

Song-Nian Hu

List of Publications by Year in descending order

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267
papers

18,932
citations

19608

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all docs

273
docs citations

273
times ranked

25339
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome of the Giant Panda Roundworm Illuminates Its Host Shift and Parasitic Adaptation. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 366-381.	3.0	13
2	Improvements of immune genes and intestinal microbiota composition of turbot (<i>Scophthalmus</i>) Tj ETQq0 0 0 rgBTJ Overlock 10 Tf 50	1.7	19
3	VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. <i>Nucleic Acids Research</i> , 2022, 50, D888-D897.	6.5	18
4	Monitoring microbial communities in intensive care units over one year in China. <i>Science of the Total Environment</i> , 2022, 811, 152353.	3.9	10
5	The Dissemination of NDM-1 in <i>Acinetobacter baumannii</i> Strains. <i>Current Microbiology</i> , 2022, 79, 117.	1.0	3
6	gcCov: Linked open data for global coronavirus studies. , 2022, 1, 92-95.		2
7	Amplicon-based sequencing and co-occurrence network analysis reveals notable differences of microbial community structure in healthy and dandruff scalps. <i>BMC Genomics</i> , 2022, 23, 312.	1.2	2
8	Genomic Characterization of a Uropathogenic <i>Escherichia coli</i> ST405 Isolate Harboring blaCTX-M-15-Encoding IncFIA-FIB Plasmid, blaCTX-M-24-Encoding IncI1 Plasmid, and Phage-Like Plasmid. <i>Frontiers in Microbiology</i> , 2022, 13, 845045.	1.5	2
9	Identification of a Putative CodY Regulon in the Gram-Negative Phylum Synergistetes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7911.	1.8	0
10	Complete sequences of two new KPC-harboring plasmids in <i>Klebsiella pneumoniae</i> ST11 strains in China. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 24, 114-120.	0.9	3
11	Genetic tracing of HCoV-19 for the re-emerging outbreak of COVID-19 in Beijing, China. <i>Protein and Cell</i> , 2021, 12, 4-6.	4.8	13
12	A Method for Estimating 24-Hour Urinary Sodium Excretion by Casual Urine Specimen in Chinese Hypertensive Patients. <i>American Journal of Hypertension</i> , 2021, 34, 718-728.	1.0	6
13	Association of CYP3A5 Gene Polymorphisms and Amlodipine-Induced Peripheral Edema in Chinese Han Patients with Essential Hypertension. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 189-197.	0.4	6
14	Selection for Cheaper Amino Acids Drives Nucleotide Usage at the Start of Translation in Eukaryotic Genes. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 949-957.	3.0	4
15	Evolutionary analysis and lineage designation of SARS-CoV-2 genomes. <i>Science Bulletin</i> , 2021, 66, 2297-2311.	4.3	26
16	Identifying Two Novel Clusters in Calcium Oxalate Stones With Urinary Tract Infection Using 16S rDNA Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 723781.	1.8	3
17	Improved 93-11 Genome and Time-Course Transcriptome Expand Resources for Rice Genomics. <i>Frontiers in Plant Science</i> , 2021, 12, 769700.	1.7	4
18	Genomic and transcriptome identification of fluconazole-resistant genes for <i>Trichosporon asahii</i> . <i>Medical Mycology</i> , 2020, 58, 393-400.	0.3	5

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19	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 161-172.	3.0	18
20	Identification of a <i>SCN4A</i> mutation in a large Chinese family with atypical normokalemic periodic paralysis using whole-exome sequencing. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095364.	0.4	1
21	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
22	A fine-scale map of genome-wide recombination in divergent <i>Escherichia coli</i> population. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	3
23	Genetic factors related to the widespread dissemination of ST11 extensively drug-resistant carbapenemase-producing <i>Klebsiella pneumoniae</i> strains within hospital. <i>Chinese Medical Journal</i> , 2020, 133, 2573-2585.	0.9	4
24	Structural and Functional Annotation of Transposable Elements Revealed a Potential Regulation of Genes Involved in Rubber Biosynthesis by TE-Derived siRNA Interference in <i>Hevea brasiliensis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 4220.	1.8	6
25	Genome Assembly and Pathway Analysis of Edible Mushroom <i>Agrocybe cylindracea</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 341-351.	3.0	18
26	The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , 2020, 21, 60.	3.8	104
27	Gene family expansion of pinewood nematode to detoxify its host defence chemicals. <i>Molecular Ecology</i> , 2020, 29, 940-955.	2.0	23
28	Semi-rational mutagenesis of an industrial <i>Streptomyces fungicidicus</i> strain for improved enduracidin productivity. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 3459-3471.	1.7	5
29	5-Hydroxymethylcytosine signatures in circulating cell-free DNA as diagnostic and predictive biomarkers for coronary artery disease. <i>Clinical Epigenetics</i> , 2020, 12, 17.	1.8	15
30	A Reference Genome of <i>Bursaphelenchus mucronatus</i> Provides New Resources for Revealing Its Displacement by Pinewood Nematode. <i>Genes</i> , 2020, 11, 570.	1.0	10
31	Post-transcriptional regulation of several biological processes involved in latex production in <i>Hevea brasiliensis</i> . <i>PeerJ</i> , 2020, 8, e8932.	0.9	9
32	Sequencing of Chinese castor lines reveals genetic signatures of selection and yield-associated loci. <i>Nature Communications</i> , 2019, 10, 3418.	5.8	26
33	Genome structure and evolution of <i>Antirrhinum majus</i> L. <i>Nature Plants</i> , 2019, 5, 174-183.	4.7	85
34	Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. <i>Nucleic Acids Research</i> , 2019, 47, W270-W275.	6.5	564
35	Fine-Tuning of MiR528 Accumulation Modulates Flowering Time in Rice. <i>Molecular Plant</i> , 2019, 12, 1103-1113.	3.9	67
36	Transcriptomic profiling reveals MEP pathway contributing to ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>BMC Genomics</i> , 2019, 20, 383.	1.2	52

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37	Genome-wide analysis in <i>Hevea brasiliensis</i> laticifers revealed species-specific post-transcriptional regulations of several redox-related genes. <i>Scientific Reports</i> , 2019, 9, 5701.	1.6	13
38	Enhancement of oxidative stress contributes to increased pathogenicity of the invasive pine wood nematode. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180323.	1.8	24
39	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
40	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
41	Plant editosome database: a curated database of RNA editosome in plants. <i>Nucleic Acids Research</i> , 2019, 47, D170-D174.	6.5	38
42	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
43	PacBio full-length cDNA sequencing integrated with RNA-seq reads drastically improves the discovery of splicing transcripts in rice. <i>Plant Journal</i> , 2019, 97, 296-305.	2.8	90
44	REDO: RNA Editing Detection in Plant Organelles Based on Variant Calling Results. <i>Journal of Computational Biology</i> , 2018, 25, 509-516.	0.8	24
45	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
46	A novel antisense long noncoding RNA, <i>twisted leaf</i> , maintains leaf blade flattening by regulating its associated sense <i>MYB</i> gene in rice. <i>New Phytologist</i> , 2018, 218, 774-788.	3.5	96
47	MVP: a microbe-phage interaction database. <i>Nucleic Acids Research</i> , 2018, 46, D700-D707.	6.5	82
48	Comparative analysis of the <i>Monochamus alternatus</i> immune system. <i>Insect Science</i> , 2018, 25, 581-603.	1.5	15
49	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
50	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
51	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 397-404.	3.0	46
52	RGAAT: A Reference-based Genome Assembly and Annotation Tool for New Genomes and Upgrade of Known Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 373-381.	3.0	15
53	Complete Genomic Analysis of a Kingdom-Crossing <i>Klebsiella variicola</i> Isolate. <i>Frontiers in Microbiology</i> , 2018, 9, 2428.	1.5	10
54	Oral Microbiota Community Dynamics Associated With Oral Squamous Cell Carcinoma Staging. <i>Frontiers in Microbiology</i> , 2018, 9, 862.	1.5	211

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55	Immune tolerance of vector beetle to its partner plant parasitic nematode modulated by its insect parasitic nematode. <i>FASEB Journal</i> , 2018, 32, 4862-4877.	0.2	12
56	Impact of growth pH and glucose concentrations on the CodY regulatory network in <i>Streptococcus salivarius</i> . <i>BMC Genomics</i> , 2018, 19, 386.	1.2	3
57	Identification of a G2-like transcription factor, OsPHL3, functions as a negative regulator of flowering in rice by co-expression and reverse genetic analysis. <i>BMC Plant Biology</i> , 2018, 18, 157.	1.6	15
58	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
59	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
60	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
61	Genetic Alterations in Esophageal Tissues From Squamous Dysplasia to Carcinoma. <i>Gastroenterology</i> , 2017, 153, 166-177.	0.6	130
62	CYP2A6 Polymorphisms Associate with Outcomes of S-1 Plus Oxaliplatin Chemotherapy in Chinese Gastric Cancer Patients. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 255-262.	3.0	9
63	Comparative genome analysis of programmed DNA elimination in nematodes. <i>Genome Research</i> , 2017, 27, 2001-2014.	2.4	94
64	ISVASE: identification of sequence variant associated with splicing event using RNA-seq data. <i>BMC Bioinformatics</i> , 2017, 18, 320.	1.2	0
65	DRDB: An Online Date Palm Genomic Resource Database. <i>Frontiers in Plant Science</i> , 2017, 8, 1889.	1.7	20
66	A meta-analysis of the association of CKM gene rs8111989 polymorphism with sport performance. <i>Biology of Sport</i> , 2017, 34, 323-330.	1.7	20
67	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
68	UGT1A1*6, UGT1A7*3 and UGT1A9*1b polymorphisms are predictive markers for severe toxicity in patients with metastatic gastrointestinal cancer treated with irinotecan-based regimens. <i>Oncology Letters</i> , 2016, 12, 4231-4237.	0.8	11
69	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
70	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
71	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
72	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

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73	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. <i>Nature Communications</i> , 2016, 7, 11334.	5.8	104
74	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
75	The rubber tree genome reveals new insights into rubber production and species adaptation. <i>Nature Plants</i> , 2016, 2, 16073.	4.7	324
76	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
77	Conserved Intramolecular Interactions Maintain Myosin Interacting-Heads Motifs Explaining Tarantula Muscle Super-Relaxed State Structural Basis. <i>Journal of Molecular Biology</i> , 2016, 428, 1142-1164.	2.0	82
78	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
79	Identification and analysis of mouse non-coding RNA using transcriptome data. <i>Science China Life Sciences</i> , 2016, 59, 589-603.	2.3	10
80	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
81	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	6.5	41
82	Complete Sequence and Analysis of Coconut Palm (<i>Cocos nucifera</i>) Mitochondrial Genome. <i>PLoS ONE</i> , 2016, 11, e0163990.	1.1	33
83	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
84	Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. <i>BMC Genomics</i> , 2015, 16, 851.	1.2	39
85	A Critical Role for CLSP2 in the Modulation of Antifungal Immune Response in Mosquitoes. <i>PLoS Pathogens</i> , 2015, 11, e1004931.	2.1	61
86	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
87	Comparative genomic analysis of aspartic proteases in eight parasitic platyhelminths: Insights into functions and evolution. <i>Gene</i> , 2015, 559, 52-61.	1.0	6
88	MicroRNA profiles and potential regulatory pattern during the early stage of spermatogenesis in mice. <i>Science China Life Sciences</i> , 2015, 58, 442-450.	2.3	18
89	Evaluation of the optimal dosage of S-1 in adjuvant SOX chemotherapy for gastric cancer. <i>Oncology Letters</i> , 2015, 9, 1451-1457.	0.8	9
90	Deep sequencing analysis of microRNA expression in human melanocyte and melanoma cell lines. <i>Gene</i> , 2015, 572, 135-145.	1.0	15

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91	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
92	An integrated RNA-Seq and network study reveals a complex regulation process of rice embryo during seed germination. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 176-181.	1.0	20
93	Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <i>Salsola vermiculata</i> and tanshinone biosynthesis. <i>Plant Journal</i> , 2015, 82, 951-961.	2.8	337
94	Long Non-coding RNAs and Their Biological Roles in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 137-147.	3.0	231
95	Integrated analysis of gene expression and microRNA regulation in three leukemia-related lymphoblastic cell lines. <i>Gene</i> , 2015, 564, 39-52.	1.0	4
96	Comparison and evaluation of two exome capture kits and sequencing platforms for variant calling. <i>BMC Genomics</i> , 2015, 16, 581.	1.2	17
97	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
98	Genome-wide mapping of 5-hydroxymethylcytosine in three rice cultivars reveals its preferential localization in transcriptionally silent transposable element genes. <i>Journal of Experimental Botany</i> , 2015, 66, 6651-6663.	2.4	26
99	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
100	Transcriptomic and Physiological Insights into the Robustness of Long Filamentous Cells of <i>Methanosaeta harundinacea</i> , Prevalent in Upflow Anaerobic Sludge Blanket Granules. <i>Applied and Environmental Microbiology</i> , 2015, 81, 831-839.	1.4	15
101	Transcriptomic study of the red palm weevil <i>Rhynchophorus ferrugineus</i> embryogenesis. <i>Insect Science</i> , 2015, 22, 65-82.	1.5	15
102	Ethylene Response Factors Are Controlled by Multiple Harvesting Stresses in <i>Hevea brasiliensis</i> . <i>PLoS ONE</i> , 2015, 10, e0123618.	1.1	20
103	RNA-Seq Based De Novo Transcriptome Assembly and Gene Discovery of <i>Cistanche deserticola</i> Fleshy Stem. <i>PLoS ONE</i> , 2015, 10, e0125722.	1.1	14
104	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
105	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
106	A Comprehensive Transcriptomic Analysis of Infant and Adult Mouse Ovary. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 239-248.	3.0	20
107	RiceWiki: a wiki-based database for community curation of rice genes. <i>Nucleic Acids Research</i> , 2014, 42, D1222-D1228.	6.5	19
108	Dose-finding study on adjuvant chemotherapy with S-1 plus oxaliplatin for gastric cancer. <i>Molecular and Clinical Oncology</i> , 2014, 2, 93-98.	0.4	6

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109	Ribogenomics: the Science and Knowledge of RNA. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 57-63.	3.0	38
110	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
111	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	5.8	230
112	Adolescent Mouse Takes on An Active Transcriptomic Expression During Postnatal Cerebral Development. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 111-119.	3.0	4
113	Whole transcriptome RNA-seq analysis: tumorigenesis and metastasis of melanoma. <i>Gene</i> , 2014, 548, 234-243.	1.0	25
114	Transcriptional profiling of biomass degradation-related genes during <i>Trichoderma reesei</i> growth on different carbon sources. <i>Journal of Biotechnology</i> , 2014, 173, 59-64.	1.9	15
115	Characterization of miRNomes in Acute and Chronic Myeloid Leukemia Cell Lines. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 79-91.	3.0	26
116	XELIRI compared with FOLFIRI as a second-line treatment in patients with metastatic colorectal cancer. <i>Oncology Letters</i> , 2014, 8, 1864-1872.	0.8	4
117	De Novo Characterization of the Spleen Transcriptome of the Large Yellow Croaker (<i>Pseudosciaena</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 PLoS ONE, 2014, 9, e97471.	1.1	89
118	Sequence and Expression Analyses of Ethylene Response Factors Highly Expressed in Latex Cells from <i>Hevea brasiliensis</i> . <i>PLoS ONE</i> , 2014, 9, e99367.	1.1	21
119	Marine Sediment Bacteria Harbor Antibiotic Resistance Genes Highly Similar to Those Found in Human Pathogens. <i>Microbial Ecology</i> , 2013, 65, 975-981.	1.4	86
120	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
121	Dynamic transcriptomes of human myeloid leukemia cells. <i>Genomics</i> , 2013, 102, 250-256.	1.3	32
122	Transcriptome dynamics during human erythroid differentiation and development. <i>Genomics</i> , 2013, 102, 431-441.	1.3	22
123	Insight into the specific virulence related genes and toxin-antitoxin virulent pathogenicity islands in swine streptococcosis pathogen <i>Streptococcus equi</i> ssp. <i>zooepidemicus</i> strain ATCC35246. <i>BMC Genomics</i> , 2013, 14, 377.	1.2	23
124	Seasonally variable intestinal metagenomes of the red palm weevil (<i>Rhyncophorus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	42
125	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	13.7	603
126	Genome sequence of the date palm <i>Phoenix dactylifera</i> L. <i>Nature Communications</i> , 2013, 4, 2274.	5.8	248

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127	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
128	Digital Gene Expression Tag Profiling Analysis of the Gene Expression Patterns Regulating the Early Stage of Mouse Spermatogenesis. <i>PLoS ONE</i> , 2013, 8, e58680.	1.1	18
129	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
130	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
131	A large-scale gene discovery for the red palm weevil <i>Rhynchophorus ferrugineus</i> (Coleoptera: Tj ETQq1 1 0.784314, 29 BT /Over	1.5	29
132	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
133	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
134	EvoView, an online tool for visualizing, annotating and managing phylogenetic trees. <i>Nucleic Acids Research</i> , 2012, 40, W569-W572.	6.5	400
135	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
136	Replication-Associated Mutational Pressure (RMP) Governs Strand-Biased Compositional Asymmetry (SCA) and Gene Organization in Animal Mitochondrial Genomes. <i>Current Genomics</i> , 2012, 13, 28-36.	0.7	8
137	The genome and transcriptome of a newly described psychrophilic archaeon, <i>Methanohalobium psychrophilum</i> R15, reveal its cold adaptive characteristics. <i>Environmental Microbiology Reports</i> , 2012, 4, 633-641.	1.0	45
138	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
139	The Transcript-centric Mutations in Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 11-22.	3.0	21
140	An RNA-seq-based Gene Expression Profiling of Radiation-induced Tumorigenic Mammary Epithelial Cells. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 326-335.	3.0	10
141	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
142	Sequencing and analysis of four BAC clones containing innate immune genes from the Zhikong scallop (<i>Chlamys farreri</i>). <i>Gene</i> , 2012, 502, 9-15.	1.0	6
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