

Jun Wang

List of Publications by Year in descending order

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Version: 2024-02-01

519
papers

205,647
citations

40

189
h-index

31

428
g-index

543
all docs

543
docs citations

543
times ranked

184059
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | The enriched gut commensal <i>Faeciroseburia intestinalis</i> contributes to the anti-metabolic disorders effects of the <i>Ganoderma meroterpene</i> derivative. <i>Food Science and Human Wellness</i> , 2022, 11, 85-96. | 2.2 | 4 |
| 2 | Identification of antimicrobial peptides from the human gut microbiome using deep learning. <i>Nature Biotechnology</i> , 2022, 40, 921-931. | 9.4 | 142 |
| 3 | Comparative genomic analysis of ABC transporter genes in <i>Tenebrio molitor</i> and four other tenebrionid beetles (Coleoptera: Tenebrionidea). <i>Archives of Insect Biochemistry and Physiology</i> , 2022, , e21916. | 0.6 | 0 |
| 4 | Linkage between microbial functional genes and net N mineralisation in forest soils along an elevational gradient. <i>European Journal of Soil Science</i> , 2022, 73, . | 1.8 | 7 |
| 5 | New insights on the function of plant acyl carrier proteins from comparative and evolutionary analysis. <i>Genomics</i> , 2021, 113, 1155-1165. | 1.3 | 7 |
| 6 | Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165. | 9.4 | 676 |
| 7 | A simple and rapid method for fish sex identification based on recombinase-aided amplification and its use in <i>Cynoglossus semilaevis</i> . <i>Scientific Reports</i> , 2021, 11, 10429. | 1.6 | 3 |
| 8 | The genomic loci of specific human tRNA genes exhibit ageing-related DNA hypermethylation. <i>Nature Communications</i> , 2021, 12, 2655. | 5.8 | 10 |
| 9 | Interference of CsGPA1, the $\hat{\pm}$ -submit of G protein, reduces drought tolerance in cucumber seedlings. <i>Horticultural Plant Journal</i> , 2021, 7, 209-220. | 2.3 | 11 |
| 10 | Draft genome of the herbaceous bamboo <i>Raddia distichophylla</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 0.8 | 6 |
| 11 | Functional Genomics and Comparative Lineage-Specific Region Analyses Reveal Novel Insights into Race Divergence in <i>Verticillium dahliae</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0111821. | 1.2 | 7 |
| 12 | Integrated transcriptome provides resources and insights into the adaptive evolution of colonized brown trout (<i>Salmo trutta fario</i>) in the Tibetan Plateau. <i>Journal of the World Aquaculture Society</i> , 2020, 51, 763-774. | 1.2 | 7 |
| 13 | The Mouse Gut Microbial Biobank expands the coverage of cultured bacteria. <i>Nature Communications</i> , 2020, 11, 79. | 5.8 | 55 |
| 14 | The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. <i>Microbiome</i> , 2020, 8, 145. | 4.9 | 77 |
| 15 | The efficacy and safety of simultaneous integrated dose reduction in clinical target volume with intensity-modulated radiotherapy for patients with locally advanced esophageal squamous cell carcinoma. <i>Annals of Translational Medicine</i> , 2020, 8, 1160-1160. | 0.7 | 3 |
| 16 | The diagnostic yield of intellectual disability: combined whole genome low-coverage sequencing and medical exome sequencing. <i>BMC Medical Genomics</i> , 2020, 13, 70. | 0.7 | 11 |
| 17 | 3'-Terminal O-methylation of lung cancer miR-21-5p enhances its stability and association with Argonaute2. <i>Nucleic Acids Research</i> , 2020, 48, 7027-7040. | 6.5 | 30 |
| 18 | Seven facts and five initiatives for gut microbiome research. <i>Protein and Cell</i> , 2020, 11, 391-400. | 4.8 | 21 |

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|----|--|-----|-----------|
| 19 | Identification and Functional Study of Chitin Metabolism and Detoxification-Related Genes in <i>Glyphodes pyloalis</i> Walker (Lepidoptera: Pyralidae) Based on Transcriptome Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1904. | 1.8 | 14 |
| 20 | Substrate Application of 5-Aminolevulinic Acid Enhanced Low-temperature and Weak-light Stress Tolerance in Cucumber (<i>Cucumis sativus</i> L.). <i>Agronomy</i> , 2020, 10, 472. | 1.3 | 20 |
| 21 | Antidiabetic Effects of Gegen Qinlian Decoction via the Gut Microbiota Are Attributable to Its Key Ingredient Berberine. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 721-736. | 3.0 | 70 |
| 22 | The use of chemogenetic approaches in alcohol use disorder research and treatment. <i>Alcohol</i> , 2019, 74, 39-45. | 0.8 | 7 |
| 23 | Transcriptomic analyses reveal new genes and networks response to H5N1 influenza viruses in duck (<i>Anas platyrhynchos</i>). <i>Journal of Integrative Agriculture</i> , 2019, 18, 1460-1472. | 1.7 | 7 |
| 24 | Optogenetic control of alcohol-seeking behavior via the dorsomedial striatal circuit. <i>Neuropharmacology</i> , 2019, 155, 89-97. | 2.0 | 24 |
| 25 | Compositional and functional differences in human gut microbiome with respect to equol production and its association with blood lipid level: a cross-sectional study. <i>Gut Pathogens</i> , 2019, 11, 20. | 1.6 | 29 |
| 26 | Genome-wide copy number variation analysis identified ANO1 as a novel oncogene and prognostic biomarker in esophageal squamous cell cancer. <i>Carcinogenesis</i> , 2019, 40, 1198-1208. | 1.3 | 39 |
| 27 | Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864. | 9.4 | 219 |
| 28 | QTL mapping for 11 agronomic traits based on a genome-wide Bin-map in a large F2 population of foxtail millet (<i>Setaria italica</i> (L.) P. Beauv). <i>Molecular Breeding</i> , 2019, 39, 1. | 1.0 | 24 |
| 29 | Alcohol intake enhances glutamatergic transmission from D2 receptor-expressing afferents onto D1 receptor-expressing medium spiny neurons in the dorsomedial striatum. <i>Neuropsychopharmacology</i> , 2019, 44, 1123-1131. | 2.8 | 22 |
| 30 | Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189. | 6.1 | 149 |
| 31 | gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648. | 6.5 | 70 |
| 32 | Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. <i>Microbiome</i> , 2019, 7, 2. | 4.9 | 135 |
| 33 | A nonhuman primate model of inherited retinal disease. <i>Journal of Clinical Investigation</i> , 2019, 129, 863-874. | 3.9 | 78 |
| 34 | Comparative transcriptome analysis reveals molecular response to salinity stress of salt-tolerant and sensitive genotypes of indica rice at seedling stage. <i>Scientific Reports</i> , 2018, 8, 2085. | 1.6 | 74 |
| 35 | Bidirectional and long-lasting control of alcohol-seeking behavior by corticostriatal LTP and LTD. <i>Nature Neuroscience</i> , 2018, 21, 373-383. | 7.1 | 94 |
| 36 | Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16. | 5.9 | 717 |

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|----|--|-----|-----------|
| 37 | Massively parallel sequencing on human cleavage-stage embryos to detect chromosomal abnormality. <i>European Journal of Medical Genetics</i> , 2018, 61, 34-42. | 0.7 | 1 |
| 38 | Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. <i>European Urology</i> , 2018, 73, 322-339. | 0.9 | 130 |
| 39 | Coexisting genomic aberrations associated with lymph node metastasis in breast cancer. <i>Journal of Clinical Investigation</i> , 2018, 128, 2310-2324. | 3.9 | 22 |
| 40 | Effects of Rich-Polyphenols Extract of <i>Dendrobium loddigesii</i> on Anti-Diabetic, Anti-Inflammatory, Anti-Oxidant, and Gut Microbiota Modulation in db/db Mice. <i>Molecules</i> , 2018, 23, 3245. | 1.7 | 70 |
| 41 | Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265. | 5.9 | 483 |
| 42 | Impact of a 3-Months Vegetarian Diet on the Gut Microbiota and Immune Repertoire. <i>Frontiers in Immunology</i> , 2018, 9, 908. | 2.2 | 56 |
| 43 | Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101. | 4.9 | 109 |
| 44 | Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017, 66, 70-78. | 6.1 | 865 |
| 45 | Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017, 66, 1968-1974. | 6.1 | 370 |
| 46 | A reference gene set for sex pheromone biosynthesis and degradation genes from the diamondback moth, <i>Plutella xylostella</i> , based on genome and transcriptome digital gene expression analyses. <i>BMC Genomics</i> , 2017, 18, 219. | 1.2 | 55 |
| 47 | Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. <i>Gut</i> , 2017, 66, 980-982. | 6.1 | 56 |
| 48 | High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. <i>Microbiome</i> , 2017, 5, 43. | 4.9 | 132 |
| 49 | Obesity is associated with depot-specific alterations in adipocyte DNA methylation and gene expression. <i>Adipocyte</i> , 2017, 6, 124-133. | 1.3 | 34 |
| 50 | Alcohol induces input-specific aberrant synaptic plasticity in the rat dorsomedial striatum. <i>Neuropharmacology</i> , 2017, 123, 46-54. | 2.0 | 34 |
| 51 | Increased serum miR-7 is a promising biomarker for type 2 diabetes mellitus and its microvascular complications. <i>Diabetes Research and Clinical Practice</i> , 2017, 130, 171-179. | 1.1 | 46 |
| 52 | The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845. | 5.8 | 1,029 |
| 53 | Mapping of <i>Sihc1</i> , which controls hull color, using a high-density genetic map based on restriction site-associated DNA sequencing in foxtail millet [<i>Setaria italica</i> (L.) P. Beauv.]. <i>Molecular Breeding</i> , 2017, 37, 1. | 1.0 | 5 |
| 54 | The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017, 8, 875. | 5.8 | 572 |

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|----|--|------|-----------|
| 55 | Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976. | 9.4 | 356 |
| 56 | Association Analysis of the MHC in Lupus Nephritis. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 3383-3394. | 3.0 | 21 |
| 57 | Deep whole-genome sequencing of 90 Han Chinese genomes. <i>GigaScience</i> , 2017, 6, 1-7. | 3.3 | 36 |
| 58 | Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017, 551, 507-511. | 13.7 | 791 |
| 59 | Small RNA Activity in Archeological Barley Shows Novel Germination Inhibition in Response to Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 2555-2562. | 3.5 | 15 |
| 60 | High Prevalence of Diabetes-Predisposing Variants in MODY Genes Among Danish Women With Gestational Diabetes Mellitus. <i>Journal of the Endocrine Society</i> , 2017, 1, 681-690. | 0.1 | 32 |
| 61 | De Novo Paternal FBN1 Mutation Detected in Embryos Before Implantation. <i>Medical Science Monitor</i> , 2017, 23, 3136-3146. | 0.5 | 4 |
| 62 | Boolean analysis reveals systematic interactions among low-abundance species in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017, 13, e1005361. | 1.5 | 34 |
| 63 | Domestication drive the changes of immune and digestive system of Eurasian perch (<i>Perca fluviatilis</i>). <i>PLoS ONE</i> , 2017, 12, e0172903. | 1.1 | 12 |
| 64 | A high-density genetic map and QTL analysis of agronomic traits in foxtail millet [<i>Setaria italica</i> (L.) P. Beauv.] using RAD-seq. <i>PLoS ONE</i> , 2017, 12, e0179717. | 1.1 | 55 |
| 65 | Integrative analysis of miRNA and gene expression reveals regulatory networks in tamoxifen-resistant breast cancer. <i>Oncotarget</i> , 2016, 7, 57239-57253. | 0.8 | 30 |
| 66 | Multigenic Control of Pod Shattering Resistance in Chinese Rapeseed Germplasm Revealed by Genome-Wide Association and Linkage Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 1058. | 1.7 | 25 |
| 67 | Metagenome-wide association studies: fine-mining the microbiome. <i>Nature Reviews Microbiology</i> , 2016, 14, 508-522. | 13.6 | 356 |
| 68 | Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (<i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2016, 6, 38636. | 1.6 | 77 |
| 69 | Roux-en-Y gastric bypass surgery of morbidly obese patients induces swift and persistent changes of the individual gut microbiota. <i>Genome Medicine</i> , 2016, 8, 67. | 3.6 | 260 |
| 70 | Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016, 3, 572-584.e3. | 2.9 | 261 |
| 71 | The Asian arowana (<i>Scleropages formosus</i>) genome provides new insights into the evolution of an early lineage of teleosts. <i>Scientific Reports</i> , 2016, 6, 24501. | 1.6 | 89 |
| 72 | Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016, 48, 740-746. | 9.4 | 188 |

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|----|--|------|-----------|
| 73 | Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. <i>Nature Biotechnology</i> , 2016, 34, 531-538. | 9.4 | 273 |
| 74 | Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569. | 6.0 | 1,398 |
| 75 | Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564. | 6.0 | 1,716 |
| 76 | The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016, 9, 975-985. | 3.9 | 102 |
| 77 | DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. <i>Genome Biology</i> , 2016, 17, 92. | 3.8 | 14 |
| 78 | Novel regional age-associated DNA methylation changes within human common disease-associated loci. <i>Genome Biology</i> , 2016, 17, 193. | 3.8 | 29 |
| 79 | Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381. | 13.7 | 1,506 |
| 80 | A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161. | 5.9 | 416 |
| 81 | Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. <i>Scientific Reports</i> , 2016, 6, 22525. | 1.6 | 143 |
| 82 | Genome-wide characteristics of de novo mutations in autism. <i>Npj Genomic Medicine</i> , 2016, 1, 160271-1602710. | 1.7 | 200 |
| 83 | Genomic and oncogenic preference of HBV integration in hepatocellular carcinoma. <i>Nature Communications</i> , 2016, 7, 12992. | 5.8 | 228 |
| 84 | Genome and metagenome analyses reveal adaptive evolution of the host and interaction with the gut microbiota in the goose. <i>Scientific Reports</i> , 2016, 6, 32961. | 1.6 | 36 |
| 85 | Analysis of liver and gill miRNAs of <i>Larimichthys crocea</i> against <i>Cryptocaryon irritans</i> challenge. <i>Fish and Shellfish Immunology</i> , 2016, 59, 484-491. | 1.6 | 25 |
| 86 | Analysis of a four generation family reveals the widespread sequence-dependent maintenance of allelic DNA methylation in somatic and germ cells. <i>Scientific Reports</i> , 2016, 6, 19260. | 1.6 | 15 |
| 87 | A targeted next-generation sequencing method for identifying clinically relevant mutation profiles in lung adenocarcinoma. <i>Scientific Reports</i> , 2016, 6, 22338. | 1.6 | 49 |
| 88 | De novo mutations associated with early-onset Parkinson's disease. <i>Annals of Neurology</i> , 2016, 79, 244-256. | 2.8 | 148 |
| 89 | Effect of a long-term high-protein diet on survival, obesity development, and gut microbiota in mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2016, 310, E886-E899. | 1.8 | 55 |
| 90 | Low-pass whole-genome sequencing in clinical cytogenetics: a validated approach. <i>Genetics in Medicine</i> , 2016, 18, 940-948. | 1.1 | 138 |

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|-----|---|-----|-----------|
| 91 | SCRaMble generates designed combinatorial stochastic diversity in synthetic chromosomes. <i>Genome Research</i> , 2016, 26, 36-49. | 2.4 | 124 |
| 92 | Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363. | 4.3 | 70 |
| 93 | Sprites: detection of deletions from sequencing data by re-aligning split reads. <i>Bioinformatics</i> , 2016, 32, 1788-1796. | 1.8 | 23 |
| 94 | The <i>Sinocyclocheilus</i> cavefish genome provides insights into cave adaptation. <i>BMC Biology</i> , 2016, 14, 1. | 1.7 | 292 |
| 95 | Donor Species Richness Determines Faecal Microbiota Transplantation Success in Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 387-394. | 0.6 | 256 |
| 96 | High-Quality Exome Sequencing of Whole-Genome Amplified Neonatal Dried Blood Spot DNA. <i>PLoS ONE</i> , 2016, 11, e0153253. | 1.1 | 38 |
| 97 | Mutation analysis of Leber congenital amaurosis-associated genes in patients with retinitis pigmentosa. <i>Molecular Medicine Reports</i> , 2015, 11, 1827-1832. | 1.1 | 13 |
| 98 | Whole Exome Sequencing Identifies Frequent Somatic Mutations in Cell-Cell Adhesion Genes in Chinese Patients with Lung Squamous Cell Carcinoma. <i>Scientific Reports</i> , 2015, 5, 14237. | 1.6 | 51 |
| 99 | Performance of genetic risk factors in prediction of trichloroethylene induced hypersensitivity syndrome. <i>Scientific Reports</i> , 2015, 5, 12169. | 1.6 | 12 |
| 100 | MICA: A fast short-read aligner that takes full advantage of Many Integrated Core Architecture (MIC). <i>BMC Bioinformatics</i> , 2015, 16, S10. | 1.2 | 14 |
| 101 | A host plant genome (<i>Zizania latifolia</i>) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609. | 2.8 | 67 |
| 102 | Comparative genomic analysis reveals bilateral breast cancers are genetically independent. <i>Oncotarget</i> , 2015, 6, 31820-31829. | 0.8 | 20 |
| 103 | The Dynamic Distribution of Porcine Microbiota across Different Ages and Gastrointestinal Tract Segments. <i>PLoS ONE</i> , 2015, 10, e0117441. | 1.1 | 349 |
| 104 | A comparison of isolated circulating tumor cells and tissue biopsies using whole-genome sequencing in prostate cancer. <i>Oncotarget</i> , 2015, 6, 44781-44793. | 0.8 | 94 |
| 105 | Unique Variants in <i>OPN1LW</i> Cause Both Syndromic and Nonsyndromic X-Linked High Myopia Mapped to MYP1. , 2015, 56, 4150. | | 46 |
| 106 | Genome-wide circulating microRNA expression profiling indicates biomarkers for epilepsy. <i>Scientific Reports</i> , 2015, 5, 9522. | 1.6 | 126 |
| 107 | De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015, 33, 617-622. | 9.4 | 73 |
| 108 | Molecular Signatures of Major Depression. <i>Current Biology</i> , 2015, 25, 1146-1156. | 1.8 | 224 |

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|-----|--|-----|-----------|
| 109 | Circulating microRNAs are promising novel biomarkers for drug-resistant epilepsy. <i>Scientific Reports</i> , 2015, 5, 10201. | 1.6 | 126 |
| 110 | Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277. | 3.8 | 167 |
| 111 | RNA-seq analysis of <i>Macrobrachium rosenbergii</i> hepatopancreas in response to <i>Vibrio parahaemolyticus</i> infection. <i>Gut Pathogens</i> , 2015, 7, 6. | 1.6 | 66 |
| 112 | Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. <i>Nature Communications</i> , 2015, 6, 10131. | 5.8 | 93 |
| 113 | Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133. | 3.8 | 325 |
| 114 | Discovery, genotyping and characterization of structural variation and novel sequence at single nucleotide resolution from de novo genome assemblies on a population scale. <i>GigaScience</i> , 2015, 4, 64. | 3.3 | 30 |
| 115 | Advantage of Whole Exome Sequencing over Allele-Specific and Targeted Segment Sequencing in Detection of Novel <i>TULP1</i> Mutation in Leber Congenital Amaurosis. <i>Ophthalmic Genetics</i> , 2015, 36, 333-338. | 0.5 | 12 |
| 116 | The draft genome of Tibetan hulless barley reveals adaptive patterns to the high stressful Tibetan Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1095-1100. | 3.3 | 147 |
| 117 | Recurrent Loss of Sex Is Associated with Accumulation of Deleterious Mutations in <i>Oenothera</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 896-905. | 3.5 | 82 |
| 118 | Integrated genome sequence and linkage map of physic nut (<i>Jatropha curcas</i> L.), a biodiesel plant. <i>Plant Journal</i> , 2015, 81, 810-821. | 2.8 | 149 |
| 119 | Genome-wide profiling of HPV integration in cervical cancer identifies clustered genomic hot spots and a potential microhomology-mediated integration mechanism. <i>Nature Genetics</i> , 2015, 47, 158-163. | 9.4 | 393 |
| 120 | Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969. | 5.8 | 164 |
| 121 | Novel nonsense mutation in the <i>PTRF</i> gene underlies congenital generalized lipodystrophy in a consanguineous Saudi family. <i>European Journal of Medical Genetics</i> , 2015, 58, 216-221. | 0.7 | 31 |
| 122 | Embryo Genome Profiling by Single-Cell Sequencing for Preimplantation Genetic Diagnosis in a β -Thalassemia Family. <i>Clinical Chemistry</i> , 2015, 61, 617-626. | 1.5 | 16 |
| 123 | A Neutrality Test for Detecting Selection on DNA Methylation Using Single Methylation Polymorphism Frequency Spectrum. <i>Genome Biology and Evolution</i> , 2015, 7, 154-171. | 1.1 | 25 |
| 124 | Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528. | 5.8 | 1,062 |
| 125 | Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1257-62. | 3.3 | 159 |
| 126 | Genome Sequencing of the Perciform Fish <i>Larimichthys crocea</i> Provides Insights into Molecular and Genetic Mechanisms of Stress Adaptation. <i>PLoS Genetics</i> , 2015, 11, e1005118. | 1.5 | 230 |

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|-----|---|------|-----------|
| 127 | The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015, 21, 895-905. | 15.2 | 1,306 |
| 128 | Excess of Rare Variants in Genes that are Key Epigenetic Regulators of Spermatogenesis in the Patients with Non-Obstructive Azoospermia. <i>Scientific Reports</i> , 2015, 5, 8785. | 1.6 | 39 |
| 129 | Lanosterol reverses protein aggregation in cataracts. <i>Nature</i> , 2015, 523, 607-611. | 13.7 | 351 |
| 130 | Inference of Purifying and Positive Selection in Three Subspecies of Chimpanzees (<i>Pan troglodytes</i>) from Exome Sequencing. <i>Genome Biology and Evolution</i> , 2015, 7, 1122-1132. | 1.1 | 33 |
| 131 | Genomic Analyses Reveal Mutational Signatures and Frequently Altered Genes in Esophageal Squamous Cell Carcinoma. <i>American Journal of Human Genetics</i> , 2015, 96, 597-611. | 2.6 | 290 |
| 132 | Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530. | 9.4 | 1,064 |
| 133 | Generation of outbred Ace2 knockout mice by RNA transfection of TALENs displaying colitis reminiscent pathophysiology and inflammation. <i>Transgenic Research</i> , 2015, 24, 433-446. | 1.3 | 14 |
| 134 | Non-targeted metabolomics and lipidomics LC-MS data from maternal plasma of 180 healthy pregnant women. <i>GigaScience</i> , 2015, 4, 16. | 3.3 | 25 |
| 135 | A reliable, high-resolution and high-throughput genotyping method for HLA-DRB1. <i>Human Immunology</i> , 2015, 76, 397-401. | 1.2 | 1 |
| 136 | Effects of Maternal and Fetal Characteristics on Cell-Free Fetal DNA Fraction in Maternal Plasma. <i>Reproductive Sciences</i> , 2015, 22, 1429-1435. | 1.1 | 85 |
| 137 | Global gene expression profiling of brown to white adipose tissue transformation in sheep reveals novel transcriptional components linked to adipose remodeling. <i>BMC Genomics</i> , 2015, 16, 215. | 1.2 | 60 |
| 138 | Exome analysis identified a novel missense mutation in the CLPP gene in a consanguineous Saudi family expanding the clinical spectrum of Perrault Syndrome type-3. <i>Journal of the Neurological Sciences</i> , 2015, 353, 149-154. | 0.3 | 37 |
| 139 | Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015, 17, 690-703. | 5.1 | 2,276 |
| 140 | Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143. | 6.0 | 357 |
| 141 | Construction of high-throughput genotyped chromosome segment substitution lines in rice (<i>Oryza</i>) Tj ETQq1 _{1.0} 0.7843 ₁₄ rgBT / O | | |
| 142 | Characterization of 26 deletion CNVs reveals the frequent occurrence of micro-mutations within the breakpoint-flanking regions and frequent repair of double-strand breaks by templated insertions derived from remote genomic regions. <i>Human Genetics</i> , 2015, 134, 589-603. | 1.8 | 25 |
| 143 | lPeak: An open source tool to combine results from multiple MS/MS search engines. <i>Proteomics</i> , 2015, 15, 2916-2920. | 1.3 | 33 |
| 144 | Transcriptome profiling of brown adipose tissue during cold exposure reveals extensive regulation of glucose metabolism. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 308, E380-E392. | 1.8 | 105 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 145 | The goose genome sequence leads to insights into the evolution of waterfowl and susceptibility to fatty liver. <i>Genome Biology</i> , 2015, 16, 89. | 3.8 | 98 |
| 146 | A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108. | 9.4 | 422 |
| 147 | A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74. | 13.7 | 13,998 |
| 148 | The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015, 350, 691-694. | 6.0 | 430 |
| 149 | RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538. | 1.2 | 86 |
| 150 | Genome sequencing of adzuki bean (<i>Vigna angularis</i>) provides insight into high starch and low fat accumulation and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13213-13218. | 3.3 | 104 |
| 151 | Mutations in apoptosis-inducing factor cause X-linked recessive auditory neuropathy spectrum disorder. <i>Journal of Medical Genetics</i> , 2015, 52, 523-531. | 1.5 | 92 |
| 152 | Comparison of variations detection between whole-genome amplification methods used in single-cell resequencing. <i>GigaScience</i> , 2015, 4, 37. | 3.3 | 141 |
| 153 | Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen <i>Vibrio parahaemolyticus</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1396-1410. | 3.5 | 98 |
| 154 | The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90. | 13.7 | 1,014 |
| 155 | Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015, 6, 8212. | 5.8 | 146 |
| 156 | Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266. | 13.7 | 1,627 |
| 157 | The p.Ser267Phe variant in SLC10A1 is associated with resistance to chronic hepatitis B. <i>Hepatology</i> , 2015, 61, 1251-1260. | 3.6 | 78 |
| 158 | Genome-wide identification of RNA editing in hepatocellular carcinoma. <i>Genomics</i> , 2015, 105, 76-82. | 1.3 | 40 |
| 159 | The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72. | 9.4 | 413 |
| 160 | Peptidomics combined with cDNA library unravel the diversity of centipede venom. <i>Journal of Proteomics</i> , 2015, 114, 28-37. | 1.2 | 31 |
| 161 | An exome study of Parkinson's disease in Sardinia, a Mediterranean genetic isolate. <i>Neurogenetics</i> , 2015, 16, 55-64. | 0.7 | 20 |
| 162 | Novel recurrently mutated genes and a prognostic mutation signature in colorectal cancer. <i>Gut</i> , 2015, 64, 636-645. | 6.1 | 163 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 163 | Mutation analysis in 129 genes associated with other forms of retinal dystrophy in 157 families with retinitis pigmentosa based on exome sequencing. <i>Molecular Vision</i> , 2015, 21, 477-86. | 1.1 | 21 |
| 164 | Design and Characterization of a 52K SNP Chip for Goats. <i>PLoS ONE</i> , 2014, 9, e86227. | 1.1 | 220 |
| 165 | Genome-Wide Transcriptome and Antioxidant Analyses on Gamma-Irradiated Phases of <i>Deinococcus radiodurans</i> R1. <i>PLoS ONE</i> , 2014, 9, e85649. | 1.1 | 37 |
| 166 | Whole-Exome Sequencing for the Identification of Susceptibility Genes of Kashinâ€“Beck Disease. <i>PLoS ONE</i> , 2014, 9, e92298. | 1.1 | 14 |
| 167 | A Novel DFNA36 Mutation in TMC1 Orthologous to the Beethoven (Bth) Mouse Associated with Autosomal Dominant Hearing Loss in a Chinese Family. <i>PLoS ONE</i> , 2014, 9, e97064. | 1.1 | 61 |
| 168 | Differentially Expressed Plasma MicroRNAs and the Potential Regulatory Function of Let-7b in Chronic Thromboembolic Pulmonary Hypertension. <i>PLoS ONE</i> , 2014, 9, e101055. | 1.1 | 50 |
| 169 | Deep Sequencing of HIV-Infected Cells: Insights into Nascent Transcription and Host-Directed Therapy. <i>Journal of Virology</i> , 2014, 88, 8768-8782. | 1.5 | 41 |
| 170 | Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014, 5, 5594. | 5.8 | 135 |
| 171 | Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. <i>Genome Biology</i> , 2014, 15, 557. | 3.8 | 83 |
| 172 | The plasticity of NBS resistance genes in sorghum is driven by multiple evolutionary processes. <i>BMC Plant Biology</i> , 2014, 14, 253. | 1.6 | 49 |
| 173 | Genomes of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. <i>Genome Biology</i> , 2014, 15, 521. | 3.8 | 404 |
| 174 | The willow genome and divergent evolution from poplar after the common genome duplication. <i>Cell Research</i> , 2014, 24, 1274-1277. | 5.7 | 148 |
| 175 | Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. <i>Nature Genetics</i> , 2014, 46, 253-260. | 9.4 | 685 |
| 176 | The Genome of a Mongolian Individual Reveals the Genetic Imprints of Mongolians on Modern Human Populations. <i>Genome Biology and Evolution</i> , 2014, 6, 3122-3136. | 1.1 | 24 |
| 177 | An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014, 5, 5719. | 5.8 | 100 |
| 178 | Plasma microRNA-320, microRNA-let-7e and microRNA-21 as novel potential biomarkers for the detection of retinoblastoma. <i>Biomedical Reports</i> , 2014, 2, 424-428. | 0.9 | 55 |
| 179 | The <i>Opisthorchis viverrini</i> genome provides insights into life in the bile duct. <i>Nature Communications</i> , 2014, 5, 4378. | 5.8 | 144 |
| 180 | Exome sequencing reveals CHM mutations in six families with atypical choroideremia initially diagnosed as retinitis pigmentosa. <i>International Journal of Molecular Medicine</i> , 2014, 34, 573-577. | 1.8 | 28 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 181 | The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014, 5, 2957. | 5.8 | 437 |
| 182 | Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. <i>Cell Research</i> , 2014, 24, 701-712. | 5.7 | 123 |
| 183 | The <scp>OMSSAP</scp>ercolator: <scp>A</scp>n automated tool to validate <scp>OMSSA</scp> results. <i>Proteomics</i> , 2014, 14, 1011-1014. | 1.3 | 13 |
| 184 | IQuant: An automated pipeline for quantitative proteomics based upon isobaric tags. <i>Proteomics</i> , 2014, 14, 2280-2285. | 1.3 | 253 |
| 185 | Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320. | 6.0 | 895 |
| 186 | Variation and association to diabetes in 2000 full mtDNA sequences mined from an exome study in a Danish population. <i>European Journal of Human Genetics</i> , 2014, 22, 1040-1045. | 1.4 | 26 |
| 187 | Addendum: Independent optical excitation of distinct neural populations. <i>Nature Methods</i> , 2014, 11, 972-972. | 9.0 | 33 |
| 188 | Adaptations to a Subterranean Environment and Longevity Revealed by the Analysis of Mole Rat Genomes. <i>Cell Reports</i> , 2014, 8, 1354-1364. | 2.9 | 162 |
| 189 | DADS Suppresses Human Esophageal Xenograft Tumors through RAF/MEK/ERK and Mitochondria-Dependent Pathways. <i>International Journal of Molecular Sciences</i> , 2014, 15, 12422-12441. | 1.8 | 33 |
| 190 | Comparative genomic data of the Avian Phylogenomics Project. <i>GigaScience</i> , 2014, 3, 26. | 3.3 | 117 |
| 191 | Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27. | 3.3 | 72 |
| 192 | Dietary history contributes to enterotype-like clustering and functional metagenomic content in the intestinal microbiome of wild mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2703-10. | 3.3 | 144 |
| 193 | Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17. | 3.3 | 582 |
| 194 | Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014, 15, R39. | 13.9 | 245 |
| 195 | Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014, 15, R56. | 13.9 | 87 |
| 196 | Independent optical excitation of distinct neural populations. <i>Nature Methods</i> , 2014, 11, 338-346. | 9.0 | 1,879 |
| 197 | Identification of genomic alterations in oesophageal squamous cell cancer. <i>Nature</i> , 2014, 509, 91-95. | 13.7 | 903 |
| 198 | Activating hotspot L205R mutation in <i>PRKACA</i> and adrenal Cushingâ€™s syndrome. <i>Science</i> , 2014, 344, 913-917. | 6.0 | 193 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 199 | Spider genomes provide insight into composition and evolution of venom and silk. <i>Nature Communications</i> , 2014, 5, 3765. | 5.8 | 235 |
| 200 | Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794. | 13.5 | 363 |
| 201 | The Genome of the Netherlands: design, and project goals. <i>European Journal of Human Genetics</i> , 2014, 22, 221-227. | 1.4 | 246 |
| 202 | A large-scale screen for coding variants predisposing to psoriasis. <i>Nature Genetics</i> , 2014, 46, 45-50. | 9.4 | 183 |
| 203 | Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014, 24, 604-615. | 2.4 | 356 |
| 204 | Influenza H7N9 and H9N2 Viruses: Coexistence in Poultry Linked to Human H7N9 Infection and Genome Characteristics. <i>Journal of Virology</i> , 2014, 88, 3423-3431. | 1.5 | 93 |
| 205 | Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014, 46, 88-92. | 9.4 | 227 |
| 206 | Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767. | 6.0 | 2,096 |
| 207 | Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4859-68. | 3.3 | 1,123 |
| 208 | sapFinder: an R/Bioconductor package for detection of variant peptides in shotgun proteomics experiments. <i>Bioinformatics</i> , 2014, 30, 3136-3138. | 1.8 | 25 |
| 209 | Comparison of distinct transcriptional expression patterns of flavonoid biosynthesis in Cabernet Sauvignon grapes from east and west China. <i>Plant Physiology and Biochemistry</i> , 2014, 84, 45-56. | 2.8 | 26 |
| 210 | Camelid genomes reveal evolution and adaptation to desert environments. <i>Nature Communications</i> , 2014, 5, 5188. | 5.8 | 299 |
| 211 | Sequencing-based approach identified three new susceptibility loci for psoriasis. <i>Nature Communications</i> , 2014, 5, 4331. | 5.8 | 67 |
| 212 | Transcriptional Pause Release Is a Rate-Limiting Step for Somatic Cell Reprogramming. <i>Cell Stem Cell</i> , 2014, 15, 574-588. | 5.2 | 60 |
| 213 | Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014, 46, 701-706. | 9.4 | 93 |
| 214 | Marked methylation changes in intestinal genes during the perinatal period of preterm neonates. <i>BMC Genomics</i> , 2014, 15, 716. | 1.2 | 65 |
| 215 | Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. <i>Genome Biology</i> , 2014, 15, 408. | 3.8 | 173 |
| 216 | Comparative population genomics reveals the domestication history of the peach, <i>Prunus persica</i> , and human influences on perennial fruit crops. <i>Genome Biology</i> , 2014, 15, 415. | 3.8 | 134 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 217 | MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. <i>Genome Biology</i> , 2014, 15, 419. | 3.8 | 87 |
| 218 | SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014, 30, 1660-1666. | 1.8 | 826 |
| 219 | Complementary symbiont contributions to plant decomposition in a fungus-farming termite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14500-14505. | 3.3 | 243 |
| 220 | Pregnancy-Induced Metabolic Phenotype Variations in Maternal Plasma. <i>Journal of Proteome Research</i> , 2014, 13, 1527-1536. | 1.8 | 84 |
| 221 | Mutations of 60 known causative genes in 157 families with retinitis pigmentosa based on exome sequencing. <i>Human Genetics</i> , 2014, 133, 1255-1271. | 1.8 | 148 |
| 222 | The 3,000 rice genomes project: new opportunities and challenges for future rice research. <i>GigaScience</i> , 2014, 3, 8. | 3.3 | 337 |
| 223 | A chromosomal genomics approach to assess and validate the <i>desi</i> and <i>kabuli</i> draft chickpea genome assemblies. <i>Plant Biotechnology Journal</i> , 2014, 12, 778-786. | 4.1 | 54 |
| 224 | Direct ChIP-bisulfite sequencing reveals a role of H3K27me3 mediating aberrant hypermethylation of promoter CpG islands in cancer cells. <i>Genomics</i> , 2014, 103, 204-210. | 1.3 | 37 |
| 225 | Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014, 46, 567-572. | 9.4 | 883 |
| 226 | Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828. | 9.4 | 909 |
| 227 | An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841. | 9.4 | 1,664 |
| 228 | Evaluation of a target region capture sequencing platform using monogenic diabetes as a study-model. <i>BMC Genetics</i> , 2014, 15, 13. | 2.7 | 51 |
| 229 | Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. <i>Nature</i> , 2014, 512, 194-197. | 13.7 | 904 |
| 230 | A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014, 512, 190-193. | 13.7 | 338 |
| 231 | The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173. | 6.0 | 436 |
| 232 | Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966. | 5.8 | 124 |
| 233 | The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930. | 5.8 | 918 |
| 234 | Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6672-6677. | 3.3 | 146 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 235 | Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636. | 5.8 | 371 |
| 236 | Targeted next-generation sequencing as a comprehensive test for patients with and female carriers of DMD/BMD: a multi-population diagnostic study. <i>European Journal of Human Genetics</i> , 2014, 22, 110-118. | 1.4 | 66 |
| 237 | Altered Serum MicroRNAs as Novel Diagnostic Biomarkers for Atypical Coronary Artery Disease. <i>PLoS ONE</i> , 2014, 9, e107012. | 1.1 | 36 |
| 238 | Correction: The genome sequence of the ground tit <i>Pseudopodoces humilis</i> provides insights into its adaptation to high altitude. <i>Genome Biology</i> , 2014, 15, R33. | 13.9 | 1 |
| 239 | Single-base-resolution methylomes of <i>populus trichocarpa</i> reveal the association between DNA methylation and drought stress. <i>BMC Genetics</i> , 2014, 15, S9. | 2.7 | 123 |
| 240 | Genomic methylation patterns in archaeological barley show de-methylation as a time-dependent diagenetic process. <i>Scientific Reports</i> , 2014, 4, 5559. | 1.6 | 63 |
| 241 | Omics-based interpretation of synergism in a soil-derived cellulose-degrading microbial community. <i>Scientific Reports</i> , 2014, 4, 5288. | 1.6 | 39 |
| 242 | A complete ancient RNA genome: identification, reconstruction and evolutionary history of archaeological Barley Stripe Mosaic Virus. <i>Scientific Reports</i> , 2014, 4, 4003. | 1.6 | 86 |
| 243 | Two-Step Source Tracing Strategy of <i>Yersinia pestis</i> and Its Historical Epidemiology in a Specific Region. <i>PLoS ONE</i> , 2014, 9, e85374. | 1.1 | 9 |
| 244 | The South Asian Genome. <i>PLoS ONE</i> , 2014, 9, e102645. | 1.1 | 43 |
| 245 | Divergence of Gene Body DNA Methylation and Evolution of Plant Duplicate Genes. <i>PLoS ONE</i> , 2014, 9, e110357. | 1.1 | 48 |
| 246 | SOAPfuse: an algorithm for identifying fusion transcripts from paired-end RNA-Seq data. <i>Genome Biology</i> , 2013, 14, R12. | 13.9 | 197 |
| 247 | TIMP1 overexpression mediates resistance of MCF-7 human breast cancer cells to fulvestrant and down-regulates progesterone receptor expression. <i>Tumor Biology</i> , 2013, 34, 3839-3851. | 0.8 | 18 |
| 248 | Decoding the <i>Ascaris suum</i> Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods – Unprecedented Prospects for Fundamental and Applied Research. , 2013, , 287-314. | | 1 |
| 249 | Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013, 31, 759-765. | 9.4 | 340 |
| 250 | Metagenome-wide analysis of antibiotic resistance genes in a large cohort of human gut microbiota. <i>Nature Communications</i> , 2013, 4, 2151. | 5.8 | 606 |
| 251 | Comparative genomics of parasitic silkworm microsporidia reveal an association between genome expansion and host adaptation. <i>BMC Genomics</i> , 2013, 14, 186. | 1.2 | 127 |
| 252 | Mutation in the <i>SYNJ1</i> Gene Associated with Autosomal Recessive, Early-Onset Parkinsonism. <i>Human Mutation</i> , 2013, 34, 1208-1215. | 1.1 | 276 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 253 | Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246. | 9.4 | 1,049 |
| 254 | Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , 2013, 56, 298-310. | 2.9 | 119 |
| 255 | Genome sequencing of 161 <i>Mycobacterium tuberculosis</i> isolates from China identifies genes and intergenic regions associated with drug resistance. <i>Nature Genetics</i> , 2013, 45, 1255-1260. | 9.4 | 426 |
| 256 | Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. <i>Nature Communications</i> , 2013, 4, 2320. | 5.8 | 405 |
| 257 | The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567. | 2.8 | 75 |
| 258 | Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546. | 13.7 | 3,641 |
| 259 | A method for noninvasive detection of fetal large deletions/duplications by low coverage massively parallel sequencing. <i>Prenatal Diagnosis</i> , 2013, 33, 584-590. | 1.1 | 103 |
| 260 | Genetic Analysis and Preliminary Mapping of a Highly Male-Sterile Gene in Foxtail Millet (<i>Setaria italica</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T | 1.7 | 18 |
| 261 | Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , 2013, 4, 2212. | 5.8 | 213 |
| 262 | Whole-genome and whole-exome sequencing of bladder cancer identifies frequent alterations in genes involved in sister chromatid cohesion and segregation. <i>Nature Genetics</i> , 2013, 45, 1459-1463. | 9.4 | 400 |
| 263 | Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199. | 9.0 | 442 |
| 264 | Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. <i>American Journal of Human Genetics</i> , 2013, 93, 852-864. | 2.6 | 284 |
| 265 | Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq1 1 0.784314 rgBT /Ov | 9.4 | 479 |
| 266 | Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. <i>Gastroenterology</i> , 2013, 145, 339-347. | 0.6 | 149 |
| 267 | Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797. | 5.8 | 286 |
| 268 | Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2013, 93, 1072-1086. | 2.6 | 124 |
| 269 | A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225. | 9.4 | 472 |
| 270 | Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. <i>BMC Genomics</i> , 2013, 14, 646. | 1.2 | 47 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 271 | Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10. | 3.3 | 582 |
| 272 | Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. <i>BMC Genomics</i> , 2013, 14, 579. | 1.2 | 186 |
| 273 | Obligate mutualism within a host drives the extreme specialization of a fig wasp genome. <i>Genome Biology</i> , 2013, 14, R141. | 13.9 | 85 |
| 274 | A Short-Read Multiplex Sequencing Method for Reliable, Cost-Effective and High-Throughput Genotyping in Large-Scale Studies. <i>Human Mutation</i> , 2013, 34, 1715-1720. | 1.1 | 45 |
| 275 | Detection of Clinically Relevant Genetic Variants in Autism Spectrum Disorder by Whole-Genome Sequencing. <i>American Journal of Human Genetics</i> , 2013, 93, 249-263. | 2.6 | 429 |
| 276 | Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <i>Nature Communications</i> , 2013, 4, 1595. | 5.8 | 190 |
| 277 | The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408. | 2.4 | 832 |
| 278 | Genome of the Chinese tree shrew. <i>Nature Communications</i> , 2013, 4, 1426. | 5.8 | 284 |
| 279 | Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460. | 6.0 | 522 |
| 280 | The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58. | 9.4 | 731 |
| 281 | The microbiome explored: recent insights and future challenges. <i>Nature Reviews Microbiology</i> , 2013, 11, 213-217. | 13.6 | 162 |
| 282 | HIVID: An efficient method to detect HBV integration using low coverage sequencing. <i>Genomics</i> , 2013, 102, 338-344. | 1.3 | 94 |
| 283 | Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. <i>Science</i> , 2013, 339, 1063-1067. | 6.0 | 230 |
| 284 | Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90. | 13.7 | 700 |
| 285 | Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. <i>Nature Genetics</i> , 2013, 45, 563-566. | 9.4 | 141 |
| 286 | <i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95. | 13.7 | 714 |
| 287 | Integrated detection of both 5-mC and 5-hmC by high-throughput tag sequencing technology highlights methylation reprogramming of bivalent genes during cellular differentiation. <i>Epigenetics</i> , 2013, 8, 421-430. | 1.3 | 31 |
| 288 | Haplotype-assisted accurate non-invasive fetal whole genome recovery through maternal plasma sequencing. <i>Genome Medicine</i> , 2013, 5, 18. | 3.6 | 36 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 289 | The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013, 45, 701-706. | 9.4 | 409 |
| 290 | Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. <i>Nature Genetics</i> , 2013, 45, 67-71. | 9.4 | 303 |
| 291 | Recalibrating <i>Equus</i> evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78. | 13.7 | 717 |
| 292 | The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013, 45, 776-783. | 9.4 | 327 |
| 293 | SOAPfusion: a robust and effective computational fusion discovery tool for RNA-seq reads. <i>Bioinformatics</i> , 2013, 29, 2971-2978. | 1.8 | 23 |
| 294 | High Occurrence of Functional New Chimeric Genes in Survey of Rice Chromosome 3 Short Arm Genome Sequences. <i>Genome Biology and Evolution</i> , 2013, 5, 1038-1048. | 1.1 | 11 |
| 295 | RNA sequencing reveals the complex regulatory network in the maize kernel. <i>Nature Communications</i> , 2013, 4, 2832. | 5.8 | 252 |
| 296 | Genetic Recombination Is Targeted towards Gene Promoter Regions in Dogs. <i>PLoS Genetics</i> , 2013, 9, e1003984. | 1.5 | 198 |
| 297 | The Wilms Tumor Gene, <i>Wt1</i> , Is Critical for Mouse Spermatogenesis via Regulation of Sertoli Cell Polarity and Is Associated with Non-Obstructive Azoospermia in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003645. | 1.5 | 109 |
| 298 | Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. <i>PLoS Genetics</i> , 2013, 9, e1003530. | 1.5 | 112 |
| 299 | Dissecting yield-associated loci in super hybrid rice by resequencing recombinant inbred lines and improving parental genome sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14492-14497. | 3.3 | 155 |
| 300 | SOAPindel: Efficient identification of indels from short paired reads. <i>Genome Research</i> , 2013, 23, 195-200. | 2.4 | 115 |
| 301 | Bajji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013, 4, 2708. | 5.8 | 93 |
| 302 | Integrative analyses of gene expression and DNA methylation profiles in breast cancer cell line models of tamoxifen-resistance indicate a potential role of cells with stem-like properties. <i>Breast Cancer Research</i> , 2013, 15, R119. | 2.2 | 46 |
| 303 | A population model for genotyping indels from next-generation sequence data. <i>Nucleic Acids Research</i> , 2013, 41, e46-e46. | 6.5 | 12 |
| 304 | Mutations in <i>ABCB6</i> Cause Dyschromatosis Universalis Hereditaria. <i>Journal of Investigative Dermatology</i> , 2013, 133, 2221-2228. | 0.3 | 80 |
| 305 | Genome sequence of ground tit <i>Pseudopodoces humilis</i> and its adaptation to high altitude. <i>Genome Biology</i> , 2013, 14, R29. | 13.9 | 81 |
| 306 | Comprehensive Mutation Analysis by Whole-Exome Sequencing in 41 Chinese Families With Leber Congenital Amaurosis. , 2013, 54, 4351. | | 93 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 307 | Six Mutations in AAGAB Confirm Its Pathogenic Role in Chinese Punctate Palmoplantar Keratoderma Patients. <i>Journal of Investigative Dermatology</i> , 2013, 133, 2631-2634. | 0.3 | 11 |
| 308 | Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858. | 5.8 | 229 |
| 309 | Lack of evidence for existence of noncanonical RNA editing. <i>Nature Biotechnology</i> , 2013, 31, 19-20. | 9.4 | 87 |
| 310 | Whole-exome sequencing identifies a polymorphism in the BMP5 gene associated with SSRI treatment response in major depression. <i>Journal of Psychopharmacology</i> , 2013, 27, 915-920. | 2.0 | 31 |
| 311 | Draft genome sequence of the mulberry tree <i>Morus notabilis</i> . <i>Nature Communications</i> , 2013, 4, 2445. | 5.8 | 277 |
| 312 | Whole exome sequencing of insulinoma reveals recurrent T372R mutations in YY1. <i>Nature Communications</i> , 2013, 4, 2810. | 5.8 | 137 |
| 313 | Historical variations in mutation rate in an epidemic pathogen, <i>Yersinia pestis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 577-582. | 3.3 | 373 |
| 314 | The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013, 4, 2433. | 5.8 | 217 |
| 315 | Analysis of elite variety tag SNPs reveals an important allele in upland rice. <i>Nature Communications</i> , 2013, 4, 2138. | 5.8 | 43 |
| 316 | Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013, 23, 1422-1433. | 2.4 | 457 |
| 317 | ReSeqTools: an integrated toolkit for large-scale next-generation sequencing based resequencing analysis. <i>Genetics and Molecular Research</i> , 2013, 12, 6275-6283. | 0.3 | 25 |
| 318 | Sorafenib Inhibits Epithelial-Mesenchymal Transition through an Epigenetic-Based Mechanism in Human Lung Epithelial Cells. <i>PLoS ONE</i> , 2013, 8, e64954. | 1.1 | 30 |
| 319 | Exome Sequencing of 47 Chinese Families with Cone-Rod Dystrophy: Mutations in 25 Known Causative Genes. <i>PLoS ONE</i> , 2013, 8, e65546. | 1.1 | 52 |
| 320 | An Integrated Tool to Study MHC Region: Accurate SNV Detection and HLA Genes Typing in Human MHC Region Using Targeted High-Throughput Sequencing. <i>PLoS ONE</i> , 2013, 8, e69388. | 1.1 | 63 |
| 321 | Exome Sequencing and Linkage Analysis Identified Tenascin-C (TNC) as a Novel Causative Gene in Nonsyndromic Hearing Loss. <i>PLoS ONE</i> , 2013, 8, e69549. | 1.1 | 46 |
| 322 | Exome Sequencing and Functional Analysis Identifies a Novel Mutation in EXT1 Gene That Causes Multiple Osteochondromas. <i>PLoS ONE</i> , 2013, 8, e72316. | 1.1 | 14 |
| 323 | Development of Transgenic Minipigs with Expression of Antimorphic Human Cryptochrome 1. <i>PLoS ONE</i> , 2013, 8, e76098. | 1.1 | 9 |
| 324 | Identification of CHIP as a Novel Causative Gene for Autosomal Recessive Cerebellar Ataxia. <i>PLoS ONE</i> , 2013, 8, e81884. | 1.1 | 86 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 325 | Human Gut Microbial Gene by Metagenomic Sequencing. , 2013, , 1-8. | | 1 |
| 326 | Divergent Evolutionary and Expression Patterns between Lineage Specific New Duplicate Genes and Their Parental Paralogs in Arabidopsis thaliana. PLoS ONE, 2013, 8, e72362. | 1.1 | 19 |
| 327 | Genes Contributing to Pain Sensitivity in the Normal Population: An Exome Sequencing Study. PLoS Genetics, 2012, 8, e1003095. | 1.5 | 49 |
| 328 | The genome of Prunus mume. Nature Communications, 2012, 3, 1318. | 5.8 | 441 |
| 329 | Exome sequencing identified a missense mutation of <i>EPS8L3</i> in Marie Unna hereditary hypotrichosis. Journal of Medical Genetics, 2012, 49, 727-730. | 1.5 | 19 |
| 330 | An exome sequencing pipeline for identifying and genotyping common CNVs associated with disease with application to psoriasis. Bioinformatics, 2012, 28, i370-i374. | 1.8 | 24 |
| 331 | Low frequency of DNMT3A mutations in pediatric AML, and the identification of the OCI-AML3 cell line as an in vitro model. Leukemia, 2012, 26, 371-373. | 3.3 | 34 |
| 332 | Extensive X-linked adaptive evolution in central chimpanzees. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2054-2059. | 3.3 | 79 |
| 333 | Genome interpretation and assembly—recent progress and next steps. Nature Biotechnology, 2012, 30, 1081-1083. | 9.4 | 10 |
| 334 | The genome of flax (<i>Linum usitatissimum</i>) assembled <i>de novo</i> from short shotgun sequence reads. Plant Journal, 2012, 72, 461-473. | 2.8 | 415 |
| 335 | Whole-Genome Sequencing in Autism Identifies Hot Spots for De Novo Germline Mutation. Cell, 2012, 151, 1431-1442. | 13.5 | 501 |
| 336 | Exome sequencing identifies a <i>COL14A1</i> mutation in a large Chinese pedigree with punctate palmoplantar keratoderma. Journal of Medical Genetics, 2012, 49, 563-568. | 1.5 | 34 |
| 337 | A genome triplication associated with early diversification of the core eudicots. Genome Biology, 2012, 13, R3. | 13.9 | 389 |
| 338 | Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. Genome Biology, 2012, 13, R35. | 13.9 | 113 |
| 339 | Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. Nature Genetics, 2012, 44, 765-769. | 9.4 | 785 |
| 340 | Rare inborn errors associated with chronic hepatitis B virus infection*. Hepatology, 2012, 56, 1661-1670. | 3.6 | 30 |
| 341 | Clinical application of massively parallel sequencing-based prenatal noninvasive fetal trisomy test for trisomies 21 and 18 in 11% pregnancies with mixed risk factors. Prenatal Diagnosis, 2012, 32, 1225-1232. | 1.1 | 197 |
| 342 | Systematic assessment of reduced representation bisulfite sequencing to human blood samples: A promising method for large-sample-scale epigenomic studies. Journal of Biotechnology, 2012, 157, 1-6. | 1.9 | 44 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 343 | RNA-seq analysis of prostate cancer in the Chinese population identifies recurrent gene fusions, cancer-associated long noncoding RNAs and aberrant alternative splicings. <i>Cell Research</i> , 2012, 22, 806-821. | 5.7 | 352 |
| 344 | Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398. | 13.7 | 1,190 |
| 345 | Exome sequencing identifies MVK mutations in disseminated superficial actinic porokeratosis. <i>Nature Genetics</i> , 2012, 44, 1156-1160. | 9.4 | 124 |
| 346 | Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 253-260. | 9.4 | 461 |
| 347 | A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012, 490, 55-60. | 13.7 | 5,345 |
| 348 | A comparative analysis of the intestinal metagenomes present in guinea pigs (<i>Cavia porcellus</i>) and humans (<i>Homo sapiens</i>). <i>BMC Genomics</i> , 2012, 13, 514. | 1.2 | 43 |
| 349 | Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. <i>Cell</i> , 2012, 148, 886-895. | 13.5 | 622 |
| 350 | Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885. | 13.5 | 503 |
| 351 | Deciphering neo-sex and B chromosome evolution by the draft genome of <i>Drosophila albomicans</i> . <i>BMC Genomics</i> , 2012, 13, 109. | 1.2 | 64 |
| 352 | Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. <i>BMC Genomics</i> , 2012, 13, 300. | 1.2 | 266 |
| 353 | Noninvasive Fetal Trisomy (NIFTY) test: an advanced noninvasive prenatal diagnosis methodology for fetal autosomal and sex chromosomal aneuploidies. <i>BMC Medical Genomics</i> , 2012, 5, 57. | 0.7 | 132 |
| 354 | Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012, 1, 12. | 3.3 | 99 |
| 355 | The sequence and analysis of a Chinese pig genome. <i>GigaScience</i> , 2012, 1, 16. | 3.3 | 125 |
| 356 | SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. <i>GigaScience</i> , 2012, 1, 18. | 3.3 | 4,510 |
| 357 | An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65. | 13.7 | 7,199 |
| 358 | The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54. | 13.7 | 1,966 |
| 359 | The draft genome of a diploid cotton <i>Gossypium raimondii</i> . <i>Nature Genetics</i> , 2012, 44, 1098-1103. | 9.4 | 935 |
| 360 | Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89. | 9.4 | 788 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 361 | Frequent mutations of genes encoding ubiquitin-mediated proteolysis pathway components in clear cell renal cell carcinoma. <i>Nature Genetics</i> , 2012, 44, 17-19. | 9.4 | 295 |
| 362 | Genome-wide and Caste-Specific DNA Methylomes of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Current Biology</i> , 2012, 22, 1755-1764. | 1.8 | 361 |
| 363 | Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807. | 9.4 | 577 |
| 364 | Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111. | 9.4 | 818 |
| 365 | Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225. | 9.4 | 383 |
| 366 | The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641. | 13.7 | 2,860 |
| 367 | Transcriptome and Network Changes in Climbers at Extreme Altitudes. <i>PLoS ONE</i> , 2012, 7, e31645. | 1.1 | 21 |
| 368 | Exome Sequencing Identifies Compound Heterozygous Mutations in CYP4V2 in a Pedigree with Retinitis Pigmentosa. <i>PLoS ONE</i> , 2012, 7, e33673. | 1.1 | 40 |
| 369 | MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656. | 1.1 | 208 |
| 370 | An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. <i>Science</i> , 2012, 337, 100-104. | 6.0 | 626 |
| 371 | An atlas of DNA methylomes in porcine adipose and muscle tissues. <i>Nature Communications</i> , 2012, 3, 850. | 5.8 | 152 |
| 372 | Insights into salt tolerance from the genome of <i>Thellungiella salsuginea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12219-12224. | 3.3 | 272 |
| 373 | Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811. | 9.4 | 816 |
| 374 | Comparative genomics of rhizobia nodulating soybean suggests extensive recruitment of lineage-specific genes in adaptations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8629-8634. | 3.3 | 234 |
| 375 | A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828. | 6.0 | 1,095 |
| 376 | Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527. | 3.3 | 687 |
| 377 | Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012, 30, 549-554. | 9.4 | 636 |
| 378 | Retrogenes Moved Out of the Z Chromosome in the Silkworm. <i>Journal of Molecular Evolution</i> , 2012, 74, 113-126. | 0.8 | 41 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 379 | The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012, 44, 946-949. | 9.4 | 708 |
| 380 | InterStoreDB: A Generic Integration Resource for Genetic and Genomic Data. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 345-355. | 4.1 | 13 |
| 381 | Identification of ten serum microRNAs from a genome-wide serum microRNA expression profile as novel noninvasive biomarkers for nonsmall cell lung cancer diagnosis. <i>International Journal of Cancer</i> , 2012, 130, 1620-1628. | 2.3 | 251 |
| 382 | Bisulfite Sequencing Reveals That <i>Aspergillus flavus</i> Holds a Hollow in DNA Methylation. <i>PLoS ONE</i> , 2012, 7, e30349. | 1.1 | 74 |
| 383 | SNP Calling, Genotype Calling, and Sample Allele Frequency Estimation from New-Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e37558. | 1.1 | 336 |
| 384 | An Effort to Use Human-Based Exome Capture Methods to Analyze Chimpanzee and Macaque Exomes. <i>PLoS ONE</i> , 2012, 7, e40637. | 1.1 | 28 |
| 385 | Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195. | 13.7 | 1,912 |
| 386 | Frequent mutations of chromatin remodeling genes in transitional cell carcinoma of the bladder. <i>Nature Genetics</i> , 2011, 43, 875-878. | 9.4 | 638 |
| 387 | Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. <i>Nature Biotechnology</i> , 2011, 29, 723-730. | 9.4 | 113 |
| 388 | Non-invasive prenatal assessment of trisomy 21 by multiplexed maternal plasma DNA sequencing: large scale validity study. <i>BMJ: British Medical Journal</i> , 2011, 342, c7401-c7401. | 2.4 | 641 |
| 389 | Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011, 29, 1019-1023. | 9.4 | 284 |
| 390 | Open-Source Genomic Analysis of Shiga-Toxin-Producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , 2011, 365, 718-724. | 13.9 | 392 |
| 391 | Confirmation by Exome Sequencing of the Pathogenic Role of NCSTN Mutations in Acne Inversa (Hidradenitis Suppurativa). <i>Journal of Investigative Dermatology</i> , 2011, 131, 1570-1572. | 0.3 | 78 |
| 392 | Analysis of expressed sequence tags from biodiesel plant <i>Jatropha curcas</i> embryos at different developmental stages. <i>Plant Science</i> , 2011, 181, 696-700. | 1.7 | 35 |
| 393 | Genome sequence and global sequence variation map with 5.5 million SNPs in Chinese rhesus macaque. <i>Genome Biology</i> , 2011, 12, R63. | 3.8 | 35 |
| 394 | Comprehensive comparison of three commercial human whole-exome capture platforms. <i>Genome Biology</i> , 2011, 12, R95. | 13.9 | 145 |
| 395 | The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011, 29, 735-741. | 9.4 | 699 |
| 396 | Genome-Wide Mapping of DNA Methylation in Chicken. <i>PLoS ONE</i> , 2011, 6, e19428. | 1.1 | 116 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 397 | Global Mapping of H3K4me1 and H3K4me3 Reveals the Chromatin State-Based Cell Type-Specific Gene Regulation in Human Treg Cells. PLoS ONE, 2011, 6, e27770. | 1.1 | 32 |
| 398 | Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65. | 13.7 | 991 |
| 399 | Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180. | 13.7 | 5,800 |
| 400 | Genome sequencing reveals insights into physiology and longevity of the naked mole rat. Nature, 2011, 479, 223-227. | 13.7 | 517 |
| 401 | The genome of the mesopolyploid crop species <i>Brassica rapa</i> . Nature Genetics, 2011, 43, 1035-1039. | 9.4 | 1,893 |
| 402 | Noninvasive Prenatal Diagnosis of Fetal Trisomy 18 and Trisomy 13 by Maternal Plasma DNA Sequencing. PLoS ONE, 2011, 6, e21791. | 1.1 | 243 |
| 403 | <i>Ascaris suum</i> draft genome. Nature, 2011, 479, 529-533. | 13.7 | 246 |
| 404 | The making of a new pathogen: Insights from comparative population genomics of the domesticated wheat pathogen <i>Mycosphaerella graminicola</i> and its wild sister species. Genome Research, 2011, 21, 2157-2166. | 2.4 | 191 |
| 405 | An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98. | 6.0 | 675 |
| 406 | Homozygous carriers of the G allele of rs4664447 of the glucagon gene (GCG) are characterised by decreased fasting and stimulated levels of insulin, glucagon and glucagon-like peptide (GLP)-1. Diabetologia, 2011, 54, 2820-2831. | 2.9 | 16 |
| 407 | Estimation of allele frequency and association mapping using next-generation sequencing data. BMC Bioinformatics, 2011, 12, 231. | 1.2 | 170 |
| 408 | Genome Sequence of the Spinosyns-Producing Bacterium <i>Saccharopolyspora spinosa</i> NRRL 18395. Journal of Bacteriology, 2011, 193, 5606-5606. | 1.0 | 1 |
| 409 | The genome of the leaf-cutting ant <i>Acromyrmex echinator</i> suggests key adaptations to advanced social life and fungus farming. Genome Research, 2011, 21, 1339-1348. | 2.4 | 210 |
| 410 | Genome Sequence of the Spinosyns-Producing Bacterium <i>Saccharopolyspora spinosa</i> NRRL 18395. Journal of Bacteriology, 2011, 193, 3150-3151. | 1.0 | 21 |
| 411 | Personal Genomes: For One and for All. Science, 2011, 331, 690-690. | 6.0 | 3 |
| 412 | Exome Sequencing Identifies ZNF644 Mutations in High Myopia. PLoS Genetics, 2011, 7, e1002084. | 1.5 | 164 |
| 413 | Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326. | 1.5 | 146 |
| 414 | Comparison of Gene Expression and Genome-Wide DNA Methylation Profiling between Phenotypically Normal Cloned Pigs and Conventionally Bred Controls. PLoS ONE, 2011, 6, e25901. | 1.1 | 22 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 415 | The naked mole rat genome: understanding aging through genome analysis. <i>Aging</i> , 2011, 3, 1124-1124. | 1.4 | 8 |
| 416 | Multiple gene dysfunctions lead to high cancer-susceptibility: evidences from a whole-exome sequencing study. <i>American Journal of Cancer Research</i> , 2011, 1, 562-73. | 1.4 | 4 |
| 417 | Exome sequencing and unrelated findings in the context of complex disease research: ethical and clinical implications. <i>Discovery Medicine</i> , 2011, 12, 41-55. | 0.5 | 49 |
| 418 | State of the art de novo assembly of human genomes from massively parallel sequencing data. <i>Human Genomics</i> , 2010, 4, 271. | 1.4 | 74 |
| 419 | Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. <i>Science</i> , 2010, 329, 75-78. | 6.0 | 1,339 |
| 420 | Sequencing, annotation and comparative analysis of nine BACs of giant panda (<i>Ailuropoda</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 T | 2.3 | 6 |
| 421 | Genetic diversity, molecular phylogeny and selection evidence of the silkworm mitochondria implicated by complete resequencing of 41 genomes. <i>BMC Evolutionary Biology</i> , 2010, 10, 81. | 3.2 | 40 |
| 422 | Pig genome sequence - analysis and publication strategy. <i>BMC Genomics</i> , 2010, 11, 438. | 1.2 | 132 |
| 423 | Design of association studies with pooled or unâ€ooled nextâ€generation sequencing data. <i>Genetic Epidemiology</i> , 2010, 34, 479-491. | 0.6 | 76 |
| 424 | The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317. | 13.7 | 1,058 |
| 425 | A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65. | 13.7 | 9,342 |
| 426 | Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762. | 13.7 | 750 |
| 427 | A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073. | 13.7 | 7,209 |
| 428 | Building the sequence map of the human pan-genome. <i>Nature Biotechnology</i> , 2010, 28, 57-63. | 9.4 | 237 |
| 429 | Single baseâ€resolution methylome of the silkworm reveals a sparse epigenomic map. <i>Nature Biotechnology</i> , 2010, 28, 516-520. | 9.4 | 349 |
| 430 | Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , 2010, 42, 969-972. | 9.4 | 297 |
| 431 | Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030. | 9.4 | 439 |
| 432 | Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010, 42, 1053-1059. | 9.4 | 987 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 433 | Ten years of genetics and genomics: what have we achieved and where are we heading?. <i>Nature Reviews Genetics</i> , 2010, 11, 723-733. | 7.7 | 65 |
| 434 | UCP1 Induction during Recruitment of Brown Adipocytes in White Adipose Tissue Is Dependent on Cyclooxygenase Activity. <i>PLoS ONE</i> , 2010, 5, e11391. | 1.1 | 174 |
| 435 | SilkDB v2.0: a platform for silkworm (<i>Bombyx mori</i>) genome biology. <i>Nucleic Acids Research</i> , 2010, 38, D453-D456. | 6.5 | 239 |
| 436 | Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 2010, 329, 1068-1071. | 6.0 | 420 |
| 437 | Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010, 20, 646-654. | 2.4 | 435 |
| 438 | The DNA Methylome of Human Peripheral Blood Mononuclear Cells. <i>PLoS Biology</i> , 2010, 8, e1000533. | 2.6 | 290 |
| 439 | TGM6 identified as a novel causative gene of spinocerebellar ataxias using exome sequencing. <i>Brain</i> , 2010, 133, 3510-3518. | 3.7 | 243 |
| 440 | ADD1/SREBP1c activates the PGC1- β promoter in brown adipocytes. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2010, 1801, 421-429. | 1.2 | 20 |
| 441 | Whole genome DNA methylation analysis based on high throughput sequencing technology. <i>Methods</i> , 2010, 52, 203-212. | 1.9 | 180 |
| 442 | De novo assembly of human genomes with massively parallel short read sequencing. <i>Genome Research</i> , 2010, 20, 265-272. | 2.4 | 2,516 |
| 443 | Evolutionary Transients in the Rice Transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 211-228. | 3.0 | 9 |
| 444 | Integrated Profiling of MicroRNAs and mRNAs: MicroRNAs Located on Xq27.3 Associate with Clear Cell Renal Cell Carcinoma. <i>PLoS ONE</i> , 2010, 5, e15224. | 1.1 | 573 |
| 445 | A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, . | 1.6 | 73 |
| 446 | SNP detection for massively parallel whole-genome resequencing. <i>Genome Research</i> , 2009, 19, 1124-1132. | 2.4 | 855 |
| 447 | Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm (<i>Bombyx mori</i>). <i>PLoS ONE</i> , 2010, 5, e15224. | 6.0 | 342 |
| 448 | Correlation Between Ka/Ks and Ks is Related to Substitution Model and Evolutionary Lineage. <i>Journal of Molecular Evolution</i> , 2009, 68, 414-423. | 0.8 | 71 |
| 449 | Haplotype frequencies in a sub-region of chromosome 19q13.3, related to risk and prognosis of cancer, differ dramatically between ethnic groups. <i>BMC Medical Genetics</i> , 2009, 10, 20. | 2.1 | 16 |
| 450 | The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , 2009, 460, 345-351. | 13.7 | 635 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 451 | Faster human genome sequencing. <i>Nature Biotechnology</i> , 2009, 27, 820-821. | 9.4 | 18 |
| 452 | The genome of the cucumber, <i>Cucumis sativus</i> L.. <i>Nature Genetics</i> , 2009, 41, 1275-1281. | 9.4 | 1,317 |
| 453 | SOAP2: an improved ultrafast tool for short read alignment. <i>Bioinformatics</i> , 2009, 25, 1966-1967. | 1.8 | 3,329 |
| 454 | Identification and characterization of novel amphioxus microRNAs by Solexa sequencing. <i>Genome Biology</i> , 2009, 10, R78. | 13.9 | 136 |
| 455 | The YH database: the first Asian diploid genome database. <i>Nucleic Acids Research</i> , 2009, 37, D1025-D1028. | 6.5 | 37 |
| 456 | The research progress of tiling array technology and applications. <i>Science Bulletin</i> , 2008, 53, 817-824. | 4.3 | 4 |
| 457 | 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 |
| 458 | Characterization of microRNAs in serum: a novel class of biomarkers for diagnosis of cancer and other diseases. <i>Cell Research</i> , 2008, 18, 997-1006. | 5.7 | 4,084 |
| 459 | The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65. | 13.7 | 834 |
| 460 | Gene conversion in the rice genome. <i>BMC Genomics</i> , 2008, 9, 93. | 1.2 | 42 |
| 461 | Neo-sex chromosomes in the black muntjac recapitulate incipient evolution of mammalian sex chromosomes. <i>Genome Biology</i> , 2008, 9, R98. | 13.9 | 36 |
| 462 | Analysis of 142 genes resolves the rapid diversification of the rice genus. <i>Genome Biology</i> , 2008, 9, R49. | 13.9 | 124 |
| 463 | The genome of a lepidopteran model insect, the silkworm <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1036-1045. | 1.2 | 592 |
| 464 | SOAP: short oligonucleotide alignment program. <i>Bioinformatics</i> , 2008, 24, 713-714. | 1.8 | 2,766 |
| 465 | Genome-wide assessment of worldwide chicken SNP genetic diversity indicates significant absence of rare alleles in commercial breeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17312-17317. | 3.3 | 230 |
| 466 | Recurrent Positive Selection of the <i>Drosophila</i> Hybrid Incompatibility Gene Hmr. <i>Molecular Biology and Evolution</i> , 2008, 25, 2421-2430. | 3.5 | 38 |
| 467 | New Variants of Nav1.5/SCN5A Encode Na ⁺ Channels in the Brain. <i>Journal of Neurogenetics</i> , 2008, 22, 57-75. | 0.6 | 19 |
| 468 | FGF: A web tool for Fishing Gene Family in a whole genome database. <i>Nucleic Acids Research</i> , 2007, 35, W121-W125. | 6.5 | 6 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 469 | PigGIS: Pig Genomic Informatics System. <i>Nucleic Acids Research</i> , 2007, 35, D654-D657. | 6.5 | 9 |
| 470 | Snap: an integrated SNP annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, D707-D710. | 6.5 | 36 |
| 471 | TreeFam: 2008 Update. <i>Nucleic Acids Research</i> , 2007, 36, D735-D740. | 6.5 | 294 |
| 472 | A cross-species alignment tool (CAT). <i>BMC Bioinformatics</i> , 2007, 8, 349. | 1.2 | 4 |
| 473 | 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 |
| 474 | A Glimpse of Streptococcal Toxic Shock Syndrome from Comparative Genomics of <i>S. suis</i> 2 Chinese Isolates. <i>PLoS ONE</i> , 2007, 2, e315. | 1.1 | 244 |
| 475 | Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218. | 13.7 | 1,886 |
| 476 | Identification and characterization of insect-specific proteins by genome data analysis. <i>BMC Genomics</i> , 2007, 8, 93. | 1.2 | 38 |
| 477 | BGI-RIS V2. , 2007, 406, 275-299. | | 4 |
| 478 | Detecting positive darwinian selection in brain-expressed genes during human evolution. <i>Science Bulletin</i> , 2007, 52, 324-335. | 1.7 | 3 |
| 479 | High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. <i>Plant Cell</i> , 2006, 18, 1791-1802. | 3.1 | 207 |
| 480 | KaKs_Calculator: Calculating Ka and Ks Through Model Selection and Model Averaging. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 259-263. | 3.0 | 940 |
| 481 | Mitochondrial molecular clocks and the origin of the major Otocephalan clades (Pisces: Teleostei): A new insight. <i>Gene</i> , 2006, 370, 113-124. | 1.0 | 84 |
| 482 | Detecting lineage-specific adaptive evolution of brain-expressed genes in human using rhesus macaque as outgroup. <i>Genomics</i> , 2006, 88, 745-751. | 1.3 | 111 |
| 483 | Genome-wide transcription analyses in rice using tiling microarrays. <i>Nature Genetics</i> , 2006, 38, 124-129. | 9.4 | 154 |
| 484 | The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198. | 13.7 | 53 |
| 485 | Genomic comparison of <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> by combination of suppression subtractive hybridization and DNA microarray. <i>Archives of Microbiology</i> , 2006, 186, 151-159. | 1.0 | 20 |
| 486 | TreeFam: a curated database of phylogenetic trees of animal gene families. <i>Nucleic Acids Research</i> , 2006, 34, D572-D580. | 6.5 | 465 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 487 | WEGO: a web tool for plotting GO annotations. <i>Nucleic Acids Research</i> , 2006, 34, W293-W297. | 6.5 | 2,529 |
| 488 | 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 |
| 489 | Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , 2005, 6, 70. | 1.2 | 283 |
| 490 | A Pilot Study of Transcription Unit Analysis in Rice Using Oligonucleotide Tiling-path Microarray. <i>Plant Molecular Biology</i> , 2005, 59, 137-149. | 2.0 | 17 |
| 491 | The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38. | 2.6 | 808 |
| 492 | ReAS: Recovery of Ancestral Sequences for Transposable Elements from the Unassembled Reads of a Whole Genome Shotgun. <i>PLoS Computational Biology</i> , 2005, 1, e43. | 1.5 | 93 |
| 493 | Detecting novel low-abundant transcripts in <i>Drosophila</i> . <i>Rna</i> , 2005, 11, 939-946. | 1.6 | 34 |
| 494 | Accelerated Evolution of the Pituitary Adenylate Cyclase-Activating Polypeptide Precursor Gene During Human Origin. <i>Genetics</i> , 2005, 170, 801-806. | 1.2 | 25 |
| 495 | A microarray analysis of the rice transcriptome and its comparison to <i>Arabidopsis</i> . <i>Genome Research</i> , 2005, 15, 1274-1283. | 2.4 | 112 |
| 496 | Pseudogene accumulation might promote the adaptive microevolution of <i>Yersinia pestis</i> . <i>Journal of Medical Microbiology</i> , 2005, 54, 259-268. | 0.7 | 35 |
| 497 | Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005, 15, 1258-1264. | 2.4 | 91 |
| 498 | Tiling microarray analysis of rice chromosome 10 to identify the transcriptome and relate its expression to chromosomal architecture. <i>Genome Biology</i> , 2005, 6, R52. | 13.9 | 41 |
| 499 | A Comparison of Rice Chloroplast Genomes. <i>Plant Physiology</i> , 2004, 135, 412-420. | 2.3 | 142 |
| 500 | 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 |
| 501 | 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 |
| 502 | ChickVD: a sequence variation database for the chicken genome. <i>Nucleic Acids Research</i> , 2004, 33, D438-D441. | 6.5 | 33 |
| 503 | SilkDB: a knowledgebase for silkworm biology and genomics. <i>Nucleic Acids Research</i> , 2004, 33, D399-D402. | 6.5 | 158 |
| 504 | The analysis of large-scale gene expression correlated to the phase changes of the migratory locust. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17611-17615. | 3.3 | 197 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 505 | Neutral evolution of 'non-coding' complementary DNAs. <i>Nature</i> , 2004, 431, 1-2. | 13.7 | 127 |
| 506 | A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722. | 13.7 | 391 |
| 507 | 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 |
| 508 | A Draft Sequence for the Genome of the Domesticated Silkworm (<i>Bombyx mori</i>). <i>Science</i> , 2004, 306, 1937-1940. | 6.0 | 994 |
| 509 | Mouse transcriptome: neutral evolution of 'non-coding' complementary DNAs. <i>Nature</i> , 2004, 431, 1 p following 757; discussion following 757. | 13.7 | 86 |
| 510 | Vertebrate gene predictions and the problem of large genes. <i>Nature Reviews Genetics</i> , 2003, 4, 741-749. | 7.7 | 56 |
| 511 | 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 |
| 512 | A Statistical Approach Designed for Finding Mathematically Defined Repeats in Shotgun Data and Determining the Length Distribution of Clone-Inserts. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 43-51. | 3.0 | 7 |
| 513 | 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 |
| 514 | Evolution and Variation of the SARS-CoV Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 216-225. | 3.0 | 16 |
| 515 | RePS: A Sequence Assembler That Masks Exact Repeats Identified from the Shotgun Data. <i>Genome Research</i> , 2002, 12, 824-831. | 2.4 | 62 |
| 516 | Compositional Gradients in Gramineae Genes. <i>Genome Research</i> , 2002, 12, 851-856. | 2.4 | 166 |
| 517 | 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 |
| 518 | Genomic organization, transcript variants and comparative analysis of the human nucleoporin 155 (NUP155) gene. <i>Gene</i> , 2002, 288, 9-18. | 1.0 | 9 |
| 519 | A draft sequence of the rice (<i>Oryza sativa</i> ssp.indica) genome. <i>Science Bulletin</i> , 2001, 46, 1937-1942. | 1.7 | 35 |