

Song-Nian Hu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

267
papers

13,544
citations

53
h-index

109
g-index

273
ext. papers

16,642
ext. citations

6.5
avg, IF

5.96
L-index

#	Paper	IF	Citations
267	Improvements of immune genes and intestinal microbiota composition of turbot (<i>Scophthalmus maximus</i>) with dietary oregano oil and probiotics. <i>Aquaculture</i> , 2022 , 547, 737442	4.4	3
266	The Dissemination of NDM-1 in <i>Acinetobacter baumannii</i> Strains.. <i>Current Microbiology</i> , 2022 , 79, 117	2.4	
265	gcCov: Linked open data for global coronavirus studies 2022 , 1, 92-95		1
264	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	4.5	0
263	Genomic Characterization of a Uropathogenic ST405 Isolate Harboring -Encoding IncFIA-FIB Plasmid, -Encoding IncI1 Plasmid, and Phage-Like Plasmid.. <i>Frontiers in Microbiology</i> , 2022 , 13, 845045	5.7	
262	A fine-scale map of genome-wide recombination in divergent <i>Escherichia coli</i> population. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
261	Improved 93-11 Genome and Time-Course Transcriptome Expand Resources for Rice Genomics.. <i>Frontiers in Plant Science</i> , 2021 , 12, 769700	6.2	0
260	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	5.9	0
259	Monitoring microbial communities in intensive care units over one year in China.. <i>Science of the Total Environment</i> , 2021 , 811, 152353	10.2	0
258	Selection for Cheaper Amino Acids Drives Nucleotide Usage at the Start of Translation in Eukaryotic Genes. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	1
257	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	3.4	3
256	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	7.2	8
255	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	2.3	2
254	Association of Gene Polymorphisms and Amlodipine-Induced Peripheral Edema in Chinese Han Patients with Essential Hypertension. <i>Pharmacogenomics and Personalized Medicine</i> , 2021 , 14, 189-197	2.1	2
253	Genome of the Giant Panda Roundworm Illuminates Its Host Shift and Parasitic Adaptation. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	2
252	Evolutionary analysis and lineage designation of SARS-CoV-2 genomes. <i>Science Bulletin</i> , 2021 , 66, 2297-2316	33.6	12
251	VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2

250	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	2.9	1
249	Structural and Functional Annotation of Transposable Elements Revealed a Potential Regulation of Genes Involved in Rubber Biosynthesis by TE-Derived siRNA Interference in. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	3
248	Genome Assembly and Pathway Analysis of Edible Mushroom <i>Agrocybe cylindracea</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 341-351	6.5	5
247	The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , 2020 , 21, 60	18.3	39
246	Gene family expansion of pinewood nematode to detoxify its host defence chemicals. <i>Molecular Ecology</i> , 2020 , 29, 940-955	5.7	8
245	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	5.7	3
244	5-Hydroxymethylcytosine signatures in circulating cell-free DNA as diagnostic and predictive biomarkers for coronary artery disease. <i>Clinical Epigenetics</i> , 2020 , 12, 17	7.7	7
243	A Reference Genome of Provides New Resources for Revealing Its Displacement by Pinewood Nematode. <i>Genes</i> , 2020 , 11,	4.2	4
242	Post-transcriptional regulation of several biological processes involved in latex production in. <i>PeerJ</i> , 2020 , 8, e8932	3.1	4
241	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 161-172	6.5	9
240	Identification of a mutation in a large Chinese family with atypical normokalemic periodic paralysis using whole-exome sequencing. <i>Journal of International Medical Research</i> , 2020 , 48, 300060520953643	1.4	
239	Abundant Taxa and Favorable Pathways in the Microbiome of Soda-Saline Lakes in Inner Mongolia. <i>Frontiers in Microbiology</i> , 2020 , 11, 1740	5.7	7
238	Genomic and transcriptome identification of fluconazole-resistant genes for <i>Trichosporon asahii</i> . <i>Medical Mycology</i> , 2020 , 58, 393-400	3.9	3
237	Genome structure and evolution of <i>Antirrhinum majus</i> L. <i>Nature Plants</i> , 2019 , 5, 174-183	11.5	39
236	Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. <i>Nucleic Acids Research</i> , 2019 , 47, W270-W275	20.1	188
235	Fine-Tuning of MiR528 Accumulation Modulates Flowering Time in Rice. <i>Molecular Plant</i> , 2019 , 12, 1103-1113	11.13	30
234	Transcriptomic profiling reveals MEP pathway contributing to ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>BMC Genomics</i> , 2019 , 20, 383	4.5	20
233	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	4.9	12

232	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	5.8	16
231	The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. <i>Molecular Plant</i> , 2019 , 12, 402-409	14.4	26
230	Sequencing of Chinese castor lines reveals genetic signatures of selection and yield-associated loci. <i>Nature Communications</i> , 2019 , 10, 3418	17.4	14
229	The apricot (L.) genome elucidates Rosaceae evolution and beta-carotenoid synthesis. <i>Horticulture Research</i> , 2019 , 6, 128	7.7	48
228	Plant editosome database: a curated database of RNA editosome in plants. <i>Nucleic Acids Research</i> , 2019 , 47, D170-D174	20.1	20
227	Editome Disease Knowledgebase (EDK): a curated knowledgebase of editome-disease associations in human. <i>Nucleic Acids Research</i> , 2019 , 47, D78-D83	20.1	20
226	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	6.9	50
225	REDO: RNA Editing Detection in Plant Organelles Based on Variant Calling Results. <i>Journal of Computational Biology</i> , 2018 , 25, 509-516	1.7	7
224	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	3.6	142
223	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> , 2018 , 218, 774-788	9.8	34
222	MVP: a microbe-phage interaction database. <i>Nucleic Acids Research</i> , 2018 , 46, D700-D707	20.1	31
221	Comparative analysis of the <i>Monochamus alternatus</i> immune system. <i>Insect Science</i> , 2018 , 25, 581-603	3.6	10
220	ICG: a wiki-driven knowledgebase of internal control genes for RT-qPCR normalization. <i>Nucleic Acids Research</i> , 2018 , 46, D121-D126	20.1	37
219	Oral Microbiota Community Dynamics Associated With Oral Squamous Cell Carcinoma Staging. <i>Frontiers in Microbiology</i> , 2018 , 9, 862	5.7	119
218	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	0.9	6
217	Impact of growth pH and glucose concentrations on the CodY regulatory network in <i>Streptococcus salivarius</i> . <i>BMC Genomics</i> , 2018 , 19, 386	4.5	2
216	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	5.3	7
215	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> , 2018 , 59, 1990-2003	4.9	23

214	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	15.5	31
213	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018 , 16, 397-404	6.5	25
212	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	6.5	7
211	Complete Genomic Analysis of a Kingdom-Crossing Isolate. <i>Frontiers in Microbiology</i> , 2018 , 9, 2428	5.7	7
210	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> , 2017 , 7, 4-24	2.7	21
209	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	4	69
208	Genetic Alterations in Esophageal Tissues From Squamous Dysplasia to Carcinoma. <i>Gastroenterology</i> , 2017 , 153, 166-177	13.3	78
207	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	6.5	5
206	Comparative genome analysis of programmed DNA elimination in nematodes. <i>Genome Research</i> , 2017 , 27, 2001-2014	9.7	55
205	ISVASE: identification of sequence variant associated with splicing event using RNA-seq data. <i>BMC Bioinformatics</i> , 2017 , 18, 320	3.6	
204	: An Online Date Palm Genomic Resource Database. <i>Frontiers in Plant Science</i> , 2017 , 8, 1889	6.2	13
203	A meta-analysis of the association of CKM gene rs8111989 polymorphism with sport performance. <i>Biology of Sport</i> , 2017 , 34, 323-330	4.3	10
202	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. <i>Nature Communications</i> , 2016 , 7, 11334	17.4	41
201	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. <i>Nature Communications</i> , 2016 , 7, 12845	17.4	30
200	The rubber tree genome reveals new insights into rubber production and species adaptation. <i>Nature Plants</i> , 2016 , 2, 16073	11.5	209
199	Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. <i>Nucleic Acids Research</i> , 2016 , 44, W236-41	20.1	331
198	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	6.5	53
197	DNA motifs determining the accuracy of repeat duplication during CRISPR adaptation in <i>Haloarcula hispanica</i> . <i>Nucleic Acids Research</i> , 2016 , 44, 4266-77	20.1	32

196	Identification and analysis of mouse non-coding RNA using transcriptome data. <i>Science China Life Sciences</i> , 2016 , 59, 589-603	8.5	5
195	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, 560-70	3.8	18
194	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016 , 44, D1172-80	20.1	31
193	Complete Sequence and Analysis of Coconut Palm (<i>Cocos nucifera</i>) Mitochondrial Genome. <i>PLoS ONE</i> , 2016 , 11, e0163990	3.7	22
192	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,	4.8	27
191	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	2.6	8
190	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	4.9	26
189	Ascarosides coordinate the dispersal of a plant-parasitic nematode with the metamorphosis of its vector beetle. <i>Nature Communications</i> , 2016 , 7, 12341	17.4	50
188	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	3.3	19
187	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	11.5	79
186	MicroRNA profiles and potential regulatory pattern during the early stage of spermatogenesis in mice. <i>Science China Life Sciences</i> , 2015 , 58, 442-50	8.5	12
185	Evaluation of the optimal dosage of S-1 in adjuvant SOX chemotherapy for gastric cancer. <i>Oncology Letters</i> , 2015 , 9, 1451-1457	2.6	9
184	Deep sequencing analysis of microRNA expression in human melanocyte and melanoma cell lines. <i>Gene</i> , 2015 , 572, 135-145	3.8	13
183	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	4.5	27
182	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, 176-81	3.4	14
181	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> , 2015 , 82, 951-961	6.9	233
180	Long non-coding RNAs and their biological roles in plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 137-47	6.5	157
179	Integrated analysis of gene expression and microRNA regulation in three leukemia-related lymphoblastic cell lines. <i>Gene</i> , 2015 , 564, 39-52	3.8	3

178	Comparison and evaluation of two exome capture kits and sequencing platforms for variant calling. <i>BMC Genomics</i> , 2015 , 16, 581	4.5	15
177	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	4.9	22
176	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, 6651-63	7	19
175	Metatranscriptomic analyses of plant cell wall polysaccharide degradation by microorganisms in the cow rumen. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1375-86	4.8	114
174	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, 831-9	4.8	12
173	Transcriptomic study of the red palm weevil <i>Rhynchophorus ferrugineus</i> embryogenesis. <i>Insect Science</i> , 2015 , 22, 65-82	3.6	9
172	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	4.5	36
171	Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. <i>BMC Genomics</i> , 2015 , 16, 851	4.5	30
170	A Critical Role for CLSP2 in the Modulation of Antifungal Immune Response in Mosquitoes. <i>PLoS Pathogens</i> , 2015 , 11, e1004931	7.6	44
169	Profiling microRNA expression during multi-staged date palm (<i>Phoenix dactylifera</i> L.) fruit development. <i>Genomics</i> , 2015 , 105, 242-51	4.3	26
168	Comparative genomic analysis of aspartic proteases in eight parasitic platyhelminths: insights into functions and evolution. <i>Gene</i> , 2015 , 559, 52-61	3.8	3
167	Ethylene Response Factors Are Controlled by Multiple Harvesting Stresses in <i>Hevea brasiliensis</i> . <i>PLoS ONE</i> , 2015 , 10, e0123618	3.7	17
166	RNA-Seq Based De Novo Transcriptome Assembly and Gene Discovery of <i>Cistanche deserticola</i> Fleshy Stem. <i>PLoS ONE</i> , 2015 , 10, e0125722	3.7	9
165	Transcriptomic analysis reveals key regulators of mammaryogenesis and the pregnancy-lactation cycle. <i>Science China Life Sciences</i> , 2014 , 57, 340-355	8.5	19
164	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014 , 5, 5110	17.4	156
163	Adolescent mouse takes on an active transcriptomic expression during postnatal cerebral development. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 111-9	6.5	3
162	Whole transcriptome RNA-seq analysis: tumorigenesis and metastasis of melanoma. <i>Gene</i> , 2014 , 548, 234-43	3.8	20
161	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	3.7	14

160	Characterization of miRNomes in acute and chronic myeloid leukemia cell lines. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 79-91	6.5	19
159	XELIRI compared with FOLFIRI as a second-line treatment in patients with metastatic colorectal cancer. <i>Oncology Letters</i> , 2014 , 8, 1864-1872	2.6	2
158	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	3.7	30
157	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, 1180-8	4.8	85
156	A comprehensive transcriptomic analysis of infant and adult mouse ovary. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 239-48	6.5	16
155	RiceWiki: a wiki-based database for community curation of rice genes. <i>Nucleic Acids Research</i> , 2014 , 42, D1222-8	20.1	18
154	Dose-finding study on adjuvant chemotherapy with S-1 plus oxaliplatin for gastric cancer. <i>Molecular and Clinical Oncology</i> , 2014 , 2, 93-98	1.6	6
153	Ribogenomics: the science and knowledge of RNA. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 57-63	6.5	10
152	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> , 2014 , 9, e97471	3.7	73
151	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	3.7	20
150	Marine sediment bacteria harbor antibiotic resistance genes highly similar to those found in human pathogens. <i>Microbial Ecology</i> , 2013 , 65, 975-81	4.4	59
149	Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <i>Science China Life Sciences</i> , 2013 , 56, 1-12	8.5	33
148	Dynamic transcriptomes of human myeloid leukemia cells. <i>Genomics</i> , 2013 , 102, 250-6	4.3	26
147	Transcriptome dynamics during human erythroid differentiation and development. <i>Genomics</i> , 2013 , 102, 431-441	4.3	19
146	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	4.5	19
145	Seasonally variable intestinal metagenomes of the red palm weevil (<i>Rhynchophorus ferrugineus</i>). <i>Environmental Microbiology</i> , 2013 , 15, 3020-9	5.2	33
144	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013 , 496, 57-63	50.4	483
143	Genome sequence of the date palm <i>Phoenix dactylifera</i> L. <i>Nature Communications</i> , 2013 , 4, 2274	17.4	189

142	The small RNA profile in latex from <i>Hevea brasiliensis</i> trees is affected by tapping panel dryness. <i>Tree Physiology</i> , 2013 , 33, 1084-98	4.2	29
141	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	3.7	18
140	The complete mitochondrial genome of <i>Gossypium hirsutum</i> and evolutionary analysis of higher plant mitochondrial genomes. <i>PLoS ONE</i> , 2013 , 8, e69476	3.7	37
139	Regulation of MIR genes in response to abiotic stress in <i>Hevea brasiliensis</i> . <i>International Journal of Molecular Sciences</i> , 2013 , 14, 19587-604	6.3	23
138	A large-scale gene discovery for the red palm weevil <i>Rhynchophorus ferrugineus</i> (Coleoptera: Curculionidae). <i>Insect Science</i> , 2013 , 20, 689-702	3.6	14
137	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	3.7	49
136	Acquisition of hydrogenosomal presequences: examples from <i>Trichomonas vaginalis</i> . <i>FEMS Microbiology Letters</i> , 2012 , 330, 127-31	2.9	1
135	The genome and transcriptome of a newly described psychrophilic archaeon, <i>Methanlobus psychrophilus</i> R15, reveal its cold adaptive characteristics. <i>Environmental Microbiology Reports</i> , 2012 , 4, 633-41	3.7	38
134	Distinct contributions of replication and transcription to mutation rate variation of human genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 4-10	6.5	25
133	The transcript-centric mutations in human genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 11-22	6.5	17
132	An RNA-seq-based gene expression profiling of radiation-induced tumorigenic mammary epithelial cells. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 326-35	6.5	9
131	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	9.8	145
130	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	3.8	5
129	Evolutional and functional analysis of a serine protease in <i>Spodoptera litura</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2012 , 81, 121-35	2.3	
128	Molecular identification of <i>Diphyllbothrium latum</i> and a brief review of diphyllbothriosis in China. <i>Acta Parasitologica</i> , 2012 , 57, 293-6	1.7	11
127	The association between H3K4me3 and antisense transcription. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 74-81	6.5	11
126	Comparative analyses of H3K4 and H3K27 trimethylations between the mouse cerebrum and testis. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 82-93	6.5	18
125	Transcriptome comparison between honey bee queen- and worker-destined larvae. <i>Insect Biochemistry and Molecular Biology</i> , 2012 , 42, 665-73	4.5	59

124	Complete genome and transcriptomes of <i>Streptococcus parasanguinis</i> FW213: phylogenetic relations and potential virulence mechanisms. <i>PLoS ONE</i> , 2012 , 7, e34769	3.7	13
123	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	3.7	56
122	Transposable-element associated small RNAs in <i>Bombyx mori</i> genome. <i>PLoS ONE</i> , 2012 , 7, e36599	3.7	20
121	On the molecular mechanism of GC content variation among eubacterial genomes. <i>Biology Direct</i> , 2012 , 7, 2	7.2	72
120	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, 617-26	4.6	35
119	Large-scale collection and annotation of gene models for date palm (<i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012 , 79, 521-36	4.6	21
118	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	6	125
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