

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

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19	The genome sequence of <i>Salmonella enterica</i> serovar Choleraesuis, a highly invasive and resistant zoonotic pathogen. <i>Nucleic Acids Research</i> , 2005, 33, 1690-1698.	6.5	193
20	Comparative transcriptome analysis of transporters, phytohormone and lipid metabolism pathways in response to arsenic stress in rice (<i>Oryza sativa</i>). <i>New Phytologist</i> , 2012, 195, 97-112.	3.5	193
21	A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. <i>Genomics</i> , 2010, 96, 259-265.	1.3	184
22	Arginine methylation mediated by the <i>Arabidopsis</i> homolog of PRMT5 is essential for proper pre-mRNA splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19114-19119.	3.3	174
23	Plasmid-mediated quinolone resistance determinants qnr and aac(6')-Ib-cr in extended-spectrum β -lactamase-producing <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 61, 1003-1006.	1.3	169
24	Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002869.	1.5	167
25	A Comparison of Rice Chloroplast Genomes. <i>Plant Physiology</i> , 2004, 135, 412-420.	2.3	142
26	Evolution and pathogenesis of <i>Staphylococcus aureus</i> : lessons learned from genotyping and comparative genomics. <i>FEMS Microbiology Reviews</i> , 2008, 32, 23-37.	3.9	133
27	Genetic Alterations in Esophageal Tissues From Squamous Dysplasia to Carcinoma. <i>Gastroenterology</i> , 2017, 153, 166-177.	0.6	130
28	The Silkworm (<i>Bombyx mori</i>) microRNAs and Their Expressions in Multiple Developmental Stages. <i>PLoS ONE</i> , 2008, 3, e2997.	1.1	130
29	Transcriptome-wide N ⁶ -methyladenosine profiling of rice callus and leaf reveals the presence of tissue-specific competitors involved in selective mRNA modification. <i>RNA Biology</i> , 2014, 11, 1180-1188.	1.5	126
30	Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6026-E6035.	3.3	126
31	Environmental Adaptation: Genomic Analysis of the Piezotolerant and Psychrotolerant Deep-Sea Iron Reducing Bacterium <i>Shewanella piezotolerans</i> WP3. <i>PLoS ONE</i> , 2008, 3, e1937.	1.1	123
32	On the molecular mechanism of GC content variation among eubacterial genomes. <i>Biology Direct</i> , 2012, 7, 2.	1.9	121
33	The apricot (<i>Prunus armeniaca</i> L.) genome elucidates Rosaceae evolution and beta-carotenoid synthesis. <i>Horticulture Research</i> , 2019, 6, 128.	2.9	119
34	Rapid growth of a hepatocellular carcinoma and the driving mutations revealed by cell-population genetic analysis of whole-genome data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12042-12047.	3.3	117
35	Genomic Analysis of the Multidrug-Resistant <i>Acinetobacter baumannii</i> Strain MDR-ZJ06 Widely Spread in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4506-4512.	1.4	116
36	Rice Expression Database (RED): An integrated RNA-Seq-derived gene expression database for rice. <i>Journal of Genetics and Genomics</i> , 2017, 44, 235-241.	1.7	114

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

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55	MVP: a microbe-phage interaction database. <i>Nucleic Acids Research</i> , 2018, 46, D700-D707.	6.5	82
56	The Complete Chloroplast and Mitochondrial Genome Sequences of <i>Boea hygrometrica</i> : Insights into the Evolution of Plant Organellar Genomes. <i>PLoS ONE</i> , 2012, 7, e30531.	1.1	79
57	Complete Genome Sequence of the Metabolically Versatile Halophilic Archaeon <i>Haloferax mediterranei</i> , a Poly(3-Hydroxybutyrate-3-Hydroxyvalerate) Producer. <i>Journal of Bacteriology</i> , 2012, 194, 4463-4464.	1.0	75
58	Comparative analysis of mitochondrial genomes between a wheat K-type cytoplasmic male sterility (CMS) line and its maintainer line. <i>BMC Genomics</i> , 2011, 12, 163.	1.2	73
59	Ascarosides coordinate the dispersal of a plant-parasitic nematode with the metamorphosis of its vector beetle. <i>Nature Communications</i> , 2016, 7, 12341.	5.8	69
60	Functional Annotation and Analysis of Expressed Sequence Tags from the Hepatopancreas of Mitten Crab (<i>Eriocheir sinensis</i>). <i>Marine Biotechnology</i> , 2009, 11, 317-326.	1.1	68
61	Pyrosequencing the <i>Bemisia tabaci</i> Transcriptome Reveals a Highly Diverse Bacterial Community and a Robust System for Insecticide Resistance. <i>PLoS ONE</i> , 2012, 7, e35181.	1.1	67
62	Fine-Tuning of MiR528 Accumulation Modulates Flowering Time in Rice. <i>Molecular Plant</i> , 2019, 12, 1103-1113.	3.9	67
63	Identification of microRNA in the protist <i>Trichomonas vaginalis</i> . <i>Genomics</i> , 2009, 93, 487-493.	1.3	61
64	A Critical Role for CLSP2 in the Modulation of Antifungal Immune Response in Mosquitoes. <i>PLoS Pathogens</i> , 2015, 11, e1004931.	2.1	61
65	The Complete Mitochondrial Genome of <i>Gossypium hirsutum</i> and Evolutionary Analysis of Higher Plant Mitochondrial Genomes. <i>PLoS ONE</i> , 2013, 8, e69476.	1.1	58
66	An efficient procedure for plant organellar genome assembly, based on whole genome data from the 454 GS FLX sequencing platform. <i>Plant Methods</i> , 2011, 7, 38.	1.9	56
67	Biomonitoring for traditional herbal medicinal products using DNA metabarcoding and single molecule, real-time sequencing. <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 488-497.	5.7	55
68	Comparative Transcriptome Analysis of the Accessory Sex Gland and Testis from the Chinese Mitten Crab (<i>Eriocheir sinensis</i>). <i>PLoS ONE</i> , 2013, 8, e53915.	1.1	54
69	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	13.7	53
70	Discovery of immune-related genes in Chinese mitten crab (<i>Eriocheir sinensis</i>) by expressed sequence tag analysis of haemocytes. <i>Aquaculture</i> , 2009, 287, 297-303.	1.7	53
71	Transcriptomic profiling reveals MEP pathway contributing to ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>BMC Genomics</i> , 2019, 20, 383.	1.2	52
72	wapRNA: a web-based application for the processing of RNA sequences. <i>Bioinformatics</i> , 2011, 27, 3076-3077.	1.8	51

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73	ICG: a wiki-driven knowledgebase of internal control genes for RT-qPCR normalization. <i>Nucleic Acids Research</i> , 2018, 46, D121-D126.	6.5	49
74	Proteomic profiling of rice embryos from a hybrid rice cultivar and its parental lines. <i>Proteomics</i> , 2008, 8, 4808-4821.	1.3	48
75	De novo transcriptome analysis of <i>Medicago falcata</i> reveals novel insights about the mechanisms underlying abiotic stress-responsive pathway. <i>BMC Genomics</i> , 2015, 16, 818.	1.2	48
76	De Novo Sequencing and Transcriptome Analysis of <i>Pleurotus eryngii</i> subsp. <i>tuoliensis</i> (Bailinggu) Mycelia in Response to Cold Stimulation. <i>Molecules</i> , 2016, 21, 560.	1.7	48
77	Comparative analysis of ESTs in response to drought stress in chickpea (<i>C. arietinum</i> L.). <i>Biochemical and Biophysical Research Communications</i> , 2008, 376, 578-583.	1.0	46
78	Transcript profiles of <i>Panax quinquefolius</i> from flower, leaf and root bring new insights into genes related to ginsenosides biosynthesis and transcriptional regulation. <i>Physiologia Plantarum</i> , 2010, 138, 134-149.	2.6	46
79	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 397-404.	3.0	46
80	Analysis of immune-relevant genes expressed in red sea bream (<i>Chrysophrys major</i>) spleen. <i>Aquaculture</i> , 2004, 240, 115-130.	1.7	45
81	The genome and transcriptome of a newly described psychrophilic archaeon, <i>Methanohalobium psychrophilum</i> R15, reveal its cold adaptive characteristics. <i>Environmental Microbiology Reports</i> , 2012, 4, 633-641.	1.0	45
82	Tung Tree (<i>Vernicia fordii</i> , Hemsl.) Genome and Transcriptome Sequencing Reveals Co-Ordinate Up-Regulation of Fatty Acid β -Oxidation and Triacylglycerol Biosynthesis Pathways During Eleostearic Acid Accumulation in Seeds. <i>Plant and Cell Physiology</i> , 2018, 59, 1990-2003.	1.5	45
83	Transcriptomic insight into the immune defenses in the ghost moth, <i>Hepialus xiaojinensis</i> , during an <i>Ophiocordyceps sinensis</i> fungal infection. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 64, 1-15.	1.2	44
84	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. <i>Nature Communications</i> , 2016, 7, 12845.	5.8	43
85	Chasing relationships between nutrition and reproduction: A comparative transcriptome analysis of hepatopancreas and testis from <i>Eriocheir sinensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 227-234.	0.4	42
86	How Do Variable Substitution Rates Influence K_a and K_s Calculations?. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 116-127.	3.0	42
87	Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <i>Science China Life Sciences</i> , 2013, 56, 1-12.	2.3	42
88	Seasonally variable intestinal metagenomes of the red palm weevil (<i>Rhinocorymbus hynchophorus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	42
89	Differential gene expression in an elite hybrid rice cultivar (<i>Oryza sativa</i> , L) and its parental lines based on SAGE data. <i>BMC Plant Biology</i> , 2007, 7, 49.	1.6	41
90	Transcriptomic profiling of mature embryo from an elite super-hybrid rice LYP9 and its parental lines. <i>BMC Plant Biology</i> , 2008, 8, 114.	1.6	41

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91	DNA motifs determining the accuracy of repeat duplication during CRISPR adaptation in <i>Haloarcula hispanica</i> . <i>Nucleic Acids Research</i> , 2016, 44, 4266-4277.	6.5	41
92	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	6.5	41
93	The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. <i>Molecular Plant</i> , 2019, 12, 402-409.	3.9	41
94	De novo Transcriptome Analysis Reveals Distinct Defense Mechanisms by Young and Mature Leaves of <i>Hevea brasiliensis</i> (Para Rubber Tree). <i>Scientific Reports</i> , 2016, 6, 33151.	1.6	40
95	The calcium-dependent protein kinase (CDPK) and CDPK-related kinase gene families in <i>Hevea brasiliensis</i> comparison with five other plant species in structure, evolution, and expression. <i>FEBS Open Bio</i> , 2017, 7, 4-24.	1.0	40
96	High-throughput sequencing-based gene profiling on multi-staged fruit development of date palm (<i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012, 78, 617-626.	2.0	39
97	Transcriptome and Expression Profiling Analysis of the Hemocytes Reveals a Large Number of Immune-Related Genes in Mud Crab <i>Scylla paramamosain</i> during <i>Vibrio parahaemolyticus</i> Infection. <i>PLoS ONE</i> , 2014, 9, e114500.	1.1	39
98	Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. <i>BMC Genomics</i> , 2015, 16, 851.	1.2	39
99	Identification of Genes Involved in Immune Response, Microsatellite, and SNP Markers from Expressed Sequence Tags Generated from Hemocytes of Freshwater Pearl Mussel (<i>Hyriopsis cumingii</i>). <i>Marine Biotechnology</i> , 2009, 11, 520-530.	1.1	38
100	The small RNA profile in latex from <i>Hevea brasiliensis</i> trees is affected by tapping panel dryness. <i>Tree Physiology</i> , 2013, 33, 1084-1098.	1.4	38
101	Ribogenomics: the Science and Knowledge of RNA. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 57-63.	3.0	38
102	Plant editosome database: a curated database of RNA editosome in plants. <i>Nucleic Acids Research</i> , 2019, 47, D170-D174.	6.5	38
103	Novel microRNAs in silkworm (<i>Bombyx mori</i>). <i>Functional and Integrative Genomics</i> , 2010, 10, 405-415.	1.4	37
104	Evolution of genes on the <i>Salmonella</i> Virulence plasmid phylogeny revealed from sequencing of the virulence plasmids of <i>S. enterica</i> serotype Dublin and comparative analysis. <i>Genomics</i> , 2008, 92, 339-343.	1.3	36
105	Analysis of CYP3A4 genetic polymorphisms in Han Chinese. <i>Journal of Human Genetics</i> , 2011, 56, 415-422.	1.1	36
106	Identification of Immune Genes of the Agamaki Clam (<i>Sinonovacula constricta</i>) by Sequencing and Bioinformatic Analysis of ESTs. <i>Marine Biotechnology</i> , 2010, 12, 282-291.	1.1	35
107	Complete Genome Sequence of <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> Strain ATCC 35246. <i>Journal of Bacteriology</i> , 2011, 193, 5583-5584.	1.0	34
108	A novel DNA sequence periodicity decodes nucleosome positioning. <i>Nucleic Acids Research</i> , 2008, 36, 6228-6236.	6.5	33

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109	Involvement of the GP63 protease in infection of <i>Trichomonas vaginalis</i> . <i>Parasitology Research</i> , 2011, 109, 71-79.	0.6	33
110	Complete Sequence and Analysis of Coconut Palm (<i>Cocos nucifera</i>) Mitochondrial Genome. <i>PLoS ONE</i> , 2016, 11, e0163990.	1.1	33
111	A discovery of novel microRNAs in the silkworm (<i>Bombyx mori</i>) genome. <i>Genomics</i> , 2009, 94, 438-444.	1.3	32
112	Complete Genome Analysis of <i>Sulfobacillus acidophilus</i> Strain TPY, Isolated from a Hydrothermal Vent in the Pacific Ocean. <i>Journal of Bacteriology</i> , 2011, 193, 5555-5556.	1.0	32
113	Dynamic transcriptomes of human myeloid leukemia cells. <i>Genomics</i> , 2013, 102, 250-256.	1.3	32
114	Special fasciculiform cataract caused by a mutation in the gammaD-crystallin gene. <i>Molecular Vision</i> , 2004, 10, 233-9.	1.1	32
115	The <i>Bryopsis hypnoides</i> Plastid Genome: Multimeric Forms and Complete Nucleotide Sequence. <i>PLoS ONE</i> , 2011, 6, e14663.	1.1	31
116	Complete Genome Sequence of <i>Bifidobacterium longum</i> subsp. <i>longum</i> BBMN68, a New Strain from a Healthy Chinese Centenarian. <i>Journal of Bacteriology</i> , 2011, 193, 787-788.	1.0	31
117	Distinct Contributions of Replication and Transcription to Mutation Rate Variation of Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 4-10.	3.0	31
118	Profiling microRNA expression during multi-staged date palm (<i>Phoenix dactylifera</i> L.) fruit development. <i>Genomics</i> , 2015, 105, 242-251.	1.3	31
119	A chymotrypsin-like serine protease cDNA involved in food protein digestion in the common cutworm, <i>Spodoptera litura</i> : Cloning, characterization, developmental and induced expression patterns, and localization. <i>Journal of Insect Physiology</i> , 2010, 56, 788-799.	0.9	30
120	Discovery, Identification and Comparative Analysis of Non-Specific Lipid Transfer Protein (nsLtp) Family in Solanaceae. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 229-237.	3.0	30
121	Complete nucleotide sequence of pH11, an IncHI2 plasmid conferring multi-antibiotic resistance and multi-heavy metal resistance genes in a clinical <i>Klebsiella pneumoniae</i> isolate. <i>Plasmid</i> , 2016, 86, 26-31.	0.4	30
122	A complete mitochondrial genome of wheat (<i>Triticum aestivum</i> cv. Chinese Yumai), and fast evolving mitochondrial genes in higher plants. <i>Journal of Genetics</i> , 2009, 88, 299-307.	0.4	29
123	Complete Genome Sequence of the Pathogenic Bacterium <i>Riemerella anatipestifer</i> Strain RA-GD. <i>Journal of Bacteriology</i> , 2011, 193, 2896-2897.	1.0	28
124	Identification of genetic variations associated with epsilon-poly-lysine biosynthesis in <i>Streptomyces albus</i> ZPM by genome sequencing. <i>Scientific Reports</i> , 2015, 5, 9201.	1.6	28
125	Editome Disease Knowledgebase (EDK): a curated knowledgebase of editome-disease associations in human. <i>Nucleic Acids Research</i> , 2019, 47, D78-D83.	6.5	28
126	Complete nucleotide sequence of plasmid plca36 isolated from <i>Lactobacillus casei</i> Zhang. <i>Plasmid</i> , 2008, 60, 131-135.	0.4	27

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127	A Novel Role for Minimal Introns: Routing mRNAs to the Cytosol. <i>PLoS ONE</i> , 2010, 5, e10144.	1.1	27
128	Identification and Analysis of Muscle-Related Protein Isoforms Expressed in the White Muscle of the Mandarin Fish (<i>Siniperca chuatsi</i>). <i>Marine Biotechnology</i> , 2011, 13, 151-162.	1.1	27
129	Regulation of MIR Genes in Response to Abiotic Stress in <i>Hevea brasiliensis</i> . <i>International Journal of Molecular Sciences</i> , 2013, 14, 19587-19604.	1.8	27
130	Identification and analysis of house-keeping and tissue-specific genes based on RNA-seq data sets across 15 mouse tissues. <i>Gene</i> , 2016, 576, 560-570.	1.0	27
131	Abundant Taxa and Favorable Pathways in the Microbiome of Soda-Saline Lakes in Inner Mongolia. <i>Frontiers in Microbiology</i> , 2020, 11, 1740.	1.5	27
132	BIGpre: A Quality Assessment Package for Next-Generation Sequencing Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 238-244.	3.0	26
133	Large-scale collection and annotation of gene models for date palm (<i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012, 79, 521-536.	2.0	26
134	Transcriptomic analysis reveals key regulators of mammogenesis and the pregnancy-lactation cycle. <i>Science China Life Sciences</i> , 2014, 57, 340-355.	2.3	26
135	Characterization of miRNomes in Acute and Chronic Myeloid Leukemia Cell Lines. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 79-91.	3.0	26
136	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
137	Sequencing of Chinese castor lines reveals genetic signatures of selection and yield-associated loci. <i>Nature Communications</i> , 2019, 10, 3418.	5.8	26
138	Evolutionary analysis and lineage designation of SARS-CoV-2 genomes. <i>Science Bulletin</i> , 2021, 66, 2297-2311.	4.3	26
139	A Comparative Transcriptomic Analysis of Uveal Melanoma and Normal Uveal Melanocyte. <i>PLoS ONE</i> , 2011, 6, e16516.	1.1	25
140	Whole transcriptome RNA-seq analysis: tumorigenesis and metastasis of melanoma. <i>Gene</i> , 2014, 548, 234-243.	1.0	25
141	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
142	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
143	Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. <i>BMC Genomics</i> , 2009, 10, 117.	1.2	23
144	An evolutionary analysis of trypanosomatid GP63 proteases. <i>Parasitology Research</i> , 2011, 109, 1075-1084.	0.6	23

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