

# Jun Yu

## List of Publications by Year in descending order

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189  
papers

37,623  
citations

41344

49  
h-index

3487

182  
g-index

199  
all docs

199  
docs citations

199  
times ranked

42470  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	A Draft Sequence of the Rice Genome ( <i>Oryza sativa</i> L. ssp. <i>indica</i> ). <i>Science</i> , 2002, 296, 79-92.	12.6	3,146
3	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
4	KaKs_Calculator 2.0: A Toolkit Incorporating Gamma-Series Methods and Sliding Window Strategies. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 77-80.	6.9	1,301
5	KaKs_Calculator: Calculating Ka and Ks Through Model Selection and Model Averaging. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 259-263.	6.9	940
6	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	5.6	808
7	A Brief Review on the Mechanisms of miRNA Regulation. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 147-154.	6.9	711
8	Genome sequence and genetic diversity of the common carp, <i>Cyprinus carpio</i> . <i>Nature Genetics</i> , 2014, 46, 1212-1219.	21.4	576
9	The Complete Chloroplast Genome Sequence of Date Palm ( <i>Phoenix dactylifera</i> L.). <i>PLoS ONE</i> , 2010, 5, e12762.	2.5	255
10	On the nature of human housekeeping genes. <i>Trends in Genetics</i> , 2008, 24, 481-484.	6.7	249
11	Genome sequence of the date palm <i>Phoenix dactylifera</i> L. <i>Nature Communications</i> , 2013, 4, 2274.	12.8	248
12	A Complete Sequence of the <i>T. tengcongensis</i> Genome. <i>Genome Research</i> , 2002, 12, 689-700.	5.5	209
13	The analysis of large-scale gene expression correlated to the phase changes of the migratory locust. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17611-17615.	7.1	197
14	A transcriptomic analysis of superhybrid rice <i>LYP9</i> and its parents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7695-7701.	7.1	184
15	A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. <i>Genomics</i> , 2010, 96, 259-265.	2.9	184
16	Compositional Gradients in Gramineae Genes. <i>Genome Research</i> , 2002, 12, 851-856.	5.5	166
17	Evolution of alternative splicing after gene duplication. <i>Genome Research</i> , 2006, 16, 182-189.	5.5	141
18	The Silkworm ( <i>Bombyx mori</i> ) microRNAs and Their Expressions in Multiple Developmental Stages. <i>PLoS ONE</i> , 2008, 3, e2997.	2.5	130

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19	Neutral evolution of $\sim$ non-coding $\hat{\epsilon}$ ™ complementary DNAs. <i>Nature</i> , 2004, 431, 1-2.	27.8	127
20	How many human genes can be defined as housekeeping with current expression data?. <i>BMC Genomics</i> , 2008, 9, 172.	2.8	125
21	On the molecular mechanism of GC content variation among eubacterial genomes. <i>Biology Direct</i> , 2012, 7, 2.	4.6	121
22	The next-generation sequencing technology and application. <i>Protein and Cell</i> , 2010, 1, 520-536.	11.0	112
23	The complete chloroplast genome provides insight into the evolution and polymorphism of <i>Panax ginseng</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 696.	3.6	112
24	LncRNAWiki: harnessing community knowledge in collaborative curation of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2015, 43, D187-D192.	14.5	110
25	DNA Microarray Analysis of Genome Dynamics in <i>Yersinia pestis</i> : Insights into Bacterial Genome Microevolution and Niche Adaptation. <i>Journal of Bacteriology</i> , 2004, 186, 5138-5146.	2.2	109
26	The Rice Mitochondrial Genomes and Their Variations. <i>Plant Physiology</i> , 2006, 140, 401-410.	4.8	103
27	$\hat{\beta}$ -MYN: a new algorithm for estimating $K_a$ and $K_s$ with consideration of variable substitution rates. <i>Biology Direct</i> , 2009, 4, 20.	4.6	99
28	Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005, 15, 1258-1264.	5.5	91
29	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.	3.3	91
30	Serial Analysis of Gene Expression Study of a Hybrid Rice Strain (LYP9) and Its Parental Cultivars. <i>Plant Physiology</i> , 2005, 138, 1216-1231.	4.8	86
31	Mouse transcriptome: neutral evolution of 'non-coding' complementary DNAs. <i>Nature</i> , 2004, 431, 1 p following 757; discussion following 757.	27.8	86
32	Biological Databases for Human Research. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 55-63.	6.9	84
33	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.	2.5	79
34	Inactivated SARS-CoV Vaccine Prepared from Whole Virus Induces a High Level of Neutralizing Antibodies in BALB/c Mice. <i>DNA and Cell Biology</i> , 2004, 23, 391-394.	1.9	78
35	Computing $K_a$ and $K_s$ with a consideration of unequal transitional substitutions. <i>BMC Evolutionary Biology</i> , 2006, 6, 44.	3.2	78
36	Minimal Introns Are Not "Junk". <i>Genome Research</i> , 2002, 12, 1185-1189.	5.5	74

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37	Genetic variation and metabolic pathway intricacy govern the active compound content and quality of the Chinese medicinal plant <i>Lonicera japonica</i> thunb. <i>BMC Genomics</i> , 2012, 13, 195.	2.8	74
38	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.	2.8	73
39	Correlation Between Ka/Ks and Ks is Related to Substitution Model and Evolutionary Lineage. <i>Journal of Molecular Evolution</i> , 2009, 68, 414-423.	1.8	71
40	An Integrated Analysis of miRNA and mRNA Expressions in Non-Small Cell Lung Cancers. <i>PLoS ONE</i> , 2011, 6, e26502.	2.5	71
41	A Brief Review of Software Tools for Pangenomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 73-76.	6.9	66
42	A Mitochondrial Genome Sequence of the Tibetan Antelope ( <i>Pantholops hodgsonii</i> ). <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 5-17.	6.9	60
43	The next-generation sequencing technology: A technology review and future perspective. <i>Science China Life Sciences</i> , 2010, 53, 44-57.	4.9	57
44	Sampling SNPs. <i>Nature Genetics</i> , 2000, 26, 13-14.	21.4	56
45	Vertebrate gene predictions and the problem of large genes. <i>Nature Reviews Genetics</i> , 2003, 4, 741-749.	16.3	56
46	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.	4.3	56
47	Adaptive clustering algorithm for community detection in complex networks. <i>Physical Review E</i> , 2008, 78, 046115.	2.1	54
48	Most of the Human Genome Is Transcribed. <i>Genome Research</i> , 2001, 11, 1975-1977.	5.5	53
49	Codon Deviation Coefficient: a novel measure for estimating codon usage bias and its statistical significance. <i>BMC Bioinformatics</i> , 2012, 13, 43.	2.6	53
50	A proteomic study on postdiapaused embryonic development of brine shrimp ( <i>Artemia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	2.2	50
51	Proteomic profiling of rice embryos from a hybrid rice cultivar and its parental lines. <i>Proteomics</i> , 2008, 8, 4808-4821.	2.2	48
52	Fatal Infection with Influenza A (H5N1) Virus in China. <i>New England Journal of Medicine</i> , 2006, 354, 2731-2732.	27.0	47
53	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 397-404.	6.9	46
54	Systematic analysis of intron size and abundance parameters in diverse lineages. <i>Science China Life Sciences</i> , 2013, 56, 968-974.	4.9	43

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55	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. <i>Nature Communications</i> , 2016, 7, 12845.	12.8	43
56	How Do Variable Substitution Rates Influence Ka and Ks Calculations?. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 116-127.	6.9	42
57	Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <i>Science China Life Sciences</i> , 2013, 56, 1-12.	4.9	42
58	Seasonally variable intestinal metagenomes of the red palm weevil ( <i>Rhynchophorus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.8	42
59	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.	3.6	41
60	Transcriptomic profiling of mature embryo from an elite super-hybrid rice LYP9 and its parental lines. <i>BMC Plant Biology</i> , 2008, 8, 114.	3.6	41
61	GC content variability of eubacteria is governed by the pol III $\beta'$ subunit. <i>Biochemical and Biophysical Research Communications</i> , 2007, 356, 20-25.	2.1	40
62	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.	3.9	39
63	Ribogenomics: the Science and Knowledge of RNA. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 57-63.	6.9	38
64	Novel microRNAs in silkworm ( <i>Bombyx mori</i> ). <i>Functional and Integrative Genomics</i> , 2010, 10, 405-415.	3.5	37
65	Mitochondrial genome sequences of <i>Artemia tibetiana</i> and <i>Artemia urmiana</i> : assessing molecular changes for high plateau adaptation. <i>Science China Life Sciences</i> , 2013, 56, 440-452.	4.9	37
66	A gene catalogue for post-diapause development of an anhydrobiotic arthropod <i>Artemia franciscana</i> . <i>BMC Genomics</i> , 2009, 10, 52.	2.8	36
67	MicroRNA expression profiling of the fifth-instar posterior silk gland of <i>Bombyx mori</i> . <i>BMC Genomics</i> , 2014, 15, 410.	2.8	36
68	Pseudogene accumulation might promote the adaptive microevolution of <i>Yersinia pestis</i> . <i>Journal of Medical Microbiology</i> , 2005, 54, 259-268.	1.8	35
69	Evaluation of Six Methods for Estimating Synonymous and Nonsynonymous Substitution Rates. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 173-181.	6.9	34
70	A novel DNA sequence periodicity decodes nucleosome positioning. <i>Nucleic Acids Research</i> , 2008, 36, 6228-6236.	14.5	33
71	Involvement of the GP63 protease in infection of <i>Trichomonas vaginalis</i> . <i>Parasitology Research</i> , 2011, 109, 71-79.	1.6	33
72	Complete Sequence and Analysis of Coconut Palm ( <i>Cocos nucifera</i> ) Mitochondrial Genome. <i>PLoS ONE</i> , 2016, 11, e0163990.	2.5	33

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73	A comparative analysis of divergently-paired genes (DPGs) among <i>Drosophila</i> and vertebrate genomes. <i>BMC Evolutionary Biology</i> , 2009, 9, 55.	3.2	32
74	A discovery of novel microRNAs in the silkworm ( <i>Bombyx mori</i> ) genome. <i>Genomics</i> , 2009, 94, 438-444.	2.9	32
75	Diverse LEA (late embryogenesis abundant) and LEA-like genes and their responses to hypersaline stress in post-diapause embryonic development of <i>Artemia franciscana</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2011, 160, 32-39.	1.6	32
76	Compositional dynamics of guanine and cytosine content in prokaryotic genomes. <i>Research in Microbiology</i> , 2007, 158, 363-370.	2.1	31
77	Distinct Contributions of Replication and Transcription to Mutation Rate Variation of Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 4-10.	6.9	31
78	Profiling microRNA expression during multi-staged date palm ( <i>Phoenix dactylifera</i> L.) fruit development. <i>Genomics</i> , 2015, 105, 242-251.	2.9	31
79	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.	0.7	29
80	Comparative Analysis of Eubacterial DNA Polymerase III Alpha Subunits. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 203-211.	6.9	28
81	DNA barcoding provides distinction between <i>Radix Astragali</i> and its adulterants. <i>Science China Life Sciences</i> , 2010, 53, 992-999.	4.9	28
82	Replication-associated purine asymmetry may contribute to strand-biased gene distribution. <i>Genomics</i> , 2007, 90, 186-194.	2.9	27
83	A Novel Role for Minimal Introns: Routing mRNAs to the Cytosol. <i>PLoS ONE</i> , 2010, 5, e10144.	2.5	27
84	PMirP: A pre-microRNA prediction method based on structure-sequence hybrid features. <i>Artificial Intelligence in Medicine</i> , 2010, 49, 127-132.	6.5	26
85	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.	3.9	26
86	Transcriptomic analysis reveals key regulators of mammogenesis and the pregnancy-lactation cycle. <i>Science China Life Sciences</i> , 2014, 57, 340-355.	4.9	26
87	The Rice Genome Knowledgebase (RGKbase): an annotation database for rice comparative genomics and evolutionary biology. <i>Nucleic Acids Research</i> , 2012, 41, D1199-D1205.	14.5	25
88	An evolutionary analysis of trypanosomatid GP63 proteases. <i>Parasitology Research</i> , 2011, 109, 1075-1084.	1.6	23
89	Comparative Analyses of H3K4 and H3K27 Trimethylations Between the Mouse Cerebrum and Testis. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 82-93.	6.9	22
90	Identification of Human HK Genes and Gene Expression Regulation Study in Cancer from Transcriptomics Data Analysis. <i>PLoS ONE</i> , 2013, 8, e54082.	2.5	22

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91	Flexibility and Symmetry of Prokaryotic Genome Rearrangement Reveal Lineage-Associated Core-Gene-Defined Genome Organizational Frameworks. <i>MBio</i> , 2014, 5, e01867.	4.1	22
92	Transcriptome sequencing of essential marine brown and red algal species in China and its significance in algal biology and phylogeny. <i>Acta Oceanologica Sinica</i> , 2014, 33, 1-12.	1.0	22
93	The Organelle Genomes of Hassawi Rice ( <i>Oryza sativa</i> L.) and Its Hybrid in Saudi Arabia: Genome Variation, Rearrangement, and Origins. <i>PLoS ONE</i> , 2012, 7, e42041.	2.5	22
94	The Transcript-centric Mutations in Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 11-22.	6.9	21
95	The quest for a unified view of bacterial land colonization. <i>ISME Journal</i> , 2014, 8, 1358-1369.	9.8	21
96	A large-scale gene discovery for the red palm weevil <i>Rhynchophorus ferrugineus</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	21
97	Phylogenetic Analysis of Brine Shrimp ( <i>Artemia</i> ) in China Using DNA Barcoding. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 155-162.	6.9	20
98	A novel mechanism of epigenetic regulation: Nucleosome-space occupancy. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 884-889.	2.1	20
99	A pangenomic study of <i>Bacillus thuringiensis</i> . <i>Journal of Genetics and Genomics</i> , 2011, 38, 567-576.	3.9	20
100	On the Organizational Dynamics of the Genetic Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 21-29.	6.9	20
101	Phylogeny of C4-Photosynthesis Enzymes Based on Algal Transcriptomic and Genomic Data Supports an Archaeal/Proteobacterial Origin and Multiple Duplication for Most C4-Related Genes. <i>PLoS ONE</i> , 2014, 9, e110154.	2.5	20
102	A Comprehensive Transcriptomic Analysis of Infant and Adult Mouse Ovary. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 239-248.	6.9	20
103	Evolution of Complex Thallus Alga: Genome Sequencing of <i>Saccharina japonica</i> . <i>Frontiers in Genetics</i> , 2019, 10, 378.	2.3	20
104	Modeling Transcriptome Based on Transcript-Sampling Data. <i>PLoS ONE</i> , 2008, 3, e1659.	2.5	20
105	Nucleotide compositional asymmetry between the leading and lagging strands of eubacterial genomes. <i>Research in Microbiology</i> , 2010, 161, 838-846.	2.1	19
106	RiceWiki: a wiki-based database for community curation of rice genes. <i>Nucleic Acids Research</i> , 2014, 42, D1222-D1228.	14.5	19
107	Gene Identification and Expression Analysis of 86,136 Expressed Sequence Tags (EST) from the Rice Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 26-42.	6.9	18
108	A Scenario on the Stepwise Evolution of the Genetic Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 143-151.	6.9	18

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109	MTD: a mammalian transcriptomic database to explore gene expression and regulation. <i>Briefings in Bioinformatics</i> , 2017, 18, 28-36.	6.5	18
110	Genome Assembly and Pathway Analysis of Edible Mushroom <i>Agrocybe cylindracea</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 341-351.	6.9	18
111	Both Size and GC-Content of Minimal Introns Are Selected in Human Populations. <i>PLoS ONE</i> , 2011, 6, e17945.	2.5	18
112	On the core bacterial flora of <i>Ixodes persulcatus</i> (Taiga tick). <i>PLoS ONE</i> , 2017, 12, e0180150.	2.5	18
113	A Content-Centric Organization of the Genetic Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 1-6.	6.9	17
114	Transposon-Derived and Satellite-Derived Repetitive Sequences Play Distinct Functional Roles in Mammalian Intron Size Expansion. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9758.	1.2	17
115	Molecular Dynamics Simulation of the Complex PBP-2x with Drug Cefuroxime to Explore the Drug Resistance Mechanism of <i>Streptococcus suis</i> R61. <i>PLoS ONE</i> , 2012, 7, e35941.	2.5	17
116	Evolution and Variation of the SARS-CoV Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 216-225.	6.9	16
117	Complete Genome Sequences of the SARS-CoV: the BJ Group (Isolates BJ01-BJ04). <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 180-192.	6.9	15
118	Transcriptomic study of the red palm weevil <i>Rhynchophorus ferrugineus</i> embryogenesis. <i>Insect Science</i> , 2015, 22, 65-82.	3.0	15
119	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	6.9	15
120	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.	6.9	15
121	Comparing the whole-genome-shotgun and map-based sequences of the rice genome. <i>Trends in Plant Science</i> , 2006, 11, 387-391.	8.8	14
122	Genome-wide mapping of conserved microRNAs and their host transcripts in <i>Tribolium castaneum</i> . <i>Journal of Genetics and Genomics</i> , 2008, 35, 349-355.	3.9	14
123	Hydroxyurea-induced global transcriptional suppression in mouse ES cells. <i>Carcinogenesis</i> , 2010, 31, 1661-1668.	2.8	13
124	Modeling compositional dynamics based on GC and purine contents of protein-coding sequences. <i>Biology Direct</i> , 2010, 5, 63.	4.6	13
125	VCGDB: a dynamic genome database of the Chinese population. <i>BMC Genomics</i> , 2014, 15, 265.	2.8	13
126	The Elements of Data Sharing. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 1-4.	6.9	13



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127	Thousands of Novel Transcripts Identified in Mouse Cerebrum, Testis, and ES Cells Based on ribo-minus RNA Sequencing. <i>Frontiers in Genetics</i> , 2011, 2, 93.	2.3	12
128	WikiCell: A Unified Resource Platform for Human Transcriptomics Research. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 357-362.	2.0	12
129	The Association Between H3K4me3 and Antisense Transcription. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 74-81.	6.9	12
130	Sequence Signatures of Nucleosome Positioning in <i>Caenorhabditis elegans</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 92-102.	6.9	11
131	Strand-biased Gene Distribution in Bacteria Is Related to both Horizontal Gene Transfer and Strand-biased Nucleotide Composition. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 186-196.	6.9	11
132	Comparative analysis on transcriptome sequencings of six <i>Sargassum</i> species in China. <i>Acta Oceanologica Sinica</i> , 2014, 33, 37-44.	1.0	11
133	Endogenous viral elements in algal genomes. <i>Acta Oceanologica Sinica</i> , 2014, 33, 102-107.	1.0	11
134	A comprehensive crop genome research project: the Superhybrid Rice Genome Project in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1023-1034.	4.0	10
135	DNA sequencing leads to genomics progress in China. <i>Science China Life Sciences</i> , 2011, 54, 290-292.	4.9	10
136	An RNA-seq-based Gene Expression Profiling of Radiation-induced Tumorigenic Mammary Epithelial Cells. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 326-335.	6.9	10
137	BIGrat: a repeat resolver for pyrosequencing-based re-sequencing with Newbler. <i>BMC Research Notes</i> , 2012, 5, 567.	1.4	10
138	Gene and Genome Parameters of Mammalian Liver Circadian Genes (LCGs). <i>PLoS ONE</i> , 2012, 7, e46961.	2.5	10
139	Predicting the Function of 4-Coumarate:CoA Ligase (LJ4CL1) in <i>Lonicera japonica</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 2386-2399.	4.1	10
140	The bacterial RNA ligase RtcB accelerates the repair process of fragmented rRNA upon releasing the antibiotic stress. <i>Science China Life Sciences</i> , 2020, 63, 251-258.	4.9	10
141	Evolutionary Transients in the Rice Transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 211-228.	6.9	9
142	Transcriptome-Wide Analysis of SAME Superfamily to Novelty Phosphoethanolamine N-Methyltransferase Copy in <i>Lonicera japonica</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 521-534.	4.1	9
143	Gene expression profiling in porcine mammary gland during lactation and identification of breed-and developmental-stage-specific genes. <i>Science in China Series C: Life Sciences</i> , 2006, 49, 26-36.	1.3	8
144	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.	1.6	8

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145	The Pendulum Model for Genome Compositional Dynamics: from the Four Nucleotides to the Twenty Amino Acids. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 175-180.	6.9	8
146	Phylogenomic analysis of transcriptomic sequences of mitochondria and chloroplasts of essential brown algae (Phaeophyceae) in China. <i>Acta Oceanologica Sinica</i> , 2014, 33, 94-101.	1.0	8
147	Comparative analysis of four essential Gracilariaceae species in China based on whole transcriptomic sequencing. <i>Acta Oceanologica Sinica</i> , 2014, 33, 54-62.	1.0	8
148	Analysis of <i>Saccharina japonica</i> transcriptome using the high-throughput DNA sequencing technique and its vanadium-dependent haloperoxidase gene. <i>Acta Oceanologica Sinica</i> , 2014, 33, 27-36.	1.0	8
149	Compositional Variability and Mutation Spectra of Monophyletic SARS-CoV-2 Clades. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 648-663.	6.9	8
150	A comprehensive analysis of protein phosphatases in rice and Arabidopsis. <i>Plant Systematics and Evolution</i> , 2010, 289, 111-126.	0.9	7
151	A complete genome assembly of <i>Glaciecola mesophila</i> sp. nov. sequenced by using BIGIS-4 sequencer system. <i>Science China Life Sciences</i> , 2011, 54, 835-840.	4.9	7
152	LCGbase: A Comprehensive Database for Lineage-Based Co-regulated Genes. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8540.	1.2	7
153	Life on Two Tracks. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 123-126.	6.9	7
154	De novo sequencing and comparative analysis of three red algal species of Family Solieriaceae to discover putative genes associated with carrageenan biosynthesis. <i>Acta Oceanologica Sinica</i> , 2014, 33, 45-53.	1.0	7
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