

# Jun Yu

## List of Publications by Year in descending order

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189  
papers

37,623  
citations

41344

49  
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3487

182  
g-index

199  
all docs

199  
docs citations

199  
times ranked

42470  
citing authors

#	ARTICLE	IF	CITATIONS
1	Roles of host small RNAs in the evolution and host tropism of coronaviruses. <i>Briefings in Bioinformatics</i> , 2021, 22, 1096-1105.	6.5	2
2	On the ultimate finishing line of the Human Genome Project. <i>Innovation(China)</i> , 2021, 2, 100133.	9.1	3
3	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
4	Transcriptomic and Proteomic Analysis of Mannitol-metabolism-associated Genes in <i>Saccharina japonica</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 415-429.	6.9	5
5	From Mutation Signature to Molecular Mechanism in the RNA World: A Case of SARS-CoV-2. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 627-639.	6.9	4
6	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
7	The Elements of Data Sharing. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 1-4.	6.9	13
8	Compositional Variability and Mutation Spectra of Monophyletic SARS-CoV-2 Clades. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 648-663.	6.9	8
9	Evolution of Complex Thallus Alga: Genome Sequencing of <i>Saccharina japonica</i> . <i>Frontiers in Genetics</i> , 2019, 10, 378.	2.3	20
10	Meta-analysis Reveals Potential Influence of Oxidative Stress on the Airway Microbiomes of Cystic Fibrosis Patients. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 590-602.	6.9	4
11	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 397-404.	6.9	46
12	A Time for Celebration: 40th Anniversary of GSC and 15th Anniversary of BIG, CAS. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 387-388.	6.9	0
13	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
14	MTD: a mammalian transcriptomic database to explore gene expression and regulation. <i>Briefings in Bioinformatics</i> , 2017, 18, 28-36.	6.5	18
15	Complete mitochondrial genome and phylogenetic analysis of <i>Ixodes persulcatus</i> (taiga tick). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 3-4.	0.4	3
16	A Step Forward in Precision Medicine on "One Belt One Road". <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 219.	6.9	0
17	MicroRNA Expression in Multistage Date Fruit Development. <i>Methods in Molecular Biology</i> , 2017, 1638, 339-351.	0.9	0
18	ISVASE: identification of sequence variant associated with splicing event using RNA-seq data. <i>BMC Bioinformatics</i> , 2017, 18, 320.	2.6	0

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19	On the core bacterial flora of <i>Ixodes persulcatus</i> (Taiga tick). PLoS ONE, 2017, 12, e0180150.	2.5	18
20	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. BMC Biotechnology, 2016, 16, 47.	3.3	91
21	Precision Medicine: What Do We Expect in the Scope of Basic Biomedical Sciences?. Genomics, Proteomics and Bioinformatics, 2016, 14, 1-3.	6.9	3
22	Precision Medicine: What Challenges Are We Facing?. Genomics, Proteomics and Bioinformatics, 2016, 14, 253-261.	6.9	15
23	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. Nature Communications, 2016, 7, 12845.	12.8	43
24	Complete Sequence and Analysis of Coconut Palm ( <i>Cocos nucifera</i> ) Mitochondrial Genome. PLoS ONE, 2016, 11, e0163990.	2.5	33
25	A Brief Review of Software Tools for Pangenomics. Genomics, Proteomics and Bioinformatics, 2015, 13, 73-76.	6.9	66
26	LncRNAWiki: harnessing community knowledge in collaborative curation of human long non-coding RNAs. Nucleic Acids Research, 2015, 43, D187-D192.	14.5	110
27	Profiling microRNA expression during multi-staged date palm ( <i>Phoenix dactylifera</i> L.) fruit development. Genomics, 2015, 105, 242-251.	2.9	31
28	Plastid-LCGbase: a collection of evolutionarily conserved plastid-associated gene pairs. Nucleic Acids Research, 2015, 43, D990-D995.	14.5	4
29	Transcriptome-Wide Analysis of SAME Superfamily to Novelty Phosphoethanolamine N-Methyltransferase Copy in <i>Lonicera japonica</i> . International Journal of Molecular Sciences, 2015, 16, 521-534.	4.1	9
30	Biological Databases for Human Research. Genomics, Proteomics and Bioinformatics, 2015, 13, 55-63.	6.9	84
31	KGCAK: a K-mer based database for genome-wide phylogeny and complexity evaluation. Biology Direct, 2015, 10, 53.	4.6	5
32	LCGserver: A Webserver for Exploring Evolutionary Trajectory of Gene Orders in a Large Number of Genomes. OMICS A Journal of Integrative Biology, 2015, 19, 574-577.	2.0	0
33	Transcriptomic study of the red palm weevil <i>Rhynchophorus ferrugineus</i> embryogenesis. Insect Science, 2015, 22, 65-82.	3.0	15
34	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. PLoS ONE, 2014, 9, e110154.	2.5	20
35	Predicting the Function of 4-Coumarate:CoA Ligase (LJ4CL1) in <i>Lonicera japonica</i> . International Journal of Molecular Sciences, 2014, 15, 2386-2399.	4.1	10
36	A Comprehensive Transcriptomic Analysis of Infant and Adult Mouse Ovary. Genomics, Proteomics and Bioinformatics, 2014, 12, 239-248.	6.9	20

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37	RiceWiki: a wiki-based database for community curation of rice genes. <i>Nucleic Acids Research</i> , 2014, 42, D1222-D1228.	14.5	19
38	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
39	Ribogenomics: the Science and Knowledge of RNA. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 57-63.	6.9	38
40	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
41	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
42	Phylogenomic analysis of transcriptomic sequences of mitochondria and chloroplasts for marine red algae (Rhodophyta) in China. <i>Acta Oceanologica Sinica</i> , 2014, 33, 86-93.	1.0	3
43	Tryptophan synthase of Phaeophyceae originated from the secondary host nucleus. <i>Acta Oceanologica Sinica</i> , 2014, 33, 63-72.	1.0	0
44	The discovery of archaea origin phosphomannomutase in algae based on the algal transcriptome. <i>Acta Oceanologica Sinica</i> , 2014, 33, 108-113.	1.0	2
45	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
46	Comparative analysis on transcriptome sequencings of six Sargassum species in China. <i>Acta Oceanologica Sinica</i> , 2014, 33, 37-44.	1.0	11
47	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
48	Endogenous viral elements in algal genomes. <i>Acta Oceanologica Sinica</i> , 2014, 33, 102-107.	1.0	11
49	Transcriptome-wide evolutionary analysis on essential brown algae (Phaeophyceae) in China. <i>Acta Oceanologica Sinica</i> , 2014, 33, 13-19.	1.0	7
50	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
51	Origin and evolution of alginate-c5-mannuronan-epimerase gene based on transcriptomic analysis of brown algae. <i>Acta Oceanologica Sinica</i> , 2014, 33, 73-85.	1.0	6
52	Transcriptome characterization of <i>Ishige okamurae</i> (Phaeophyceae) shows strong environmental acclimation. <i>Acta Oceanologica Sinica</i> , 2014, 33, 20-26.	1.0	5
53	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
54	The quest for a unified view of bacterial land colonization. <i>ISME Journal</i> , 2014, 8, 1358-1369.	9.8	21

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55	Genome sequence and genetic diversity of the common carp, <i>Cyprinus carpio</i> . <i>Nature Genetics</i> , 2014, 46, 1212-1219.	21.4	576
56	VCGDB: a dynamic genome database of the Chinese population. <i>BMC Genomics</i> , 2014, 15, 265.	2.8	13
57	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
58	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
59	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
60	Complete genome sequence of methicillin-sensitive <i>Staphylococcus aureus</i> containing a heterogeneous staphylococcal cassette chromosome element. <i>Science China Life Sciences</i> , 2013, 56, 268-274.	4.9	0
61	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
62	Seasonally variable intestinal metagenomes of the red palm weevil ( <i>Rhynchophorus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.8	42
63	Does the Genetic Code Have A Eukaryotic Origin?. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 41-55.	6.9	2
64	Genome sequence of the date palm <i>Phoenix dactylifera</i> L. <i>Nature Communications</i> , 2013, 4, 2274.	12.8	248
65	Systematic analysis of intron size and abundance parameters in diverse lineages. <i>Science China Life Sciences</i> , 2013, 56, 968-974.	4.9	43
66	Improved picoliter-sized micro-reactors for high-throughput biological analysis. <i>Science China Life Sciences</i> , 2013, 56, 1134-1141.	4.9	0
67	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
68	Functional Networking of Human Divergently Paired Genes (DPGs). <i>PLoS ONE</i> , 2013, 8, e78896.	2.5	3
69	A large-scale gene discovery for the red palm weevil <i>Rhynchophorus ferrugineus</i> (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overl	3.0	29
70	LCGbase: A Comprehensive Database for Lineage-Based Co-regulated Genes. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8540.	1.2	7
71	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
72	A New Definition of Modularity for Community Detection in Complex Networks. <i>Chinese Physics Letters</i> , 2012, 29, 098901.	3.3	5

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73	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
74	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
75	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
76	The Transcript-centric Mutations in Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 11-22.	6.9	21
77	Has a New Start"Open Access. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 1-3.	6.9	1
78	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
79	WikiCell: A Unified Resource Platform for Human Transcriptomics Research. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 357-362.	2.0	12
80	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
81	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
82	The Association Between H3K4me3 and Antisense Transcription. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 74-81.	6.9	12
83	Challenges to the Common Dogma. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 55-57.	6.9	6
84	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
85	Life on Two Tracks. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 123-126.	6.9	7
86	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
87	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
88	Latest notable achievements in genomics. <i>Science China Life Sciences</i> , 2012, 55, 645-648.	4.9	1
89	BIGrat: a repeat resolver for pyrosequencing-based re-sequencing with Newbler. <i>BMC Research Notes</i> , 2012, 5, 567.	1.4	10
90	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

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91	A Novel Autosomal Dominant Inclusion Body Myopathy Linked to 7q22.1-31.1. <i>PLoS ONE</i> , 2012, 7, e39288.	2.5	4
92	Gene and Genome Parameters of Mammalian Liver Circadian Genes (LCGs). <i>PLoS ONE</i> , 2012, 7, e46961.	2.5	10
93	On the molecular mechanism of GC content variation among eubacterial genomes. <i>Biology Direct</i> , 2012, 7, 2.	4.6	121
94	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
95	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
96	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
97	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
98	A pangenomic study of <i>Bacillus thuringiensis</i> . <i>Journal of Genetics and Genomics</i> , 2011, 38, 567-576.	3.9	20
99	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
100	On the Organizational Dynamics of the Genetic Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 21-29.	6.9	20
101	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
102	Involvement of the GP63 protease in infection of <i>Trichomonas vaginalis</i> . <i>Parasitology Research</i> , 2011, 109, 71-79.	1.6	33
103	An evolutionary analysis of trypanosomatid GP63 proteases. <i>Parasitology Research</i> , 2011, 109, 1075-1084.	1.6	23
104	Exploration of the binding mode of $\beta$ -type small acid soluble proteins (SASPs) with DNA. <i>Journal of Molecular Modeling</i> , 2011, 17, 3183-3193.	1.8	2
105	DNA sequencing leads to genomics progress in China. <i>Science China Life Sciences</i> , 2011, 54, 290-292.	4.9	10
106	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
107	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
108	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

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109	Both Size and GC-Content of Minimal Introns Are Selected in Human Populations. PLoS ONE, 2011, 6, e17945.	2.5	18
110	The Disequilibrium of Nucleosomes Distribution along Chromosomes Plays a Functional and Evolutionarily Role in Regulating Gene Expression. PLoS ONE, 2011, 6, e23219.	2.5	6
111	An Integrated Analysis of miRNA and mRNA Expressions in Non-Small Cell Lung Cancers. PLoS ONE, 2011, 6, e26502.	2.5	71
112	Novel microRNAs in silkworm ( <i>Bombyx mori</i> ). Functional and Integrative Genomics, 2010, 10, 405-415.	3.5	37
113	A comprehensive analysis of protein phosphatases in rice and Arabidopsis. Plant Systematics and Evolution, 2010, 289, 111-126.	0.9	7
114	The next-generation sequencing technology and application. Protein and Cell, 2010, 1, 520-536.	11.0	112
115	The next-generation sequencing technology: A technology review and future perspective. Science China Life Sciences, 2010, 53, 44-57.	4.9	57
116	DNA barcoding provides distinction between <i>Radix Astragali</i> and its adulterants. Science China Life Sciences, 2010, 53, 992-999.	4.9	28
117	PMirP: A pre-microRNA prediction method based on structure-sequence hybrid features. Artificial Intelligence in Medicine, 2010, 49, 127-132.	6.5	26
118	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
119	A Novel Role for Minimal Introns: Routing mRNAs to the Cytosol. PLoS ONE, 2010, 5, e10144.	2.5	27
120	Hydroxyurea-induced global transcriptional suppression in mouse ES cells. Carcinogenesis, 2010, 31, 1661-1668.	2.8	13
121	Modeling compositional dynamics based on GC and purine contents of protein-coding sequences. Biology Direct, 2010, 5, 63.	4.6	13
122	A novel mechanism of epigenetic regulation: Nucleosome-space occupancy. Biochemical and Biophysical Research Communications, 2010, 391, 884-889.	2.1	20
123	Nucleotide compositional asymmetry between the leading and lagging strands of eubacterial genomes. Research in Microbiology, 2010, 161, 838-846.	2.1	19
124	A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. Genomics, 2010, 96, 259-265.	2.9	184
125	KaKs_Calculator 2.0: A Toolkit Incorporating Gamma-Series Methods and Sliding Window Strategies. Genomics, Proteomics and Bioinformatics, 2010, 8, 77-80.	6.9	1,301
126	Sequence Signatures of Nucleosome Positioning in <i>Caenorhabditis elegans</i> . Genomics, Proteomics and Bioinformatics, 2010, 8, 92-102.	6.9	11

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127	Evolutionary Transients in the Rice Transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 211-228.	6.9	9
128	The Complete Chloroplast Genome Sequence of Date Palm ( <i>Phoenix dactylifera</i> L.). <i>PLoS ONE</i> , 2010, 5, e12762.	2.5	255
129	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
130	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
131	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
132	HRGD: a database for mining potential heterosis-related genes in plants. <i>Plant Molecular Biology</i> , 2009, 69, 255-260.	3.9	6
133	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
134	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
135	A discovery of novel microRNAs in the silkworm ( <i>Bombyx mori</i> ) genome. <i>Genomics</i> , 2009, 94, 438-444.	2.9	32
136	Î <sup>3</sup> -MYN: a new algorithm for estimating Ka and Ks with consideration of variable substitution rates. <i>Biology Direct</i> , 2009, 4, 20.	4.6	99
137	How Do Variable Substitution Rates Influence Ka and Ks Calculations?. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 116-127.	6.9	42
138	A Brief Review on the Mechanisms of miRNA Regulation. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 147-154.	6.9	711
139	Proteomic profiling of rice embryos from a hybrid rice cultivar and its parental lines. <i>Proteomics</i> , 2008, 8, 4808-4821.	2.2	48
140	How many human genes can be defined as housekeeping with current expression data?. <i>BMC Genomics</i> , 2008, 9, 172.	2.8	125
141	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
142	On the nature of human housekeeping genes. <i>Trends in Genetics</i> , 2008, 24, 481-484.	6.7	249
143	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
144	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

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145	A novel DNA sequence periodicity decodes nucleosome positioning. <i>Nucleic Acids Research</i> , 2008, 36, 6228-6236.	14.5	33
146	Adaptive clustering algorithm for community detection in complex networks. <i>Physical Review E</i> , 2008, 78, 046115.	2.1	54
147	Modeling Transcriptome Based on Transcript-Sampling Data. <i>PLoS ONE</i> , 2008, 3, e1659.	2.5	20
148	The Silkworm ( <i>Bombyx mori</i> ) microRNAs and Their Expressions in Multiple Developmental Stages. <i>PLoS ONE</i> , 2008, 3, e2997.	2.5	130
149	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
150	Compositional dynamics of guanine and cytosine content in prokaryotic genomes. <i>Research in Microbiology</i> , 2007, 158, 363-370.	2.1	31
151	Replication-associated purine asymmetry may contribute to strand-biased gene distribution. <i>Genomics</i> , 2007, 90, 186-194.	2.9	27
152	GC content variability of eubacteria is governed by the pol III $\epsilon$ subunit. <i>Biochemical and Biophysical Research Communications</i> , 2007, 356, 20-25.	2.1	40
153	A Content-Centric Organization of the Genetic Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 1-6.	6.9	17
154	A Scenario on the Stepwise Evolution of the Genetic Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 143-151.	6.9	18
155	A proteomic study on postdiapaused embryonic development of brine shrimp ( <i>Artemia</i> ). <i>Trends in Plant Science</i> , 2007, 12, 10-14.	2.2	50
156	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
157	Evolution of alternative splicing after gene duplication. <i>Genome Research</i> , 2006, 16, 182-189.	5.5	141
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