

# Song-Nian Hu

## List of Publications by Citations

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267  
papers

13,544  
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53  
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273  
ext. papers

16,642  
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6.5  
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5.96  
L-index

#	Paper	IF	Citations
267	A draft sequence of the rice genome ( <i>Oryza sativa</i> L. ssp. indica). <i>Science</i> , <b>2002</b> , 296, 79-92	33.3	2356
266	The Genomes of <i>Oryza sativa</i> : a history of duplications. <i>PLoS Biology</i> , <b>2005</b> , 3, e38	9.7	695
265	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , <b>2013</b> , 496, 57-63	50.4	483
264	A brief review on the mechanisms of miRNA regulation. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2009</b> , 7, 147-54	6.5	461
263	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , <b>2004</b> , 432, 717-22	50.4	341
262	Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W236-41	20.1	331
261	EvolView, an online tool for visualizing, annotating and managing phylogenetic trees. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W569-72	20.1	258
260	Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <i>Salvia miltiorrhiza</i> and tanshinone biosynthesis. <i>Plant Journal</i> , <b>2015</b> , 82, 951-961	6.9	233
259	The rubber tree genome reveals new insights into rubber production and species adaptation. <i>Nature Plants</i> , <b>2016</b> , 2, 16073	11.5	209
258	On the nature of human housekeeping genes. <i>Trends in Genetics</i> , <b>2008</b> , 24, 481-4	8.5	194
257	Genome sequence of the date palm <i>Phoenix dactylifera</i> L. <i>Nature Communications</i> , <b>2013</b> , 4, 2274	17.4	189
256	A complete sequence of the <i>T. tengcongensis</i> genome. <i>Genome Research</i> , <b>2002</b> , 12, 689-700	9.7	189
255	Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W270-W275	20.1	188
254	The genome sequence of <i>Salmonella enterica</i> serovar Choleraesuis, a highly invasive and resistant zoonotic pathogen. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 1690-8	20.1	170
253	Long non-coding RNAs and their biological roles in plants. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2015</b> , 13, 137-47	6.5	157
252	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , <b>2014</b> , 5, 5110	17.4	156
251	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> , <b>2012</b> , 195, 97-112	9.8	145

250	Plasmid-mediated quinolone resistance determinants qnr and aac(69-Ib-cr in extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> in China. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2008</b> , 61, 1003-6	5.1	143
249	Analysis of gut microbiota diversity and auxiliary diagnosis as a biomarker in patients with schizophrenia: A cross-sectional study. <i>Schizophrenia Research</i> , <b>2018</b> , 197, 470-477	3.6	142
248	Arginine methylation mediated by the Arabidopsis 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> , <b>2010</b> , 107, 19114-9	11.5	135
247	A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. <i>Genomics</i> , <b>2010</b> , 96, 259-65	4.3	135
246	Comparative analysis of the genomes of two field isolates of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002869	6	125
245	A comparison of rice chloroplast genomes. <i>Plant Physiology</i> , <b>2004</b> , 135, 412-20	6.6	124
244	Oral Microbiota Community Dynamics Associated With Oral Squamous Cell Carcinoma Staging. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 862	5.7	119
243	Metatranscriptomic analyses of plant cell wall polysaccharide degradation by microorganisms in the cow rumen. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 1375-86	4.8	114
242	Evolution and pathogenesis of <i>Staphylococcus aureus</i> : lessons learned from genotyping and comparative genomics. <i>FEMS Microbiology Reviews</i> , <b>2008</b> , 32, 23-37	15.1	111
241	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> , <b>2011</b> , 108, 12042-7	11.5	110
240	Genomic analysis of the multidrug-resistant <i>Acinetobacter baumannii</i> strain MDR-ZJ06 widely spread in China. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2011</b> , 55, 4506-12	5.9	105
239	The silkworm ( <i>Bombyx mori</i> ) microRNAs and their expressions in multiple developmental stages. <i>PLoS ONE</i> , <b>2008</b> , 3, e2997	3.7	105
238	Environmental adaptation: genomic analysis of the piezotolerant and psychrotolerant deep-sea iron reducing bacterium <i>Shewanella piezotolerans</i> WP3. <i>PLoS ONE</i> , <b>2008</b> , 3, e1937	3.7	101
237	The rice mitochondrial genomes and their variations. <i>Plant Physiology</i> , <b>2006</b> , 140, 401-10	6.6	91
236	Transcriptome-wide N <sup>6</sup> -methyladenosine profiling of rice callus and leaf reveals the presence of tissue-specific competitors involved in selective mRNA modification. <i>RNA Biology</i> , <b>2014</b> , 11, 1180-8	4.8	85
235	A novel OxyR sensor and regulator of hydrogen peroxide stress with one cysteine residue in <i>Deinococcus radiodurans</i> . <i>PLoS ONE</i> , <b>2008</b> , 3, e1602	3.7	85
234	A complete sequence and transcriptomic analyses of date palm ( <i>Phoenix dactylifera</i> L.) mitochondrial genome. <i>PLoS ONE</i> , <b>2012</b> , 7, e37164	3.7	82
233	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> , <b>2016</b> , 113, E6026-E6035	11.5	79

232	Genetic Alterations in Esophageal Tissues From Squamous Dysplasia to Carcinoma. <i>Gastroenterology</i> , <b>2017</b> , 153, 166-177	13.3	78
231	A genome-wide microsatellite polymorphism database for the indica and japonica rice. <i>DNA Research</i> , <b>2007</b> , 14, 37-45	4.5	73
230	De novo characterization of the spleen transcriptome of the large yellow croaker ( <i>Pseudosciaena crocea</i> ) and analysis of the immune relevant genes and pathways involved in the antiviral response. <i>PLoS ONE</i> , <b>2014</b> , 9, e97471	3.7	73
229	On the molecular mechanism of GC content variation among eubacterial genomes. <i>Biology Direct</i> , <b>2012</b> , 7, 2	7.2	72
228	Salmonella paratyphi C: genetic divergence from Salmonella choleraesuis and pathogenic convergence with Salmonella typhi. <i>PLoS ONE</i> , <b>2009</b> , 4, e4510	3.7	72
227	Metagenomic insights into the fibrolytic microbiome in yak rumen. <i>PLoS ONE</i> , <b>2012</b> , 7, e40430	3.7	71
226	Identification of differentially expressed genes in human lung squamous cell carcinoma using suppression subtractive hybridization. <i>Cancer Letters</i> , <b>2004</b> , 212, 83-93	9.9	70
225	Rice Expression Database (RED): An integrated RNA-Seq-derived gene expression database for rice. <i>Journal of Genetics and Genomics</i> , <b>2017</b> , 44, 235-241	4	69
224	Complete genome sequence of <i>Lactobacillus casei</i> Zhang, a new probiotic strain isolated from traditional homemade koumiss in Inner Mongolia, China. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 5268-9	3.5	68
223	The complete chloroplast and mitochondrial genome sequences of <i>Boea hygrometrica</i> : insights into the evolution of plant organellar genomes. <i>PLoS ONE</i> , <b>2012</b> , 7, e30531	3.7	66
222	Complete genome sequence of the metabolically versatile halophilic archaeon <i>Haloferax mediterranei</i> , a poly(3-hydroxybutyrate-co-3-hydroxyvalerate) producer. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 4463-4	3.5	63
221	Functional annotation and analysis of expressed sequence tags from the hepatopancreas of mitten crab ( <i>Eriocheir sinensis</i> ). <i>Marine Biotechnology</i> , <b>2009</b> , 11, 317-26	3.4	62
220	Comparative analysis of mitochondrial genomes between a wheat K-type cytoplasmic male sterility (CMS) line and its maintainer line. <i>BMC Genomics</i> , <b>2011</b> , 12, 163	4.5	60
219	Marine sediment bacteria harbor antibiotic resistance genes highly similar to those found in human pathogens. <i>Microbial Ecology</i> , <b>2013</b> , 65, 975-81	4.4	59
218	Transcriptome comparison between honey bee queen- and worker-destined larvae. <i>Insect Biochemistry and Molecular Biology</i> , <b>2012</b> , 42, 665-73	4.5	59
217	Pyrosequencing the <i>Bemisia tabaci</i> transcriptome reveals a highly diverse bacterial community and a robust system for insecticide resistance. <i>PLoS ONE</i> , <b>2012</b> , 7, e35181	3.7	56
216	Identification of microRNA in the protist <i>Trichomonas vaginalis</i> . <i>Genomics</i> , <b>2009</b> , 93, 487-93	4.3	56
215	Comparative genome analysis of programmed DNA elimination in nematodes. <i>Genome Research</i> , <b>2017</b> , 27, 2001-2014	9.7	55

214	Conserved Intramolecular Interactions Maintain Myosin Interacting-Heads Motifs Explaining Tarantula Muscle Super-Relaxed State Structural Basis. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 1142-1164	6.5	53
213	wapRNA: a web-based application for the processing of RNA sequences. <i>Bioinformatics</i> , <b>2011</b> , 27, 3076-77.2		51
212	Ascarosides coordinate the dispersal of a plant-parasitic nematode with the metamorphosis of its vector beetle. <i>Nature Communications</i> , <b>2016</b> , 7, 12341	17.4	50
211	PacBio full-length cDNA sequencing integrated with RNA-seq reads drastically improves the discovery of splicing transcripts in rice. <i>Plant Journal</i> , <b>2019</b> , 97, 296-305	6.9	50
210	Comparative transcriptome analysis of the accessory sex gland and testis from the Chinese mitten crab ( <i>Eriocheir sinensis</i> ). <i>PLoS ONE</i> , <b>2013</b> , 8, e53915	3.7	49
209	The apricot (L.) genome elucidates Rosaceae evolution and beta-carotenoid synthesis. <i>Horticulture Research</i> , <b>2019</b> , 6, 128	7.7	48
208	Proteomic profiling of rice embryos from a hybrid rice cultivar and its parental lines. <i>Proteomics</i> , <b>2008</b> , 8, 4808-21	4.8	47
207	An efficient procedure for plant organellar genome assembly, based on whole genome data from the 454 GS FLX sequencing platform. <i>Plant Methods</i> , <b>2011</b> , 7, 38	5.8	45
206	Discovery of immune-related genes in Chinese mitten crab ( <i>Eriocheir sinensis</i> ) by expressed sequence tag analysis of haemocytes. <i>Aquaculture</i> , <b>2009</b> , 287, 297-303	4.4	45
205	A Critical Role for CLSP2 in the Modulation of Antifungal Immune Response in Mosquitoes. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004931	7.6	44
204	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , <b>2006</b> , 440, 1194-8	50.4	43
203	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> , <b>2010</b> , 138, 134-49	4.6	42
202	Analysis of immune-relevant genes expressed in red sea bream ( <i>Chrysophrys major</i> ) spleen. <i>Aquaculture</i> , <b>2004</b> , 240, 115-130	4.4	42
201	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. <i>Nature Communications</i> , <b>2016</b> , 7, 11334	17.4	41
200	Comparative analysis of ESTs in response to drought stress in chickpea ( <i>C. arietinum</i> L.). <i>Biochemical and Biophysical Research Communications</i> , <b>2008</b> , 376, 578-83	3.4	41
199	Genome structure and evolution of <i>Antirrhinum majus</i> L. <i>Nature Plants</i> , <b>2019</b> , 5, 174-183	11.5	39
198	The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , <b>2020</b> , 21, 60	18.3	39
197	The genome and transcriptome of a newly described psychrophilic archaeon, <i>Methanolobus psychrophilus</i> R15, reveal its cold adaptive characteristics. <i>Environmental Microbiology Reports</i> , <b>2012</b> , 4, 633-41	3.7	38

196	ICG: a wiki-driven knowledgebase of internal control genes for RT-qPCR normalization. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D121-D126	20.1	37
195	The complete mitochondrial genome of <i>Gossypium hirsutum</i> and evolutionary analysis of higher plant mitochondrial genomes. <i>PLoS ONE</i> , <b>2013</b> , 8, e69476	3.7	37
194	Novel microRNAs in silkworm ( <i>Bombyx mori</i> ). <i>Functional and Integrative Genomics</i> , <b>2010</b> , 10, 405-15	3.8	37
193	Transcriptomic profiling of mature embryo from an elite super-hybrid rice LYP9 and its parental lines. <i>BMC Plant Biology</i> , <b>2008</b> , 8, 114	5.3	37
192	De novo transcriptome analysis of <i>Medicago falcata</i> reveals novel insights about the mechanisms underlying abiotic stress-responsive pathway. <i>BMC Genomics</i> , <b>2015</b> , 16, 818	4.5	36
191	High-throughput sequencing-based gene profiling on multi-staged fruit development of date palm ( <i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , <b>2012</b> , 78, 617-26	4.6	35
190	A novel antisense long noncoding RNA, TWISTED LEAF, maintains leaf blade flattening by regulating its associated sense R2R3-MYB gene in rice. <i>New Phytologist</i> , <b>2018</b> , 218, 774-788	9.8	34
189	Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <i>Science China Life Sciences</i> , <b>2013</b> , 56, 1-12	8.5	33
188	Seasonally variable intestinal metagenomes of the red palm weevil ( <i>Rhynchophorus ferrugineus</i> ). <i>Environmental Microbiology</i> , <b>2013</b> , 15, 3020-9	5.2	33
187	Identification of immune genes of the Agamaki clam ( <i>Sinonovacula constricta</i> ) by sequencing and bioinformatic analysis of ESTs. <i>Marine Biotechnology</i> , <b>2010</b> , 12, 282-91	3.4	33
186	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> , <b>2007</b> , 7, 49	5.3	33
185	DNA motifs determining the accuracy of repeat duplication during CRISPR adaptation in <i>Haloarcula hispanica</i> . <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 4266-77	20.1	32
184	MVP: a microbe-phage interaction database. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D700-D707	20.1	31
183	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D1172-80	20.1	31
182	Biomonitoring for traditional herbal medicinal products using DNA metabarcoding and single molecule, real-time sequencing. <i>Acta Pharmaceutica Sinica B</i> , <b>2018</b> , 8, 488-497	15.5	31
181	Fine-Tuning of MiR528 Accumulation Modulates Flowering Time in Rice. <i>Molecular Plant</i> , <b>2019</b> , 12, 1103-1113	14.3	30
180	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. <i>Nature Communications</i> , <b>2016</b> , 7, 12845	17.4	30
179	Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. <i>BMC Genomics</i> , <b>2015</b> , 16, 851	4.5	30

178	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> , <b>2014</b> , 9, e114500	3.7	30
177	Evolution of genes on the Salmonella Virulence plasmid phylogeny revealed from sequencing of the virulence plasmids of <i>S. enterica</i> serotype Dublin and comparative analysis. <i>Genomics</i> , <b>2008</b> , 92, 339-43	4.3	30
176	The small RNA profile in latex from <i>Hevea brasiliensis</i> trees is affected by tapping panel dryness. <i>Tree Physiology</i> , <b>2013</b> , 33, 1084-98	4.2	29
175	Analysis of CYP3A4 genetic polymorphisms in Han Chinese. <i>Journal of Human Genetics</i> , <b>2011</b> , 56, 415-22	4.3	29
174	A discovery of novel microRNAs in the silkworm ( <i>Bombyx mori</i> ) genome. <i>Genomics</i> , <b>2009</b> , 94, 438-44	4.3	29
173	A novel DNA sequence periodicity decodes nucleosome positioning. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 6228-36	20.1	29
172	Special fasciculiform cataract caused by a mutation in the gammaD-crystallin gene. <i>Molecular Vision</i> , <b>2004</b> , 10, 233-9	2.3	29
171	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> , <b>2015</b> , 64, 1-15	4.5	27
170	The <i>Bryopsis hypnoides</i> plastid genome: multimeric forms and complete nucleotide sequence. <i>PLoS ONE</i> , <b>2011</b> , 6, e14663	3.7	27
169	A novel role for minimal introns: routing mRNAs to the cytosol. <i>PLoS ONE</i> , <b>2010</b> , 5, e10144	3.7	27
168	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> , <b>2009</b> , 11, 520-30	3.4	27
167	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> , <b>2011</b> , 193, 787-8	3.5	27
166	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> , <b>2016</b> , 21,	4.8	27
165	The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. <i>Molecular Plant</i> , <b>2019</b> , 12, 402-409	14.4	26
164	Dynamic transcriptomes of human myeloid leukemia cells. <i>Genomics</i> , <b>2013</b> , 102, 250-6	4.3	26
163	Profiling microRNA expression during multi-staged date palm ( <i>Phoenix dactylifera</i> L.) fruit development. <i>Genomics</i> , <b>2015</b> , 105, 242-51	4.3	26
162	Complete genome analysis of <i>Sulfobacillus acidophilus</i> strain TPY, isolated from a hydrothermal vent in the Pacific Ocean. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5555-6	3.5	26
161	Complete genome sequence of the pathogenic bacterium <i>Riemerella anatipestifer</i> strain RA-GD. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2896-7	3.5	26

160	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> , <b>2010</b> , 56, 788-99	2.4	26
159	Complete nucleotide sequence of plasmid plca36 isolated from <i>Lactobacillus casei</i> Zhang. <i>Plasmid</i> , <b>2008</b> , 60, 131-5	3.3	26
158	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> , <b>2016</b> , 6, 33151	4.9	26
157	Distinct contributions of replication and transcription to mutation rate variation of human genomes. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2012</b> , 10, 4-10	6.5	25
156	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> , <b>2009</b> , 4, 227-34	2	25
155	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2018</b> , 16, 397-404	6.5	25
154	Involvement of the GP63 protease in infection of <i>Trichomonas vaginalis</i> . <i>Parasitology Research</i> , <b>2011</b> , 109, 71-9	2.4	24
153	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> , <b>2011</b> , 13, 151-62	3.4	24
152	Complete genome sequence of <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> strain ATCC 35246. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5583-4	3.5	24
151	Tung Tree ( <i>Vernicia fordii</i> , Hemsl.) Genome and Transcriptome Sequencing Reveals Co-Ordinate Up-Regulation of Fatty Acid Oxidation and Triacylglycerol Biosynthesis Pathways During Eleostearic Acid Accumulation in Seeds. <i>Plant and Cell Physiology</i> , <b>2018</b> , 59, 1990-2003	4.9	23
150	Regulation of MIR genes in response to abiotic stress in <i>Hevea brasiliensis</i> . <i>International Journal of Molecular Sciences</i> , <b>2013</b> , 14, 19587-604	6.3	23
149	A comparative transcriptomic analysis of uveal melanoma and normal uveal melanocyte. <i>PLoS ONE</i> , <b>2011</b> , 6, e16516	3.7	23
148	Identification of genetic variations associated with epsilon-poly-lysine biosynthesis in <i>Streptomyces albulus</i> ZPM by genome sequencing. <i>Scientific Reports</i> , <b>2015</b> , 5, 9201	4.9	22
147	BIGpre: a quality assessment package for next-generation sequencing data. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2011</b> , 9, 238-44	6.5	22
146	Discovery, identification and comparative analysis of non-specific lipid transfer protein (nsLtp) family in Solanaceae. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2010</b> , 8, 229-37	6.5	22
145	Complete Sequence and Analysis of Coconut Palm ( <i>Cocos nucifera</i> ) Mitochondrial Genome. <i>PLoS ONE</i> , <b>2016</b> , 11, e0163990	3.7	22
144	The calcium-dependent protein kinase (CDPK) and CDPK-related kinase gene families in -comparison with five other plant species in structure, evolution, and expression. <i>FEBS Open Bio</i> , <b>2017</b> , 7, 4-24	2.7	21
143	Large-scale collection and annotation of gene models for date palm ( <i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , <b>2012</b> , 79, 521-36	4.6	21



142	An evolutionary analysis of trypanosomatid GP63 proteases. <i>Parasitology Research</i> , <b>2011</b> , 109, 1075-84	2.4	21
141	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> , <b>2009</b> , 88, 299-307	1.2	21
140	Transcriptomic profiling reveals MEP pathway contributing to ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>BMC Genomics</i> , <b>2019</b> , 20, 383	4.5	20
139	Whole transcriptome RNA-seq analysis: tumorigenesis and metastasis of melanoma. <i>Gene</i> , <b>2014</b> , 548, 234-43	3.8	20
138	Transposable-element associated small RNAs in <i>Bombyx mori</i> genome. <i>PLoS ONE</i> , <b>2012</b> , 7, e36599	3.7	20
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