Non-Specific Lipid Transfer Protein (nsLtp) Family in Solanaceae. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 229-237. | 3.0 | 30 |
| 121 | Complete nucleotide sequence of pH11, an IncHI2 plasmid conferring multi-antibiotic resistance and multi-heavy metal resistance genes in a clinical <i>Klebsiella pneumoniae</i> isolate. <i>Plasmid</i> , 2016, 86, 26-31. | 0.4 | 30 |
| 122 | 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 |
| 123 | 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 |
| 124 | Identification of genetic variations associated with epsilon-poly-lysine biosynthesis in <i>Streptomyces albus</i> ZPM by genome sequencing. <i>Scientific Reports</i> , 2015, 5, 9201. | 1.6 | 28 |
| 125 | Editome Disease Knowledgebase (EDK): a curated knowledgebase of editome-disease associations in human. <i>Nucleic Acids Research</i> , 2019, 47, D78-D83. | 6.5 | 28 |
| 126 | Complete nucleotide sequence of plasmid plca36 isolated from <i>Lactobacillus casei</i> Zhang. <i>Plasmid</i> , 2008, 60, 131-135. | 0.4 | 27 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | A Novel Role for Minimal Introns: Routing mRNAs to the Cytosol. <i>PLoS ONE</i> , 2010, 5, e10144. | 1.1 | 27 |
| 128 | Identification and Analysis of Muscle-Related Protein Isoforms Expressed in the White Muscle of the Mandarin Fish (<i>Siniperca chuatsi</i>). <i>Marine Biotechnology</i> , 2011, 13, 151-162. | 1.1 | 27 |
| 129 | Regulation of MIR Genes in Response to Abiotic Stress in <i>Hevea brasiliensis</i> . <i>International Journal of Molecular Sciences</i> , 2013, 14, 19587-19604. | 1.8 | 27 |
| 130 | Identification and analysis of house-keeping and tissue-specific genes based on RNA-seq data sets across 15 mouse tissues. <i>Gene</i> , 2016, 576, 560-570. | 1.0 | 27 |
| 131 | Abundant Taxa and Favorable Pathways in the Microbiome of Soda-Saline Lakes in Inner Mongolia. <i>Frontiers in Microbiology</i> , 2020, 11, 1740. | 1.5 | 27 |
| 132 | BIGpre: A Quality Assessment Package for Next-Generation Sequencing Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 238-244. | 3.0 | 26 |
| 133 | Large-scale collection and annotation of gene models for date palm (<i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012, 79, 521-536. | 2.0 | 26 |
| 134 | Transcriptomic analysis reveals key regulators of mammogenesis and the pregnancy-lactation cycle. <i>Science China Life Sciences</i> , 2014, 57, 340-355. | 2.3 | 26 |
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