

CAP3: A DNA Sequence Assembly Program

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A Parallel Euler Approach for Large-Scale Biological Sequence Assembly. , 0, , .		2
2	Gene Index analysis of the human genome estimates approximately 120,000 genes. Nature Genetics, 2000, 25, 239-240.	9.4	262
3	Human proton/oligopeptide transporter (POT) genes: Identification of putative human genes using bioinformatics. AAPS PharmSci, 2000, 2, 76-97.	1.3	45
4	The TIGR Gene Indices: reconstruction and representation of expressed gene sequences. Nucleic Acids Research, 2000, 28, 141-145.	6.5	312
5	An optimized protocol for analysis of EST sequences. Nucleic Acids Research, 2000, 28, 3657-3665.	6.5	121
6	Identification of human chromosome 22 transcribed sequences with ORF expressed sequence tags. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 12690-12693.	3.3	70
7	Anchoring of rice BAC clones to the rice genetic map in silico. Nucleic Acids Research, 2000, 28, 3636-3641.	6.5	40
8	RESOURCERER: a database for annotating and linking microarray resources within and across species. Genome Biology, 2001, 2, software0002.1.	13.9	99
9	Functional annotation of a full-length mouse cDNA collection. Nature, 2001, 409, 685-690.	13.7	653
10	The TIGR Gene Indices: analysis of gene transcript sequences in highly sampled eukaryotic species. Nucleic Acids Research, 2001, 29, 159-164.	6.5	413
11	Genomic analysis of orthologous mouse and human olfactory receptor loci. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 7390-7395.	3.3	94
12	Genome of Lumpy Skin Disease Virus. Journal of Virology, 2001, 75, 7122-7130.	1.5	269
13	The libraries that made SUCEST. Genetics and Molecular Biology, 2001, 24, 1-7.	0.6	146
14	In silico characterization and expression analyses of sugarcane putative sucrose non-fermenting-1 (SNF1) related kinases. Genetics and Molecular Biology, 2001, 24, 35-41.	0.6	6
15	In silico differential display of defense-related expressed sequence tags from sugarcane tissues infected with diazotrophic endophytes. Genetics and Molecular Biology, 2001, 24, 103-111.	0.6	28
16	Bioinformatics of the sugarcane EST project. Genetics and Molecular Biology, 2001, 24, 9-15.	0.6	21
18	Automated processing of raw DNA sequence data. IEEE Engineering in Medicine and Biology Magazine, 2001, 20, 41-48.	1.1	2
19	Sequence Evaluation of Four Pooled-Tissue Normalized Bovine cDNA Libraries and Construction of a Gene Index for Cattle. Genome Research, 2001, 11, 626-630.	2.4	98

#	ARTICLE	IF	CITATIONS
20	trEST, trGEN and Hits: access to databases of predicted protein sequences. <i>Nucleic Acids Research</i> , 2001, 29, 148-151.	6.5	27
21	Assembly of the Working Draft of the Human Genome with GigAssembler. <i>Genome Research</i> , 2001, 11, 1541-1548.	2.4	113
22	Fragment assembly with double-barreled data. <i>Bioinformatics</i> , 2001, 17, S225-S233.	1.8	97
23	A new approach to fragment assembly in DNA sequencing. , 2001, , .		36
24	Chapter 20. Bioinformatics in the drug discovery process. <i>Annual Reports in Medicinal Chemistry</i> , 2001, 36, 201-210.	0.5	1
25	Genome Sequence of a Baculovirus Pathogenic for <i>Culex nigripalpus</i> . <i>Journal of Virology</i> , 2001, 75, 11157-11165.	1.5	155
26	GBuilder--An Application for the Visualization and Integration of EST Cluster Data. <i>Genome Research</i> , 2001, 11, 179-184.	2.4	8
27	An Eulerian path approach to DNA fragment assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9748-9753.	3.3	1,094
28	The Genomes of Sheeppox and Goatpox Viruses. <i>Journal of Virology</i> , 2002, 76, 6054-6061.	1.5	285
29	The Genome of Swinepox Virus. <i>Journal of Virology</i> , 2002, 76, 783-790.	1.5	93
30	Annotated Expressed Sequence Tags and cDNA Microarrays for Studies of Brain and Behavior in the Honey Bee. <i>Genome Research</i> , 2002, 12, 555-566.	2.4	253
31	Cross-Referencing Eukaryotic Genomes: TIGR Orthologous Gene Alignments (TOGA). <i>Genome Research</i> , 2002, 12, 493-502.	2.4	134
32	A Computer-Based Method of Selecting Clones for a Full-Length cDNA Project: Simultaneous Collection of Negligibly Redundant and Variant cDNAs. <i>Genome Research</i> , 2002, 12, 1127-1134.	2.4	28
33	Exploring root symbiotic programs in the model legume <i>Medicago truncatula</i> using EST analysis. <i>Nucleic Acids Research</i> , 2002, 30, 5579-5592.	6.5	193
34	Splicing graphs and EST assembly problem. <i>Bioinformatics</i> , 2002, 18, S181-S188.	1.8	172
35	UniBLAST: a system to filter, cluster, and display BLAST results and assign unique gene annotation. <i>Bioinformatics</i> , 2002, 18, 1268-1268.	1.8	9
36	Xena, a Full-Length Basal Retroelement from Tetraodontid Fish. <i>Molecular Biology and Evolution</i> , 2002, 19, 247-255.	3.5	29
37	Comparison of RNA Expression Profiles Based on Maize Expressed Sequence Tag Frequency Analysis and Micro-Array Hybridization. <i>Plant Physiology</i> , 2002, 128, 896-910.	2.3	96

#	ARTICLE	IF	CITATIONS
38	Identification of mixups among DNA sequencing plates. <i>Bioinformatics</i> , 2002, 18, 1418-1426.	1.8	6
39	Fast algorithms for large-scale genome alignment and comparison. <i>Nucleic Acids Research</i> , 2002, 30, 2478-2483.	6.5	931
40	ARACHNE: A Whole-Genome Shotgun Assembler. <i>Genome Research</i> , 2002, 12, 177-189.	2.4	508
41	Assaying gene content in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9568-9572.	3.3	33
42	Space and time efficient parallel algorithms and software for EST clustering. , 0, , .		2
43	A compilation of soybean ESTs: generation and analysis. <i>Genome</i> , 2002, 45, 329-338.	0.9	133
44	Parallel EST clustering. , 2002, , .		4
45	Analysis of gene expression in rose petals using expressed sequence tags. <i>FEBS Letters</i> , 2002, 515, 35-38.	1.3	78
46	An integrated genetic, radiation hybrid, physical and transcription map of a region of distal mouse chromosome 12, including an imprinted locus and the "Legs at odd angles"™ (Loa) mutation. <i>Gene</i> , 2002, 283, 71-82.	1.0	6
47	Differential expression and genetic variation of hepatic messenger RNAs from genetically lean and fat chickens. <i>Gene</i> , 2002, 299, 235-243.	1.0	20
48	Oliz, a suite of Perl scripts that assist in the design of microarrays using 50mer oligonucleotides from the 3' untranslated region. <i>BMC Bioinformatics</i> , 2002, 3, 27.	1.2	20
49	Making sense of EST sequences by CLOBBing them. <i>BMC Bioinformatics</i> , 2002, 3, 31.	1.2	86
50	IL-4 dependent alternatively-activated macrophages have a distinctive in vivo gene expression phenotype. <i>BMC Immunology</i> , 2002, 3, 7.	0.9	290
51	Genome sequence assembly: algorithms and issues. <i>Computer</i> , 2002, 35, 47-54.	1.2	60
52	The River Blindness Genome Project. <i>Trends in Parasitology</i> , 2002, 18, 86-90.	1.5	18
53	Application Domains: Agri-Food and Genomics. , 0, , 127-143.		0
54	DNA Technologies: Sequencing Technology. , 0, , 165-208.		0
55	Genomic organization and regulation of three Cecropin genes in <i>Anopheles gambiae</i> . <i>Insect Molecular Biology</i> , 2002, 11, 517-525.	1.0	37

#	ARTICLE	IF	CITATIONS
56	Evidence of en bloc duplication in vertebrate genomes. <i>Nature Genetics</i> , 2002, 31, 100-105.	9.4	247
57	The Genome of Camelpox Virus. <i>Virology</i> , 2002, 295, 1-9.	1.1	84
58	Microarray data quality analysis: lessons from the AFGC project. Arabidopsis Functional Genomics Consortium. <i>Plant Molecular Biology</i> , 2002, 48, 119-132.	2.0	76
59	A semiautomated approach to gene discovery through expressed sequence tag data mining: Discovery of new human transporter genes. <i>AAPS PharmSci</i> , 2003, 5, 1-18.	1.3	15
60	The complete genome sequence of the avian pathogen <i>Mycoplasma gallisepticum</i> strain Rlow. <i>Microbiology (United Kingdom)</i> , 2003, 149, 2307-2316.	0.7	204
61	trap: Tandem Repeat Assembly Program produces improved shotgun assemblies of repetitive sequences. <i>Computer Methods and Programs in Biomedicine</i> , 2003, 70, 47-59.	2.6	11
62	Transcriptome characterization of the dimorphic and pathogenic fungus <i>Paracoccidioides brasiliensis</i> by EST analysis. <i>Yeast</i> , 2003, 20, 263-271.	0.8	74
63	Genotype to phenotype: a technological challenge. <i>Annals of Applied Biology</i> , 2003, 142, 33-39.	1.3	18
64	TACC1 and TOGAP Aurora A protein complex in breast cancer. <i>Oncogene</i> , 2003, 22, 8102-8116.	2.6	99
65	Massive parallelism, randomness and genomic advances. <i>Nature Genetics</i> , 2003, 33, 219-227.	9.4	68
66	Transcriptome analysis of the acoelomate human parasite <i>Schistosoma mansoni</i> . <i>Nature Genetics</i> , 2003, 35, 148-157.	9.4	433
67	Bioinformatics goes back to the future. <i>Nature Reviews Molecular Cell Biology</i> , 2003, 4, 157-162.	16.1	12
68	Application of Microarray Technology in Environmental and Comparative Physiology. <i>Annual Review of Physiology</i> , 2003, 65, 231-259.	5.6	153
69	Sequence analysis of a rainbow trout cDNA library and creation of a gene index. <i>Cytogenetic and Genome Research</i> , 2003, 102, 347-354.	0.6	97
70	Induced expression of pathogenesis-related protein genes in soybean by wounding and the <i>Phytophthora sojae</i> cell wall glucan elicitor. <i>Physiological and Molecular Plant Pathology</i> , 2003, 63, 141-149.	1.3	58
71	Laser-Capture Microdissection, a Tool for the Global Analysis of Gene Expression in Specific Plant Cell Types: Identification of Genes Expressed Differentially in Epidermal Cells or Vascular Tissues of Maize[W]. <i>Plant Cell</i> , 2003, 15, 583-596.	3.1	368
72	Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : Implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8007-8012.	3.3	341
73	TEPP, a new gene specifically expressed in testis, prostate, and placenta and well conserved in chordates. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 1209-1215.	1.0	11

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74	Mining single-nucleotide polymorphisms from hexaploid wheat ESTs. <i>Genome</i> , 2003, 46, 431-437.	0.9	167
75	Whole genome shotgun sequencing guided by bioinformatics pipelines—an optimized approach for an established technique. <i>Journal of Biotechnology</i> , 2003, 106, 121-133.	1.9	25
76	Immune gene discovery by expressed sequence tags generated from hemocytes of the bacteria-challenged oyster, <i>Crassostrea gigas</i> . <i>Gene</i> , 2003, 303, 139-145.	1.0	221
77	Comparison of gene representation in midguts from two phytophagous insects, <i>Bombyx mori</i> and <i>Ips pini</i> , using expressed sequence tags. <i>Gene</i> , 2003, 316, 127-136.	1.0	46
78	Cohen Syndrome Is Caused by Mutations in a Novel Gene, COH1, Encoding a Transmembrane Protein with a Presumed Role in Vesicle-Mediated Sorting and Intracellular Protein Transport. <i>American Journal of Human Genetics</i> , 2003, 72, 1359-1369.	2.6	321
79	The T Cell Surface—How Well Do We Know It?. <i>Immunity</i> , 2003, 19, 213-223.	6.6	31
80	Genomic evidence for the absence of a functional cholesteryl ester transfer protein gene in mice and rats. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2003, 135, 219-229.	0.7	64
81	Expressed sequence tags: alternative or complement to whole genome sequences?. <i>Trends in Plant Science</i> , 2003, 8, 321-329.	4.3	263
82	Pilot survey of expressed sequence tags (ESTs) from the asexual blood stages of <i>Plasmodium vivax</i> in human patients. <i>Malaria Journal</i> , 2003, 2, 21.	0.8	7
83	Development of a Molecular Tool for the Diagnosis of Leprosis, a Major Threat to Citrus Production in the Americas. <i>Plant Disease</i> , 2003, 87, 1317-1321.	0.7	87
84	BioNotes: a system for biosequence annotation. , 0, , .		1
85	Systems-wide chicken DNA microarrays, gene expression profiling, and discovery of functional genes. <i>Poultry Science</i> , 2003, 82, 939-951.	1.5	102
86	Space and time efficient parallel algorithms and software for EST clustering. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2003, 14, 1209-1221.	4.0	26
87	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. <i>Genome Research</i> , 2003, 13, 2725-2735.	2.4	254
88	A divide-and-conquer approach to fragment assembly. <i>Bioinformatics</i> , 2003, 19, 22-29.	1.8	24
89	ESTAP—an automated system for the analysis of EST data. <i>Bioinformatics</i> , 2003, 19, 1720-1722.	1.8	46
90	PCAP: A Whole-Genome Assembly Program. <i>Genome Research</i> , 2003, 13, 2164-2170.	2.4	237
91	Digital extractor: analysis of digital differential display output. <i>Bioinformatics</i> , 2003, 19, 1594-1595.	1.8	8

#	ARTICLE	IF	CITATIONS
92	EST analysis of genes expressed by the zygomycete pathogen <i>Conidiobolus coronatus</i> during growth on insect cuticle. <i>Microbiology (United Kingdom)</i> , 2003, 149, 1893-1900.	0.7	51
93	GenoPlante-Info (GPI): a collection of databases and bioinformatics resources for plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 179-182.	6.5	29
94	Cytogenetics, conserved synteny and evolution of chicken fucosyltransferase genes compared to human. <i>Cytogenetic and Genome Research</i> , 2003, 103, 111-121.	0.6	7
95	DNA Sequence-Based "Bar Codes" for Tracking the Origins of Expressed Sequence Tags from a Maize cDNA Library Constructed Using Multiple mRNA Sources. <i>Plant Physiology</i> , 2003, 133, 475-481.	2.3	38
96	A novel algorithm for computational identification of contaminated EST libraries. <i>Nucleic Acids Research</i> , 2003, 31, 1067-1074.	6.5	75
97	Expressed Sequence Tag Analysis of the Human Pathogen <i>Paracoccidioides brasiliensis</i> Yeast Phase: Identification of Putative Homologues of <i>Candida albicans</i> Virulence and Pathogenicity Genes. <i>Eukaryotic Cell</i> , 2003, 2, 34-48.	3.4	185
98	Comparative Analyses of Potato Expressed Sequence Tag Libraries. <i>Plant Physiology</i> , 2003, 131, 419-429.	2.3	174
99	TRAIT (TRANscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003, 19, 661-662.	1.8	4
100	Transcript Mapping and Genome Annotation of Ascidian mtDNA Using EST Data. <i>Genome Research</i> , 2003, 13, 2203-2212.	2.4	32
101	Efficient clustering of large EST data sets on parallel computers. <i>Nucleic Acids Research</i> , 2003, 31, 2963-2974.	6.5	69
102	Amino acid substitutions in the thyroglobulin gene are associated with susceptibility to human and murine autoimmune thyroid disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15119-15124.	3.3	169
103	TIGR Gene Indices clustering tools (TGICL): a software system for fast clustering of large EST datasets. <i>Bioinformatics</i> , 2003, 19, 651-652.	1.8	1,741
104	Genome of Bovine Herpesvirus 5. <i>Journal of Virology</i> , 2003, 77, 10339-10347.	1.5	136
105	ZmDB, an integrated database for maize genome research. <i>Nucleic Acids Research</i> , 2003, 31, 244-247.	6.5	33
106	MtDB: a database for personalized data mining of the model legume <i>Medicago truncatula</i> transcriptome. <i>Nucleic Acids Research</i> , 2003, 31, 196-201.	6.5	61
107	Redundancy based detection of sequence polymorphisms in expressed sequence tag data using autoSNP. <i>Bioinformatics</i> , 2003, 19, 421-422.	1.8	156
108	Mining for Single Nucleotide Polymorphisms and Insertions/Deletions in Maize Expressed Sequence Tag Data. <i>Plant Physiology</i> , 2003, 132, 84-91.	2.3	263
109	Genome Sequencing, Assembly and Gene Prediction in Fungi. <i>Applied Mycology and Biotechnology</i> , 2003, 3, 65-81.	0.3	1

#	ARTICLE	IF	CITATIONS
110	Expressed sequence tag (EST) analysis of two subspecies of <i>Metarhizium anisopliae</i> reveals a plethora of secreted proteins with potential activity in insect hosts. <i>Microbiology (United Kingdom)</i> , 2003, 149, 239-247.	0.7	133
111	Parallel hierarchical adaptive genetic algorithm for fragment assembly. , 0, , .		9
112	EST Pipeline System: Detailed and Automated EST Data Processing and Mining. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 236-242.	3.0	12
113	Using the TIGR Gene Index Databases for Biological Discovery. <i>Current Protocols in Bioinformatics</i> , 2003, 3, Unit 1.6.	25.8	4
114	Antimicrobial Resistance Markers of Class 1 and Class 2 Integron-bearing <i>Escherichia coli</i> from Irrigation Water and Sediments. <i>Emerging Infectious Diseases</i> , 2003, 9, 822-826.	2.0	92
115	GenFlow: generic flow for integration, management and analysis of molecular biology data. <i>Genetics and Molecular Biology</i> , 2004, 27, 691-695.	0.6	3
116	Gene Expression Profiling of Purified Rat Retinal Ganglion Cells. , 2004, 45, 2503.		36
117	Transposon-Mediated Sequencing. , 2004, 255, 197-210.		1
118	Using the TIGR Assembler in Shotgun Sequencing Projects. , 2004, 255, 279-294.		17
119	A strategy for assembling the maize (<i>Zea mays</i> L.) genome. <i>Bioinformatics</i> , 2004, 20, 140-147.	1.8	55
120	The TIGR Gene Indices: clustering and assembling EST and known genes and integration with eukaryotic genomes. <i>Nucleic Acids Research</i> , 2004, 33, D71-D74.	6.5	189
121	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. <i>Nucleic Acids Research</i> , 2004, 32, 3977-3983.	6.5	77
122	Saci-1, -2, and -3 and Perere, Four Novel Retrotransposons with High Transcriptional Activities from the Human Parasite <i>Schistosoma mansoni</i> . <i>Journal of Virology</i> , 2004, 78, 2967-2978.	1.5	57
123	'We are gathered here today' – EST cluster databases. <i>Briefings in Bioinformatics</i> , 2004, 5, 284-286.	3.2	0
124	PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries. <i>Nucleic Acids Research</i> , 2004, 32, 484D-488.	6.5	80
125	Construction and Evaluation of cDNA Libraries for Large-Scale Expressed Sequence Tag Sequencing in Wheat (<i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 595-608.	1.2	57
126	The Genome of Canarypox Virus. <i>Journal of Virology</i> , 2004, 78, 353-366.	1.5	167
127	Identifying differentially expressed genes in the mammalian retina and the retinal pigment epithelium by suppression subtractive hybridization. <i>Cytogenetic and Genome Research</i> , 2004, 106, 74-81.	0.6	12

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128	Systems biology of the 2-cell mouse embryo. <i>Cytogenetic and Genome Research</i> , 2004, 105, 240-250.	0.6	128
129	EST-PAGE--managing and analyzing EST data. <i>Bioinformatics</i> , 2004, 20, 286-288.	1.8	26
130	Molecular cloning of ten distinct hypervariable regions from the cellulose synthase gene superfamily in aspen trees. <i>Tree Physiology</i> , 2004, 24, 543-550.	1.4	29
131	Relocalization of Nuclear ALY Proteins to the Cytoplasm by the Tomato Bushy Stunt Virus P19 Pathogenicity Protein. <i>Plant Physiology</i> , 2004, 135, 2411-2423.	2.3	88
132	A Populus EST resource for plant functional genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13951-13956.	3.3	278
133	Shotgun Sequence Assembly. <i>Advances in Computers</i> , 2004, 60, 193-248.	1.2	20
134	PlantGDB, plant genome database and analysis tools. <i>Nucleic Acids Research</i> , 2004, 32, 354D-359.	6.5	193
135	The Diatom EST Database. <i>Nucleic Acids Research</i> , 2004, 33, D344-D347.	6.5	75
136	Characterization of the Maize Endosperm Transcriptome and Its Comparison to the Rice Genome. <i>Genome Research</i> , 2004, 14, 1932-1937.	2.4	80
137	Genomes of the Parapoxviruses Orf Virus and Bovine Papular Stomatitis Virus. <i>Journal of Virology</i> , 2004, 78, 168-177.	1.5	247
138	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	2.3	287
139	Genomics of Economically Significant <i>Aspergillus</i> and <i>Fusarium</i> Species. <i>Applied Mycology and Biotechnology</i> , 2004, 4, 249-283.	0.3	19
140	The Genome Sequence of <i>Mycoplasma hyopneumoniae</i> Strain 232, the Agent of Swine Mycoplasmosis. <i>Journal of Bacteriology</i> , 2004, 186, 7123-7133.	1.0	233
141	Virtual-SAGE: A New Approach to EST Data Analysis. <i>DNA Research</i> , 2004, 11, 145-152.	1.5	4
142	Chicken single nucleotide polymorphism identification and selection for genetic mapping. <i>Poultry Science</i> , 2004, 83, 1925-1931.	1.5	14
143	Fragment assembly with short reads. <i>Bioinformatics</i> , 2004, 20, 2067-2074.	1.8	166
144	Over 20% of human transcripts might form sense-antisense pairs. <i>Nucleic Acids Research</i> , 2004, 32, 4812-4820.	6.5	287
145	EST clustering error evaluation and correction. <i>Bioinformatics</i> , 2004, 20, 2973-2984.	1.8	68

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146	A transcriptomics resource for wheat functional genomics. <i>Plant Biotechnology Journal</i> , 2004, 2, 495-506.	4.1	60
147	Sequence composition, organization, and evolution of the core Triticeae genome. <i>Plant Journal</i> , 2004, 40, 500-511.	2.8	204
148	Characterization of open reading frame-expressed sequence tags generated from <i>Bos indicus</i> and <i>B. taurus</i> mammary gland cDNA libraries. <i>Animal Genetics</i> , 2004, 35, 213-219.	0.6	5
149	Gene conversion: a mechanism for generation of heterogeneity in the <i>tprK</i> gene of <i>Treponema pallidum</i> during infection. <i>Molecular Microbiology</i> , 2004, 52, 1579-1596.	1.2	137
150	Genomics of cellulose biosynthesis in poplars. <i>New Phytologist</i> , 2004, 164, 53-61.	3.5	119
151	Large-scale identification of genes in the fungus <i>Hebeloma cylindrosporum</i> paves the way to molecular analyses of ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2004, 164, 505-513.	3.5	40
152	<i>Aspergillus flavus</i> expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops. <i>FEMS Microbiology Letters</i> , 2004, 237, 333-340.	0.7	76
153	<i>Eimeria tenella</i> sporozoites and merozoites differentially express glycosylphosphatidylinositol-anchored variant surface proteins. <i>Molecular and Biochemical Parasitology</i> , 2004, 135, 123-132.	0.5	67
154	A survey of <i>Leishmania braziliensis</i> genome by shotgun sequencing. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 81-86.	0.5	20
155	DNA microarrays for comparative genomics and analysis of gene expression in <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2004, 138, 183-194.	0.5	21
156	Optimal cDNA microarray design using expressed sequence tags for organisms with limited genomic information. <i>BMC Bioinformatics</i> , 2004, 5, 191.	1.2	21
157	From biomedicine to natural history research: EST resources for ambystomatid salamanders. <i>BMC Genomics</i> , 2004, 5, 54.	1.2	79
158	Microarrays for global expression constructed with a low redundancy set of 27,500 sequenced cDNAs representing an array of developmental stages and physiological conditions of the soybean plant. <i>BMC Genomics</i> , 2004, 5, 73.	1.2	91
159	FunnyBase: a systems level functional annotation of <i>Fundulus</i> ESTs for the analysis of gene expression. <i>BMC Genomics</i> , 2004, 5, 96.	1.2	30
160	Expression of a glycine decarboxylase complex H-protein in non-photosynthetic tissues of <i>Populus tremuloides</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1676, 266-272.	2.4	8
161	Monitoring of Gene Expression Profiles and Isolation of Candidate Genes Involved in Pollination and Fertilization in Rice (<i>Oryza Sativa</i> L.) with a 10K cDNA Microarray. <i>Plant Molecular Biology</i> , 2004, 54, 471-487.	2.0	66
162	Suppression subtractive hybridization-mediated transcriptome analysis from multiple tissues of aspen (<i>Populus tremuloides</i>) altered in phenylpropanoid metabolism. <i>Planta</i> , 2004, 219, 694-704.	1.6	35
163	Identification of genes preferentially expressed in the pathogenic yeast phase of <i>Paracoccidioides brasiliensis</i> , using suppression subtraction hybridization and differential macroarray analysis. <i>Molecular Genetics and Genomics</i> , 2004, 271, 667-677.	1.0	67

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164	Study of simple sequence repeat (SSR) markers from wheat expressed sequence tags (ESTs). <i>Theoretical and Applied Genetics</i> , 2004, 109, 800-805.	1.8	155
165	Robust simple sequence repeat markers for spruce (<i>Picea</i> spp.) from expressed sequence tags. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1283-1294.	1.8	181
166	Phylogenetic Analysis of Ciona intestinalis Gene Superfamilies Supports the Hypothesis of Successive Gene Expansions. <i>Journal of Molecular Evolution</i> , 2004, 58, 168-181.	0.8	38
167	Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from <i>Trichoderma reesei</i> . <i>FEMS Microbiology Letters</i> , 2004, 230, 275-282.	0.7	20
168	Functional Genomics in Chickens: Development of Integrated-Systems Microarrays for Transcriptional Profiling and Discovery of Regulatory Pathways. <i>Comparative and Functional Genomics</i> , 2004, 5, 253-261.	2.0	58
169	A cDNA microarray from the telencephalon of juvenile male and female zebra finches. <i>Journal of Neuroscience Methods</i> , 2004, 138, 199-206.	1.3	42
170	SUPERCONTIGS: a contig scaffolding tool. , 0, , .		0
171	Functional Proteomics Mapping of a Human Signaling Pathway. <i>Genome Research</i> , 2004, 14, 1324-1332.	2.4	278
172	Microarray analysis for identification of Plasmodium-refractoriness candidate genes in mosquitoes. <i>Genome</i> , 2004, 47, 1061-1070.	0.9	11
173	Changes in gene expression during meristem activation processes in <i>Solanum tuberosum</i> with a focus on the regulation of an auxin response factor gene*. <i>Journal of Experimental Botany</i> , 2004, 55, 613-622.	2.4	78
174	A first generation physical map of the medaka genome in BACs essential for positional cloning and clone-by-clone based genomic sequencing. <i>Mechanisms of Development</i> , 2004, 121, 903-913.	1.7	32
175	Genome-wide mutagenesis of <i>Zea mays</i> L. using RescueMu transposons. <i>Genome Biology</i> , 2004, 5, R82.	13.9	66
176	A genome annotation-driven approach to cloning the human ORFeome. <i>Genome Biology</i> , 2004, 5, R84.	13.9	38
177	An <i>Ambystoma mexicanum</i> EST sequencing project: analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries. <i>Genome Biology</i> , 2004, 5, R67.	13.9	67
178	Versatile and open software for comparing large genomes. <i>Genome Biology</i> , 2004, 5, R12.	13.9	4,989
179	Duplicated Spot 14 genes in the chicken: characterization and identification of polymorphisms associated with abdominal fat traits. <i>Gene</i> , 2004, 332, 79-88.	1.0	47
180	The identification of genes from the oyster <i>Crassostrea gigas</i> that are differentially expressed in progeny exhibiting opposed susceptibility to summer mortality. <i>Gene</i> , 2004, 343, 211-220.	1.0	127
181	expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops. <i>FEMS Microbiology Letters</i> , 2004, 237, 333-340.	0.7	77

#	ARTICLE	IF	CITATIONS
182	Insight into <i>Trichoderma reesei</i> 's genome content, organization and evolution revealed through BAC library characterization. <i>Fungal Genetics and Biology</i> , 2004, 41, 1077-1087.	0.9	22
183	<i>Pneumocystis</i> : unraveling the cloak of obscurity. <i>Trends in Microbiology</i> , 2004, 12, 243-249.	3.5	47
184	Identification and characterization of the β -l-arabinofuranosidase B of <i>Fusarium oxysporum</i> f. sp. <i>dianthi</i> . <i>Physiological and Molecular Plant Pathology</i> , 2004, 64, 201-208.	1.3	16
185	Analysis of genes isolated from lipopolysaccharide-stimulated rainbow trout (<i>Oncorhynchus mykiss</i>) macrophages. <i>Molecular Immunology</i> , 2004, 41, 1199-1210.	1.0	92
186	Identification of a fatty acid Δ^{11} -desaturase from the microalga <i>Thalassiosira pseudonana</i> 1. <i>FEBS Letters</i> , 2004, 563, 28-34.	1.3	39
187	Mining EST databases to resolve evolutionary events in major crop species. <i>Genome</i> , 2004, 47, 868-876.	0.9	310
188	Expressed Sequence Tags: Medium-Throughput Protocols<I>. , 2004, 270, 075-092.		63
189	Expressed Sequence Tags: Analysis and Annotation<I>. , 2004, 270, 093-126.		11
190	Functional Genomic Analysis of the Rice Blast Fungus <i>Magnaporthe grisea</i> . <i>Applied Mycology and Biotechnology</i> , 2004, , 331-352.	0.3	3
191	Biological Sequence Assembly and Alignment. , 2005, , 243-261.		0
192	Assembling DNA Fragments with a Distributed Genetic Algorithm. , 2005, , 285-302.		3
193	Alignment of Optical Maps. <i>Lecture Notes in Computer Science</i> , 2005, , 489-504.	1.0	1
194	Characterization of a Novel Member of the Family <i>Closteroviridae</i> from <i>Mentha</i> spp.. <i>Phytopathology</i> , 2005, 95, 1043-1048.	1.1	24
195	Isolation and annotation of 10828 putative full length cDNAs from indica rice. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 445.	1.3	17
196	HarvEST. , 2005, 406, 161-177.		33
197	Seventy-five EST-linked Atlantic salmon (<i>Salmo salar</i> L.) microsatellite markers and their cross-amplification in five salmonid species. <i>Molecular Ecology Notes</i> , 2005, 5, 282-288.	1.7	34
198	Microsatellite markers for <i>Vaccinium</i> from EST and genomic libraries. <i>Molecular Ecology Notes</i> , 2005, 5, 657-660.	1.7	70
199	Transcriptomic study of apricot fruit (<i>Prunus armeniaca</i>) ripening among 13 006 expressed sequence tags. <i>Physiologia Plantarum</i> , 2005, 125, 281-292.	2.6	76

#	ARTICLE	IF	CITATIONS
200	A set of testis-specific novel genes collected from a collection of Korean Native Chicken ESTs. <i>Animal Genetics</i> , 2005, 36, 346-348.	0.6	16
201	Morphological and molecular characterization of the sudden-death syndrome pathogen of soybean in Brazil. <i>Plant Pathology</i> , 2005, 54, 53-65.	1.2	18
202	Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63. <i>Plant Journal</i> , 2005, 42, 772-780.	2.8	39
203	The chloroplast ClpP complex in <i>Chlamydomonas reinhardtii</i> contains an unusual high molecular mass subunit with a large apical domain. <i>FEBS Journal</i> , 2005, 272, 5558-5571.	2.2	32
204	Differential expression and molecular characterisation of Lmo7, Myo1e, Sash1, and Mcoln2 genes in Btk-defective B-cells. <i>Cellular Immunology</i> , 2005, 235, 46-55.	1.4	40
205	Maize cystatins respond to developmental cues, cold stress and drought. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005, 1729, 186-199.	2.4	73
206	An oligonucleotide microarray for transcriptome analysis of <i>Schistosoma mansoni</i> and its application/use to investigate gender-associated gene expression. <i>Molecular and Biochemical Parasitology</i> , 2005, 141, 1-13.	0.5	100
207	ESTree db: a Tool for Peach Functional Genomics. <i>BMC Bioinformatics</i> , 2005, 6, S16.	1.2	38
208	ParPEST: a pipeline for EST data analysis based on parallel computing. <i>BMC Bioinformatics</i> , 2005, 6, S9.	1.2	32
209	XenDB: Full length cDNA prediction and cross species mapping in <i>Xenopus laevis</i> . <i>BMC Genomics</i> , 2005, 6, 123.	1.2	5
210	EST analysis in <i>Ginkgo biloba</i> : an assessment of conserved developmental regulators and gymnosperm specific genes. <i>BMC Genomics</i> , 2005, 6, 143.	1.2	34
211	A rigorous method for multigenic families' functional annotation: the peptidyl arginine deiminase (PADs) proteins family example. <i>BMC Genomics</i> , 2005, 6, 153.	1.2	34
212	ASAP: Amplification, sequencing & annotation of plastomes. <i>BMC Genomics</i> , 2005, 6, 176.	1.2	61
213	GC-compositional strand bias around transcription start sites in plants and fungi. <i>BMC Genomics</i> , 2005, 6, 26.	1.2	67
214	Marine Genomics: A clearing-house for genomic and transcriptomic data of marine organisms. <i>BMC Genomics</i> , 2005, 6, 34.	1.2	34
215	Genomic organization, annotation, and ligand-receptor inferences of chicken chemokines and chemokine receptor genes based on comparative genomics. <i>BMC Genomics</i> , 2005, 6, 45.	1.2	57
216	Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , 2005, 6, 70.	1.2	283
217	Expressed sequence tags (ESTs) and simple sequence repeat (SSR) markers from octoploid strawberry (<i>Fragaria x ananassa</i>). <i>BMC Plant Biology</i> , 2005, 5, 12.	1.6	48

#	ARTICLE	IF	CITATIONS
218	Generation and analysis of 9792 EST sequences from cold acclimated oat, <i>Avena sativa</i> . <i>BMC Plant Biology</i> , 2005, 5, 18.	1.6	52
219	Pscroph, a parasitic plant EST database enriched for parasite associated transcripts. <i>BMC Plant Biology</i> , 2005, 5, 24.	1.6	37
220	Floral gene resources from basal angiosperms for comparative genomics research. <i>BMC Plant Biology</i> , 2005, 5, 5.	1.6	100
221	Development of real-time diagnostic assays specific for <i>Mycoplasma mycoides</i> subspecies <i>mycoides</i> Small Colony. <i>Veterinary Microbiology</i> , 2005, 111, 51-58.	0.8	19
222	Mutation of E1 glycoprotein of classical swine fever virus affects viral virulence in swine. <i>Virology</i> , 2005, 343, 116-127.	1.1	54
223	Generation and analysis of expressed sequence tags from the salt-tolerant mangrove species <i>Avicennia marina</i> (Forsk) Vierh.. <i>Theoretical and Applied Genetics</i> , 2005, 110, 416-424.	1.8	90
224	Identification and mapping of SNPs from ESTs in sunflower. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1532-1544.	1.8	97
225	Characteristics of the tomato nuclear genome as determined by sequencing undermethylated EcoRI digested fragments. <i>Theoretical and Applied Genetics</i> , 2005, 112, 72-84.	1.8	19
226	Coffee and tomato share common gene repertoires as revealed by deep sequencing of seed and cherry transcripts. <i>Theoretical and Applied Genetics</i> , 2005, 112, 114-130.	1.8	102
227	Candidate gene database and transcript map for peach, a model species for fruit trees. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1419-1428.	1.8	71
228	Analysis of expressed sequence tags from <i>Musa acuminata</i> ssp. <i>burmannicoides</i> , var. <i>Calcutta</i> (AA) leaves submitted to temperature stresses. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1517-1522.	1.8	30
229	Comparative analysis of expressed sequence tags from cold-acclimated and non-acclimated leaves of <i>Rhododendron catawbiense</i> Michx. <i>Planta</i> , 2005, 221, 406-416.	1.6	81
230	Isogene specific oligo arrays reveal multifaceted changes in gene expression during grape berry (<i>Vitis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	246
231	Cycloheximide treatment of cotton ovules alters the abundance of specific classes of mRNAs and generates novel ESTs for microarray expression profiling. <i>Molecular Genetics and Genomics</i> , 2005, 274, 477-493.	1.0	21
232	A comparative analysis of transcript abundance using SAGE and Affymetrix arrays. <i>Functional and Integrative Genomics</i> , 2005, 5, 163-174.	1.4	36
233	Frequency, type, distribution and annotation of simple sequence repeats in Rosaceae ESTs. <i>Functional and Integrative Genomics</i> , 2005, 5, 136-143.	1.4	90
234	Comparative analysis of expressed sequence tags from different organs of <i>Vitis vinifera</i> L.. <i>Functional and Integrative Genomics</i> , 2005, 5, 208-217.	1.4	44
235	The effect of replicate number and image analysis method on sweetpotato [<i>Ipomoea batatas</i> (L.) Lam.] cDNA microarray results. <i>Plant Molecular Biology Reporter</i> , 2005, 23, 367-381.	1.0	1

#	ARTICLE	IF	CITATIONS
236	Expressed sequence tags from the phytopathogenic fungus <i>Botrytis cinerea</i> . <i>European Journal of Plant Pathology</i> , 2005, 111, 139-146.	0.8	20
237	Comparative Analysis of Expressed Sequence Tags of Conifers and Angiosperms Reveals Sequences Specifically Conserved in Conifers. <i>Plant Molecular Biology</i> , 2005, 59, 895-907.	2.0	42
238	Endosperm-preferred Expression of Maize Genes as Revealed by Transcriptome-wide Analysis of Expressed Sequence Tags. <i>Plant Molecular Biology</i> , 2005, 59, 363-374.	2.0	28
239	The transcriptome of <i>Toxoplasma gondii</i> . <i>BMC Biology</i> , 2005, 3, 26.	1.7	167
240	A novel strategy for the identification of toxinlike structures in spider venom. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 131-140.	1.5	95
241	The anti-HIV cyanovirin-N domain is evolutionarily conserved and occurs as a protein module in eukaryotes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 670-678.	1.5	62
242	Proteome analysis of early somatic embryogenesis in <i>Picea glauca</i> . <i>Proteomics</i> , 2005, 5, 461-473.	1.3	166
243	Including mutations from conceptually translated expressed sequence tags into orthologous proteins improves the preliminary assignment of peptide mass fingerprints on non-model genomes. <i>Proteomics</i> , 2005, 5, 2769-2777.	1.3	4
244	Single Nucleotide Polymorphism discovery and genotyping within the chicken <i>Tapasin</i> gene. <i>Italian Journal of Animal Science</i> , 2005, 4, 103-105.	0.8	0
246	EST clustering: a short tutorial. , 2005, , .		0
247	Microarray analysis of selection lines from outbred populations to identify genes involved with nematode parasite resistance in sheep. <i>Physiological Genomics</i> , 2005, 21, 59-69.	1.0	103
248	<i>Satellyptus</i> : analysis and database of microsatellites from ESTs of <i>Eucalyptus</i> . <i>Genetics and Molecular Biology</i> , 2005, 28, 589-600.	0.6	22
249	Natural antisense transcripts associated with genes involved in eye development. <i>Human Molecular Genetics</i> , 2005, 14, 913-923.	1.4	101
250	Support vector machines for separation of mixed plant-pathogen EST collections based on codon usage. <i>Bioinformatics</i> , 2005, 21, 1383-1388.	1.8	23
251	Identification and Genomic Characterization of a New Virus (<i>Tymoviridae</i> Family) Associated with Citrus Sudden Death Disease. <i>Journal of Virology</i> , 2005, 79, 3028-3037.	1.5	76
252	Analysis of expressed sequence tags from the ectoparasitic nematode <i>Xiphinema index</i> . <i>Nematology</i> , 2005, 7, 95-104.	0.2	26
253	GARSA: genomic analysis resources for sequence annotation. <i>Bioinformatics</i> , 2005, 21, 4302-4303.	1.8	20
254	Comparative EST Analyses in Plant Systems. <i>Methods in Enzymology</i> , 2005, 395, 400-418.	0.4	22

#	ARTICLE	IF	CITATIONS
255	Virus-Induced Gene Silencing-Based Functional Characterization of Genes Associated with Powdery Mildew Resistance in Barley. <i>Plant Physiology</i> , 2005, 138, 2155-2164.	2.3	245
256	Expedito: A Pipeline for Designing Primers Using Human Gene Structure and Livestock Animal EST Information. <i>Journal of Heredity</i> , 2005, 96, 80-82.	1.0	9
257	TRANSPARENT LEAF AREA1 Encodes a Secreted Proteolipid Required for Anther Maturation, Morphogenesis, and Differentiation during Leaf Development in Maize. <i>Plant Cell</i> , 2005, 17, 730-745.	3.1	16
258	Genome of Deerpox Virus. <i>Journal of Virology</i> , 2005, 79, 966-977.	1.5	55
259	Transcription and Histone Modifications in the Recombination-Free Region Spanning a Rice Centromere[W]. <i>Plant Cell</i> , 2005, 17, 3227-3238.	3.1	107
260	Large-Scale Identification of Expressed Sequence Tags Involved in Rice and Rice Blast Fungus Interaction. <i>Plant Physiology</i> , 2005, 138, 105-115.	2.3	96
261	A graph based algorithm for generating EST consensus sequences. <i>Bioinformatics</i> , 2005, 21, 1371-1375.	1.8	18
262	The planarian <i>Schmidtea mediterranea</i> as a model for epigenetic germ cell specification: Analysis of ESTs from the hermaphroditic strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18491-18496.	3.3	140
263	The E2 Glycoprotein of Classical Swine Fever Virus Is a Virulence Determinant in Swine. <i>Journal of Virology</i> , 2005, 79, 3787-3796.	1.5	131
264	Molecular Characterization of the Capsid Gene of Two Serotypes of Turkey Astroviruses. <i>Avian Diseases</i> , 2005, 49, 514-519.	0.4	28
265	Moving Toward a Systems Biology Approach to the Study of Fungal Pathogenesis in the Rice Blast Fungus <i>Magnaporthe grisea</i> . <i>Advances in Applied Microbiology</i> , 2005, 57, 177-215.	1.3	18
266	Diatomics: Toward Diatom Functional Genomics. <i>Journal of Nanoscience and Nanotechnology</i> , 2005, 5, 5-14.	0.9	17
267	Bioinformatic Tools for Gene and Protein Sequence Analysis. , 2005, , 387-407.		1
268	ESTmapper: Efficiently Aligning DNA Sequences to Genomes. , 0, , .		4
269	Expressed Sequence Tag-Linked Microsatellites as a Source of Gene-Associated Polymorphisms for Detecting Signatures of Divergent Selection in Atlantic Salmon (<i>Salmo salar</i> L.). <i>Molecular Biology and Evolution</i> , 2005, 22, 1067-1076.	3.5	252
270	Molecular Characterization of Maize Acetylcholinesterase. A Novel Enzyme Family in the Plant Kingdom. <i>Plant Physiology</i> , 2005, 138, 1359-1371.	2.3	70
271	Comparative Plant Genomics Resources at PlantGDB. <i>Plant Physiology</i> , 2005, 139, 610-618.	2.3	95
272	Gene Discovery and Expression Profile Analysis through Sequencing of Expressed Sequence Tags from Different Developmental Stages of the Chytridiomycete <i>Blastocladiella emersonii</i> . <i>Eukaryotic Cell</i> , 2005, 4, 455-464.	3.4	21

#	ARTICLE	IF	CITATIONS
273	Quality assessment of maize assembled genomic islands (MAGs) and large-scale experimental verification of predicted genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12282-12287.	3.3	67
274	Transcriptome analysis of the aphid bacteriocyte, the symbiotic host cell that harbors an endocellular mutualistic bacterium, <i>Buchnera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5477-5482.	3.3	212
275	Profile and Analysis of Gene Expression Changes during Early Development in Germinating Spores of <i>Ceratopteris richardii</i> . <i>Plant Physiology</i> , 2005, 138, 1734-1745.	2.3	70
276	The animal sialyltransferases and sialyltransferase-related genes: a phylogenetic approach. <i>Glycobiology</i> , 2005, 15, 805-817.	1.3	264
277	Exploring the Genome of <i>Trypanosoma vivax</i> through GSS and In Silico Comparative Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 116-128.	1.0	4
278	An updated catalogue of salivary gland transcripts in the adult female mosquito, <i>Anopheles gambiae</i> . <i>Journal of Experimental Biology</i> , 2005, 208, 3971-3986.	0.8	173
279	BACCardI—a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. <i>Bioinformatics</i> , 2005, 21, 853-859.	1.8	32
280	ESTminer: a suite of programs for gene and allele identification. <i>Bioinformatics</i> , 2005, 21, 691-693.	1.8	10
281	Transcriptional Profiles of the Human Pathogenic Fungus <i>Paracoccidioides brasiliensis</i> in Mycelium and Yeast Cells. <i>Journal of Biological Chemistry</i> , 2005, 280, 24706-24714.	1.6	169
282	Diagnostic Evaluation of a Real-Time Reverse Transcriptase PCR Assay for Detection of Classical Swine Fever Virus. <i>Journal of Clinical Microbiology</i> , 2005, 43, 468-471.	1.8	36
283	Comparative Genomics of the Pennate Diatom <i>Phaeodactylum tricornutum</i> . <i>Plant Physiology</i> , 2005, 137, 500-513.	2.3	122
284	The Maize Root Transcriptome by Serial Analysis of Gene Expression. <i>Plant Physiology</i> , 2005, 138, 1700-1710.	2.3	62
285	Identification of genes that are differentially expressed in hemocytes of the Pacific blue shrimp (<i>Litopenaeus stylirostris</i>) surviving an infection with <i>Vibrio penaeicida</i> . <i>Physiological Genomics</i> , 2005, 21, 174-183.	1.0	64
286	Assembling DNA Fragments with Parallel Algorithms. , 0, , .		10
287	SNPServer: a real-time SNP discovery tool. <i>Nucleic Acids Research</i> , 2005, 33, W493-W495.	6.5	56
288	Identification of a Long-Chain Polyunsaturated Fatty Acid Acyl-Coenzyme A Synthetase from the Diatom <i>Thalassiosira pseudonana</i> . <i>Plant Physiology</i> , 2005, 138, 402-408.	2.3	51
289	Analyzing the potato abiotic stress transcriptome using expressed sequence tags. <i>Genome</i> , 2005, 48, 598-605.	0.9	60
290	EST Data Mining and Applications in Fungal Genomics. <i>Applied Mycology and Biotechnology</i> , 2005, 5, 33-70.	0.3	0

#	ARTICLE	IF	CITATIONS
291	Comparative Genomics of Foot-and-Mouth Disease Virus. <i>Journal of Virology</i> , 2005, 79, 6487-6504.	1.5	410
292	A comparative survey, by expressed sequence tag analysis, of genes expressed in peach leaves infected with Plum pox virus (PPV) and free from PPV. <i>Canadian Journal of Plant Pathology</i> , 2005, 27, 410-419.	0.8	12
293	The SOL Genomics Network. A Comparative Resource for Solanaceae Biology and Beyond. <i>Plant Physiology</i> , 2005, 138, 1310-1317.	2.3	398
294	Expression analysis and physical mapping of low-molecular-weight glutenin loci in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Genome</i> , 2005, 48, 401-410.	0.9	16
295	Animal Phylogenomics: Multiple Interspecific Genome Comparisons. <i>Methods in Enzymology</i> , 2005, 395, 104-133.	0.4	6
297	Genomic structure of eight porcine chemokine receptors and intergene sharing of an exon between CCR1 and XCR1. <i>Gene</i> , 2005, 349, 55-66.	1.0	12
298	Natterins, a new class of proteins with kininogenase activity characterized from fish venom. <i>Biochimie</i> , 2005, 87, 687-699.	1.3	108
299	Differential gene expression by <i>Metarhizium anisopliae</i> growing in root exudate and host (<i>Manduca</i>) Tj ETQq1 1 0.784314 rgBT /Over... <i>Biology</i> , 2005, 42, 704-718.	0.9	142
300	A 7872 cDNA microarray and its use in bovine functional genomics. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 235-245.	0.5	52
301	Gene expression profiling of avian macrophage activation. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 289-299.	0.5	63
302	An ancient transcriptional regulatory linkage. <i>Developmental Biology</i> , 2005, 281, 299-308.	0.9	53
303	Protein interaction mapping: A <i>Drosophila</i> case study. <i>Genome Research</i> , 2005, 15, 376-384.	2.4	509
304	Comparative bioinformatic analysis of genes expressed in common bean (<i>Phaseolus vulgaris</i> L.) seedlings. <i>Genome</i> , 2005, 48, 562-570.	0.9	50
305	Generating a Genome Assembly with PCAP. <i>Current Protocols in Bioinformatics</i> , 2005, 11, Unit11.3.	25.8	19
307	Analysis of expressed sequence tags of the water flea <i>Daphnia magna</i> . <i>Genome</i> , 2005, 48, 606-609.	0.9	68
308	The dog and rat olfactory receptor repertoires. <i>Genome Biology</i> , 2005, 6, R83.	13.9	138
309	<i>Anopheles gambiae</i> genome reannotation through synthesis of ab initio and comparative gene prediction algorithms. <i>Genome Biology</i> , 2006, 7, R24.	13.9	18
310	Large-scale gene discovery in the pea aphid <i>Acyrtosiphon pisum</i> (Hemiptera). <i>Genome Biology</i> , 2006, 7, R21.	13.9	123

#	ARTICLE	IF	CITATIONS
311	Development of the GENIPOL European Flounder (<i>Platichthys flesus</i>) Microarray and Determination of Temporal Transcriptional Responses to Cadmium at Low Dose.. <i>Environmental Science & Technology</i> , 2006, 40, 6479-6488.	4.6	81
312	Single Nucleotide Polymorphism Discovery in the Avian Tapasin Gene. <i>Poultry Science</i> , 2006, 85, 606-612.	1.5	7
313	Large-Scale DNA Sequence Assembly by Using Computing Grid. , 2006, , .		0
314	A hitchhiker's guide to expressed sequence tag (EST) analysis. <i>Briefings in Bioinformatics</i> , 2006, 8, 6-21.	3.2	235
315	Molecular structure and organization of the wheat genomic manganese superoxide dismutase gene. <i>Genome</i> , 2006, 49, 209-218.	0.9	18
316	Gene expression profiles underlying alternative caste phenotypes in a highly eusocial bee, <i>Melipona quadrifasciata</i> . <i>Insect Molecular Biology</i> , 2006, 15, 33-44.	1.0	42
317	EGAssembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. <i>Nucleic Acids Research</i> , 2006, 34, W459-W462.	6.5	139
318	Bioinformatics Packages for Sequence Analysis. <i>Applied Mycology and Biotechnology</i> , 2006, 6, 143-160.	0.3	8
319	Heuristically Tuned GA to Solve Genome Fragment Assembly Problem. , 0, , .		17
320	Differential gene expression in egg cells and zygotes suggests that the transcriptome is restructured before the first zygotic division in tobacco. <i>FEBS Letters</i> , 2006, 580, 1747-1752.	1.3	82
321	Hcc-2, a novel mammalian ER thioredoxin that is differentially expressed in hepatocellular carcinoma. <i>FEBS Letters</i> , 2006, 580, 2216-2226.	1.3	24
322	Some aspects of the venom proteome of the Colubridae snake <i>Philodryas olfersii</i> revealed from a Duvernoy's (venom) gland transcriptome. <i>FEBS Letters</i> , 2006, 580, 4417-4422.	1.3	108
323	Functional study of hot pepper 26S proteasome subunit RPN7 induced by Tobacco mosaic virus from nuclear proteome analysis. <i>Biochemical and Biophysical Research Communications</i> , 2006, 351, 405-411.	1.0	47
324	Duplication and extensive remodeling shaped POTE family genes encoding proteins containing ankyrin repeat and coiled coil domains. <i>Gene</i> , 2006, 366, 238-245.	1.0	42
325	Microarray analysis of differential gene expression in the liver of lean and fat chickens. <i>Gene</i> , 2006, 372, 162-170.	1.0	67
326	Structural organization and expression of human MTUS1, a candidate 8p22 tumor suppressor gene encoding a family of angiotensin II AT2 receptor-interacting proteins, ATIP. <i>Gene</i> , 2006, 380, 127-136.	1.0	82
327	<i>Penaeus monodon</i> gene discovery project: The generation of an EST collection and establishment of a database. <i>Gene</i> , 2006, 384, 104-112.	1.0	149
328	Transcriptome analysis of expressed sequence tags from the venom glands of the fish <i>Thalassophryne nattereri</i> . <i>Biochimie</i> , 2006, 88, 693-699.	1.3	67

#	ARTICLE	IF	CITATIONS
329	An annotated catalog of salivary gland transcripts from <i>Ixodes scapularis</i> ticks. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 111-129.	1.2	340
330	Comparative genomics of insect juvenile hormone biosynthesis. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 366-374.	1.2	71
331	The sialotranscriptome of adult male <i>Anopheles gambiae</i> mosquitoes. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 570-575.	1.2	45
332	Nucleotide sequence of Blackberry yellow vein associated virus, a novel member of the <i>Closteroviridae</i> . <i>Virus Research</i> , 2006, 116, 196-200.	1.1	19
333	Construction, database integration, and application of an <i>Oenothera</i> EST library. <i>Genomics</i> , 2006, 88, 372-380.	1.3	12
334	Sequencing and analysis of 14,842 expressed sequence tags of burma mangrove, <i>Bruguiera gymnorrhiza</i> . <i>Plant Science</i> , 2006, 171, 234-241.	1.7	32
335	Identification of transcripts related to high egg production in the chicken hypothalamus and pituitary gland. <i>Theriogenology</i> , 2006, 66, 1274-1283.	0.9	37
336	Bothrops jararaca venom gland transcriptome: Analysis of the gene expression pattern. <i>Toxicon</i> , 2006, 48, 437-461.	0.8	118
337	Identification and characterization of a resistance gene analog (RGA) from the <i>Caricaceae</i> Dumort family. <i>Revista Brasileira De Fruticultura</i> , 2006, 28, 458-462.	0.2	2
338	Abundantly expressed genes in pig adipose tissue: An expressed sequence tag approach. <i>Journal of Animal Science</i> , 2006, 84, 2673-2683.	0.2	34
339	Discovery of eight novel divergent homologs expressed in cattle placenta. <i>Physiological Genomics</i> , 2006, 25, 405-413.	1.0	30
340	Brazilian coffee genome project: an EST-based genomic resource. <i>Brazilian Journal of Plant Physiology</i> , 2006, 18, 95-108.	0.5	112
341	Generation and analysis of expressed sequence tags from <i>Botrytis cinerea</i> . <i>Biological Research</i> , 2006, 39, 367-76.	1.5	14
343	MGOS: A Resource for Studying <i>Magnaporthe grisea</i> and <i>Oryza sativa</i> Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1055-1061.	1.4	24
345	Chicken genomics resource: sequencing and annotation of 35,407 ESTs from single and multiple tissue cDNA libraries and CAP3 assembly of a chicken gene index. <i>Physiological Genomics</i> , 2006, 25, 514-524.	1.0	60
346	Bioinformatic analysis of expressed sequence tags from sporophyte of <i>Porphyra yezoensis</i> (<i>Bagiaceae</i>). <i>Tj ETQq1 1 0,784314,rgBT /Over</i>	1.8	18
347	LegumeDB1 bioinformatics resource: comparative genomic analysis and novel cross-genera marker identification in lupin and pasture legume species. <i>Genome</i> , 2006, 49, 689-699.	0.9	9
349	Development of EST-SSRs in <i>Cucumis sativus</i> from sequence database. <i>Molecular Ecology Notes</i> , 2006, 6, 1234-1236.	1.7	46

#	ARTICLE	IF	CITATIONS
350	Mitogenomics and phylogenomics reveal priapulid worms as extant models of the ancestral Ecdysozoan. <i>Evolution & Development</i> , 2006, 8, 502-510.	1.1	88
351	Cloning and Expressional Studies of the Voltage-dependent Anion Channel Gene from <i>Brassica rapa</i> L.. <i>Journal of Integrative Plant Biology</i> , 2006, 48, 197-203.	4.1	6
352	Draft Assembly and Annotation of the <i>Pneumocystis carinii</i> Genome. <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, S89-S91.	0.8	31
353	Large-Scale Characterization of Introns in the <i>Pneumocystis carinii</i> Genome. <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, S151-S153.	0.8	8
354	Genomics of hybrid poplar (<i>Populus trichocarpa</i> × <i>P. deltoides</i>) interacting with forest tent caterpillars (<i>Malacosoma disstria</i>): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences. <i>Molecular Ecology</i> , 2006, 15, 1275-1297.	2.0	183
355	The molecular ecologist's guide to expressed sequence tags. <i>Molecular Ecology</i> , 2006, 16, 907-924.	2.0	326
356	Development of polymorphic expressed sequence tag-derived microsatellites for the extension of the genetic linkage map of the black tiger shrimp (<i>Penaeus monodon</i>). <i>Animal Genetics</i> , 2006, 37, 363-368.	0.6	55
357	Comparative genomic analysis of phytopathogenic fungi using expressed sequence tag (EST) collections. <i>Molecular Plant Pathology</i> , 2006, 7, 61-70.	2.0	36
358	Bioinformatic analysis of expressed sequence tags derived from a compatible <i>Alternaria brassicicola</i> - <i>Brassica oleracea</i> interaction. <i>Molecular Plant Pathology</i> , 2006, 7, 113-124.	2.0	30
359	Yellow vein-affected blackberries and the presence of a novel Crinivirus. <i>Plant Pathology</i> , 2006, 55, 607-613.	1.2	13
360	Conifer defence against insects: microarray gene expression profiling of Sitka spruce (<i>Picea</i>) transcriptome. <i>Plant, Cell and Environment</i> , 2006, 29, 1545-1570.	2.8	221
361	Creating hierarchical models of protein families based on Expressed Sequence Tags: The analysis pipeline. <i>Analytica Chimica Acta</i> , 2006, 564, 123-132.	2.6	0
362	Phylogenetic and mutational analyses reveal key residues for UDP-glucuronic acid binding and activity of β 1,3-glucuronosyltransferase I (GlcAT-I). <i>Protein Science</i> , 2006, 15, 1667-1678.	3.1	16
363	Dirigent Proteins in Conifer Defense: Gene Discovery, Phylogeny, and Differential Wound- and Insect-induced Expression of a Family of DIR and DIR-like Genes in Spruce (<i>Picea</i> spp.). <i>Plant Molecular Biology</i> , 2006, 60, 21-40.	2.0	160
364	Generation and analysis of expressed sequence tags from the mangrove plant, <i>Acanthus ebracteatus</i> Vahl. <i>Tree Genetics and Genomes</i> , 2006, 2, 196-201.	0.6	21
365	Conserved ortholog sets in forest trees. <i>Tree Genetics and Genomes</i> , 2006, 3, 61-70.	0.6	22
366	Comparative analysis of genes expressed in regenerating intestine and non-eviscerated intestine of <i>Apostichopus japonicus</i> Selenka (Aspidochirotrida: Stichopodidae) and cloning of ependymin gene. <i>Hydrobiologia</i> , 2006, 571, 109-122.	1.0	22
367	Mint virus X: a novel potexvirus associated with symptoms in 'Variegata'™ mint. <i>Archives of Virology</i> , 2006, 151, 143-153.	0.9	12

#	ARTICLE	IF	CITATIONS
368	Ethylene in induced conifer defense: cDNA cloning, protein expression, and cellular and subcellular localization of 1-aminocyclopropane-1-carboxylate oxidase in resin duct and phenolic parenchyma cells. <i>Planta</i> , 2006, 224, 865-877.	1.6	74
369	The <i>Macrostomum lignano</i> EST database as a molecular resource for studying platyhelminth development and phylogeny. <i>Development Genes and Evolution</i> , 2006, 216, 695-707.	0.4	25
370	Detection of putative secreted proteins in the plant-parasitic nematode <i>Heterodera schachtii</i> . <i>Parasitology Research</i> , 2006, 98, 414-424.	0.6	46
371	Putative fasciclin-like arabinogalactan-proteins (FLA) in wheat (<i>Triticum aestivum</i>) and rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlook 478-494.	1.0	96
372	Human-specific nonsense mutations identified by genome sequence comparisons. <i>Human Genetics</i> , 2006, 119, 169-178.	1.8	32
373	The Frequency of Eubacterium-to-Eukaryote Lateral Gene Transfers Shows Significant Cross-Taxa Variation Within Amoebozoa. <i>Journal of Molecular Evolution</i> , 2006, 63, 801-814.	0.8	27
374	The complete DNA sequence of the mitochondrial genome of the dermatophyte fungus <i>Epidermophyton floccosum</i> . <i>Current Genetics</i> , 2006, 49, 302-308.	0.8	16
375	Construction of a watermelon BAC library and identification of SSRs anchored to melon or <i>Arabidopsis</i> genomes. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1553-1562.	1.8	49
376	Characterisation of single nucleotide polymorphisms in sugarcane ESTs. <i>Theoretical and Applied Genetics</i> , 2006, 113, 331-343.	1.8	58
377	Identification of a novel virulence determinant within the E2 structural glycoprotein of classical swine fever virus. <i>Virology</i> , 2006, 355, 94-101.	1.1	72
378	<i>Parastrongyloides trichosuri</i> , a nematode parasite of mammals that is uniquely suited to genetic analysis. <i>International Journal for Parasitology</i> , 2006, 36, 453-466.	1.3	65
379	Extense variant gene family repertoire overlap in Western Amazon <i>Plasmodium falciparum</i> isolates. <i>Molecular and Biochemical Parasitology</i> , 2006, 150, 157-165.	0.5	35
380	Differential transcription profiles in <i>Trypanosoma cruzi</i> associated with clinical forms of Chagas disease: Maxicircle NADH dehydrogenase subunit 7 gene truncation in asymptomatic patient isolates. <i>Molecular and Biochemical Parasitology</i> , 2006, 150, 236-248.	0.5	31
381	Phylogenetic diversification of glycogen synthase kinase 3/SHAGGY-like kinase genes in plants. <i>BMC Plant Biology</i> , 2006, 6, 3.	1.6	55
382	Testing the neutral theory of molecular evolution using genomic data: a comparison of the human and bovine transcriptome. <i>Genetics Selection Evolution</i> , 2006, 38, 321.	1.2	7
383	IsoSVM—distinguishing isoforms and paralogs on the protein level. <i>BMC Bioinformatics</i> , 2006, 7, 110.	1.2	16
384	QualitySNP: a pipeline for detecting single nucleotide polymorphisms and insertions/deletions in EST data from diploid and polyploid species. <i>BMC Bioinformatics</i> , 2006, 7, 438.	1.2	127
385	SNP-PHAGE—High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006, 7, 468.	1.2	29

#	ARTICLE	IF	CITATIONS
386	JUICE: a data management system that facilitates the analysis of large volumes of information in an EST project workflow. <i>BMC Bioinformatics</i> , 2006, 7, 513.	1.2	9
387	GO-Diff: mining functional differentiation between EST-based transcriptomes. <i>BMC Bioinformatics</i> , 2006, 7, 72.	1.2	16
388	The monosaccharide transporter gene family in land plants is ancient and shows differential subfamily expression and expansion across lineages. <i>BMC Evolutionary Biology</i> , 2006, 6, 64.	3.2	58
389	A wing expressed sequence tag resource for <i>Bicyclus anynana</i> butterflies, an evo-devo model. <i>BMC Genomics</i> , 2006, 7, 130.	1.2	85
390	CMD: a Cotton Microsatellite Database resource for <i>Gossypium</i> genomics. <i>BMC Genomics</i> , 2006, 7, 132.	1.2	102
391	Production and utilization of a high-density oligonucleotide microarray in channel catfish, <i>Ictalurus punctatus</i> . <i>BMC Genomics</i> , 2006, 7, 134.	1.2	37
392	Wheat EST resources for functional genomics of abiotic stress. <i>BMC Genomics</i> , 2006, 7, 149.	1.2	100
393	Generation, annotation and analysis of ESTs from <i>Trichoderma harzianum</i> CECT 2413. <i>BMC Genomics</i> , 2006, 7, 193.	1.2	60
394	Identification and analysis of gene families from the duplicated genome of soybean using EST sequences. <i>BMC Genomics</i> , 2006, 7, 204.	1.2	21
395	Analysis and functional annotation of expressed sequence tags from the fall armyworm <i>Spodoptera frugiperda</i> . <i>BMC Genomics</i> , 2006, 7, 264.	1.2	16
396	Establishment of a pipeline to analyse non-synonymous SNPs in <i>Bos taurus</i> . <i>BMC Genomics</i> , 2006, 7, 298.	1.2	21
397	Generation and analysis of large-scale expressed sequence tags (ESTs) from a full-length enriched cDNA library of porcine backfat tissue. <i>BMC Genomics</i> , 2006, 7, 36.	1.2	28
398	Gene expression profiling of Na ⁺ -ve sheep genetically resistant and susceptible to gastrointestinal nematodes. <i>BMC Genomics</i> , 2006, 7, 42.	1.2	78
399	Comparative salivary gland transcriptomics of sandfly vectors of visceral leishmaniasis. <i>BMC Genomics</i> , 2006, 7, 52.	1.2	148
400	A multispecies comparison of the metazoan 3'-processing downstream elements and the CstF-64 RNA recognition motif. <i>BMC Genomics</i> , 2006, 7, 55.	1.2	44
401	What is the future of electrophoresis in large-scale genomic sequencing?. <i>Electrophoresis</i> , 2006, 27, 3689-3702.	1.3	35
402	<i>Lachesis muta</i> (Viperidae) cDNAs Reveal Diverging Pit Viper Molecules and Scaffolds Typical of Cobra (Elapidae) Venoms: Implications for Snake Toxin Repertoire Evolution. <i>Genetics</i> , 2006, 173, 877-889.	1.2	117
403	Phytome: a platform for plant comparative genomics. <i>Nucleic Acids Research</i> , 2006, 34, D724-D730.	6.5	35

#	ARTICLE	IF	CITATIONS
404	Molecular Characterization and Phylogeny of U2AF35 Homologs in Plants. <i>Plant Physiology</i> , 2006, 140, 624-636.	2.3	46
405	Function and evolution of a gene family encoding odorant binding-like proteins in a social insect, the honey bee (<i>Apis mellifera</i>). <i>Genome Research</i> , 2006, 16, 1404-1413.	2.4	315
406	Mining the EST Databases to Determine Evolutionary Events in the Legumes and Grasses. , 2005, , 163-181.		3
407	SEAN: SNP prediction and display program utilizing EST sequence clusters. <i>Bioinformatics</i> , 2006, 22, 495-496.	1.8	31
408	Analysis of expressed sequence tags from <i>Cryptomeria japonica</i> pollen reveals novel pollen-specific transcripts. <i>Tree Physiology</i> , 2006, 26, 1517-1528.	1.4	22
409	Identification of human tRNA:m5C methyltransferase catalysing intron-dependent m5C formation in the first position of the anticodon of the $\text{pre-tRNA}_{\text{left(CAA)}}^{\text{Leu}}$. <i>Nucleic Acids Research</i> , 2006, 34, 6034-6043.	6.5	162
410	Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcription and organismic complexity. <i>Genome Research</i> , 2006, 16, 922-933.	2.4	40
411	Analyses of Expressed Sequence Tags from Apple. <i>Plant Physiology</i> , 2006, 141, 147-166.	2.3	246
412	Water stress-responsive genes in loblolly pine (<i>Pinus taeda</i>) roots identified by analyses of expressed sequence tag libraries. <i>Tree Physiology</i> , 2006, 26, 1-16.	1.4	84
413	Vitamin K-dependent proteins in <i>Ciona intestinalis</i> , a basal chordate lacking a blood coagulation cascade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15794-15799.	3.3	31
414	Genome of Invertebrate Iridescent Virus Type 3 (Mosquito Iridescent Virus). <i>Journal of Virology</i> , 2006, 80, 8439-8449.	1.5	68
415	Using global genome approaches to address problems in cod mariculture1. <i>ICES Journal of Marine Science</i> , 2006, 63, 393-399.	1.2	16
416	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	2.4	138
417	Isolation, Characterization, and Ecology of Cold-Active, Chemolithotrophic, Sulfur-Oxidizing Bacteria from Perennially Ice-Covered Lake Fryxell, Antarctica. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5562-5568.	1.4	70
418	Evolution and expression of chimeric POTE-actin genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17885-17890.	3.3	42
419	A transcriptome analysis of the <i>Aedes aegypti</i> vitellogenic fat body. <i>Journal of Insect Science</i> , 2006, 6, 1-26.	0.6	18
420	Large-Scale cis-Element Detection by Analysis of Correlated Expression and Sequence Conservation between <i>Arabidopsis</i> and <i>Brassica oleracea</i> Å. <i>Plant Physiology</i> , 2006, 142, 1589-1602.	2.3	50
421	Physical map-assisted whole-genome shotgun sequence assemblies. <i>Genome Research</i> , 2006, 16, 768-775.	2.4	27

#	ARTICLE	IF	CITATIONS
422	Just one cross appears capable of dramatically altering the population biology of a eukaryotic pathogen like <i>Toxoplasma gondii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10514-10519.	3.3	112
423	An algorithm for assembly of ordered restriction maps from single DNA molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15770-15775.	3.3	164
424	<i>Paenibacillus</i> sp. Strain JDR-2 and XynA 1 : a Novel System for Methylglucuronoxylan Utilization. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1496-1506.	1.4	57
425	Genome of Horsepox Virus. <i>Journal of Virology</i> , 2006, 80, 9244-9258.	1.5	122
426	Assembling genomes on large-scale parallel computers. , 2006, , .		3
427	Six new cellulose synthase genes from <i>Eucalyptus</i> are associated with primary and secondary cell wall biosynthesis. <i>Tree Physiology</i> , 2006, 26, 545-556.	1.4	89
428	Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. <i>Genome Research</i> , 2006, 16, 1334-1338.	2.4	233
429	Alignment of Optical Maps. <i>Journal of Computational Biology</i> , 2006, 13, 442-462.	0.8	76
430	Genomic analysis of hostâ€“pathogen interaction between <i>Fusarium graminearum</i> and wheat during early stages of disease development. <i>Microbiology (United Kingdom)</i> , 2006, 152, 1877-1890.	0.7	44
431	Genome of Crocodilepox Virus. <i>Journal of Virology</i> , 2006, 80, 4978-4991.	1.5	60
432	Gene discovery and annotation using LCM-454 transcriptome sequencing. <i>Genome Research</i> , 2006, 17, 69-73.	2.4	321
433	Transcriptome Analysis of <i>Aspergillus nidulans</i> Exposed to Camptothecin-Induced DNA Damage. <i>Eukaryotic Cell</i> , 2006, 5, 1688-1704.	3.4	26
434	Transcriptome Analysis in Response to Heat Shock and Cadmium in the Aquatic Fungus <i>Blastocladiella emersonii</i> . <i>Eukaryotic Cell</i> , 2007, 6, 1053-1062.	3.4	29
435	Sampling the <i>Arabidopsis</i> Transcriptome with Massively Parallel Pyrosequencing. <i>Plant Physiology</i> , 2007, 144, 32-42.	2.3	298
436	Organization of the Mitochondrial Genome in the Dinoflagellate <i>Amphidinium carterae</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 1528-1536.	3.5	56
437	ZIPK: A Unique Case of Murine-Specific Divergence of a Conserved Vertebrate Gene. <i>PLoS Genetics</i> , 2007, 3, e180.	1.5	17
438	Identification of Cold-Induced Genes in Cereal Crops and <i>Arabidopsis</i> Through Comparative Analysis of Multiple EST Sets. , 2007, , 48-65.		4
439	Transcriptional profiling of <i>Ovis aries</i> identifies <i>Ovar-DQA1</i> allele frequency differences between nematode-resistant and susceptible selection lines. <i>Physiological Genomics</i> , 2007, 30, 253-261.	1.0	29

#	ARTICLE	IF	CITATIONS
440	An insight into the sialome of the oriental rat flea, <i>Xenopsylla cheopis</i> (Rots). <i>BMC Genomics</i> , 2007, 8, 102.	1.2	70
441	PlantGDB: a resource for comparative plant genomics. <i>Nucleic Acids Research</i> , 2007, 36, D959-D965.	6.5	246
442	Wheat Estimated Transcript Server (WhETS): a tool to provide best estimate of hexaploid wheat transcript sequence. <i>Nucleic Acids Research</i> , 2007, 35, W148-W151.	6.5	14
443	SNP mining porcine ESTs with MAVIANT, a novel tool for SNP evaluation and annotation. <i>Bioinformatics</i> , 2007, 23, i387-i391.	1.8	29
444	Chapter 11 Genome Sequencing and Assembly. <i>Perspectives in Bioanalysis</i> , 2007, , 327-355.	0.3	2
445	Temporal Gene Expression Profiling of the Wheat Leaf Rust Pathosystem Using cDNA Microarray Reveals Differences in Compatible and Incompatible Defence Pathways. <i>International Journal of Plant Genomics</i> , 2007, 2007, 1-13.	2.2	35
446	Muc5b and Muc5ac are the major oligomeric mucins in equine airway mucus. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2007, 292, L1396-L1404.	1.3	29
447	Analyses of expressed sequence tags from an agarophyte, <i>Gracilaria changii</i> (Gracilariales), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 0.9 34	0.9	34
448	The TIGR Plant Transcript Assemblies database. <i>Nucleic Acids Research</i> , 2007, 35, D846-D851.	6.5	173
449	Aminocyclopropane Carboxylic Acid Synthase Is a Regulated Step in Ethylene-Dependent Induced Conifer Defense. Full-Length cDNA Cloning of a Multigene Family, Differential Constitutive, and Wound- and Insect-Induced Expression, and Cellular and Subcellular Localization in Spruce and Douglas Fir. <i>Plant Physiology</i> , 2007, 143, 410-424.	2.3	54
450	Common Functions for Diverse Small RNAs of Land Plants. <i>Plant Cell</i> , 2007, 19, 1750-1769.	3.1	387
451	SHARCGS, a fast and highly accurate short-read assembly algorithm for de novo genomic sequencing. <i>Genome Research</i> , 2007, 17, 1697-1706.	2.4	230
452	In Search of Microarray Design Decision Support System. , 2007, , .		0
453	Fuzzy Classification of Genome Sequences Prior to Assembly Based on Similarity Measures. , 2007, , .		1
454	Ultraviolet A-specific induction of anthocyanin biosynthesis in the swollen hypocotyls of turnip (<i>Brassica rapa</i>). <i>Journal of Experimental Botany</i> , 2007, 58, 1771-1781.	2.4	102
455	MAKER: An easy-to-use annotation pipeline designed for emerging model organism genomes. <i>Genome Research</i> , 2008, 18, 188-196.	2.4	1,564
456	A Survey of Expressed Sequence Tags from the Rainbow Trout (<i>Oncorhynchus Mykiss</i>) Pituitary. <i>Animal Biotechnology</i> , 2007, 18, 213-230.	0.7	3
457	Co-ordinated gene expression during phases of dormancy release in raspberry (<i>Rubus idaeus</i> L.) buds. <i>Journal of Experimental Botany</i> , 2007, 58, 1035-1045.	2.4	187

#	ARTICLE	IF	CITATIONS
458	Contributions and perspectives of chicken genomics in Brazil: from biological model to export commodity. <i>World's Poultry Science Journal</i> , 2007, 63, 597-610.	1.4	3
459	ESTpass: a web-based server for processing and annotating expressed sequence tag (EST) sequences. <i>Nucleic Acids Research</i> , 2007, 35, W159-W162.	6.5	30
460	A novel non-protein-coding infection-specific gene family is clustered throughout the genome of <i>Phytophthora infestans</i> . <i>Microbiology (United Kingdom)</i> , 2007, 153, 747-759.	0.7	27
461	Evolution of Cinnamate/Cooumarate Carboxyl Methyltransferases and Their Role in the Biosynthesis of Methylcinnamate. <i>Plant Cell</i> , 2007, 19, 3212-3229.	3.1	66
462	GoSh: a web-based database for goat and sheep EST sequences. <i>Bioinformatics</i> , 2007, 23, 1043-1045.	1.8	8
463	Insights into the immune transcriptome of the shrimp <i>Litopenaeus vannamei</i> : tissue-specific expression profiles and transcriptomic responses to immune challenge. <i>Physiological Genomics</i> , 2007, 29, 44-56.	1.0	120
464	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, W143-W147.	6.5	60
465	Large Gene Family Expansion and Variable Selective Pressures for Cathepsin B in Aphids. <i>Molecular Biology and Evolution</i> , 2007, 25, 5-17.	3.5	75
466	Nearly Identical Paralogs: Implications for Maize (<i>Zea mays</i> L.) Genome Evolution. <i>Genetics</i> , 2007, 175, 429-439.	1.2	60
467	Transcriptome profiling of <i>Paracoccidioides brasiliensis</i> yeast-phase cells recovered from infected mice brings new insights into fungal response upon host interaction. <i>Microbiology (United Kingdom)</i> , 2007, 153, 4194-4207.	0.7	86
468	Transcriptome Analysis of The Sugarcane Genome For Crop Improvement. , 2007, , 483-494.		3
469	N-Linked Glycosylation Status of Classical Swine Fever Virus Strain Brescia E2 Glycoprotein Influences Virulence in Swine. <i>Journal of Virology</i> , 2007, 81, 924-933.	1.5	84
470	Nutrition-induced ketosis alters metabolic and signaling gene networks in liver of periparturient dairy cows. <i>Physiological Genomics</i> , 2007, 32, 105-116.	1.0	292
471	Selective Cysteine Protease Inhibition Contributes to Blood-feeding Success of the Tick <i>Ixodes scapularis</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 29256-29263.	1.6	95
472	Expressed Sequence Tags from <i>Phytophthora sojae</i> Reveal Genes Specific to Development and Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 781-793.	1.4	59
473	Association of CAPN1 and CAST gene polymorphisms with meat tenderness in <i>Bos taurus</i> beef cattle from Argentina. <i>Genetics and Molecular Biology</i> , 2007, 30, 1064-1069.	0.6	48
474	Sensitivity and Speed of Induced Defense of Cabbage (<i>Brassica oleracea</i> L.): Dynamics of BoLOX Expression Patterns During Insect and Pathogen Attack. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1332-1345.	1.4	89
475	Characterization of a U.S. Isolate of Beet black scorch virus. <i>Phytopathology</i> , 2007, 97, 1245-1254.	1.1	21

#	ARTICLE	IF	CITATIONS
476	Bioinformatics Support for Genome-Sequencing Projects. , 0, , 25-55.		0
477	High-performance Computing Methods for Computational Genomics. , 2007, , .		0
478	Distinct profiles of expressed sequence tags during intestinal regeneration in the sea cucumber <i>Holothuria glaberrima</i> . <i>Physiological Genomics</i> , 2007, 31, 203-215.	1.0	60
479	Strawberry chlorotic fleck: Identification and characterization of a novel Closterovirus associated with the disease. <i>Virus Research</i> , 2007, 124, 88-94.	1.1	23
480	Identification and characterization of Raspberry mottle virus, a novel member of the Closteroviridae. <i>Virus Research</i> , 2007, 127, 26-33.	1.1	59
481	Urochordate whole body regeneration inaugurates a diverse innate immune signaling profile. <i>Developmental Biology</i> , 2007, 312, 131-146.	0.9	38
482	A combined bioinformatics and chemoinformatics approach for the development of new antiparasitic drugs. <i>Genomics</i> , 2007, 89, 36-43.	1.3	38
483	Microarray and suppression subtractive hybridization analyses of gene expression in <i>Puccinellia tenuiflora</i> after exposure to NaHCO ₃ . <i>Plant Science</i> , 2007, 173, 309-320.	1.7	15
484	Identification by suppression subtractive hybridization and expression analysis of <i>Medicago truncatula</i> putative defence genes in response to <i>Orobanche crenata</i> parasitization. <i>Physiological and Molecular Plant Pathology</i> , 2007, 70, 49-59.	1.3	37
485	Isolation of salinity tolerant genes from the mangrove plant, <i>Bruguiera cylindrica</i> by using suppression subtractive hybridization (SSH) and bacterial functional screening. <i>Aquatic Botany</i> , 2007, 86, 117-122.	0.8	36
486	Phylogeny-directed structural analysis of the <i>Arabidopsis</i> PsbS protein. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 464-470.	1.0	13
487	Cloning, expression, and biochemical characterization of a new histone deacetylase-like protein from <i>Thermus caldophilus</i> GK24. <i>Biochemical and Biophysical Research Communications</i> , 2007, 361, 55-61.	1.0	5
488	Spidroins from the Brazilian spider <i>Nephilengys cruentata</i> (Araneae: Nephilidae). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2007, 147, 597-606.	0.7	22
489	DNA microarray technology in toxicogenomics of aquatic models: Methods and applications. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2007, 145, 5-14.	1.3	31
490	Immune gene discovery by expressed sequence tag analysis of spleen in the duck (<i>Anas platyrhynchos</i>). <i>Developmental and Comparative Immunology</i> , 2007, 31, 272-285.	1.0	23
491	Identification of immune-relevant genes in histoincompatible rejecting colonies of the tunicate <i>Botryllus schlosseri</i> . <i>Developmental and Comparative Immunology</i> , 2007, 31, 889-902.	1.0	17
492	Transcriptome analysis of gills from the white shrimp <i>Litopenaeus vannamei</i> infected with White Spot Syndrome Virus. <i>Fish and Shellfish Immunology</i> , 2007, 23, 459-472.	1.6	104
493	Identification of a novel C-type lectin gene in Japanese flounder, <i>Paralichthys olivaceus</i> . <i>Fish and Shellfish Immunology</i> , 2007, 23, 1089-1094.	1.6	28

#	ARTICLE	IF	CITATIONS
512	Gene profiling for studying the mechanism of aflatoxin biosynthesis in <i>Aspergillus flavus</i> and <i>A. parasiticus</i> . <i>Food Additives and Contaminants</i> , 2007, 24, 1035-1042.	2.0	21
513	Identification of stress-responsive genes in an indica rice (<i>Oryza sativa</i> L.) using ESTs generated from drought-stressed seedlings. <i>Journal of Experimental Botany</i> , 2007, 58, 253-265.	2.4	127
514	A New Local Search Algorithm for the DNA Fragment Assembly Problem. <i>Lecture Notes in Computer Science</i> , 2007, , 1-12.	1.0	30
515	Dothideomycete "Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i> ". <i>Plant Cell</i> , 2007, 19, 3347-3368.	3.1	235
516	GDR (Genome Database for Rosaceae): integrated web-database for Rosaceae genomics and genetics data. <i>Nucleic Acids Research</i> , 2007, 36, D1034-D1040.	6.5	170
517	Efficient assembling of genome fragments using genetic algorithm enhanced by heuristic search. , 2007, , .		0
518	The <i>Dugesia ryukyuensis</i> Database as a Molecular Resource for Studying Switching of the Reproductive System. <i>Zoological Science</i> , 2007, 24, 31-37.	0.3	26
519	Characterization of an EST Database for the Perennial Weed Leafy Spurge: An Important Resource for Weed Biology Research. <i>Weed Science</i> , 2007, 55, 193-203.	0.8	51
520	Genome Assembly, Rearrangement, and Repeats. <i>Chemical Reviews</i> , 2007, 107, 3391-3406.	23.0	23
521	Plant Genomic Sequencing Using Gene-Enriched Libraries. <i>Chemical Reviews</i> , 2007, 107, 3377-3390.	23.0	5
522	SmedGD: the <i>Schmidtea mediterranea</i> genome database. <i>Nucleic Acids Research</i> , 2007, 36, D599-D606.	6.5	251
523	Gene expression responses of European flounder (<i>Platichthys flesus</i>) to 17- β estradiol. <i>Toxicology Letters</i> , 2007, 168, 236-248.	0.4	86
524	Identification of stress-induced genes from the drought-tolerant plant <i>Prosopis juliflora</i> (Swartz) DC. through analysis of expressed sequence tags. <i>Genome</i> , 2007, 50, 470-478.	0.9	29
525	Development, characterization, and comparative analysis of polymorphism at common bean SSR loci isolated from genic and genomic sources. <i>Genome</i> , 2007, 50, 266-277.	0.9	85
526	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. <i>PLoS ONE</i> , 2007, 2, e1326.	1.1	945
527	Genes associated with hypersensitive response (HR) in the citrus EST database (CitEST). <i>Genetics and Molecular Biology</i> , 2007, 30, 943-956.	0.6	16
528	PR gene families of citrus: their organ specific-biotic and abiotic inducible expression profiles based on ESTs approach. <i>Genetics and Molecular Biology</i> , 2007, 30, 917-930.	0.6	24
529	Terpene production in the peel of sweet orange fruits. <i>Genetics and Molecular Biology</i> , 2007, 30, 841-847.	0.6	7

#	ARTICLE	IF	CITATIONS
530	Differentially expressed stress-related genes in the compatible citrus-Citrus leprosis virus interaction. <i>Genetics and Molecular Biology</i> , 2007, 30, 980-990.	0.6	22
531	Gene projects: a genome web tool for ongoing mining and annotation applied to CitEST. <i>Genetics and Molecular Biology</i> , 2007, 30, 1030-1036.	0.6	8
532	Frequency and distribution of microsatellites from ESTs of citrus. <i>Genetics and Molecular Biology</i> , 2007, 30, 1009-1018.	0.6	37
533	Signaling pathways in a Citrus EST database. <i>Genetics and Molecular Biology</i> , 2007, 30, 734-751.	0.6	2
534	A genetic framework for flowering-time pathways in Citrus spp.. <i>Genetics and Molecular Biology</i> , 2007, 30, 769-779.	0.6	16
535	Putative resistance genes in the CitEST database. <i>Genetics and Molecular Biology</i> , 2007, 30, 931-942.	0.6	8
536	Phytophthora parasitica transcriptome, a new concept in the understanding of the citrus gummosis. <i>Genetics and Molecular Biology</i> , 2007, 30, 997-1008.	0.6	11
537	Bioinformatics for the Citrus EST Project (CitEST). <i>Genetics and Molecular Biology</i> , 2007, 30, 1024-1029.	0.6	7
538	Analysis of expressed sequence tags from Citrus sinensis L. Osbeck infected with Xylella fastidiosa. <i>Genetics and Molecular Biology</i> , 2007, 30, 957-964.	0.6	11
539	Differential expression of genes identified from Poncirus trifoliata tissue inoculated with CTV through EST analysis and in silico hybridization. <i>Genetics and Molecular Biology</i> , 2007, 30, 972-979.	0.6	19
540	Identification of protein kinase SNF1 in CitEST. <i>Genetics and Molecular Biology</i> , 2007, 30, 866-871.	0.6	1
541	Genetic machinery for RNA silencing and defense against viruses in Citrus. <i>Genetics and Molecular Biology</i> , 2007, 30, 991-996.	0.6	0
542	Cell Cycle Genes PEDF and CDKN1C in Growing Deer Antlers. <i>Anatomical Record</i> , 2007, 290, 994-1004.	0.8	16
543	Cloning and characterization of two glutathione <i>S</i> -transferase cDNAs in the spruce budworm, <i>Choristoneura fumiferana</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2007, 66, 146-157.	0.6	8
544	cDNA representational difference analysis used in the identification of genes expressed by <i>Trichophyton rubrum</i> during contact with keratin. <i>Microbes and Infection</i> , 2007, 9, 1415-1421.	1.0	27
545	Development of bioinformatic tools to support EST-sequencing, in silico- and microarray-based transcriptome profiling in mycorrhizal symbioses. <i>Phytochemistry</i> , 2007, 68, 19-32.	1.4	49
546	Dirigent proteins in conifer defense II: Extended gene discovery, phylogeny, and constitutive and stress-induced gene expression in spruce (<i>Picea</i> spp.). <i>Phytochemistry</i> , 2007, 68, 1975-1991.	1.4	116
547	Assembling genomes on large-scale parallel computers. <i>Journal of Parallel and Distributed Computing</i> , 2007, 67, 1240-1255.	2.7	26

#	ARTICLE	IF	CITATIONS
548	Hemi-nested touchdown PCR combined with primer-template mismatch PCR for rapid isolation and sequencing of low molecular weight glutenin subunit gene family from a hexaploid wheat BAC library. <i>BMC Genetics</i> , 2007, 8, 18.	2.7	16
549	The venom gland transcriptome of the Desert Massasauga Rattlesnake (<i>Sistrurus catenatus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.0	107
550	Gene knockdown by RNAi in the pea aphid <i>Acyrtosiphon pisum</i> . <i>BMC Biotechnology</i> , 2007, 7, 63.	1.7	190
551	The mitochondrial genome from the thermal dimorphic fungus <i>Paracoccidioides brasiliensis</i> . <i>Yeast</i> , 2007, 24, 607-616.	0.8	33
552	Viral metagenomics. <i>Reviews in Medical Virology</i> , 2007, 17, 115-131.	3.9	247
553	EST-SSRs as a resource for population genetic analyses. <i>Heredity</i> , 2007, 99, 125-132.	1.2	499
554	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. <i>Molecular Psychiatry</i> , 2007, 12, 74-86.	4.1	386
555	Microarray analysis of <i>Fusarium graminearum</i> -induced wheat genes: identification of organ-specific and differentially expressed genes. <i>Plant Biotechnology Journal</i> , 2007, 5, 38-49.	4.1	88
556	Development, characterization and utilization of microsatellite markers in pigeonpea. <i>Plant Breeding</i> , 2007, 126, 130-136.	1.0	85
557	Isolation and characterization of <i>cgchi3</i> , a nodule-specific gene from <i>Casuarina glauca</i> encoding a class III chitinase. <i>Physiologia Plantarum</i> , 2007, 130, 418-426.	2.6	21
558	TOPO TA is A-OK: a test of phylogenetic bias in fungal environmental clone library construction. <i>Environmental Microbiology</i> , 2007, 9, 1329-1334.	1.8	60
559	Rare actinomycete bacteria from the shallow water sediments of the Trondheim fjord, Norway: isolation, diversity and biological activity. <i>Environmental Microbiology</i> , 2007, 9, 2756-2764.	1.8	163
560	Arsenite oxidation by a chemoautotrophic moderately acidophilic <i>Thiomonas</i> sp.: from the strain isolation to the gene study. <i>Environmental Microbiology</i> , 2008, 10, 228-237.	1.8	103
561	Sequence analysis and molecular characterization of larval midgut cDNA transcripts encoding peptidases from the yellow mealworm, <i>Tenebrio molitor</i> L.. <i>Insect Molecular Biology</i> , 2007, 16, 455-468.	1.0	72
562	Hepatopancreatic multi-€ transcript expression patterns in the crayfish <i>Cherax quadricarinatus</i> during the moult cycle. <i>Insect Molecular Biology</i> , 2007, 16, 661-674.	1.0	35
563	Archaeal diversity in naturally occurring and impacted environments from a tropical region. <i>Journal of Applied Microbiology</i> , 2007, 103, 141-151.	1.4	29
564	Genes differentially expressed in <i>Theobroma cacao</i> associated with resistance to witches' broom disease caused by <i>Crinipellis pernicioso</i> . <i>Molecular Plant Pathology</i> , 2007, 8, 279-292.	2.0	48
565	Generation of a wheat leaf rust, <i>Puccinia triticina</i> , EST database from stage-specific cDNA libraries. <i>Molecular Plant Pathology</i> , 2007, 8, 451-467.	2.0	49

#	ARTICLE	IF	CITATIONS
566	ANALYSES OF EXPRESSED SEQUENCE TAGS FROM SARGASSUM BINDERI (PHAEOPHYTA). <i>Journal of Phycology</i> , 2007, 43, 528-534.	1.0	28
567	Microsatellite-enriched genomic libraries as a source of polymorphic loci for <i>Schistosoma mansoni</i> . <i>Molecular Ecology Notes</i> , 2007, 7, 263-265.	1.7	19
568	Mining and characterizing microsatellites in <i>Cucumis melo</i> expressed sequence tags from sequence database. <i>Molecular Ecology Notes</i> , 2007, 7, 281-283.	1.7	39
569	Analysis of gene expression in cotton fiber initials. <i>BMC Plant Biology</i> , 2007, 7, 22.	1.6	124
570	An EST database from saffron stigmas. <i>BMC Plant Biology</i> , 2007, 7, 53.	1.6	56
571	Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. <i>BMC Plant Biology</i> , 2007, 7, 66.	1.6	91
572	ESTs from a wild <i>Arachis</i> species for gene discovery and marker development. <i>BMC Plant Biology</i> , 2007, 7, 7.	1.6	112
573	Tracembler " software for in-silico chromosome walking in unassembled genomes. <i>BMC Bioinformatics</i> , 2007, 8, 151.	1.2	12
574	A novel approach to sequence validating protein expression clones with automated decision making. <i>BMC Bioinformatics</i> , 2007, 8, 198.	1.2	6
575	CATMA, a comprehensive genome-scale resource for silencing and transcript profiling of <i>Arabidopsis</i> genes. <i>BMC Bioinformatics</i> , 2007, 8, 400.	1.2	46
576	SAT, a flexible and optimized Web application for SSR marker development. <i>BMC Bioinformatics</i> , 2007, 8, 465.	1.2	39
577	The Personal Sequence Database: a suite of tools to create and maintain web-accessible sequence databases. <i>BMC Bioinformatics</i> , 2007, 8, 479.	1.2	3
578	Minimus: a fast, lightweight genome assembler. <i>BMC Bioinformatics</i> , 2007, 8, 64.	1.2	354
579	ESTuber db: an online database for <i>Tuber borchii</i> EST sequences. <i>BMC Bioinformatics</i> , 2007, 8, S13.	1.2	9
580	Origin and diversification of the basic helix-loop-helix gene family in metazoans: insights from comparative genomics. <i>BMC Evolutionary Biology</i> , 2007, 7, 33.	3.2	263
581	A cricket Gene Index: a genomic resource for studying neurobiology, speciation, and molecular evolution. <i>BMC Genomics</i> , 2007, 8, 109.	1.2	32
582	Sequence-indexed mutations in maize using the UniformMu transposon-tagging population. <i>BMC Genomics</i> , 2007, 8, 116.	1.2	124
583	Transcriptome analysis of the venom gland of the Mexican scorpion <i>Hadrurus gertschi</i> (Arachnida: Tj ETQq1 1 0.784314 rgBT/Overlock	1.2	128

#	ARTICLE	IF	CITATIONS
584	Generation and analysis of ESTs from the eastern oyster, <i>Crassostrea virginica</i> Gmelin and identification of microsatellite and SNP markers. <i>BMC Genomics</i> , 2007, 8, 157.	1.2	65
585	Gender-specific selection on codon usage in plant genomes. <i>BMC Genomics</i> , 2007, 8, 169.	1.2	27
586	Towards the ictalurid catfish transcriptome: generation and analysis of 31,215 catfish ESTs. <i>BMC Genomics</i> , 2007, 8, 177.	1.2	70
587	Identification of unannotated exons of low abundance transcripts in <i>Drosophila melanogaster</i> and cloning of a new serine protease gene upregulated upon injury. <i>BMC Genomics</i> , 2007, 8, 249.	1.2	9
588	TrED: the <i>Trichophyton rubrum</i> Expression Database. <i>BMC Genomics</i> , 2007, 8, 250.	1.2	27
589	cDNA sequences reveal considerable gene prediction inaccuracy in the <i>Plasmodium falciparum</i> genome. <i>BMC Genomics</i> , 2007, 8, 255.	1.2	50
590	Inference of transcriptional regulation using gene expression data from the bovine and human genomes. <i>BMC Genomics</i> , 2007, 8, 265.	1.2	7
591	Expressed sequence tags of the anther smut fungus, <i>Microbotryum violaceum</i> , identify mating and pathogenicity genes. <i>BMC Genomics</i> , 2007, 8, 272.	1.2	30
592	Analysis of 13000 unique Citrus clusters associated with fruit quality, production and salinity tolerance. <i>BMC Genomics</i> , 2007, 8, 31.	1.2	64
593	Analysis and functional annotation of expressed sequence tags (ESTs) from multiple tissues of oil palm (<i>Elaeis guineensis</i> Jacq.). <i>BMC Genomics</i> , 2007, 8, 381.	1.2	47
594	Lactation transcriptomics in the Australian marsupial, <i>Macropus eugenii</i> : transcript sequencing and quantification. <i>BMC Genomics</i> , 2007, 8, 417.	1.2	50
595	Genomic resources for <i>Myzus persicae</i> : EST sequencing, SNP identification, and microarray design. <i>BMC Genomics</i> , 2007, 8, 423.	1.2	116
596	High throughput SNP discovery and genotyping in grapevine (<i>Vitis vinifera</i> L.) by combining a re-sequencing approach and SNPlex technology. <i>BMC Genomics</i> , 2007, 8, 424.	1.2	227
597	AphanoDB: a genomic resource for <i>Aphanomyces</i> pathogens. <i>BMC Genomics</i> , 2007, 8, 471.	1.2	43
598	Comparative genomic characterization of citrus-associated <i>Xylella fastidiosa</i> strains. <i>BMC Genomics</i> , 2007, 8, 474.	1.2	25
599	Simple sequence repeats in zebra finch (<i>Taeniopygia guttata</i>) expressed sequence tags: a new resource for evolutionary genetic studies of passerines. <i>BMC Genomics</i> , 2007, 8, 52.	1.2	52
600	An annotated catalogue of salivary gland transcripts in the adult female mosquito, <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2007, 8, 6.	1.2	219
601	Expressed Sequence Tags from the oomycete <i>Plasmopara halstedii</i> , an obligate parasite of the sunflower. <i>BMC Microbiology</i> , 2007, 7, 110.	1.3	9

#	ARTICLE	IF	CITATIONS
602	Mutations in the carboxyl terminal region of E2 glycoprotein of classical swine fever virus are responsible for viral attenuation in swine. <i>Virology</i> , 2007, 364, 371-382.	1.1	51
603	Insulin and gender: An insulin-like gene expressed exclusively in the androgenic gland of the male crayfish. <i>General and Comparative Endocrinology</i> , 2007, 150, 326-336.	0.8	157
604	Molecular detection of Papaya meleira virus in the latex of <i>Carica papaya</i> by RT-PCR. <i>Journal of Virological Methods</i> , 2007, 146, 305-310.	1.0	27
605	Single nucleotide polymorphisms identification in expressed genes of <i>Schistosoma mansoni</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 154, 134-140.	0.5	22
606	Identification of midgut microvillar proteins from <i>Tenebrio molitor</i> and <i>Spodoptera frugiperda</i> by cDNA library screenings with antibodies. <i>Journal of Insect Physiology</i> , 2007, 53, 1112-1124.	0.9	37
607	The chicken RH map: current state of progress and microchromosome mapping. <i>Cytogenetic and Genome Research</i> , 2007, 117, 14-21.	0.6	22
608	Automated Discovery of Single Nucleotide Polymorphism and Simple Sequence Repeat Molecular Genetic Markers. , 2007, 406, 473-494.		11
609	TCP Transcription Factors Predate the Emergence of Land Plants. <i>Journal of Molecular Evolution</i> , 2007, 65, 23-33.	0.8	213
610	Strong Heterogeneity in Nucleotidic Composition and Codon Bias in the Pea Aphid (<i>Acyrtosiphon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 413-424.	0.8	11
611	Archaeal Communities in a Tropical Estuarine Ecosystem: Guanabara Bay, Brazil. <i>Microbial Ecology</i> , 2007, 54, 460-468.	1.4	50
612	Generation, annotation, and analysis of ESTs from four different <i>Trichoderma</i> strains grown under conditions related to biocontrol. <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 853-862.	1.7	39
613	Effects of water-deficit stress on the transcriptomes of developing immature ear and tassel in maize. <i>Plant Cell Reports</i> , 2007, 26, 2137-2147.	2.8	50
614	Brazilian Vaccinia virus strains show genetic polymorphism at the ati gene. <i>Virus Genes</i> , 2007, 35, 531-539.	0.7	16
615	Caraparu virus (group C Orthobunyavirus): sequencing and phylogenetic analysis based on the conserved region 3 of the RNA polymerase gene. <i>Virus Genes</i> , 2007, 35, 681-684.	0.7	6
616	Characterization of EST-SSRs in loblolly pine and spruce. <i>Tree Genetics and Genomes</i> , 2007, 3, 251-259.	0.6	33
617	Identification of genes associated with flesh morphogenesis during grapevine fruit development. <i>Plant Molecular Biology</i> , 2007, 63, 307-323.	2.0	78
618	A collection of 10,096 indica rice full-length cDNAs reveals highly expressed sequence divergence between <i>Oryza sativa indica</i> and japonica subspecies. <i>Plant Molecular Biology</i> , 2007, 65, 403-415.	2.0	55
619	Structure of genetic diversity among common bean (<i>Phaseolus vulgaris</i> L.) varieties of Mesoamerican and Andean origins using new developed microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 1747-1762.	0.8	65

#	ARTICLE	IF	CITATIONS
620	Estimating the Efficiency of Fish Cross-Species cDNA Microarray Hybridization. <i>Marine Biotechnology</i> , 2007, 9, 491-499.	1.1	25
621	Natural infection of <i>Alternanthera tenella</i> (Amaranthaceae) by a new potyvirus. <i>Archives of Virology</i> , 2007, 152, 2095-2099.	0.9	3
622	Gene transcript and metabolite profiling of elicitor-induced opium poppy cell cultures reveals the coordinate regulation of primary and secondary metabolism. <i>Planta</i> , 2007, 225, 1085-1106.	1.6	98
623	The olig family: phylogenetic analysis and early gene expression in <i>Xenopus tropicalis</i> . <i>Development Genes and Evolution</i> , 2007, 217, 485-497.	0.4	13
624	Validation of in silico-predicted genic SNPs in white clover (<i>Trifolium repens</i> L.), an outbreeding allopolyploid species. <i>Molecular Genetics and Genomics</i> , 2007, 277, 413-425.	1.0	23
625	The CBF gene family in hexaploid wheat and its relationship to the phylogenetic complexity of cereal CBFs. <i>Molecular Genetics and Genomics</i> , 2007, 277, 533-554.	1.0	148
626	Analysis of EST sequences suggests recent origin of allotetraploid colonial and creeping bentgrasses. <i>Molecular Genetics and Genomics</i> , 2007, 278, 197-209.	1.0	22
627	Disarming and sequencing of <i>Agrobacterium rhizogenes</i> strain K599 (NCPPB2659) plasmid pRi2659. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2007, 43, 521-535.	0.9	43
628	DNA fragment assembly using a grid-based genetic algorithm. <i>Computers and Operations Research</i> , 2008, 35, 2776-2790.	2.4	35
629	Seeding strategies and recombination operators for solving the DNA fragment assembly problem. <i>Information Processing Letters</i> , 2008, 108, 94-100.	0.4	15
630	Transcriptional profiles of immature ears and tassels in maize at early stage of water stress. <i>Biologia Plantarum</i> , 2008, 52, 754-758.	1.9	12
631	Expression profiling of salinity-alkali stress responses by large-scale expressed sequence tag analysis in <i>Tamarix hispida</i> . <i>Plant Molecular Biology</i> , 2008, 66, 245-258.	2.0	51
632	Expressed sequence tag analysis and development of gene associated markers in a near-isogenic plant system of <i>Eragrostis curvula</i> . <i>Plant Molecular Biology</i> , 2008, 67, 1-10.	2.0	51
633	Gene expression in diplosporous and sexual <i>Eragrostis curvula</i> genotypes with differing ploidy levels. <i>Plant Molecular Biology</i> , 2008, 67, 11-23.	2.0	53
634	Sugar levels modulate sorbitol dehydrogenase expression in maize. <i>Plant Molecular Biology</i> , 2008, 68, 203-213.	2.0	29
635	Transcriptome analysis approaches for the isolation of trichome-specific genes from the medicinal plant <i>Cistus creticus</i> subsp. <i>creticus</i> . <i>Plant Molecular Biology</i> , 2008, 68, 633-651.	2.0	41
636	Nucleotide sequence of the tripartite <i>Fragaria chiloensis</i> cryptic virus and presence of the virus in the Americas. <i>Virus Genes</i> , 2008, 36, 267-272.	0.7	30
637	Molecular characterization of the genes coding for glycoprotein and L protein of lymphocytic choriomeningitis virus strain MX. <i>Virus Genes</i> , 2008, 37, 31-38.	0.7	9

#	ARTICLE	IF	CITATIONS
638	Differential Responses of Wheat Inhibitor-like Genes to Hessian Fly, <i>Mayetiola destructor</i> , Attacks During Compatible and Incompatible Interactions. <i>Journal of Chemical Ecology</i> , 2008, 34, 1005-1012.	0.9	22
639	Bacterial communities of the marine sponges <i>Hymeniacidon heliophila</i> and <i>Polymastia janeirensis</i> and their environment in Rio de Janeiro, Brazil. <i>Marine Biology</i> , 2008, 155, 135-146.	0.7	25
640	Isolation of mycoparasitic-related transcripts by SSH during interaction of the mycoparasite <i>Stachybotrys elegans</i> with its host <i>Rhizoctonia solani</i> . <i>Current Genetics</i> , 2008, 53, 67-80.	0.8	27
641	Guarana (<i>Paullinia cupana</i> var. <i>sorbilis</i>), an anciently consumed stimulant from the Amazon rain forest: the seeded-fruit transcriptome. <i>Plant Cell Reports</i> , 2008, 27, 117-124.	2.8	47
642	A guanylyl cyclase-like gene is associated with <i>Gibberella</i> ear rot resistance in maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 116, 465-479.	1.8	25
643	Molecular characterization and genomic organization of low molecular weight glutenin subunit genes at the Glu-3 loci in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 116, 953-966.	1.8	68
644	SSRs and INDELS mined from the sunflower EST database: abundance, polymorphisms, and cross-taxa utility. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1021-1029.	1.8	117
645	ESTs analyses of <i>Lampetra japonica</i> liver and comparison transcriptome with the jawed vertebrates. <i>Science in China Series C: Life Sciences</i> , 2008, 51, 27-37.	1.3	3
646	Evolution of the Genes Encoding Seed Storage Proteins in Sugarcane and Maize. <i>Tropical Plant Biology</i> , 2008, 1, 108-119.	1.0	3
647	The shrunken genome of <i>Arabidopsis thaliana</i> . <i>Plant Systematics and Evolution</i> , 2008, 273, 257-271.	0.3	35
648	Complete nucleotide sequence of an isolate of coleus vein necrosis virus from verbena. <i>Archives of Virology</i> , 2008, 153, 381-384.	0.9	7
649	Characterization of a flowering cherry strain of Cherry necrotic rusty mottle virus. <i>Archives of Virology</i> , 2008, 153, 973-978.	0.9	16
650	Pollution-Affected Fish Hepatic Transcriptome and Its Expression Patterns on Exposure to Cadmium. <i>Marine Biotechnology</i> , 2008, 10, 250-261.	1.1	26
651	Comparative Analysis of Expressed Sequence Tag (EST) Libraries in the Seagrass <i>Zostera marina</i> Subjected to Temperature Stress. <i>Marine Biotechnology</i> , 2008, 10, 297-309.	1.1	55
652	Rainbow Smelt (<i>Osmerus mordax</i>) Genomic Library and EST Resources. <i>Marine Biotechnology</i> , 2008, 10, 487-91.	1.1	21
653	Preparation and Analysis of an Expressed Sequence Tag Library from the Toxic Dinoflagellate <i>Alexandrium catenella</i> . <i>Marine Biotechnology</i> , 2008, 10, 692-700.	1.1	40
654	EST and Mitochondrial DNA Sequences Support a Distinct Pacific Form of Salmon Louse, <i>Lepeophtheirus salmonis</i> . <i>Marine Biotechnology</i> , 2008, 10, 741-749.	1.1	50
655	The nuclear genome of <i>Brachypodium distachyon</i> : analysis of BAC end sequences. <i>Functional and Integrative Genomics</i> , 2008, 8, 135-147.	1.4	83

#	ARTICLE	IF	CITATIONS
656	Transposable elements in <i>Coffea</i> (Gentianales: Rubiaceae) transcripts and their role in the origin of protein diversity in flowering plants. <i>Molecular Genetics and Genomics</i> , 2008, 279, 385-401.	1.0	19
657	Evolution of non-specific lipid transfer protein (nsLTP) genes in the Poaceae family: their duplication and diversity. <i>Molecular Genetics and Genomics</i> , 2008, 279, 481-497.	1.0	24
658	Exploring the transcriptome of the burrowing nematode <i>Radopholus similis</i> . <i>Molecular Genetics and Genomics</i> , 2008, 280, 1-17.	1.0	53
659	Expressed sequence tags (ESTs) from immune tissues of turbot (<i>Scophthalmus maximus</i>) challenged with pathogens. <i>BMC Veterinary Research</i> , 2008, 4, 37.	0.7	61
660	Generation of a non-small cell lung cancer transcriptome microarray. <i>BMC Medical Genomics</i> , 2008, 1, 20.	0.7	18
661	HaploSNPer: a web-based allele and SNP detection tool. <i>BMC Genetics</i> , 2008, 9, 23.	2.7	37
662	A comprehensive analysis of normal variation and disease-causing mutations in the human <i>DSPP</i> gene. <i>Human Mutation</i> , 2008, 29, 1392-1404.	1.1	85
663	Farnesoic acid O-methyl transferase (FAMeT) isoforms: Conserved traits and gene expression patterns related to caste differentiation in the stingless bee, <i>Melipona scutellaris</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2008, 67, 97-106.	0.6	24
664	Low-coverage massively parallel pyrosequencing of cDNAs enables proteomics in non-model species: Comparison of a species-specific database generated by pyrosequencing with databases from related species for proteome analysis of pea chloroplast envelopes. <i>Journal of Biotechnology</i> , 2008, 136, 44-53.	1.9	60
665	Generation and analysis of expressed sequence tags from a NaHCO ₃ -treated <i>Limonium bicolor</i> cDNA library. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 977-986.	2.8	25
666	An insight into the salivary transcriptome and proteome of the soft tick and vector of epizootic bovine abortion, <i>Ornithodoros coriaceus</i> . <i>Journal of Proteomics</i> , 2008, 71, 493-512.	1.2	84
667	Expression of Genes Associated with Retinoid Metabolism in the Trout Ovarian Follicle1. <i>Biology of Reproduction</i> , 2008, 79, 570-577.	1.2	22
668	Phylogenetic Analysis of the Plant-specific Zinc Finger Homeobox and Mini Zinc Finger Gene Families. <i>Journal of Integrative Plant Biology</i> , 2008, 50, 1031-1045.	4.1	82
669	Global Identification of Significantly Expressed Genes in Developing Endosperm of Rice by Expression Sequence Tags and cDNA Array Approaches. <i>Journal of Integrative Plant Biology</i> , 2008, 50, 1078-1088.	4.1	9
670	AN EVOLUTIONARY EXPRESSED SEQUENCE TAG ANALYSIS OF DROSOPHILA SPERMATHECA GENES. Evolution; <i>International Journal of Organic Evolution</i> , 2008, 62, 2936-2947.	1.1	67
671	A cDNA microarray for the three-spined stickleback, <i>Gasterosteus aculeatus</i> L., and analysis of the interactive effects of oestradiol and dibenzanthracene exposures. <i>Journal of Fish Biology</i> , 2008, 72, 2133-2153.	0.7	34
672	Genomic resources and microarrays for the common carp <i>Cyprinus carpio</i> L.. <i>Journal of Fish Biology</i> , 2008, 72, 2095-2117.	0.7	60
673	The GENIPOL European flounder <i>Platichthys flesus</i> L. toxicogenomics microarray: application for investigation of the response to furunculosis vaccination. <i>Journal of Fish Biology</i> , 2008, 72, 2154-2169.	0.7	19

#	ARTICLE	IF	CITATIONS
674	Genetic mapping of sex determination in a wild strawberry, <i>Fragaria virginiana</i> , reveals earliest form of sex chromosome. <i>Heredity</i> , 2008, 101, 507-517.	1.2	159
675	The <i>Pristionchus pacificus</i> genome provides a unique perspective on nematode lifestyle and parasitism. <i>Nature Genetics</i> , 2008, 40, 1193-1198.	9.4	310
676	The <i>Lmgpi15</i> gene, encoding a component of the glycosylphosphatidylinositol anchor biosynthesis pathway, is required for morphogenesis and pathogenicity in <i>Leptosphaeria maculans</i> . <i>New Phytologist</i> , 2008, 179, 1105-1120.	3.5	12
677	RcDhn5, a cold acclimation-responsive dehydrin from <i>Rhododendron catawbiense</i> rescues enzyme activity from dehydration effects in vitro and enhances freezing tolerance in <i>RcDhn5</i> -overexpressing <i>Arabidopsis</i> plants. <i>Physiologia Plantarum</i> , 2008, 134, 583-597.	2.6	78
678	Serine proteases identified from a <i>Costelytra zealandica</i> (White) (Coleoptera: Scarabaeidae) midgut EST library and their expression through insect development. <i>Insect Molecular Biology</i> , 2008, 17, 247-259.	1.0	17
679	Characterization and expression of the odorant-binding protein 7 gene in <i>Anopheles stephensi</i> and comparative analysis among five mosquito species. <i>Insect Molecular Biology</i> , 2008, 17, 631-645.	1.0	16
680	The G α subunit BCG1, the phospholipase C (BcPLC1) and the calcineurin phosphatase co-ordinately regulate gene expression in the grey mould fungus <i>Botrytis cinerea</i> . <i>Molecular Microbiology</i> , 2008, 67, 1027-1050.	1.2	99
681	A family of GHF5 endo- β -glucanases in the migratory plant-parasitic nematode <i>Radopholus similis</i> . <i>Plant Pathology</i> , 2008, 57, 581-590.	1.2	36
682	ReRep: Computational detection of repetitive sequences in genome survey sequences (GSS). <i>BMC Bioinformatics</i> , 2008, 9, 366.	1.2	11
683	Large-scale identification of polymorphic microsatellites using an in silico approach. <i>BMC Bioinformatics</i> , 2008, 9, 374.	1.2	65
684	EST2uni: an open, parallel tool for automated EST analysis and database creation, with a data mining web interface and microarray expression data integration. <i>BMC Bioinformatics</i> , 2008, 9, 5.	1.2	54
685	Version VI of the ESTree db: an improved tool for peach transcriptome analysis. <i>BMC Bioinformatics</i> , 2008, 9, S9.	1.2	22
686	Validation of an NSP-based (negative selection pattern) gene family identification strategy. <i>BMC Bioinformatics</i> , 2008, 9, S2.	1.2	5
687	Evolutionary history of the alpha2,8-sialyltransferase (ST8Sia) gene family: Tandem duplications in early deuterostomes explain most of the diversity found in the vertebrate ST8Sia genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 258.	3.2	48
688	Sequencing and analysis of the gene-rich space of cowpea. <i>BMC Genomics</i> , 2008, 9, 103.	1.2	98
689	Detection and validation of single feature polymorphisms in cowpea (<i>Vigna unguiculata</i> L. Walp) using a soybean genome array. <i>BMC Genomics</i> , 2008, 9, 107.	1.2	35
690	The Songbird Neurogenomics (SoNG) Initiative: Community-based tools and strategies for study of brain gene function and evolution. <i>BMC Genomics</i> , 2008, 9, 131.	1.2	126
691	Novel and nodulation-regulated microRNAs in soybean roots. <i>BMC Genomics</i> , 2008, 9, 160.	1.2	283

#	ARTICLE	IF	CITATIONS
692	Stage-specific gene expression during urediniospore germination in <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . BMC Genomics, 2008, 9, 203.	1.2	53
693	Insight into the sialome of the castor bean tick, <i>Ixodes ricinus</i> . BMC Genomics, 2008, 9, 233.	1.2	77
694	Transcriptome analysis of <i>Loxosceles laeta</i> (Araneae, Sicariidae) spider venomous gland using expressed sequence tags. BMC Genomics, 2008, 9, 279.	1.2	110
695	WildSilkbase: An EST database of wild silkmoths. BMC Genomics, 2008, 9, 338.	1.2	38
696	Large-scale Gene Ontology analysis of plant transcriptome-derived sequences retrieved by AFLP technology. BMC Genomics, 2008, 9, 347.	1.2	22
697	A fragmented metazoan organellar genome: the two mitochondrial chromosomes of <i>Hydra magnipapillata</i> . BMC Genomics, 2008, 9, 350.	1.2	61
698	Analysis of expressed sequence tags from Actinidia: applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. BMC Genomics, 2008, 9, 351.	1.2	178
699	Development of genomic resources for <i>Citrus clementina</i> : Characterization of three deep-coverage BAC libraries and analysis of 46,000 BAC end sequences. BMC Genomics, 2008, 9, 423.	1.2	81
700	Identification of transcripts involved in meiosis and follicle formation during ovine ovary development. BMC Genomics, 2008, 9, 436.	1.2	13
701	Quality assessment parameters for EST-derived SNPs from catfish. BMC Genomics, 2008, 9, 450.	1.2	100
702	A conifer genomics resource of 200,000 spruce (<i>Picea</i> spp.) ESTs and 6,464 high-quality, sequence-finished full-length cDNAs for Sitka spruce (<i>Picea sitchensis</i>). BMC Genomics, 2008, 9, 484.	1.2	113
703	Microarray analysis identifies candidate genes for key roles in coral development. BMC Genomics, 2008, 9, 540.	1.2	119
704	A salmonid EST genomic study: genes, duplications, phylogeny and microarrays. BMC Genomics, 2008, 9, 545.	1.2	145
705	Exploring the mialome of ticks: An annotated catalogue of midgut transcripts from the hard tick, <i>Dermacentor variabilis</i> (Acari: Ixodidae). BMC Genomics, 2008, 9, 552.	1.2	109
706	Analysis of 4,664 high-quality sequence-finished poplar full-length cDNA clones and their utility for the discovery of genes responding to insect feeding. BMC Genomics, 2008, 9, 57.	1.2	68
707	Development and validation of a gene expression oligo microarray for the gilthead sea bream (<i>Sparus</i>) Tj ETQq1 1 0,784314 rgBT /Over 1.2 55	1.2	55
708	Coral life history and symbiosis: Functional genomic resources for two reef building Caribbean corals, <i>Acropora palmata</i> and <i>Montastraea faveolata</i> . BMC Genomics, 2008, 9, 97.	1.2	122
709	Evaluation of the bacterial diversity in the feces of cattle using 16S rDNA bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP). BMC Microbiology, 2008, 8, 125.	1.3	982

#	ARTICLE	IF	CITATIONS
710	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, <i>Thellungiella halophila</i> . <i>BMC Plant Biology</i> , 2008, 8, 115.	1.6	57
711	Development and mapping of Simple Sequence Repeat markers for pearl millet from data mining of Expressed Sequence Tags. <i>BMC Plant Biology</i> , 2008, 8, 119.	1.6	114
712	Identification of precursor transcripts for 6 novel miRNAs expands the diversity on the genomic organisation and expression of miRNA genes in rice. <i>BMC Plant Biology</i> , 2008, 8, 123.	1.6	46
713	Analysis of non-TIR NBS-LRR resistance gene analogs in <i>Musa acuminata</i> Colla: Isolation, RFLP marker development, and physical mapping. <i>BMC Plant Biology</i> , 2008, 8, 15.	1.6	63
714	Construction of nested genetic core collections to optimize the exploitation of natural diversity in <i>Vitis vinifera</i> L. subsp <i>sativa</i> . <i>BMC Plant Biology</i> , 2008, 8, 31.	1.6	109
715	A blackberry (<i>Rubus</i> L.) expressed sequence tag library for the development of simple sequence repeat markers. <i>BMC Plant Biology</i> , 2008, 8, 69.	1.6	32
716	TriMEDB: A database to integrate transcribed markers and facilitate genetic studies of the tribe Triticeae. <i>BMC Plant Biology</i> , 2008, 8, 72.	1.6	18
717	<i>Eimeria tenella</i> : Analysis of differentially expressed genes in the monensin- and maduramicin-resistant lines using cDNA array. <i>Experimental Parasitology</i> , 2008, 119, 264-271.	0.5	14
718	Stage-specific gene expression in <i>Teladorsagia circumcincta</i> (Nematoda: Strongylida) infective larvae and early parasitic stages. <i>International Journal for Parasitology</i> , 2008, 38, 829-838.	1.3	40
719	Analysis of transcripts and proteins expressed in the salivary glands of Hessian fly (<i>Mayetiola</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	61
720	Tag-encoded pyrosequencing analysis of bacterial diversity in a single soil type as affected by management and land use. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2762-2770.	4.2	418
721	The mitochondrial genome of the phytopathogenic basidiomycete <i>Moniliophthora perniciosa</i> is 109kb in size and contains a stable integrated plasmid. <i>Mycological Research</i> , 2008, 112, 1136-1152.	2.5	87
722	Comparison of genome structure between white clover and <i>Medicago truncatula</i> supports homoeologous group nomenclature based on conserved synteny. <i>Genome</i> , 2008, 51, 905-911.	0.9	17
723	A comparative gene index for the white sturgeon <i>Acipenser transmontanus</i> . <i>Marine Genomics</i> , 2008, 1, 15-21.	0.4	3
724	<i>Histoplasma capsulatum</i> proteome response to decreased iron availability. <i>Proteome Science</i> , 2008, 6, 36.	0.7	12
725	Identification of differentially expressed ovarian genes during primary and early secondary oocyte growth in coho salmon, <i>Oncorhynchus kisutch</i> . <i>Reproductive Biology and Endocrinology</i> , 2008, 6, 2.	1.4	133
726	<i>Lutzomyia longipalpis</i> s.l. in Brazil and the impact of the Sao Francisco River in the speciation of this sand fly vector. <i>Parasites and Vectors</i> , 2008, 1, 16.	1.0	32
727	Differential Gene Expression Between the Biotrophic-Like and Saprotrophic Mycelia of the Witches' Broom Pathogen <i>Moniliophthora perniciosa</i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 891-908.	1.4	50

#	ARTICLE	IF	CITATIONS
728	A New Arenavirus in a Cluster of Fatal Transplant-Associated Diseases. <i>New England Journal of Medicine</i> , 2008, 358, 991-998.	13.9	650
729	Genetic Evaluation of EST-SSRs Derived from <i>Gossypium herbaceum</i> . <i>Acta Agronomica Sinica</i> , 2008, 34, 2085-2091.	0.3	9
730	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , 2008, 9, R161.	13.9	71
731	Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Biology</i> , 2008, 9, R45.	13.9	82
732	Naturally occurring feline leukemia virus subgroup A and B infections in urban domestic cats. <i>Journal of General Virology</i> , 2008, 89, 2799-2805.	1.3	27
733	Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008, 18, 1851-1858.	2.4	2,275
734	A Bioinformatician's Guide to Metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 557-578.	2.9	361
735	A Phylogenomic Investigation into the Origin of Metazoa. <i>Molecular Biology and Evolution</i> , 2008, 25, 664-672.	3.5	259
737	An insight into the sialome of the soft tick, <i>Ornithodoros parkeri</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1-21.	1.2	105
738	An insight into the sialome of the blood-sucking bug <i>Triatoma infestans</i> , a vector of Chagas's disease. <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 213-232.	1.2	114
739	Identification and genomic structure of chemosensory proteins (CSP) and odorant binding proteins (OBP) genes expressed in foreleg tarsi of the swallowtail butterfly <i>Papilio xuthus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 969-976.	1.2	56
740	Acquisition of uncharacterized sequences from <i>Candidatus Liberibacter</i> , an unculturable bacterium, using an improved genomic walking method. <i>Molecular and Cellular Probes</i> , 2008, 22, 30-37.	0.9	24
741	Comparative ORESTES-sampling of transcriptomes of immune-challenged <i>Biomphalaria glabrata</i> snails. <i>Journal of Invertebrate Pathology</i> , 2008, 99, 192-203.	1.5	44
742	Anti-lipopolysaccharide factor in <i>Litopenaeus vannamei</i> (LvALF): A broad spectrum antimicrobial peptide essential for shrimp immunity against bacterial and fungal infection. <i>Molecular Immunology</i> , 2008, 45, 1916-1925.	1.0	180
743	Molecular diversity of Brazilian strains of porcine circovirus type 2 (PCV-2). <i>Research in Veterinary Science</i> , 2008, 85, 197-200.	0.9	10
744	Peanut genes identified during initial phase of <i>Cercosporidium personatum</i> infection. <i>Plant Science</i> , 2008, 174, 78-87.	1.7	18
745	Molecular and biochemical characterization of defense responses in ginseng (<i>Panax quinquefolius</i>) roots challenged with <i>Fusarium equiseti</i> . <i>Physiological and Molecular Plant Pathology</i> , 2008, 72, 10-20.	1.3	19
746	Laser capture microdissection and expressed sequence tag analysis of uredinia formed by <i>Phakopsora pachyrhizi</i> , the causal agent of Asian soybean rust. <i>Physiological and Molecular Plant Pathology</i> , 2008, 73, 163-174.	1.3	21

#	ARTICLE	IF	CITATIONS
747	A member of a new genus in the Potyviridae infects Rubus. <i>Virus Research</i> , 2008, 131, 145-151.	1.1	51
748	Expressed sequence tags (ESTs) from the salivary glands of the tick <i>Amblyomma cajennense</i> (Acari: Tj ETQq1 1 0.784314 rgBT / Overl...	0.8	64
749	Bacterial Tagâ€œEncoded FLX Amplicon Pyrosequencing (bTEFAP) for Microbiome Studies: Bacterial Diversity in the Ileum of Newly Weaned Salmonella-Infected Pigs. <i>Foodborne Pathogens and Disease</i> , 2008, 5, 459-472.	0.8	373
750	Germination-Arrest Factor (GAF): Biological properties of a novel, naturally-occurring herbicide produced by selected isolates of rhizosphere bacteria. <i>Biological Control</i> , 2008, 46, 380-390.	1.4	72
751	Large-scale expressed sequence tag analysis for the chestnut blight fungus <i>Cryphonectria parasitica</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 319-327.	0.9	27
752	The <i>Lmpma1</i> gene of <i>Leptosphaeria maculans</i> encodes a plasma membrane H ⁺ -ATPase isoform essential for pathogenicity towards oilseed rape. <i>Fungal Genetics and Biology</i> , 2008, 45, 1122-1134.	0.9	18
753	Analysis of ESTs and expression of two peroxiredoxins in the thermally stressed Antarctic bivalve <i>Laternula elliptica</i> . <i>Fish and Shellfish Immunology</i> , 2008, 25, 550-559.	1.6	43
754	The mitochondrial view of <i>Blastocladiella emersonii</i> . <i>Gene</i> , 2008, 424, 33-39.	1.0	14
755	Rapid accumulation of an interleukin 17 homolog transcript in <i>Crassostrea gigas</i> hemocytes following bacterial exposure. <i>Developmental and Comparative Immunology</i> , 2008, 32, 1099-1104.	1.0	96
756	New resources for studying the rose flowering process. <i>Genome</i> , 2008, 51, 827-837.	0.9	37
757	Genomic Resources for Immunology and Disease of Salmonid and Non-Salmonid Fish. <i>Reviews in Fisheries Science</i> , 2008, 16, 119-132.	2.1	10
758	Adaptive Evolution of Hepcidin Genes in Antarctic Notothenioid Fishes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1099-1112.	3.5	67
759	Microsatellites from kousa dogwood (<i>Cornus kousa</i>). <i>Molecular Ecology Resources</i> , 2008, 8, 780-782.	2.2	8
760	Increasing ecological inference from high throughput sequencing of fungi in the environment through a tagging approach. <i>Molecular Ecology Resources</i> , 2008, 8, 742-752.	2.2	45
761	Molecular phylogenetics of central Canadian Physidae (Pulmonata: Basommatophora). <i>Canadian Journal of Zoology</i> , 2008, 86, 10-16.	0.4	17
762	Development of a <i>Brassica</i> seed cDNA microarray. <i>Genome</i> , 2008, 51, 236-242.	0.9	25
763	A new algorithm for genome assembly from short reads. , 2008, , .		1
764	Multiple Models for Rosaceae Genomics. <i>Plant Physiology</i> , 2008, 147, 985-1003.	2.3	291

#	ARTICLE	IF	CITATIONS
765	Isolation and characterization of two distinct classes of DXS genes in <i>Hevea brasiliensis</i> . DNA Sequence, 2008, 19, 291-300.	0.7	7
766	ESTplus: An Integrative System for Comprehensive and Customized EST Analysis and Proteomic Data Matching. , 2008, , .		2
767	Changes in the <i>Gallus gallus</i> Proteome Induced by Marek's Disease Virus. Journal of Proteome Research, 2008, 7, 4346-4358.	1.8	15
768	A low-complexity probabilistic genome assembly based on hashing functions with SNP detection. , 2008, , .		0
769	Ripening and Genotype Control Stilbene Accumulation in Healthy Grapes. Journal of Agricultural and Food Chemistry, 2008, 56, 11773-11785.	2.4	170
770	Transcript Profiling by 3'-Untranslated Region Sequencing Resolves Expression of Gene Families. Plant Physiology, 2008, 146, 32-44.	2.3	97
771	Consensus generation and variant detection by Celera Assembler. Bioinformatics, 2008, 24, 1035-1040.	1.8	100
772	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. PLoS ONE, 2008, 3, e2527.	1.1	667
773	High Degree of Transferability of 86 Newly Developed Zebra Finch EST-Linked Microsatellite Markers in 8 Bird Species. Journal of Heredity, 2008, 99, 688-693.	1.0	22
774	Parallel Implementation of the Novel Approach to Genome Assembly. , 2008, , .		0
775	A New DNA Fragment Assembly Method Based on Long Fragment Filtration. , 2008, , .		0
776	Identification of soluble secreted proteins from appressoria of <i>Colletotrichum higginsianum</i> by analysis of expressed sequence tags. Microbiology (United Kingdom), 2008, 154, 1204-1217.	0.7	52
777	Recurrent Deletions of Puroindoline Genes at the Grain Hardness Locus in Four Independent Lineages of Polyploid Wheat. Plant Physiology, 2008, 146, 200-212.	2.3	68
778	Duplication and Functional Diversification of HAP3 Genes Leading to the Origin of the Seed-Developmental Regulatory Gene, LEAFY COTYLEDON1 (LEC1), in Nonseed Plant Genomes. Molecular Biology and Evolution, 2008, 25, 1581-1592.	3.5	56
779	EnGenius™ ENVIRONMENTAL GENOME INFORMATIONAL UTILITY SYSTEM. Journal of Bioinformatics and Computational Biology, 2008, 06, 1193-1211.	0.3	4
780	EST Analysis of Hop Glandular Trichomes Identifies an O-Methyltransferase That Catalyzes the Biosynthesis of Xanthohumol. Plant Cell, 2008, 20, 186-200.	3.1	158
781	Putative identification of expressed genes associated with attachment of the zebra mussel (<i>Dreissena</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	29
782	Calcineurin-Responsive Zinc Finger Transcription Factor CRZ1 of <i>Botrytis cinerea</i> Is Required for Growth, Development, and Full Virulence on Bean Plants. Eukaryotic Cell, 2008, 7, 584-601.	3.4	147

#	ARTICLE	IF	CITATIONS
783	Generation and analysis of an <i>Eucalyptus globulus</i> cDNA library constructed from seedlings subjected to low temperature conditions. <i>Electronic Journal of Biotechnology</i> , 2008, 11, 0-0.	1.2	18
784	Differential gene expression analysis of maize leaf at heading stage in response to water-deficit stress. <i>Bioscience Reports</i> , 2008, 28, 125-134.	1.1	17
785	The effect of sequence quality on sequence alignment. <i>Bioinformatics</i> , 2008, 24, 897-900.	1.8	17
786	A Linkage Map of the Zebra Finch <i>Taeniopygia guttata</i> Provides New Insights Into Avian Genome Evolution. <i>Genetics</i> , 2008, 179, 651-667.	1.2	107
787	TreeGenes: A Forest Tree Genome Database. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-7.	2.2	89
788	Characterization of <i>Streptococcus gordonii</i> prophage PH15: complete genome sequence and functional analysis of phage-encoded integrase and endolysin. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2970-2978.	0.7	17
789	Sequence-specific reconstruction from fragmentary databases using seed sequences: implementation and validation on SAGE, proteome and generic sequencing data. <i>Bioinformatics</i> , 2008, 24, 1676-1680.	1.8	9
790	<i>Algoriphagus hitonicola</i> sp. nov., isolated from an athalassohaline lagoon. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 424-428.	0.8	32
791	Sequencing and Analysis of Approximately 40 000 Soybean cDNA Clones from a Full-Length-Enriched cDNA Library. <i>DNA Research</i> , 2008, 15, 333-346.	1.5	98
792	Comparative Analysis of Testis Protein Evolution in Rodents. <i>Genetics</i> , 2008, 179, 2075-2089.	1.2	67
793	Metagenome analysis of an extreme microbial symbiosis reveals eurythermal adaptation and metabolic flexibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17516-17521.	3.3	111
794	Transcriptome analysis and identification of regulators for long-term plasticity in <i>Aplysia kurodai</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18602-18607.	3.3	25
795	An overview of the wcd EST clustering tool. <i>Bioinformatics</i> , 2008, 24, 1542-1546.	1.8	34
796	Molecular diversity assessment of arctic and boreal <i>Agaricus</i> taxa. <i>Mycologia</i> , 2008, 100, 577-589.	0.8	40
797	Transcriptomic and genomic evolution under constant cold in Antarctic notothenioid fish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12944-12949.	3.3	243
798	The PIWI proteins SMEDWI-2 and SMEDWI-3 are required for stem cell function and piRNA expression in planarians. <i>Rna</i> , 2008, 14, 1174-1186.	1.6	207
799	A self-adaptive cellular memetic algorithm for the DNA fragment assembly problem. , 2008, , .		14
800	Identification and characterisation of resistance gene analogues from wild Chinese Vitisspecies. <i>Journal of Horticultural Science and Biotechnology</i> , 2008, 83, 345-350.	0.9	7

#	ARTICLE	IF	CITATIONS
801	cDNA Sequences for Transcription Factors and Signaling Proteins of the Hemichordate <i>Saccoglossus kowalevskii</i> : Efficacy of the Expressed Sequence Tag (EST) Approach for Evolutionary and Developmental Studies of a New Organism. <i>Biological Bulletin</i> , 2008, 214, 284-302.	0.7	47
802	Staphylococcal toxin genes in strains isolated from cows with subclinical mastitis. <i>Pesquisa Veterinaria Brasileira</i> , 2008, 28, 617-621.	0.5	13
803	Evolution of a domain conserved in microtubule-associated proteins of eukaryotes. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2008, 1, 51.	1.6	6
804	Transcriptional Changes in the Hookworm, <i>Ancylostoma caninum</i> , during the Transition from a Free-Living to a Parasitic Larva. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e130.	1.3	72
805	Use of Genomic DNA as an Indirect Reference for Identifying Gender-Associated Transcripts in Morphologically Identical, but Chromosomally Distinct, <i>Schistosoma mansoni</i> Cercariae. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e323.	1.3	17
806	Comparative 3'UTR Analysis Allows Identification of Regulatory Clusters that Drive Eph/ephrin Expression in Cancer Cell Lines. <i>PLoS ONE</i> , 2008, 3, e2780.	1.1	25
807	New microsatellite markers developed from an enriched microsatellite common bean library. <i>Pesquisa Agropecuaria Brasileira</i> , 2008, 43, 929-936.	0.9	9
808	Identificación de algunos genes asociados al proceso de germinación de la conidia al micelio en <i>Paracoccidioides brasiliensis</i> . <i>Biomedica</i> , 2009, 29, 403.	0.3	5
809	Large-scale Discovery of Gene-Enriched SNPs. <i>Plant Genome</i> , 2009, 2, .	1.6	55
810	Molecular Marker Discovery and Genetic Map Visualisation. , 2009, , 165-189.		9
811	Expressed sequence tags from rhizomes of <i>Glycyrrhiza uralensis</i> . <i>Plant Biotechnology</i> , 2009, 26, 105-107.	0.5	23
812	SplinkBES: a splinkerette-based method for generating long end sequences from large insert DNA libraries. <i>BioTechniques</i> , 2009, 47, 681-690.	0.8	1
813	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2009, 4, e6524.	1.1	568
814	Sequencing, Mapping, and Analysis of 27,455 Maize Full-Length cDNAs. <i>PLoS Genetics</i> , 2009, 5, e1000740.	1.5	145
815	Transcript Profiling Provides Evidence of Functional Divergence and Expression Networks among Ribosomal Protein Gene Paralogs in <i>Brassica napus</i> . <i>Plant Cell</i> , 2009, 21, 2203-2219.	3.1	81
816	Quantitative Proteomic Analysis of Bean Plants Infected by a Virulent and Avirulent Obligate Rust Fungus. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 19-31.	2.5	61
817	A New Parallel Asynchronous Cellular Genetic Algorithm for de Novo Genomic Sequencing. , 2009, , .		5
818	dCAS: a desktop application for cDNA sequence annotation. <i>Bioinformatics</i> , 2009, 25, 1195-1196.	1.8	47

#	ARTICLE	IF	CITATIONS
819	Bar-Coded Pyrosequencing Reveals Shared Bacterial Community Properties along the Temperature Gradients of Two Alkaline Hot Springs in Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4565-4572.	1.4	205
820	Nbl1p: A Borealin/Dasra/CSC-1-like Protein Essential for Aurora/Ipl1 Complex Function and Integrity in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2009, 20, 1772-1784.	0.9	32
821	Identification and distribution of genetic markers in three closely related taxa of the <i>Mycoplasma mycoides</i> cluster: refining the relative position and boundaries of the <i>Mycoplasma</i> sp. bovine group 7 taxon (<i>Mycoplasma leachii</i>). <i>Microbiology (United Kingdom)</i> , 2009, 155, 3775-3787.	0.7	26
822	Dr. Zompo: an online data repository for <i>Zostera marina</i> and <i>Posidonia oceanica</i> ESTs. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap009-bap009.	1.4	38
823	Bacteroidales Diversity in Ring-Billed Gulls (<i>Larus delawarensis</i>) Residing at Lake Michigan Beaches. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1525-1533.	1.4	31
824	A consensus genetic map of cowpea [<i>Vigna unguiculata</i> (L) Walp.] and synteny based on EST-derived SNPs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18159-18164.	3.3	257
825	Update of the Diatom EST Database: a new tool for digital transcriptomics. <i>Nucleic Acids Research</i> , 2009, 37, D1001-D1005.	6.5	69
826	Evolutionary Scenarios of Notch Proteins. <i>Molecular Biology and Evolution</i> , 2009, 26, 1631-1640.	3.5	24
828	<i>Arabidopsis thaliana</i> Genes Encoding Defense Signaling and Recognition Proteins Exhibit Contrasting Evolutionary Dynamics. <i>Genetics</i> , 2009, 181, 671-684.	1.2	41
829	No Rosetta Stone for a Sense Antisense Origin of Aminoacyl tRNA Synthetase Classes. <i>Molecular Biology and Evolution</i> , 2009, 26, 445-450.	3.5	14
830	Molecular Genetic Markers: Discovery, Applications, Data Storage and Visualisation. <i>Current Bioinformatics</i> , 2009, 4, 16-27.	0.7	121
831	Highly scalable genome assembly on campus grids. , 2009, , .		9
832	Use of Massive Parallel Pyrosequencing for Near Full-Length Characterization of a Unique HIV Type 1 BF Recombinant Associated with a Fatal Primary Infection. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 937-942.	0.5	24
833	Retrotransposon expression as a defining event of genome reprogramming in fertilized and cloned bovine embryos. <i>Reproduction</i> , 2009, 138, 289-299.	1.1	49
834	Stimulation of growth and changes in the hepatic transcriptome by 17 β -estradiol in the yellow perch (<i>Perca flavescens</i>). <i>Physiological Genomics</i> , 2009, 38, 261-280.	1.0	29
835	Auxin-Responsive Genes <i>AIR12</i> Code for a New Family of Plasma Membrane b-Type Cytochromes Specific to Flowering Plants. <i>Plant Physiology</i> , 2009, 150, 606-620.	2.3	50
836	Identification of the <i>Schistosoma mansoni</i> TNF-Alpha Receptor Gene and the Effect of Human TNF-Alpha on the Parasite Gene Expression Profile. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e556.	1.3	33
837	Abundantly expressed hepatic genes and their differential expression in liver of prelaying and laying geese. <i>Poultry Science</i> , 2009, 88, 1955-1962.	1.5	11

#	ARTICLE	IF	CITATIONS
838	Population Genomics of the <i>Arabidopsis thaliana</i> Flowering Time Gene Network. <i>Molecular Biology and Evolution</i> , 2009, 26, 2475-2486.	3.5	66
839	Identification of genes upregulated by pinewood nematode inoculation in Japanese red pine. <i>Tree Physiology</i> , 2009, 29, 411-421.	1.4	32
840	k-link EST clustering: evaluating error introduced by chimeric sequences under different degrees of linkage. <i>Bioinformatics</i> , 2009, 25, 2302-2308.	1.8	4
841	Expression profiling of <i>Drosophila</i> mitochondrial genes via deep mRNA sequencing. <i>Nucleic Acids Research</i> , 2009, 37, 7509-7518.	6.5	53
842	Activity, Splice Variants, Conserved Peptide Motifs, and Phylogeny of Two New α 1,3-Fucosyltransferase Families (FUT10 and FUT11). <i>Journal of Biological Chemistry</i> , 2009, 284, 4723-4738.	1.6	58
843	<i>Halomonas ilicicola</i> sp. nov., a moderately halophilic bacterium isolated from a saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 578-582.	0.8	36
844	Gnathostome Phylogenomics Utilizing Lungfish EST Sequences. <i>Molecular Biology and Evolution</i> , 2009, 26, 463-471.	3.5	45
845	De novo sequencing of plant genomes using second-generation technologies. <i>Briefings in Bioinformatics</i> , 2009, 10, 609-618.	3.2	93
846	Development of 5006 Full-Length cDNAs in Barley: A Tool for Accessing Cereal Genomics Resources. <i>DNA Research</i> , 2009, 16, 81-89.	1.5	99
847	Analysis of the <i>Nicotiana tabacum</i> Stigma/Style Transcriptome Reveals Gene Expression Differences between Wet and Dry Stigma Species. <i>Plant Physiology</i> , 2009, 149, 1211-1230.	2.3	65
848	Expressed sequence tag analysis and cDNA array establishment of <i>Nicotiana tabacum</i> : application to salinity stress. <i>Chinese Journal of Agricultural Biotechnology</i> , 2009, 6, 81-89.	0.1	3
849	AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants. <i>Nucleic Acids Research</i> , 2009, 37, D951-D953.	6.5	83
850	Expressed sequence tags of the peanut pod nematode <i>Ditylenchus africanus</i> : The first transcriptome analysis of an Anguinid nematode. <i>Molecular and Biochemical Parasitology</i> , 2009, 167, 32-40.	0.5	50
851	Isolation and sequence analysis of a small cryptic plasmid pRK10 from a corrosion inhibitor degrading strain <i>Serratia marcescens</i> ACE2. <i>Plasmid</i> , 2009, 62, 183-190.	0.4	10
852	Phosphorylation of glycogen synthase kinase-3 β in relation to diapause processing in the silkworm, <i>Bombyx mori</i> . <i>Journal of Insect Physiology</i> , 2009, 55, 593-598.	0.9	41
853	Two epsilon glutathione S-transferase cDNAs from the common cutworm, <i>Spodoptera litura</i> : Characterization and developmental and induced expression by insecticides. <i>Journal of Insect Physiology</i> , 2009, 55, 1174-1183.	0.9	55
854	Deep proteogenomics; high throughput gene validation by multidimensional liquid chromatography and mass spectrometry of proteins from the fungal wheat pathogen <i>Stagonospora nodorum</i> . <i>BMC Bioinformatics</i> , 2009, 10, 301.	1.2	33
855	JANE: efficient mapping of prokaryotic ESTs and variable length sequence reads on related template genomes. <i>BMC Bioinformatics</i> , 2009, 10, 391.	1.2	5

#	ARTICLE	IF	CITATIONS
856	Next generation transcriptomes for next generation genomes using est2assembly. BMC Bioinformatics, 2009, 10, 447.	1.2	54
857	EasyCluster: a fast and efficient gene-oriented clustering tool for large-scale transcriptome data. BMC Bioinformatics, 2009, 10, S10.	1.2	15
858	On the phylogenetic position of Myzostomida: Can 77 genes get it wrong?. BMC Evolutionary Biology, 2009, 9, 150.	3.2	52
859	Whole genome duplications and expansion of the vertebrate GATA transcription factor gene family. BMC Evolutionary Biology, 2009, 9, 207.	3.2	45
860	Emergence, development and diversification of the TGF- β signalling pathway within the animal kingdom. BMC Evolutionary Biology, 2009, 9, 28.	3.2	137
861	Evolution of C2H2-zinc finger genes revisited. BMC Evolutionary Biology, 2009, 9, 51.	3.2	28
862	Transcriptomic basis for an antiserum against <i>Micrurus corallinus</i> (coral snake) venom. BMC Genomics, 2009, 10, 112.	1.2	51
863	Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. BMC Genomics, 2009, 10, 117.	1.2	23
864	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. BMC Genomics, 2009, 10, 163.	1.2	205
865	ESTPiper – a web-based analysis pipeline for expressed sequence tags. BMC Genomics, 2009, 10, 174.	1.2	17
866	Genic regions of a large salamander genome contain long introns and novel genes. BMC Genomics, 2009, 10, 19.	1.2	81
867	Identifying genes related to choriogenesis in insect panoistic ovaries by Suppression Subtractive Hybridization. BMC Genomics, 2009, 10, 206.	1.2	47
868	Sequencing and de novo analysis of a coral larval transcriptome using 454 GSFlx. BMC Genomics, 2009, 10, 219.	1.2	405
869	Analysis of salivary transcripts and antigens of the sand fly <i>Phlebotomus arabicus</i> . BMC Genomics, 2009, 10, 282.	1.2	79
870	Gene expression profiling via LongSAGE in a non-model plant species: a case study in seeds of <i>Brassica napus</i> . BMC Genomics, 2009, 10, 295.	1.2	19
871	Generation and analysis of a 29,745 unique Expressed Sequence Tags from the Pacific oyster (<i>Crassostrea gigas</i>) assembled into a publicly accessible database: the GigasDatabase. BMC Genomics, 2009, 10, 341.	1.2	127
872	Characterization of the <i>Zoarces viviparus</i> liver transcriptome using massively parallel pyrosequencing. BMC Genomics, 2009, 10, 345.	1.2	65
873	Grapevine cell early activation of specific responses to DIMEB, a resveratrol elicitor. BMC Genomics, 2009, 10, 363.	1.2	54

#	ARTICLE	IF	CITATIONS
874	Complexity of the MSG gene family of <i>Pneumocystis carinii</i> . BMC Genomics, 2009, 10, 367.	1.2	39
875	Generation, annotation, and analysis of ESTs from midgut tissue of adult female <i>Anopheles stephensi</i> mosquitoes. BMC Genomics, 2009, 10, 386.	1.2	8
876	Mining for single nucleotide polymorphisms in pig genome sequence data. BMC Genomics, 2009, 10, 4.	1.2	32
877	PAVE: Program for assembling and viewing ESTs. BMC Genomics, 2009, 10, 400.	1.2	24
878	Generation and analysis of expressed sequence tags from six developing xylem libraries in <i>Pinus radiata</i> D. Don. BMC Genomics, 2009, 10, 41.	1.2	71
879	Comparative analyses of genotype dependent expressed sequence tags and stress-responsive transcriptome of chickpea wilt illustrate predicted and unexpected genes and novel regulators of plant immunity. BMC Genomics, 2009, 10, 415.	1.2	57
880	Comparative EST transcript profiling of peach fruits under different post-harvest conditions reveals candidate genes associated with peach fruit quality. BMC Genomics, 2009, 10, 423.	1.2	63
881	Transcriptome analysis of the central nervous system of the mollusc <i>Lymnaea stagnalis</i> . BMC Genomics, 2009, 10, 451.	1.2	70
882	Global characterization of <i>Artemisia annua</i> glandular trichome transcriptome using 454 pyrosequencing. BMC Genomics, 2009, 10, 465.	1.2	197
883	A new procedure for determining the genetic basis of a physiological process in a non-model species, illustrated by cold induced angiogenesis in the carp. BMC Genomics, 2009, 10, 490.	1.2	8
884	Fourmidable: a database for ant genomics. BMC Genomics, 2009, 10, 5.	1.2	38
885	EST and microarray analysis of horn development in <i>Onthophagus</i> beetles. BMC Genomics, 2009, 10, 504.	1.2	38
886	A comprehensive resource of drought- and salinity- responsive ESTs for gene discovery and marker development in chickpea (<i>Cicer arietinum</i> L.). BMC Genomics, 2009, 10, 523.	1.2	199
887	Development and bin mapping of a Rosaceae Conserved Ortholog Set (COS) of markers. BMC Genomics, 2009, 10, 562.	1.2	61
888	Transcriptomic response of the mycoparasitic fungus <i>Trichoderma atroviride</i> to the presence of a fungal prey. BMC Genomics, 2009, 10, 567.	1.2	141
889	The salivary gland transcriptome of the neotropical malaria vector <i>Anopheles darlingi</i> reveals accelerated evolution of genes relevant to hematophagy. BMC Genomics, 2009, 10, 57.	1.2	71
890	Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics, 2009, 10, 582.	1.2	570
891	Large-scale identification of odorant-binding proteins and chemosensory proteins from expressed sequence tags in insects. BMC Genomics, 2009, 10, 632.	1.2	213

#	ARTICLE	IF	CITATIONS
892	Desiccation survival in an Antarctic nematode: molecular analysis using expressed sequenced tags. BMC Genomics, 2009, 10, 69.	1.2	76
893	Environmental stresses inhibit splicing in the aquatic fungus <i>Blastocladiella emersonii</i> . BMC Microbiology, 2009, 9, 231.	1.3	13
894	Targeted isolation, sequence assembly and characterization of two white spruce (<i>Picea glauca</i>) BAC clones for terpenoid synthase and cytochrome P450 genes involved in conifer defence reveal insights into a conifer genome. BMC Plant Biology, 2009, 9, 106.	1.6	55
895	Computational annotation of genes differentially expressed along olive fruit development. BMC Plant Biology, 2009, 9, 128.	1.6	88
896	Construction of 12 EST libraries and characterization of a 12,226 EST dataset for chicory (<i>Cichorium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Biology, 2009, 9, 14.	1.6	12
897	SolEST database: a "one-stop shop" approach to the study of Solanaceae transcriptomes. BMC Plant Biology, 2009, 9, 142.	1.6	17
898	A new genomic resource dedicated to wood formation in <i>Eucalyptus</i> . BMC Plant Biology, 2009, 9, 36.	1.6	54
899	GarlicESTdb: an online database and mining tool for garlic EST sequences. BMC Plant Biology, 2009, 9, 61.	1.6	25
900	Ontology-oriented retrieval of putative microRNAs in <i>Vitis vinifera</i> via GrapeMiRNA: a web database of de novo predicted grape microRNAs. BMC Plant Biology, 2009, 9, 82.	1.6	8
901	Optimization and comparison of different methods for RNA isolation for cDNA library construction from the reindeer lichen <i>Cladonia rangiferina</i> . BMC Research Notes, 2009, 2, 204.	0.6	14
902	Intragenic tandem repeats in <i>Daphnia magna</i> : structure, function and distribution. BMC Research Notes, 2009, 2, 206.	0.6	8
903	Characterization of an Atlantic cod (<i>Gadus morhua</i>) embryonic stem cell cDNA library. BMC Research Notes, 2009, 2, 74.	0.6	4
904	Perl module and PISE wrappers for the integrated analysis of sequence data and SNP features. BMC Research Notes, 2009, 2, 92.	0.6	7
905	Development of a live attenuated antigenic marker classical swine fever vaccine. Virology, 2009, 384, 106-113.	1.1	35
906	Alteration of the N-linked glycosylation condition in E1 glycoprotein of Classical Swine Fever Virus strain Brescia alters virulence in swine. Virology, 2009, 386, 210-216.	1.1	28
907	Advanced in silico analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance – Fundamental insights toward biotechnological outcomes. Biotechnology Advances, 2009, 27, 439-448.	6.0	29
908	MLST analysis reveals a highly conserved core genome among poultry isolates of <i>Clostridium septicum</i> . Anaerobe, 2009, 15, 99-106.	1.0	26
909	Identification, characterization and expression of sex-related genes in testes of the giant tiger shrimp <i>Penaeus monodon</i> . Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2009, 152, 66-76.	0.8	82

#	ARTICLE	IF	CITATIONS
910	Cloning, characterization and expression of two glutathione <i>S</i> -transferase cDNAs in the spruce budworm, <i>Choristoneura fumiferana</i> . Archives of Insect Biochemistry and Physiology, 2009, 70, 44-56.	0.6	3
911	Characterization of a deep-coverage carrot (<i>Daucus carota</i> L.) BAC library and initial analysis of BAC-end sequences. Molecular Genetics and Genomics, 2009, 281, 273-288.	1.0	41
912	EST sequencing of blood-fed and Leishmania-infected midgut of <i>Lutzomyia longipalpis</i> , the principal visceral leishmaniasis vector in the Americas. Molecular Genetics and Genomics, 2009, 282, 307-317.	1.0	27
913	Analysis of Genes Isolated from Plated Hemocytes of the Pacific Oyster, <i>Crassostrea gigas</i> . Marine Biotechnology, 2009, 11, 24-44.	1.1	52
914	Microbial analysis of backflowed injection water from a nitrate-treated North Sea oil reservoir. Journal of Industrial Microbiology and Biotechnology, 2009, 36, 439-450.	1.4	53
915	Full-Length Enriched cDNA Library Construction from Tissues Related to Energy Metabolism in Pigs. Molecules and Cells, 2009, 28, 529-536.	1.0	7
916	Isolation and characterization of floral transcripts from mangosteen (<i>Garcinia mangostana</i> L.). Trees - Structure and Function, 2009, 23, 899-910.	0.9	0
917	Hydrocarbon degradation by <i>Dietzia</i> sp. A14101 isolated from an oil reservoir model column. Antonie Van Leeuwenhoek, 2009, 96, 459-469.	0.7	45
918	Cloning and sequencing of the breakpoint regions of inversion 5g fixed in <i>Drosophila buzzatii</i> . Chromosoma, 2009, 118, 349-360.	1.0	12
919	Integrative placement and orientation of non-redundant SSR loci in cotton linkage groups by deficiency analysis. Molecular Breeding, 2009, 23, 693-707.	1.0	18
920	In silico cloning and characterization of p8 homolog cDNA from common urchin (<i>Paracentrotus</i>) Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 3	1.0	7
921	dbEST-derived SSR markers in sea urchin (<i>Hemicentrotus pulcherrimus</i>). Conservation Genetics, 2009, 10, 729-731.	0.8	9
922	Eight SSR loci from Oyster <i>Crassostrea gigas</i> EST database and cross-species amplification in <i>C. Aplicatula</i> . Conservation Genetics, 2009, 10, 1013-1015.	0.8	6
923	Eleven polymorphic simple sequence repeat markers from expressed sequence tags of Pacific oyster <i>Crassostrea gigas</i> EST database. Conservation Genetics, 2009, 10, 1773-1775.	0.8	6
924	Development of EST-SSRs in scallop (<i>PatinopectenÂyessoensis</i>) from sequence database. Conservation Genetics, 2009, 10, 1129-1131.	0.8	12
925	Development of polymorphic EST-derived SSR markers for the shrimp, <i>Fenneropenaeus chinensis</i> . Conservation Genetics, 2009, 10, 1455-1457.	0.8	5
926	A panel of polymorphic EST-derived microsatellite loci for the small yellow croaker (<i>Larimichthys</i>) Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 3	0.8	9
927	Highly Conserved UFD1 Proteins Among Eukaryotes Exhibit Considerable C-Terminus Diversity in Different Taxa. Plant Molecular Biology Reporter, 2009, 27, 439-447.	1.0	3

#	ARTICLE	IF	CITATIONS
928	Development and functional annotation of an 11,303-EST collection from Eucalyptus for studies of cold tolerance. <i>Tree Genetics and Genomes</i> , 2009, 5, 317-327.	0.6	29
929	Repertoire of leaf expressed sequence tags (ESTs) and partial characterization of stress-related and membrane transporter genes from mulberry (<i>Morus indica</i> L.). <i>Tree Genetics and Genomes</i> , 2009, 5, 359-374.	0.6	20
930	Comparative analysis of expressed sequence tags from tissues in ripening stages of peach (<i>Prunus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	27
931	Transcription analysis of apple fruit development using cDNA microarrays. <i>Tree Genetics and Genomes</i> , 2009, 5, 685-698.	0.6	31
932	Expressed sequence tag analysis of phyllosomas and hemocytes of Japanese spiny lobster <i>Panulirus japonicus</i> . <i>Fisheries Science</i> , 2009, 75, 195-206.	0.7	5
933	Computational Biology Methods and Their Application to the Comparative Genomics of Endocellular Symbiotic Bacteria of Insects. <i>Biological Procedures Online</i> , 2009, 11, 52-78.	1.4	6
934	Comparative mapping of DNA sequences in rye (<i>Secale cereale</i> L.) in relation to the rice genome. <i>Theoretical and Applied Genetics</i> , 2009, 118, 371-384.	1.8	56
935	The genomic architecture of disease resistance in lettuce. <i>Theoretical and Applied Genetics</i> , 2009, 118, 565-580.	1.8	66
936	Development of chickpea EST-SSR markers and analysis of allelic variation across related species. <i>Theoretical and Applied Genetics</i> , 2009, 118, 591-608.	1.8	153
937	The 1-deoxy-d-xylulose 5-phosphate synthase gene co-localizes with a major QTL affecting monoterpene content in grapevine. <i>Theoretical and Applied Genetics</i> , 2009, 118, 653-669.	1.8	144
938	Exploration and mapping of microsatellite markers from subtracted drought stress ESTs in <i>Sorghum bicolor</i> (L.) Moench. <i>Theoretical and Applied Genetics</i> , 2009, 118, 703-717.	1.8	47
939	Development and genetic mapping of microsatellite markers from genome survey sequences in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2009, 118, 1121-1131.	1.8	157
940	Development and analysis of EST-SSRs for flax (<i>Linum usitatissimum</i> L.). <i>Theoretical and Applied Genetics</i> , 2009, 119, 53-63.	1.8	152
941	Exploiting rice's sorghum synteny for targeted development of EST-SSRs to enrich the sorghum genetic linkage map. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1193-1204.	1.8	73
942	The promoter of the <i>Arabidopsis thaliana</i> BAN gene is active in proanthocyanidin-accumulating cells of the <i>Brassica napus</i> seed coat. <i>Plant Cell Reports</i> , 2009, 28, 601-617.	2.8	45
943	The Pig Genome Database (PiGenome): an integrated database for pig genome research. <i>Mammalian Genome</i> , 2009, 20, 60-66.	1.0	14
944	ANEXdb: an integrated animal ANnotation and microarray EXpression database. <i>Mammalian Genome</i> , 2009, 20, 768-777.	1.0	28
945	The first genome-level transcriptome of the wood-degrading fungus <i>Phanerochaete chrysosporium</i> grown on red oak. <i>Current Genetics</i> , 2009, 55, 273-286.	0.8	53

#	ARTICLE	IF	CITATIONS
946	The secreted salivary proteome of the pea aphid <i>Acyrtosiphon pisum</i> characterised by mass spectrometry. <i>Proteomics</i> , 2009, 9, 2457-2467.	1.3	224
947	Construction of an adult barnacle (<i>Balanus amphitrite</i>) cDNA library and selection of reference genes for quantitative RT-PCR studies. <i>BMC Molecular Biology</i> , 2009, 10, 62.	3.0	30
948	Microarray and cDNA sequence analysis of transcription during nerve-dependent limb regeneration. <i>BMC Biology</i> , 2009, 7, 1.	1.7	203
949	Parallel metatranscriptome analyses of host and symbiont gene expression in the gut of the termite <i>Reticulitermes flavipes</i> . <i>Biotechnology for Biofuels</i> , 2009, 2, 25.	6.2	198
950	Haplotype divergence in <i>Beta vulgaris</i> and microsynteny with sequenced plant genomes. <i>Plant Journal</i> , 2009, 57, 14-26.	2.8	19
951	The <i>Aedes aegypti</i> larval transcriptome: a comparative perspective with emphasis on trypsins and the domain structure of peritrophins. <i>Insect Molecular Biology</i> , 2009, 18, 33-44.	1.0	65
952	Genes related to immunity, as expressed in the alfalfa leafcutting bee, <i>Megachile rotundata</i> , during pathogen challenge. <i>Insect Molecular Biology</i> , 2009, 18, 785-794.	1.0	9
953	PVY ^{NTN} elicits a diverse gene expression response in different potato genotypes in the first 12Ah after inoculation. <i>Molecular Plant Pathology</i> , 2009, 10, 263-275.	2.0	97
954	Candidate effector gene identification in the ascomycete fungal phytopathogen <i>Venturia inaequalis</i> by expressed sequence tag analysis. <i>Molecular Plant Pathology</i> , 2009, 10, 431-448.	2.0	33
955	Identification and functional characterization of effectors in expressed sequence tags from various life cycle stages of the potato cyst nematode <i>Globodera pallida</i> . <i>Molecular Plant Pathology</i> , 2009, 10, 815-828.	2.0	96
956	Reliability of mCP method for identification of <i>Clostridium perfringens</i> from faecal polluted aquatic environments. <i>Journal of Applied Microbiology</i> , 2009, 108, 1994-2002.	1.4	11
957	Widespread transcriptional changes pre-empt the critical pelagic-benthic transition in the vetigastropod <i>Haliotis asinina</i> . <i>Molecular Ecology</i> , 2009, 18, 1006-1025.	2.0	55
958	Molecular phylogenetic biodiversity assessment of arctic and boreal ectomycorrhizal <i>Lactarius</i> (Russulales; Basidiomycota) in Alaska, based on soil and sporocarp DNA. <i>Molecular Ecology</i> , 2009, 18, 2213-2227.	2.0	59
959	A high-density transcript linkage map of barley derived from a single population. <i>Heredity</i> , 2009, 103, 110-117.	1.2	119
960	The RAB Family GTPase Rab1A from <i>Plasmodium falciparum</i> Defines a Unique Paralog Shared by Chromalveolates and Rhizaria. <i>Journal of Eukaryotic Microbiology</i> , 2009, 56, 348-356.	0.8	25
961	Targeted single nucleotide polymorphism (SNP) discovery in a highly polyploid plant species using 454 sequencing. <i>Plant Biotechnology Journal</i> , 2009, 7, 347-354.	4.1	134
962	Single nucleotide polymorphism discovery in barley using autoSNPdb. <i>Plant Biotechnology Journal</i> , 2009, 7, 326-333.	4.1	56
963	Disclosing arbuscular mycorrhizal fungal biodiversity in soil through a land-use gradient using a pyrosequencing approach. <i>Environmental Microbiology</i> , 2010, 12, 2165-2179.	1.8	313

#	ARTICLE	IF	CITATIONS
964	From Conservation Genetics to Conservation Genomics. <i>Annals of the New York Academy of Sciences</i> , 2009, 1162, 357-368.	1.8	102
965	Transcriptome analysis of <i>Medicago truncatula</i> leaf senescence: similarities and differences in metabolic and transcriptional regulations as compared with <i>Arabidopsis</i> , nodule senescence and nitric oxide signalling. <i>New Phytologist</i> , 2009, 181, 563-575.	3.5	52
966	Massively parallel 454 sequencing indicates hyperdiverse fungal communities in temperate <i>Quercus macrocarpa</i> phyllosphere. <i>New Phytologist</i> , 2009, 184, 438-448.	3.5	414
967	Poplar defense against insects: genome analysis, full-length cDNA cloning, and transcriptome and protein analysis of the poplar Kunitz-type protease inhibitor family. <i>New Phytologist</i> , 2009, 184, 865-884.	3.5	49
968	Bioremediation of metal contamination in the Plankenburg River, Western Cape, South Africa. <i>International Biodeterioration and Biodegradation</i> , 2009, 63, 559-568.	1.9	22
969	The Sequence Analysis and Management System "SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. <i>Journal of Biotechnology</i> , 2009, 140, 3-12.	1.9	37
970	Bothrops insularis venomomics: A proteomic analysis supported by transcriptomic-generated sequence data. <i>Journal of Proteomics</i> , 2009, 72, 241-255.	1.2	86
971	Sequence assembly. <i>Computational Biology and Chemistry</i> , 2009, 33, 121-136.	1.1	39
972	Whole genome assembly from 454 sequencing output via modified DNA graph concept. <i>Computational Biology and Chemistry</i> , 2009, 33, 224-230.	1.1	18
973	TriFLDB: A Database of Clustered Full-Length Coding Sequences from Triticeae with Applications to Comparative Grass Genomics. <i>Plant Physiology</i> , 2009, 150, 1135-1146.	2.3	86
974	Development and Characterization of Expressed Sequence Tag-Derived Microsatellite Markers for the Wheat Stem Rust Fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> . <i>Phytopathology</i> , 2009, 99, 282-289.	1.1	45
975	Fractured genes: a novel genomic arrangement involving new split inteins and a new homing endonuclease family. <i>Nucleic Acids Research</i> , 2009, 37, 2560-2573.	6.5	86
976	GENE EXPRESSION PROFILING IN ATLANTIC COD (<i>GADUS MORHUA</i> L.) FROM TWO CONTAMINATED SITES USING A CUSTOM-MADE cDNA MICROARRAY. <i>Environmental Toxicology and Chemistry</i> , 2009, 28, 1711.	2.2	31
977	Canine Distemper Virus in a Crab-eating Fox (<i>Cerdocyon thous</i>) in Brazil: Case Report and Phylogenetic Analyses. <i>Journal of Wildlife Diseases</i> , 2009, 45, 527-530.	0.3	28
978	Comparative Analysis of <i>Trypanosoma rangeli</i> Histone H2A Gene Intergenic Region with Distinct Intraspecific Lineage Markers. <i>Vector-Borne and Zoonotic Diseases</i> , 2009, 9, 449-456.	0.6	8
979	On the Morphology and Mitochondrial DNA Barcoding of the Flesh Fly <i>Sarcophaga</i> (<i>Liopygia</i>) <i>argyrostoma</i> (Robineau-Desvoidy, 1830) (Diptera: Sarcophagidae) " An important Species in Forensic Entomology. <i>Annales Zoologici</i> , 2009, 59, 465-493.	0.1	30
980	Insight into the Sialome of the Black Fly, <i>Simulium vittatum</i> . <i>Journal of Proteome Research</i> , 2009, 8, 1474-1488.	1.8	49
981	Transcriptome analysis of a spontaneous mutant in sweet orange [<i>Citrus sinensis</i> (L.) Osbeck] during fruit development. <i>Journal of Experimental Botany</i> , 2009, 60, 801-813.	2.4	68

#	ARTICLE	IF	CITATIONS
982	Cloud technologies for bioinformatics applications. , 2009, , .		52
983	Does <i>Botrytis cinerea</i> Ignore H ₂ O ₂ -Induced Oxidative Stress During Infection? Characterization of <i>Botrytis</i> Activator Protein 1. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 987-998.	1.4	148
984	Ice-binding proteins from enoki and shiitake mushrooms. <i>Cryobiology</i> , 2009, 58, 151-156.	0.3	40
985	NOD-like subfamily of the nucleotide-binding domain and leucine-rich repeat containing family receptors and their expression in channel catfish. <i>Developmental and Comparative Immunology</i> , 2009, 33, 991-999.	1.0	121
986	Molecular cloning and nucleotide sequence analysis of genes from a cDNA library of the scorpion <i>Tityus discrepans</i> . <i>Biochimie</i> , 2009, 91, 1010-1019.	1.3	58
987	Identification of the cellulose synthase genes from the Oomycete <i>Saprolegnia monoica</i> and effect of cellulose synthesis inhibitors on gene expression and enzyme activity. <i>Fungal Genetics and Biology</i> , 2009, 46, 759-767.	0.9	27
988	Evolutionary analysis of orthologous cDNA sequences from cultured and symbiotic dinoflagellate symbionts of reef-building corals (Dinophyceae: Symbiodinium). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 67-74.	0.4	34
989	Gene discovery from an ovary cDNA library of oriental river prawn <i>Macrobrachium nipponense</i> by ESTs annotation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 111-120.	0.4	27
990	Sampling the skin transcriptome of the North Atlantic right whale. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 154-158.	0.4	4
991	Bioinformatic analysis of expressed sequence tags from grass shrimp <i>Palaemonetes pugio</i> exposed to environmental stressors. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 187-195.	0.4	11
992	Characterization and expression of NADPH oxidase in LPS-, poly(I:C)- and zymosan-stimulated trout (<i>Oncorhynchus mykiss</i> W.) macrophages. <i>Fish and Shellfish Immunology</i> , 2009, 26, 651-661.	1.6	22
993	Identification of immune related genes in Atlantic halibut (<i>Hippoglossus hippoglossus</i> L.) following in vivo antigenic and in vitro mitogenic stimulation. <i>Fish and Shellfish Immunology</i> , 2009, 27, 729-738.	1.6	17
994	Identification of genes responsive to salt stress on <i>Tamarix hispida</i> roots. <i>Gene</i> , 2009, 433, 65-71.	1.0	41
995	The RIL family of small GTPases is an ancient eukaryotic invention probably functionally associated with the flagellar apparatus. <i>Gene</i> , 2009, 442, 63-72.	1.0	29
996	Varied truncation and clustering characterize some short repeats identified in micronucleus-specific DNA of <i>Tetrahymena thermophila</i> . <i>Gene</i> , 2009, 448, 174-179.	1.0	0
997	Cloning and characterization of cDNA sequences encoding for new venom peptides of the Brazilian scorpion <i>Opisthacanthus cayaporum</i> . <i>Toxicon</i> , 2009, 54, 252-261.	0.8	78
998	Identification of differentially expressed genes during flower opening by suppression subtractive hybridization and cDNA microarray analysis in <i>Eustoma grandiflorum</i> . <i>Scientia Horticulturae</i> , 2009, 122, 129-133.	1.7	8
999	Contributions of functional genomics and proteomics to the study of immune responses in the Pacific white leg shrimp <i>Litopenaeus vannamei</i> . <i>Veterinary Immunology and Immunopathology</i> , 2009, 128, 110-118.	0.5	46

#	ARTICLE	IF	CITATIONS
1000	A comparative analysis of serpin genes in the silkworm genome. <i>Genomics</i> , 2009, 93, 367-375.	1.3	100
1001	Identification of genes associated with cold acclimation in perennial ryegrass. <i>Journal of Plant Physiology</i> , 2009, 166, 1436-1445.	1.6	46
1002	Bioinformatic analysis of abundant, gender-enriched transcripts of adult <i>Ascaris suum</i> (Nematoda) using a semi-automated workflow platform. <i>Molecular and Cellular Probes</i> , 2009, 23, 205-217.	0.9	16
1003	Genomic sequence encoding diversity segments of the pig TCR β chain gene demonstrates productivity of highly diversified repertoire. <i>Molecular Immunology</i> , 2009, 46, 1212-1221.	1.0	25
1004	Identification and sequencing of remnant messenger RNAs found in domestic swine (<i>Sus scrofa</i>) fresh ejaculated spermatozoa. <i>Animal Reproduction Science</i> , 2009, 113, 143-155.	0.5	71
1005	Transcriptome-Based Identification of Candidate Membrane Proteins. <i>Methods in Molecular Biology</i> , 2009, 528, 37-56.	0.4	0
1006	Mining SNPs from DNA Sequence Data; Computational Approaches to SNP Discovery and Analysis. <i>Methods in Molecular Biology</i> , 2009, 578, 73-91.	0.4	16
1007	Sequence Comparison Tools. , 2009, , 13-37.		4
1008	Generation and analysis of transcriptomic resources for a model system on the rise: the sea anemone <i>Aiptasia pallida</i> and its dinoflagellate endosymbiont. <i>BMC Genomics</i> , 2009, 10, 258.	1.2	169
1009	Transcriptome analysis of <i>Taenia solium</i> cysticerci using Open Reading Frame ESTs (ORESTES). <i>Parasites and Vectors</i> , 2009, 2, 35.	1.0	24
1010	Abundance and distribution of <i>Corallorhiza odontorhiza</i> reflect variations in climate and ectomycorrhizae. <i>Ecological Monographs</i> , 2009, 79, 619-635.	2.4	72
1011	New Technologies for Ultra-High Throughput Genotyping in Plants. <i>Methods in Molecular Biology</i> , 2009, 513, 19-39.	0.4	107
1013	Mining for SNPs and SSRs Using SNPServer, dbSNP and SSR Taxonomy Tree. <i>Methods in Molecular Biology</i> , 2009, 537, 303-321.	0.4	20
1014	Transcriptome analysis of functional differentiation between haploid and diploid cells of <i>Emiliania huxleyi</i> , a globally significant photosynthetic calcifying cell. <i>Genome Biology</i> , 2009, 10, R114.	13.9	105
1016	Genome assembly reborn: recent computational challenges. <i>Briefings in Bioinformatics</i> , 2009, 10, 354-366.	3.2	291
1017	DryadLINQ for Scientific Analyses. , 2009, , .		30
1018	Transcriptome Analysis and Identification of Genes Related to Immune Function in Skin of the Chinese Brown Frog. <i>Zoological Science</i> , 2009, 26, 80.	0.3	25
1019	PMMR: A Method for Masking Repeats in DNA Fragment Assembly. , 2009, , .		2

#	ARTICLE	IF	CITATIONS
1020	Profiling the T-cell receptor beta-chain repertoire by massively parallel sequencing. <i>Genome Research</i> , 2009, 19, 1817-1824.	2.4	361
1021	Comparative Assessment of DNA Assemblers for Assembling Expressed Sequence Tags. , 2009, , .		1
1022	Opportunistic heterotrophy in gametophytes of the homosporous fern <i>Ceratopteris richardii</i> . <i>Botany</i> , 2009, 87, 799-806.	0.5	10
1023	Molecular characterization of complement factor I reveals constitutive expression in channel catfish. <i>Fish and Shellfish Immunology</i> , 2009, 27, 529-534.	1.6	17
1024	Gene expression analysis of the biocontrol fungus <i>Trichoderma harzianum</i> in the presence of tomato plants, chitin, or glucose using a high-density oligonucleotide microarray. <i>BMC Microbiology</i> , 2009, 9, 217.	1.3	58
1025	Transcriptome profiling of <i>Streptococcus uberis</i> -induced mastitis reveals fundamental differences between immune gene expression in the mammary gland and in a primary cell culture model. <i>Journal of Dairy Science</i> , 2009, 92, 117-129.	1.4	114
1026	Transcriptome analysis of the Amazonian viper <i>Bothrops atrox</i> venom gland using expressed sequence tags (ESTs). <i>Toxicon</i> , 2009, 53, 427-436.	0.8	53
1027	Functional Genomics in Peach. , 2009, , 259-275.		3
1028	Granules: A lightweight, streaming runtime for cloud computing with support, for Map-Reduce. , 2009, , .		43
1029	Isolation, Characterization, and Mapping of Genomic Microsatellite Markers in Sea-Island Cotton (<i>Gossypium barbadense</i>). <i>Acta Agronomica Sinica</i> , 2009, 35, 1013-1020.	0.3	2
1030	Evaluation of mitochondrial genes as DNA barcode for Basidiomycota. <i>Molecular Ecology Resources</i> , 2009, 9, 99-113.	2.2	91
1031	Characterisation of monotreme caseins reveals lineage-specific expansion of an ancestral casein locus in mammals. <i>Reproduction, Fertility and Development</i> , 2009, 21, 1015.	0.1	37
1032	Development of Drought-tolerant Canola (<i>Brassica napus</i> L.) through Genetic Modulation of ABA-mediated Stomatal Responses. <i>Crop Science</i> , 2009, 49, 1539-1554.	0.8	67
1033	Identification of phytodetritus-degrading microbial communities in sublittoral Gulf of Mexico sands. <i>Limnology and Oceanography</i> , 2009, 54, 1073-1083.	1.6	50
1034	A Key Enzyme of the Leloir Pathway Is Involved in Pathogenicity of <i>Leptosphaeria maculans</i> Toward Oilseed Rape. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 725-736.	1.4	12
1035	Computational Finishing of Large Sequence Contigs Reveals Interspersed Nested Repeats and Gene Islands in the r1-Associated Region of Maize. <i>Plant Physiology</i> , 2009, 151, 483-495.	2.3	9
1036	SNPs and entropy based hierarchical clustering method for genetic phylogeny analysis. , 2010, , .		0
1037	Quantitative Gene Expression Profiles in Real Time From Expressed Sequence Tag Databases. <i>Gene Expression</i> , 2010, 14, 321-336.	0.5	4

#	ARTICLE	IF	CITATIONS
1038	The <i>RON1/FRY1/SAL1</i> Gene Is Required for Leaf Morphogenesis and Venation Patterning in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2010, 152, 1357-1372.	2.3	91
1040	A New <i>Potyvirus</i> sp. Infects <i>Verbena</i> Exhibiting Leaf Mottling Symptoms. <i>Plant Disease</i> , 2010, 94, 1132-1136.	0.7	7
1041	Identification of novel Mlo family members in wheat and their genetic characterization. <i>Genes and Genetic Systems</i> , 2010, 85, 167-175.	0.2	40
1042	High-Performance Parallel Computing with Cloud and Cloud Technologies. , 2010, , 275-308.		18
1043	Gene ontology study of methyl jasmonate-treated and non-treated hairy roots of <i>Panax ginseng</i> to identify genes involved in secondary metabolic pathway. <i>Russian Journal of Genetics</i> , 2010, 46, 828-835.	0.2	9
1044	SSR data mined from expressed sequence tags of phytoparasitic nematodes. <i>Helminthologia</i> , 2010, 47, 8-19.	0.3	2
1045	Parallel Evolution of Nacre Building Gene Sets in Molluscs. <i>Molecular Biology and Evolution</i> , 2010, 27, 591-608.	3.5	239
1046	Gene expression profiling of the endophytic fungus <i>Neotyphodium lolii</i> in association with its host plant perennial ryegrass. <i>Australasian Plant Pathology</i> , 2010, 39, 467.	0.5	16
1047	De novo assembly of short sequence reads. <i>Briefings in Bioinformatics</i> , 2010, 11, 457-472.	3.2	167
1048	Red Microalgae: From Basic Know-How to Biotechnology. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , 205-225.	0.3	9
1049	Analysis of transposons and repeat composition of the sunflower (<i>Helianthus annuus</i> L.) genome. <i>Theoretical and Applied Genetics</i> , 2010, 120, 491-508.	1.8	47
1050	Three highly similar formate dehydrogenase genes located in the vicinity of the B4 resistance gene cluster are differentially expressed under biotic and abiotic stresses in <i>Phaseolus vulgaris</i> . <i>Theoretical and Applied Genetics</i> , 2010, 121, 87-103.	1.8	44
1051	Fine-mapping of the leaf rust Lr34 locus in <i>Triticum aestivum</i> (L.) and characterization of large germplasm collections support the ABC transporter as essential for gene function. <i>Theoretical and Applied Genetics</i> , 2010, 121, 373-384.	1.8	58
1052	High-throughput identification of genetic markers using representational oligonucleotide microarray analysis. <i>Theoretical and Applied Genetics</i> , 2010, 121, 549-565.	1.8	6
1053	Accelerated Evolutionary Rate of Housekeeping Genes in Tunicates. <i>Journal of Molecular Evolution</i> , 2010, 71, 153-167.	0.8	40
1054	Comparative Genomics of Marine Mussels (<i>Mytilus</i> spp.) Gender Associated mtDNA: Rapidly Evolving <i>atp8</i> . <i>Journal of Molecular Evolution</i> , 2010, 71, 385-400.	0.8	64
1055	EST analysis and annotation of transcripts derived from a trichome-specific cDNA library from <i>Salvia fruticosa</i> . <i>Plant Cell Reports</i> , 2010, 29, 523-534.	2.8	33
1056	Temperature and nutrient induced responses of Lake Fryxell sulfate-reducing prokaryotes and description of <i>Desulfovibrio lacusfryxellense</i> , sp. nov., a pervasive, cold-active, sulfate-reducing bacterium from Lake Fryxell, Antarctica. <i>Extremophiles</i> , 2010, 14, 357-366.	0.9	23

#	ARTICLE	IF	CITATIONS
1057	Comparative Analysis of Expressed Sequence Tags from the White-Rot Fungi (Phanerochaete) Tj ETQq0 0 0 rgBT /Overlock 1Q Tf 50 742	1.0	1
1058	Molecular characterization of the Sasanda LTR copia retrotransposon family uncovers their recent amplification in <i>Triticum aestivum</i> (L.) genome. <i>Molecular Genetics and Genomics</i> , 2010, 283, 255-271.	1.0	6
1059	Characterization of expressed sequence tags (ESTs) of pigeonpea (<i>Cajanus cajan</i> L.) and functional validation of selected genes for abiotic stress tolerance in <i>Arabidopsis thaliana</i> . <i>Molecular Genetics and Genomics</i> , 2010, 283, 273-287.	1.0	43
1060	Identification, phylogeny, and transcript profiling of ERF family genes during development and abiotic stress treatments in tomato. <i>Molecular Genetics and Genomics</i> , 2010, 284, 455-475.	1.0	189
1061	Microarray-Based Identification of Gonad Transcripts Differentially Expressed Between Lines of Pacific Oyster Selected to Be Resistant or Susceptible to Summer Mortality. <i>Marine Biotechnology</i> , 2010, 12, 326-339.	1.1	53
1062	The water-deficit stress- and red-rot-related genes in sugarcane. <i>Functional and Integrative Genomics</i> , 2010, 10, 207-214.	1.4	53
1063	Isolation and identification of Rhizoctonia-like fungi from roots of three orchid genera, <i>Paphiopedilum</i> , <i>Dendrobium</i> , and <i>Cymbidium</i> , collected in Chiang Rai and Chiang Mai provinces of Thailand. <i>Mycorrhiza</i> , 2010, 20, 459-471.	1.3	68
1064	Characterization of cultivated fungi isolated from grape marc wastes through the use of amplified rDNA restriction analysis and sequencing. <i>Journal of Microbiology</i> , 2010, 48, 297-306.	1.3	6
1065	Development of EST-based new SSR markers in seabuckthorn. <i>Physiology and Molecular Biology of Plants</i> , 2010, 16, 375-378.	1.4	30
1066	Development and characterization of 17 polymorphic microsatellite loci in the faucet snail, <i>Bithynia tentaculata</i> (Gastropoda: Caenogastropoda: Bithyniidae). <i>Conservation Genetics Resources</i> , 2010, 2, 247-250.	0.4	9
1067	Characterization of four defense-related genes up-regulated in root nodules of <i>Casuarina glauca</i> . <i>Symbiosis</i> , 2010, 50, 27-35.	1.2	11
1068	Expressed sequence tag analysis generated from a normalized full-length cDNA library of the root-knot nematode (<i>Meloidogyne incognita</i>). <i>Genes and Genomics</i> , 2010, 32, 553-562.	0.5	7
1069	Generation and analysis of expressed sequence tags from the medicinal plant <i>Salvia miltiorrhiza</i> . <i>Science China Life Sciences</i> , 2010, 53, 273-285.	2.3	33
1070	A genome-wide survey of maize lipid-related genes: candidate genes mining, digital gene expression profiling and co-location with QTL for maize kernel oil. <i>Science China Life Sciences</i> , 2010, 53, 690-700.	2.3	25
1071	Isolation and Characterization of Differentially Expressed Transcripts from the Suspension Cells of Oil Palm (<i>Elaeis guineensis</i> Jacq.) in Response to Different Concentration of Auxins. <i>Molecular Biotechnology</i> , 2010, 46, 1-19.	1.3	25
1072	Aphid Feeding Activates Expression of a Transcriptome of Oxylipin-based Defense Signals in Wheat Involved in Resistance to Herbivory. <i>Journal of Chemical Ecology</i> , 2010, 36, 260-276.	0.9	86
1073	FIDELâ€™a retrovirus-like retrotransposon and its distinct evolutionary histories in the A- and B-genome components of cultivated peanut. <i>Chromosome Research</i> , 2010, 18, 227-246.	1.0	44
1074	Genetic composition, population structure and phylogeography of the loggerhead sea turtle: colonization hypothesis for the Brazilian rookeries. <i>Conservation Genetics</i> , 2010, 11, 1467-1477.	0.8	57

#	ARTICLE	IF	CITATIONS
1075	Application of high-resolution DNA melting for genotyping and variant scanning of diploid and autotetraploid potato. <i>Molecular Breeding</i> , 2010, 25, 67-90.	1.0	54
1076	Utilization of next-generation sequencing platforms in plant genomics and genetic variant discovery. <i>Molecular Breeding</i> , 2010, 25, 553-570.	1.0	112
1077	Allele-specific expression of a weeping lovegrass gene from the lignin biosynthetic pathway, caffeoyl-coenzyme A 3-O-methyltransferase. <i>Molecular Breeding</i> , 2010, 26, 627-637.	1.0	4
1078	Molecular cloning and characterization of five genes encoding pentatricopeptide repeat proteins from Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Molecular Biology Reports</i> , 2010, 37, 801-808.	1.0	12
1079	Generation and analysis of expressed sequence tags from leaf and root of <i>Withania somnifera</i> (Ashwagandha). <i>Molecular Biology Reports</i> , 2010, 37, 893-902.	1.0	33
1080	Analysis of <i>Brassica rapa</i> ESTs: gene discovery and expression patterns of AP2/ERF family genes. <i>Molecular Biology Reports</i> , 2010, 37, 2485-2492.	1.0	35
1081	Generation and gene ontology based analysis of expressed sequence tags (EST) from a <i>Panax ginseng</i> C. A. Meyer roots. <i>Molecular Biology Reports</i> , 2010, 37, 3465-3472.	1.0	54
1082	Expressed sequence tags-based identification of genes in a biocontrol strain <i>Trichoderma asperellum</i> . <i>Molecular Biology Reports</i> , 2010, 37, 3673-3681.	1.0	37
1083	Genetic diversity and evidence for recent modular recombination in Hawaiian Citrus tristeza virus. <i>Virus Genes</i> , 2010, 40, 111-118.	0.7	72
1084	Genome sequence of the temperate bacteriophage PH10 from <i>Streptococcus oralis</i> . <i>Virus Genes</i> , 2010, 41, 450-458.	0.7	13
1085	Analysis of expressed sequence tags from Ginkgo mature foliage in China. <i>Tree Genetics and Genomes</i> , 2010, 6, 357-365.	0.6	9
1086	Multivariate analysis of digital gene expression profiles identifies a xylem signature of the vascular tissue of white spruce (<i>Picea glauca</i>). <i>Tree Genetics and Genomes</i> , 2010, 6, 601-611.	0.6	3
1087	Development, characterization, validation, and mapping of SSRs derived from <i>Theobroma cacao</i> L.â€™Moniliophthora perniciosa interaction ESTs. <i>Tree Genetics and Genomes</i> , 2010, 6, 663-676.	0.6	20
1088	Transcriptomic changes in the root of oil palm (<i>Elaeis guineensis</i> Jacq.) upon inoculation with <i>Bacillus sphaericus</i> UPMB10. <i>Tree Genetics and Genomes</i> , 2010, 6, 793-800.	0.6	12
1089	Comparative transcript analyses of the ovule, microspore, and mature pollen in <i>Brassica napus</i> . <i>Plant Molecular Biology</i> , 2010, 72, 279-299.	2.0	30
1090	An ordered EST catalogue and gene expression profiles of cassava (<i>Manihot esculenta</i>) at key growth stages. <i>Plant Molecular Biology</i> , 2010, 74, 573-590.	2.0	24
1091	Characterization of an Oxidative Stress Inducible Nonspecific Lipid Transfer Protein Coding cDNA and its Promoter from Drought Tolerant Plant <i>Prosopis juliflora</i> . <i>Plant Molecular Biology Reporter</i> , 2010, 28, 32-40.	1.0	19
1092	Isolation and Characterization of Expressed Sequence Tags (ESTs) from Cambium Tissue of Birch (<i>Betula platyphylla</i> Suk). <i>Plant Molecular Biology Reporter</i> , 2010, 28, 438-449.	1.0	24

#	ARTICLE	IF	CITATIONS
1093	In Silico and Quantitative Analyses of MADS-Box Genes in <i>Coffea arabica</i> . <i>Plant Molecular Biology Reporter</i> , 2010, 28, 460-472.	1.0	21
1094	Strategies to develop polymorphic markers for <i>Coffea arabica</i> L.. <i>Euphytica</i> , 2010, 173, 243-253.	0.6	2
1095	Discovery, phylogeny and expression patterns of AP2-like genes in maize. <i>Plant Growth Regulation</i> , 2010, 62, 51-58.	1.8	30
1096	Discovering conserved insect microRNAs from expressed sequence tags. <i>Journal of Insect Physiology</i> , 2010, 56, 1763-1769.	0.9	21
1097	Survey of genome organization and gene content of <i>Corynebacterium pseudotuberculosis</i> . <i>Microbiological Research</i> , 2010, 165, 312-320.	2.5	17
1098	Transcriptomic analyses of the avirulent protozoan parasite <i>Trypanosoma rangeli</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 174, 18-25.	0.5	32
1099	Molecular and cellular aspects of amphibian lens regeneration. <i>Progress in Retinal and Eye Research</i> , 2010, 29, 543-555.	7.3	89
1100	Structural and functional diversity of soil bacterial and fungal communities following woody plant encroachment in the southern Great Plains. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1816-1824.	4.2	72
1101	Members of soil bacterial communities sensitive to tillage and crop rotation. <i>Soil Biology and Biochemistry</i> , 2010, 42, 2111-2118.	4.2	173
1102	Suppression subtractive hybridization analysis reveals expression of conserved and novel genes in male accessory glands of the ant <i>Leptothorax gredleri</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 273.	3.2	6
1103	Unusual conservation among genes encoding small secreted salivary gland proteins from a gall midge. <i>BMC Evolutionary Biology</i> , 2010, 10, 296.	3.2	55
1104	Identification and analysis of in planta expressed genes of <i>Magnaporthe oryzae</i> . <i>BMC Genomics</i> , 2010, 11, 104.	1.2	37
1105	TobEA: an atlas of tobacco gene expression from seed to senescence. <i>BMC Genomics</i> , 2010, 11, 142.	1.2	55
1106	Discovery and application of insertion-deletion (INDEL) polymorphisms for QTL mapping of early life-history traits in Atlantic salmon. <i>BMC Genomics</i> , 2010, 11, 156.	1.2	44
1107	Transcriptome survey of the anhydrobiotic tardigrade <i>Milnesium tardigradum</i> in comparison with <i>Hypsibius dujardini</i> and <i>Richtersius coronifer</i> . <i>BMC Genomics</i> , 2010, 11, 168.	1.2	49
1108	Characterization of the ovine ribosomal protein SA gene and its pseudogenes. <i>BMC Genomics</i> , 2010, 11, 179.	1.2	8
1109	Synteny mapping between common bean and soybean reveals extensive blocks of shared loci. <i>BMC Genomics</i> , 2010, 11, 184.	1.2	100
1110	Genomic analysis of expressed sequence tags in American black bear <i>Ursus americanus</i> . <i>BMC Genomics</i> , 2010, 11, 201.	1.2	16

#	ARTICLE	IF	CITATIONS
1111	An insight into the sialome of <i>Glossina morsitans morsitans</i> . BMC Genomics, 2010, 11, 213.	1.2	76
1112	Functional genomics of mountain pine beetle (<i>Dendroctonus ponderosae</i>) midguts and fat bodies. BMC Genomics, 2010, 11, 215.	1.2	63
1113	A comparison of SNPs and microsatellites as linkage mapping markers: lessons from the zebra finch (<i>Taeniopygia guttata</i>). BMC Genomics, 2010, 11, 218.	1.2	77
1114	Transcriptome sequencing and development of an expression microarray platform for the domestic ferret. BMC Genomics, 2010, 11, 251.	1.2	35
1115	Differences in transcription between free-living and CO ₂ -activated third-stage larvae of <i>Haemonchus contortus</i> . BMC Genomics, 2010, 11, 266.	1.2	47
1116	An EST resource for tilapia based on 17 normalized libraries and assembly of 116,899 sequence tags. BMC Genomics, 2010, 11, 278.	1.2	39
1117	<i>Salmo salar</i> and <i>Esox lucius</i> full-length cDNA sequences reveal changes in evolutionary pressures on a post-tetraploidization genome. BMC Genomics, 2010, 11, 279.	1.2	163
1118	Massively parallel pyrosequencing-based transcriptome analyses of small brown planthopper (<i>Laodelphax striatellus</i>), a vector insect transmitting rice stripe virus (RSV). BMC Genomics, 2010, 11, 303.	1.2	115
1119	Population-level transcriptome sequencing of nonmodel organisms <i>Erynnis propertius</i> and <i>Papilio zelicaon</i> . BMC Genomics, 2010, 11, 310.	1.2	114
1120	Development of an oligo DNA microarray for the European sea bass and its application to expression profiling of jaw deformity. BMC Genomics, 2010, 11, 354.	1.2	37
1121	The expression of genes coding for distinct types of glycine-rich proteins varies according to the biology of three metastriate ticks, <i>Rhipicephalus (Boophilus) microplus</i> , <i>Rhipicephalus sanguineus</i> and <i>Amblyomma cajennense</i> . BMC Genomics, 2010, 11, 363.	1.2	60
1122	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. BMC Genomics, 2010, 11, 384.	1.2	161
1123	Heart transcriptome of the bank vole (<i>Myodes glareolus</i>): towards understanding the evolutionary variation in metabolic rate. BMC Genomics, 2010, 11, 390.	1.2	22
1124	Complete mitochondrial genomes of <i>Taenia multiceps</i> , <i>T. hydatigena</i> and <i>T. pisiformis</i> : additional molecular markers for a tapeworm genus of human and animal health significance. BMC Genomics, 2010, 11, 447.	1.2	122
1125	An insight into the sialotranscriptome of the brown dog tick, <i>Rhipicephalus sanguineus</i> . BMC Genomics, 2010, 11, 450.	1.2	91
1126	Transcriptome analysis of the oil-rich seed of the bioenergy crop <i>Jatropha curcas</i> L. BMC Genomics, 2010, 11, 462.	1.2	118
1127	Deep sequencing-based transcriptome profiling analysis of bacteria-challenged <i>Lateolabrax japonicus</i> reveals insight into the immune-relevant genes in marine fish. BMC Genomics, 2010, 11, 472.	1.2	189
1128	An insight into the sialotranscriptome of the West Nile mosquito vector, <i>Culex tarsalis</i> . BMC Genomics, 2010, 11, 51.	1.2	37

#	ARTICLE	IF	CITATIONS
1129	Gene discovery for the bark beetle-vectored fungal tree pathogen <i>Grosmannia clavigera</i> . <i>BMC Genomics</i> , 2010, 11, 536.	1.2	25
1130	Comparing de novo assemblers for 454 transcriptome data. <i>BMC Genomics</i> , 2010, 11, 571.	1.2	217
1131	A transcriptomic analysis of gene expression in the venom gland of the snake <i>Bothrops alternatus</i> (urutu). <i>BMC Genomics</i> , 2010, 11, 605.	1.2	55
1132	Gene discovery from <i>Jatropha curcas</i> by sequencing of ESTs from normalized and full-length enriched cDNA library from developing seeds. <i>BMC Genomics</i> , 2010, 11, 606.	1.2	59
1133	Genomic tools development for <i>Aquilegia</i> : construction of a BAC-based physical map. <i>BMC Genomics</i> , 2010, 11, 621.	1.2	13
1134	Insights into metazoan evolution from <i>alvinella pompejana</i> cDNAs. <i>BMC Genomics</i> , 2010, 11, 634.	1.2	46
1135	Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. <i>BMC Genomics</i> , 2010, 11, 650.	1.2	82
1136	The venom composition of the parasitic wasp <i>Chelonus inanitus</i> resolved by combined expressed sequence tags analysis and proteomic approach. <i>BMC Genomics</i> , 2010, 11, 693.	1.2	102
1137	Global characterization of the root transcriptome of a wild species of rice, <i>Oryza longistaminata</i> , by deep sequencing. <i>BMC Genomics</i> , 2010, 11, 705.	1.2	31
1138	Development of a EST dataset and characterization of EST-SSRs in a traditional Chinese medicinal plant, <i>Epimedium sagittatum</i> (Sieb. Et Zucc.) Maxim. <i>BMC Genomics</i> , 2010, 11, 94.	1.2	180
1139	Generation, analysis and functional annotation of expressed sequence tags from the sheepshead minnow (<i>Cyprinodon variegatus</i>). <i>BMC Genomics</i> , 2010, 11, S4.	1.2	3
1140	Alternative splicing enriched cDNA libraries identify breast cancer-associated transcripts. <i>BMC Genomics</i> , 2010, 11, S4.	1.2	10
1141	Multi-locus analysis of human infective <i>Cryptosporidium</i> species and subtypes using ten novel genetic loci. <i>BMC Microbiology</i> , 2010, 10, 213.	1.3	35
1142	Planctomycetes dominate biofilms on surfaces of the kelp <i>Laminaria hyperborea</i> . <i>BMC Microbiology</i> , 2010, 10, 261.	1.3	221
1143	Transcriptional profiling reveals the expression of novel genes in response to various stimuli in the human dermatophyte <i>Trichophyton rubrum</i> . <i>BMC Microbiology</i> , 2010, 10, 39.	1.3	49
1144	Genome-wide characterization of the biggest grass, bamboo, based on 10,608 putative full-length cDNA sequences. <i>BMC Plant Biology</i> , 2010, 10, 116.	1.6	81
1145	Candidate genes associated with bud dormancy release in blackcurrant (<i>Ribes nigrum</i> L.). <i>BMC Plant Biology</i> , 2010, 10, 202.	1.6	69
1146	Comparative genomic analysis of 1047 completely sequenced cDNAs from an <i>Arabidopsis</i> -related model halophyte, <i>Thellungiella halophila</i> . <i>BMC Plant Biology</i> , 2010, 10, 261.	1.6	38

#	ARTICLE	IF	CITATIONS
1147	The first set of EST resource for gene discovery and marker development in pigeonpea (<i>Cajanus cajan</i>) Tj ETQq0 0 QrgBT /Overlock 10 T	1.6	90
1148	A full-length enriched cDNA library and expressed sequence tag analysis of the parasitic weed, <i>Striga hermonthica</i> . <i>BMC Plant Biology</i> , 2010, 10, 55.	1.6	34
1149	Analysis of expressed sequence tags from a single wheat cultivar facilitates interpretation of tandem mass spectrometry data and discrimination of gamma gliadin proteins that may play different functional roles in flour. <i>BMC Plant Biology</i> , 2010, 10, 7.	1.6	45
1150	Uncovering the evolutionary origin of plant molecular processes: comparison of <i>Coleochaete</i> (<i>Coleochaetales</i>) and <i>Spirogyra</i> (<i>Zygnematales</i>) transcriptomes. <i>BMC Plant Biology</i> , 2010, 10, 96.	1.6	91
1151	An efficient method for developing SNP markers based on EST data combined with high resolution melting (HRM) analysis. <i>BMC Research Notes</i> , 2010, 3, 51.	0.6	17
1152	Elucidating the transcriptome of <i>Fasciola hepatica</i> – A key to fundamental and biotechnological discoveries for a neglected parasite. <i>Biotechnology Advances</i> , 2010, 28, 222-231.	6.0	119
1153	Development, characterization and utilization of genomic microsatellite markers in turmeric (<i>Curcuma longa</i> L.). <i>Biochemical Systematics and Ecology</i> , 2010, 38, 641-646.	0.6	21
1154	<i>Rhipicephalus (Boophilus) microplus</i> : Clotting time in tick-infested skin varies according to local inflammation and gene expression patterns in tick salivary glands. <i>Experimental Parasitology</i> , 2010, 124, 428-435.	0.5	29
1155	<i>Teladorsagia circumcincta</i> : Activation-associated secreted proteins in excretory/secretory products of fourth stage larvae are targets of early IgA responses in infected sheep. <i>Experimental Parasitology</i> , 2010, 125, 329-337.	0.5	29
1156	Characterization of pLAC1, a cryptic plasmid isolated from <i>Lactobacillus acidipiscis</i> and comparative analysis with its related plasmids. <i>International Journal of Food Microbiology</i> , 2010, 141, 222-228.	2.1	10
1157	Differential gene expression in bovine cells infected with wild type and leaderless foot-and-mouth disease virus. <i>Virology</i> , 2010, 404, 32-40.	1.1	37
1158	Effects of the interactions of classical swine fever virus Core protein with proteins of the SUMOylation pathway on virulence in swine. <i>Virology</i> , 2010, 407, 129-136.	1.1	35
1159	First transcriptomic analysis of the economically important parasitic nematode, <i>Trichostrongylus colubriformis</i> , using a next-generation sequencing approach. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1199-1207.	1.0	55
1160	Suppressive subtractive hybridization analysis of <i>Rhipicephalus (Boophilus) microplus</i> larval and adult transcript expression during attachment and feeding. <i>Veterinary Parasitology</i> , 2010, 167, 304-320.	0.7	36
1161	A suite of genes expressed during transition to parasitic lifestyle in the trichostrongylid nematode <i>Haemonchus contortus</i> encode potentially secreted proteins conserved in <i>Teladorsagia circumcincta</i> . <i>Veterinary Parasitology</i> , 2010, 174, 106-114.	0.7	12
1162	Transcriptome analysis of the venom glands of the Chinese wolf spider <i>Lycosa singoriensis</i> . <i>Zoology</i> , 2010, 113, 10-18.	0.6	84
1163	SNP identification, verification, and utility for population genetics in a non-model genus. <i>BMC Genetics</i> , 2010, 11, 32.	2.7	59
1164	Analysis of expressed sequence tags from <i>Prunus mume</i> flower and fruit and development of simple sequence repeat markers. <i>BMC Genetics</i> , 2010, 11, 66.	2.7	24

#	ARTICLE	IF	CITATIONS
1165	Identification of testis-relevant genes using in silico analysis from testis ESTs and cDNA microarray in the black tiger shrimp (<i>Penaeus monodon</i>). <i>BMC Molecular Biology</i> , 2010, 11, 55.	3.0	25
1166	Rapid transcriptome and proteome profiling of a non-model marine invertebrate, <i>Bugula neritina</i> . <i>Proteomics</i> , 2010, 10, 2972-2981.	1.3	46
1167	Characterization of the horseweed (<i>Conyza canadensis</i>) transcriptome using GS-FLX 454 pyrosequencing and its application for expression analysis of candidate non-target herbicide resistance genes. <i>Pest Management Science</i> , 2010, 66, 1053-1062.	1.7	112
1168	Characterization of <i>de novo</i> transcriptome for waterhemp (<i>Amaranthus tuberculatus</i>) using GS-FLX 454 pyrosequencing and its application for studies of herbicide target site genes. <i>Pest Management Science</i> , 2010, 66, 1042-1052.	1.7	89
1169	Characterization of <i>drCol 15a1b</i> : A Novel Component of the Stem Cell Niche in the Zebrafish Retina. <i>Stem Cells</i> , 2010, 28, 1399-1411.	1.4	16
1170	Seasonally dynamic fungal communities in the <i>Quercus macrocarpa</i> phyllosphere differ between urban and nonurban environments. <i>New Phytologist</i> , 2010, 186, 496-513.	3.5	185
1171	Phylogenetic and ecological analyses of soil and sporocarp DNA sequences reveal high diversity and strong habitat partitioning in the boreal ectomycorrhizal genus <i>Russula</i> (Russulales). <i>Journal of Ecology</i> , 2010, 98, 475-497.	1.0	10
1172	Specific resistances against <i>Pseudomonas syringae</i> effectors AvrB and AvrRpm1 have evolved differently in common bean (<i>Phaseolus vulgaris</i>), soybean (<i>Glycine max</i>), and <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2010, 187, 941-956.	3.5	50
1173	Transcriptome profiles of hybrid poplar (<i>Populus trichocarpa</i> × <i>deltoides</i>) reveal rapid changes in undamaged, systemic sink leaves after simulated feeding by forest tent caterpillar (<i>Malacosoma disstria</i>). <i>New Phytologist</i> , 2010, 188, 787-802.	3.5	48
1174	A major SNP resource for dissection of phenotypic and genetic variation in Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Animal Genetics</i> , 2010, 41, 39-47.	0.6	37
1175	Discovery of host defence genes in the Japanese scallop <i>Mizuhopecten yessoensis</i> Jay by expressed sequence tag analysis of kidney tissue. <i>Aquaculture Research</i> , 2010, 41, 1602-1613.	0.9	18
1176	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , 2010, 62, 898-909.	2.8	89
1177	A full-length cDNA resource for the pea aphid, <i>Acyrtosiphon pisum</i> . <i>Insect Molecular Biology</i> , 2010, 19, 23-31.	1.0	30
1178	Comparative analysis of detoxification enzymes in <i>Acyrtosiphon pisum</i> and <i>Myzus persicae</i> . <i>Insect Molecular Biology</i> , 2010, 19, 155-164.	1.0	203
1179	Analysis of expressed sequence tags for <i>Frankliniella occidentalis</i> , the western flower thrips. <i>Insect Molecular Biology</i> , 2010, 19, 537-551.	1.0	34
1180	Evolutionary variation in gene expression is associated with dimorphism in eusocial vespid wasps. <i>Insect Molecular Biology</i> , 2010, 19, 641-652.	1.0	14
1181	Finding candidate genes under positive selection in Non-model species: examples of genes involved in host specialization in pathogens. <i>Molecular Ecology</i> , 2010, 19, 292-306.	2.0	44
1182	A genetic basis for the phenotypic differentiation between siscowet and lean lake trout (<i>Salvelinus</i>). <i>Journal of Heredity</i> , 2010, 101, 140-147.	2.0	140

#	ARTICLE	IF	CITATIONS
1183	Massively parallel 454â€ sequencing of fungal communities in <i>Quercus</i> spp. ectomycorrhizas indicates seasonal dynamics in urban and rural sites. <i>Molecular Ecology</i> , 2010, 19, 41-53.	2.0	156
1184	Microbial ecological response of the intestinal flora of <i>Peromyscus maniculatus</i> and <i>P. leucopus</i> to heavy metal contamination. <i>Molecular Ecology</i> , 2010, 19, 67-80.	2.0	19
1185	The genetic basis of recessive self-colour pattern in a wild sheep population. <i>Heredity</i> , 2010, 104, 206-214.	1.2	43
1186	Generation and analysis of 10 000 ESTs from the halfâ€ smooth tongue sole <i>Cynoglossus semilaevis</i> and identification of microsatellite and SNP markers. <i>Journal of Fish Biology</i> , 2010, 76, 1190-1204.	0.7	27
1187	Expression Profile During the Development of Appressoria Induced by Hydrophobic Surfaces in <i>Magnaporthe grisea</i> Y34. <i>Journal of Phytopathology</i> , 2010, 158, 143-153.	0.5	2
1188	Molecular evolutionary analysis of seminal receptacle sperm storage organ genes of <i>Drosophila melanogaster</i> . <i>Journal of Evolutionary Biology</i> , 2010, 23, 1386-1398.	0.8	41
1189	Hepatitis B genotype G and high frequency of lamivudine-resistance mutations among human immunodeficiencyvirus/hepatitis B virus co-infected patients in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2010, 105, 770-778.	0.8	16
1190	A Transcript Accounting from Diverse Tissues of a Cultivated Strawberry. <i>Plant Genome</i> , 2010, 3, .	1.6	22
1191	In silico identification of coffee genome expressed sequences potentially associated with resistance to diseases. <i>Genetics and Molecular Biology</i> , 2010, 33, 795-806.	0.6	13
1192	CA88, a nuclear repetitive DNA sequence identified in <i>Schistosoma mansoni</i> , aids in the genotyping of nine <i>Schistosoma</i> species of medical and veterinary importance. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2010, 105, 391-397.	0.8	0
1193	The Porcelain Crab Transcriptome and PCAD, the Porcelain Crab Microarray and Sequence Database. <i>PLoS ONE</i> , 2010, 5, e9327.	1.1	21
1194	Transcriptome Profiling of a Toxic Dinoflagellate Reveals a Gene-Rich Protist and a Potential Impact on Gene Expression Due to Bacterial Presence. <i>PLoS ONE</i> , 2010, 5, e9688.	1.1	134
1195	Discovery of <i>Phytophthora infestans</i> Genes Expressed in Planta through Mining of cDNA Libraries. <i>PLoS ONE</i> , 2010, 5, e9847.	1.1	8
1196	Identification and Characterization of Full-Length cDNAs in Channel Catfish (<i>Ictalurus punctatus</i>) and Blue Catfish (<i>Ictalurus furcatus</i>). <i>PLoS ONE</i> , 2010, 5, e11546.	1.1	40
1197	A Brassica Exon Array for Whole-Transcript Gene Expression Profiling. <i>PLoS ONE</i> , 2010, 5, e12812.	1.1	27
1198	A Dual Platform Approach to Transcript Discovery for the Planarian <i>Schmidtea mediterranea</i> to Establish RNAseq for Stem Cell and Regeneration Biology. <i>PLoS ONE</i> , 2010, 5, e15617.	1.1	61
1199	Isolation and characterization of genes functionally involved in ovarian development of the giant tiger shrimp <i>Penaeus monodon</i> by suppression subtractive hybridization (SSH). <i>Genetics and Molecular Biology</i> , 2010, 33, 676-685.	0.6	18
1200	Mining SNPs from EST sequences using filters and ensemble classifiers. <i>Genetics and Molecular Research</i> , 2010, 9, 820-834.	0.3	9

#	ARTICLE	IF	CITATIONS
1201	Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean. <i>Crop Science</i> , 2010, 50, 1950-1960.	0.8	282
1202	Polymorphisms in the IGF1 gene and their effect on growth traits in Mexican beef cattle. <i>Genetics and Molecular Research</i> , 2010, 9, 875-883.	0.3	45
1203	Migration-related changes in gene expression in leg muscle of the Christmas Island red crab <i>Gecarcoidea natalis</i> : seasonal preparation for long-distance walking. <i>Journal of Experimental Biology</i> , 2010, 213, 1740-1750.	0.8	8
1204	The heterogeneous nuclear ribonucleoprotein-R is necessary for axonal β -actin mRNA translocation in spinal motor neurons. <i>Human Molecular Genetics</i> , 2010, 19, 1951-1966.	1.4	101
1205	A High-Throughput Data Mining of Single Nucleotide Polymorphisms in <i>Coffea</i> Species Expressed Sequence Tags Suggests Differential Homeologous Gene Expression in the Allotetraploid <i>Coffea arabica</i> . <i>Plant Physiology</i> , 2010, 154, 1053-1066.	2.3	61
1206	Evidence for Multiple Independent Origins of trans-Splicing in Metazoa. <i>Molecular Biology and Evolution</i> , 2010, 27, 684-693.	3.5	71
1207	An Insight into the Sialotranscriptome of <i>Simulium nigrimanum</i> , a Black Fly Associated with Fogo Selvagem in South America. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 1060-1075.	0.6	36
1208	Characterizing the Embryonic Transcriptome of the Snail <i>Ilyanassa</i> . <i>Integrative and Comparative Biology</i> , 2010, 50, 768-777.	0.9	30
1209	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , 2010, 38, e171-e171.	6.5	62
1210	Identification of genes associated with bud dormancy release in <i>Prunus persica</i> by suppression subtractive hybridization. <i>Tree Physiology</i> , 2010, 30, 655-666.	1.4	102
1211	Identification of Key Functional Residues in the Active Site of Human β 1,4-Galactosyltransferase 7. <i>Journal of Biological Chemistry</i> , 2010, 285, 37342-37358.	1.6	20
1212	Comparative Proteomics Indicates That Biosynthesis of Pectic Precursors Is Important for Cotton Fiber and <i>Arabidopsis</i> Root Hair Elongation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2019-2033.	2.5	167
1213	ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. <i>Genomics Insights</i> , 2010, 3, GEI.S4340.	3.0	26
1214	Genomics and Bioinformatics Resources for Crop Improvement. <i>Plant and Cell Physiology</i> , 2010, 51, 497-523.	1.5	177
1215	Comparative Genomic Analyses of Attenuated Strains of <i>Mycoplasma gallisepticum</i> . <i>Infection and Immunity</i> , 2010, 78, 1760-1771.	1.0	50
1216	Large-Scale Parsimony Analysis of Metazoan Indels in Protein-Coding Genes. <i>Molecular Biology and Evolution</i> , 2010, 27, 441-451.	3.5	34
1217	Growth of Bacteria on 3-Nitropropionic Acid as a Sole Source of Carbon, Nitrogen, and Energy. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3590-3598.	1.4	31
1218	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	2.4	228

#	ARTICLE	IF	CITATIONS
1219	Gene identification in <i>Phytophthora capsici</i> through expressed sequence tags. , 2010, , .		1
1220	Vertical distribution of fungal communities in tallgrass prairie soil. <i>Mycologia</i> , 2010, 102, 1027-1041.	0.8	118
1221	Developmental stage-specific gene expression profiling for a medicinal fungus <i>Cordyceps militaris</i> . <i>Mycology</i> , 2010, 1, 25-66.	2.0	30
1222	STEPWISE ORIGIN AND FUNCTIONAL DIVERSIFICATION OF THE AFL SUBFAMILY B3 GENES DURING LAND PLANT EVOLUTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 33-45.	0.3	11
1223	Studies of a Biochemical Factory: Tomato Trichome Deep Expressed Sequence Tag Sequencing and Proteomics. <i>Plant Physiology</i> , 2010, 153, 1212-1223.	2.3	117
1224	Development of a novel set of EST-SSR markers and cross-species amplification in <i>Tamarix africana</i> (Tamaricaceae). <i>American Journal of Botany</i> , 2010, 97, e45-7.	0.8	8
1225	Genome assembly quality: Assessment and improvement using the neutral indel model. <i>Genome Research</i> , 2010, 20, 675-684.	2.4	44
1226	Generation and Analysis of Expressed Sequence Tags from <i>Olea europaea</i> L.. <i>Comparative and Functional Genomics</i> , 2010, 2010, 1-9.	2.0	16
1227	The complete mitochondrial DNA sequence of the short mackerel (<i>Rastrelliger brachysoma</i>), and its phylogenetic position within Scombroidei, Perciformes. <i>Mitochondrial DNA</i> , 2010, 21, 36-47.	0.6	28
1228	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	2.6	913
1229	Discovery of a New Human Polyomavirus Associated with Trichodysplasia Spinulosa in an Immunocompromized Patient. <i>PLoS Pathogens</i> , 2010, 6, e1001024.	2.1	386
1230	Massively Parallel Sequencing and Analysis of the <i>Necator americanus</i> Transcriptome. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e684.	1.3	66
1231	Mining ESTs to Determine the Usefulness of SNPs Across Shrimp Species. <i>Animal Biotechnology</i> , 2010, 21, 100-103.	0.7	14
1232	Insights into the Evolution of Mitochondrial Genome Size from Complete Sequences of <i>Citrullus lanatus</i> and <i>Cucurbita pepo</i> (Cucurbitaceae). <i>Molecular Biology and Evolution</i> , 2010, 27, 1436-1448.	3.5	400
1233	Development and Application of Bovine and Porcine Oligonucleotide Arrays with Protein-Based Annotation. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-11.	3.0	7
1234	PEACE: Parallel Environment for Assembly and Clustering of Gene Expression. <i>Nucleic Acids Research</i> , 2010, 38, W737-W742.	6.5	7
1235	The Salivary Gland Transcriptome of the Eastern Tree Hole Mosquito, <i>Ochlerotatus triseriatus</i> . <i>Journal of Medical Entomology</i> , 2010, 47, 376-386.	0.9	17
1236	First Identification of Canine Distemper Virus in Hoary Fox (<i>Lycalopex vetulus</i>): Pathologic Aspects and Virus Phylogeny. <i>Journal of Wildlife Diseases</i> , 2010, 46, 303-305.	0.3	26

#	ARTICLE	IF	CITATIONS
1237	Cloud computing paradigms for pleasingly parallel biomedical applications. , 2010, , .		47
1238	Solving the DNA fragment assembly problem efficiently using iterative optimization with evolved hypermutations. , 2010, , .		13
1239	The ANISEED database: Digital representation, formalization, and elucidation of a chordate developmental program. <i>Genome Research</i> , 2010, 20, 1459-1468.	2.4	105
1240	The Salivary Gland Transcriptome of the Eastern Tree Hole Mosquito, <i>Ochlerotatus triseriatus</i> . <i>Journal of Medical Entomology</i> , 2010, 47, 376-386.	0.9	12
1241	Demosponge EST Sequencing Reveals a Complex Genetic Toolkit of the Simplest Metazoans. <i>Molecular Biology and Evolution</i> , 2010, 27, 2747-2756.	3.5	45
1242	From raw materials to validated system: the construction of a genomic library and microarray to interpret systemic perturbations in Northern bobwhite. <i>Physiological Genomics</i> , 2010, 42, 219-235.	1.0	55
1243	A practical guide to fungal genome projects: strategy, technology, cost and completion. <i>Mycology</i> , 2010, 1, 9-24.	2.0	13
1244	Marsupial Sequencing Projects and Bioinformatics Challenges. , 2010, , 121-132.		1
1245	Unlocking the Transcriptomes of Two Carcinogenic Parasites, <i>Clonorchis sinensis</i> and <i>Opisthorchis viverrini</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e719.	1.3	141
1246	MapReduce in the Clouds for Science. , 2010, , .		107
1247	Using the DFCI Gene Index Databases for Biological Discovery. <i>Current Protocols in Bioinformatics</i> , 2010, 29, Unit1.6.1-36.	25.8	12
1248	<i>Armillaria mellea</i> Induces a Set of Defense Genes in Grapevine Roots and One of Them Codifies a Protein with Antifungal Activity. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 485-496.	1.4	13
1249	Monitoring and identification of airborne fungi at historic locations on Ross Island, Antarctica. <i>Polar Science</i> , 2010, 4, 275-283.	0.5	25
1250	AmphiEST: Enabling comparative analysis of ESTs from five developmental stages of amphioxus. <i>Marine Genomics</i> , 2010, 3, 151-155.	0.4	6
1251	Bhalterin: Functional and structural characterization of a new thrombin-like enzyme from <i>Bothrops alternatus</i> snake venom. <i>Toxicon</i> , 2010, 55, 1365-1377.	0.8	39
1252	Characterization of proteinases from the midgut of <i>Rhipicephalus (Boophilus) microplus</i> involved in the generation of antimicrobial peptides. <i>Parasites and Vectors</i> , 2010, 3, 63.	1.0	42
1253	Germ cell specification and ovary structure in the rotifer <i>Brachionus plicatilis</i> . <i>EvoDevo</i> , 2010, 1, 5.	1.3	18
1254	Insight into the Sialome of the Bed Bug, <i>Cimex lectularius</i> . <i>Journal of Proteome Research</i> , 2010, 9, 3820-3831.	1.8	65

#	ARTICLE	IF	CITATIONS
1255	Gene expression analysis of volatile-rich male flowers of dioecious <i>Pandanus fascicularis</i> using expressed sequence tags. <i>Journal of Plant Physiology</i> , 2010, 167, 914-919.	1.6	6
1256	Identification of CYP genes in <i>Mytilus</i> (mussel) and <i>Crassostrea</i> (oyster) species: First approach to the full complement of cytochrome P450 genes in bivalves. <i>Marine Environmental Research</i> , 2010, 69, S1-S3.	1.1	47
1257	Differentially expressed genes following persistent infection with infectious pancreatic necrosis virus in vitro and in vivo. <i>Fish and Shellfish Immunology</i> , 2010, 28, 845-853.	1.6	35
1258	cDNA cloning of the immunoglobulin heavy chain genes in banded houndshark <i>Triakis scyllium</i> . <i>Fish and Shellfish Immunology</i> , 2010, 29, 854-861.	1.6	19
1259	Microarray analysis of gene expression in eastern oyster (<i>Crassostrea virginica</i>) reveals a novel combination of antimicrobial and oxidative stress host responses after dermo (<i>Perkinsus marinus</i>) challenge. <i>Fish and Shellfish Immunology</i> , 2010, 29, 921-929.	1.6	66
1260	Assembled catalog of immune-related genes from allogeneic challenged corals that unveils the participation of vWF-like transcript. <i>Developmental and Comparative Immunology</i> , 2010, 34, 630-637.	1.0	8
1261	EST analysis and identification of gonad-related genes from the normalized cDNA library of large yellow croaker, <i>Larimichthys crocea</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 89-97.	0.4	10
1262	The transcriptome of the early life history stages of the California Sea Hare <i>Aplysia californica</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 165-170.	0.4	28
1263	Comparison of gene order in the chromosome region containing a TERMINAL FLOWER 1 homolog in apricot and peach reveals microsynteny across angiosperms. <i>Plant Science</i> , 2010, 179, 390-398.	1.7	11
1264	Identification of early transcripts related to male development in chicken embryos. <i>Theriogenology</i> , 2010, 74, 1161-1178.e8.	0.9	7
1265	Patterns of gene expression in swine macrophages infected with classical swine fever virus detected by microarray. <i>Virus Research</i> , 2010, 151, 10-18.	1.1	27
1266	Tracing phylogenomic events leading to diversity of <i>Haemophilus influenzae</i> and the emergence of Brazilian Purpuric Fever (BPF)-associated clones. <i>Genomics</i> , 2010, 96, 290-302.	1.3	5
1267	A radiation hybrid map of the European sea bass (<i>Dicentrarchus labrax</i>) based on 1581 markers: Synteny analysis with model fish genomes. <i>Genomics</i> , 2010, 96, 228-238.	1.3	32
1268	Development and validation of single nucleotide polymorphism markers in the eastern oyster <i>Crassostrea virginica</i> Gmelin by mining ESTs and resequencing. <i>Aquaculture</i> , 2010, 302, 124-129.	1.7	54
1269	Digital expression profiling of novel diatom transcripts provides insight into their biological functions. <i>Genome Biology</i> , 2010, 11, R85.	13.9	97
1270	The <i>Chlorella variabilis</i> NC64A Genome Reveals Adaptation to Photosymbiosis, Coevolution with Viruses, and Cryptic Sex. <i>Plant Cell</i> , 2010, 22, 2943-2955.	3.1	441
1271	Production of a New Thiopeptide Antibiotic, TP-1161, by a Marine <i>Nocardiopsis</i> Species. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4969-4976.	1.4	149
1272	What can next generation sequencing do for you? Next generation sequencing as a valuable tool in plant research. <i>Plant Biology</i> , 2010, 12, 831-841.	1.8	140

#	ARTICLE	IF	CITATIONS
1273	A gene family-based method for interspecies comparisons of sequencing-based transcriptomes and its use in environmental adaptation analysis. <i>Journal of Genetics and Genomics</i> , 2010, 37, 205-218.	1.7	3
1274	Development of novel EST-SSR markers for cucumber (<i>Cucumis sativus</i>) and their transferability to related species. <i>Scientia Horticulturae</i> , 2010, 125, 534-538.	1.7	37
1275	High Performance Parallel Computing with Clouds and Cloud Technologies. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2010, , 20-38.	0.2	86
1276	The Mining of Citrus EST-SNP and Its Application in Cultivar Discrimination. <i>Agricultural Sciences in China</i> , 2010, 9, 179-190.	0.6	49
1277	Gene expression analysis of <i>Paracoccidioides brasiliensis</i> transition from conidium to yeast cell. <i>Medical Mycology</i> , 2010, 48, 147-154.	0.3	19
1279	Assembly of 500,000 inter-specific catfish expressed sequence tags and large scale gene-associated marker development for whole genome association studies. <i>Genome Biology</i> , 2010, 11, R8.	13.9	83
1280	Identification and Expression Analysis of Sex-Specific Expression Markers of Thai Abalone <i>Haliotis asinina</i> , Linnaeus, 1758. <i>Journal of Shellfish Research</i> , 2010, 29, 765-773.	0.3	9
1281	Identification of Genes Differentially Expressed in the Ganglia of Growing <i>Haliotis asinina</i> . <i>Journal of Shellfish Research</i> , 2010, 29, 741-752.	0.3	5
1282	Evolutionary distribution of light-harvesting complex-like proteins in photosynthetic eukaryotes. <i>Genome</i> , 2010, 53, 68-78.	0.9	31
1283	Comparative Gene Expression Analysis of Susceptible and Resistant Near-Isogenic Lines in Common Wheat Infected by <i>Puccinia triticina</i> . <i>DNA Research</i> , 2010, 17, 211-222.	1.5	59
1284	Structure and resilience of fungal communities in Alaskan boreal forest soils This article is one of a selection of papers from The Dynamics of Change in Alaska's Boreal Forests: Resilience and Vulnerability in Response to Climate Warming.. <i>Canadian Journal of Forest Research</i> , 2010, 40, 1288-1301.	0.8	84
1285	Comparison of gene order of GIGANTEA loci in yellow-poplar, monocots, and eudicots. <i>Genome</i> , 2010, 53, 533-544.	0.9	6
1286	Averaging measurement strategies for identifying single nucleotide polymorphisms from redundant data sets. , 2011, , .		0
1287	Survey and DNA Barcoding of Poaceae in Flat Rock Cedar Glades and Barrens State Natural Area, Murfreesboro, Tennessee. <i>Castanea</i> , 2011, 76, 300-310.	0.2	10
1288	An improved maximum likelihood formulation for accurate genome assembly. , 2011, , .		4
1289	Analysis of the mitochondrial haplogroups of farm and wild-living raccoon dogs in Poland. <i>Mitochondrial DNA</i> , 2011, 22, 105-110.	0.6	14
1290	Insight into the Salivary Transcriptome and Proteome of <i>Dipetalogaster maxima</i> . <i>Journal of Proteome Research</i> , 2011, 10, 669-679.	1.8	42
1291	Defining the Transcriptome Assembly and Its Use for Genome Dynamics and Transcriptome Profiling Studies in Pigeonpea (<i>Cajanus cajan</i> L.). <i>DNA Research</i> , 2011, 18, 153-164.	1.5	85

#	ARTICLE	IF	CITATIONS
1292	Construction and characterization of Japanese medaka (<i>Oryzias latipes</i>) hepatic cDNA library and its implementation to biomarker screening in aquatic toxicology. <i>Aquatic Toxicology</i> , 2011, 105, 569-575.	1.9	8
1293	Heartworm Genomics: Unprecedented Opportunities for Fundamental Molecular Insights and New Intervention Strategies. <i>Topics in Companion Animal Medicine</i> , 2011, 26, 193-199.	0.4	5
1294	A Portrait of the Transcriptome of the Neglected Trematode, <i>Fasciola gigantica</i> Biological and Biotechnological Implications. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1004.	1.3	84
1296	A transcriptomic scan for positively selected genes in two closely related marine fishes: <i>Sebastes caurinus</i> and <i>S. rastrelliger</i> . <i>Marine Genomics</i> , 2011, 4, 93-98.	0.4	11
1297	Transcriptome sequencing of a highly salt tolerant mangrove species <i>Sonneratia alba</i> using Illumina platform. <i>Marine Genomics</i> , 2011, 4, 129-136.	0.4	49
1298	In silico whole-genome EST analysis reveals 2322 novel microsatellites for the silver-lipped pearl oyster, <i>Pinctada maxima</i> . <i>Marine Genomics</i> , 2011, 4, 287-290.	0.4	11
1299	Identification of tissue-specific, abiotic stress-responsive gene expression patterns in wine grape (<i>Vitis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.65	35
1300	The complexity of <i>Rhipicephalus (Boophilus) microplus</i> genome characterised through detailed analysis of two BAC clones. <i>BMC Research Notes</i> , 2011, 4, 254.	0.6	6
1301	SNP Discovery by Transcriptome Pyrosequencing. <i>Methods in Molecular Biology</i> , 2011, 729, 225-246.	0.4	18
1302	Cloud Technologies for Bioinformatics Applications. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2011, 22, 998-1011.	4.0	50
1303	A Bioinformatics Pipeline for Sequence-Based Analyses of Fungal Biodiversity. <i>Methods in Molecular Biology</i> , 2011, 722, 141-155.	0.4	22
1304	Development of EST-SSR markers in castor bean (<i>Ricinus communis</i>) and their utilization for genetic purity testing of hybrids. <i>Genome</i> , 2011, 54, 684-691.	0.9	20
1305	CREST maps somatic structural variation in cancer genomes with base-pair resolution. <i>Nature Methods</i> , 2011, 8, 652-654.	9.0	451
1307	The draft genome and transcriptome of <i>Cannabis sativa</i> . <i>Genome Biology</i> , 2011, 12, R102.	13.9	479
1308	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011, 12, R40.	3.8	594
1309	Assessment of population structure in Pacific <i>Lepeophtheirus salmonis</i> (KrÅyer) using single nucleotide polymorphism and microsatellite genetic markers. <i>Aquaculture</i> , 2011, 320, 183-192.	1.7	29
1310	Identification of genes involved in immune response of Atlantic salmon (<i>Salmo salar</i>) to IPN virus infection, using expressed sequence tag (EST) analysis. <i>Aquaculture</i> , 2011, 318, 54-60.	1.7	32
1311	Recurrent outbreaks of viral nervous necrosis in intensively cultured barramundi (<i>Lates calcarifer</i>) due to horizontal transmission of betanodavirus and recommendations for disease control. <i>Aquaculture</i> , 2011, 319, 41-52.	1.7	26

#	ARTICLE	IF	CITATIONS
1312	EST resources and establishment and validation of a 16k cDNA microarray from Atlantic cod (<i>Gadus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	9.4	11
1313	EST analysis on the gonad development related organs and microarray screen for differentially expressed genes in mature ovary and testis of <i>Scylla paramamosain</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 150-157.	0.4	15
1314	Molecular responses of ceruloplasmin to <i>Edwardsiella ictaluri</i> infection and iron overload in channel catfish (<i>Ictalurus punctatus</i>). <i>Fish and Shellfish Immunology</i> , 2011, 30, 992-997.	1.6	22
1315	Use of suppressive subtractive hybridization to identify differentially expressed genes in ayu (<i>Plecoglossus altivelis</i>) associated with <i>Listonella anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2011, 31, 500-506.	1.6	17
1316	Prokaryotic expression, purification, and refolding of leukocyte cell-derived chemotaxin 2 and its effect on gene expression of head kidney-derived macrophages of a teleost fish, ayu (<i>Plecoglossus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.7	10
1317	Expressed sequence tags reveal genetic diversity and putative virulence factors of the pathogenic oomycete <i>Pythium insidiosum</i> . <i>Fungal Biology</i> , 2011, 115, 683-696.	1.1	53
1318	Genome-wide comparison of cyanobacterial transposable elements, potential genetic diversity indicators. <i>Gene</i> , 2011, 473, 139-149.	1.0	58
1319	cDNA cloning of porcine PKD2 gene and RNA interference in LLCâ€“PK1 cells. <i>Gene</i> , 2011, 476, 38-45.	1.0	11
1320	Cyclic Depsipeptides, Grassypeptolides D and E and Ibu-epidemethoxylyngbyastatin 3, from a Red Sea <i>Leptolyngbya</i> Cyanobacterium. <i>Journal of Natural Products</i> , 2011, 74, 1677-1685.	1.5	67
1321	Identification of Plant RAD52 Homologs and Characterization of the <i>Arabidopsis thaliana</i> RAD52-Like Genes. <i>Plant Cell</i> , 2011, 23, 4266-4279.	3.1	63
1322	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	6.0	794
1323	Novel genes differentially expressed between posterior and median silk gland identified by SAGE-aided transcriptome analysis. <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 118-124.	1.2	13
1324	Identification and tissue distribution of odorant binding protein genes in the lucerne plant bug <i>Adelphocoris lineolatus</i> (Goeze). <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 254-263.	1.2	125
1325	Representational Difference Analysis (RDA) reveals differential expression of conserved as well as novel genes during caste-specific development of the honey bee (<i>Apis mellifera</i> L.) ovary. <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 602-612.	1.2	30
1326	Transcriptome and gene expression profile of ovarian follicle tissue of the triatomine bug <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 823-831.	1.2	49
1327	An insight into the sialotranscriptome and proteome of the coarse bontlegged tick, <i>Hyalomma marginatum rufipes</i> . <i>Journal of Proteomics</i> , 2011, 74, 2892-2908.	1.2	62
1328	Phylogenomics reveals deep molluscan relationships. <i>Nature</i> , 2011, 477, 452-456.	13.7	420
1329	Blueberry latent virus: An amalgam of the Partitiviridae and Totiviridae. <i>Virus Research</i> , 2011, 155, 175-180.	1.1	76

#	ARTICLE	IF	CITATIONS
1330	Complete sequence and genetic characterization of Raspberry latent virus, a novel member of the family Reoviridae. <i>Virus Research</i> , 2011, 155, 397-405.	1.1	33
1331	Detection of diverse marine algal viruses in the South Sea regions of Korea by PCR amplification of the DNA polymerase and major capsid protein genes. <i>Virus Research</i> , 2011, 159, 43-50.	1.1	13
1332	The biology of coral metamorphosis: Molecular responses of larvae to inducers of settlement and metamorphosis. <i>Developmental Biology</i> , 2011, 353, 411-419.	0.9	76
1333	De novo transcriptome sequencing in <i>Salvia miltiorrhiza</i> to identify genes involved in the biosynthesis of active ingredients. <i>Genomics</i> , 2011, 98, 272-279.	1.3	181
1334	EST profiling of resistant and susceptible <i>Hevea</i> infected by <i>Microcyclus ulei</i> . <i>Physiological and Molecular Plant Pathology</i> , 2011, 76, 126-136.	1.3	22
1335	Mining online genomic resources in <i>Anolis carolinensis</i> facilitates rapid and inexpensive development of cross-species microsatellite markers for the <i>Anolis</i> lizard genus. <i>Molecular Ecology Resources</i> , 2011, 11, 126-133.	2.2	20
1336	Identification of genes responding to nematode infection in red grouse. <i>Molecular Ecology Resources</i> , 2011, 11, 305-313.	2.2	16
1337	PRGmatic: an efficient pipeline for collating genome-enriched second-generation sequencing data using a provisional reference genome™. <i>Molecular Ecology Resources</i> , 2011, 11, 743-748.	2.2	52
1338	Developmental Transcriptomic Features of the Carcinogenic Liver Fluke, <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1208.	1.3	72
1339	Akemetopon, a new genus containing three new species of planthoppers (Hemiptera: Fulgoroidea: Tj ETQq1 1 0.784314 rgBT /Overl	0.2	2
1340	Transposable elements in <i>Phyllostachys pubescens</i> (Poaceae) genome survey sequences and the full-length cDNA sequences, and their association with simple-sequence repeats. <i>Genetics and Molecular Research</i> , 2011, 10, 3026-3037.	0.3	6
1341	Characterization of novel developed expressed sequence tag (EST)-derived simple sequence repeat (SSR) markers and their application in diversity analysis of eggplant. <i>African Journal of Biotechnology</i> , 2011, 10, 9023-9031.	0.3	8
1342	Soybean Rust: Five Years of Research. , 0, , .		0
1343	A Genomic Approach to Study Anthocyanin Synthesis and Flower Pigmentation in Passionflowers. <i>Journal of Nucleic Acids</i> , 2011, 2011, 1-17.	0.8	22
1344	Functional characterization of three cDNA libraries from the diploid wheat <i>Triticum monoccocum</i> (AmAm) with different growth habits. <i>Cereal Research Communications</i> , 2011, 39, 475-486.	0.8	0
1345	The Barley Microarray. A Community Vision and Application to Abiotic Stress. <i>Czech Journal of Genetics and Plant Breeding</i> , 2005, 41, 144-152.	0.4	7
1346	Expressed sequenced tags profiling of resistant and susceptible Gyr x Holstein cattle infested with the tick <i>Rhipicephalus</i> (<i>Boophilus</i>) <i>microplus</i> . <i>Genetics and Molecular Research</i> , 2011, 10, 3803-3816.	0.3	7
1347	Comparing De Novo Genome Assembly: The Long and Short of It. <i>PLoS ONE</i> , 2011, 6, e19175.	1.1	95

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1348	A Deletion in Exon 9 of the LIPH Gene Is Responsible for the Rex Hair Coat Phenotype in Rabbits (<i>Oryctolagus cuniculus</i>). PLoS ONE, 2011, 6, e19281.	1.1	27
1349	Identification of Hyaloperonospora arabidopsidis Transcript Sequences Expressed during Infection Reveals Isolate-Specific Effectors. PLoS ONE, 2011, 6, e19328.	1.1	59
1350	Genome-Wide Gene Expression Profiling of Fertilization Competent Mycelium in Opposite Mating Types in the Heterothallic Fungus Podospora anserina. PLoS ONE, 2011, 6, e21476.	1.1	51
1351	Transcriptome Sequencing and De Novo Analysis for Yesso Scallop (<i>Patinopecten yessoensis</i>) Using 454 GS FLX. PLoS ONE, 2011, 6, e21560.	1.1	204
1352	Castor Bean Organelle Genome Sequencing and Worldwide Genetic Diversity Analysis. PLoS ONE, 2011, 6, e21743.	1.1	88
1353	MACSE: Multiple Alignment of Coding SEquences Accounting for Frameshifts and Stop Codons. PLoS ONE, 2011, 6, e22594.	1.1	546
1354	Generation, Annotation and Analysis of First Large-Scale Expressed Sequence Tags from Developing Fiber of <i>Gossypium barbadense</i> L. PLoS ONE, 2011, 6, e22758.	1.1	25
1355	Genome-Wide Functional Analysis of the Cotton Transcriptome by Creating an Integrated EST Database. PLoS ONE, 2011, 6, e26980.	1.1	102
1356	Novel Tools for Conservation Genomics: Comparing Two High-Throughput Approaches for SNP Discovery in the Transcriptome of the European Hake. PLoS ONE, 2011, 6, e28008.	1.1	59
1357	Antifouling Activities against Colonizer Marine Bacteria of Extracts from Marine Invertebrates Collected in the Colombian Caribbean Sea and on the Brazilian Coast (Santa Catarina). Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2011, 66, 515-526.	0.6	5
1358	Parallel Sequencing of Expressed Sequence Tags from Two Complementary DNA Libraries for High and Low Phosphorus Adaptation in Common Beans. Plant Genome, 2011, 4, .	1.6	6
1360	Bioinformatic studies of the wheat glutaredoxin gene family and functional analysis of the ROXY1 orthologues. Functional Plant Biology, 2011, 38, 25.	1.1	3
1361	Expression study on the porcine PTHLH gene and its relationship with sow teat number. Journal of Animal Breeding and Genetics, 2011, 128, 344-353.	0.8	11
1362	Differential Gene Expression in Cotton Defence Response to <i>Verticillium dahliae</i> by SSH. Journal of Phytopathology, 2011, 159, 606-615.	0.5	53
1363	cDNA representational difference analysis for identifying transcripts regulated under anhydrobiosis in the tardigrade <i>Milnesium tardigradum</i> . Journal of Zoological Systematics and Evolutionary Research, 2011, 49, 127-132.	0.6	5
1364	Large-scale transcriptome analysis in chickpea (<i>Cicer arietinum</i> L.), an orphan legume crop of the semi-arid tropics of Asia and Africa. Plant Biotechnology Journal, 2011, 9, 922-931.	4.1	250
1365	The DUF579 domain containing proteins IRX15 and IRX15a affect xylan synthesis in Arabidopsis. Plant Journal, 2011, 66, 387-400.	2.8	120
1366	Distinct evolutionary patterns of <i>Oryza glaberrima</i> deciphered by genome sequencing and comparative analysis. Plant Journal, 2011, 66, 796-805.	2.8	28

#	ARTICLE	IF	CITATIONS
1367	The biosynthesis of Caryophyllaceae-like cyclic peptides in <i>Saponaria vaccaria</i> L. from DNA-encoded precursors. <i>Plant Journal</i> , 2011, 67, 682-690.	2.8	53
1368	Revealing impaired pathways in the <i>an11</i> mutant by high-throughput characterization of <i>Petunia axillaris</i> and <i>Petunia inflata</i> transcriptomes. <i>Plant Journal</i> , 2011, 68, 11-27.	2.8	35
1369	Comparative deep transcriptional profiling of four developing oilseeds. <i>Plant Journal</i> , 2011, 68, 1014-1027.	2.8	241
1370	Narrowing down the apricot <i>Plum pox virus</i> resistance locus and comparative analysis with the peach genome syntenic region. <i>Molecular Plant Pathology</i> , 2011, 12, 535-547.	2.0	28
1371	Analysis of expressed sequence tags from Maize mosaic rhabdovirus-infected gut tissues of <i>Peregrinus maidis</i> reveals the presence of key components of insect innate immunity. <i>Insect Molecular Biology</i> , 2011, 20, 225-242.	1.0	30
1372	Molecular characterization of three genes encoding aminopeptidases N in the poplar leaf beetle <i>Chrysomela tremulae</i> . <i>Insect Molecular Biology</i> , 2011, 20, 267-278.	1.0	1
1373	Pyrosequencing the midgut transcriptome of the brown planthopper, <i>Nilaparvata lugens</i> . <i>Insect Molecular Biology</i> , 2011, 20, 745-762.	1.0	30
1374	Evolutionary and functional analyses of cytochrome P450A promoter polymorphisms in natural populations. <i>Molecular Ecology</i> , 2011, 20, 5236-5247.	2.0	21
1375	ANALYSIS OF EXPRESSED SEQUENCE TAGS FROM THE GREEN ALGA <i>DUNALIELLA SALINA</i> (CHLOROPHYTA). <i>Journal of Phycology</i> , 2011, 47, 1454-1460.	1.0	13
1376	Diverse Helotiales associated with the roots of three species of Arctic Ericaceae provide no evidence for host specificity. <i>New Phytologist</i> , 2011, 191, 515-527.	3.5	150
1377	Genomic expression dominance in the natural allopolyploid <i>Coffea arabica</i> is massively affected by growth temperature. <i>New Phytologist</i> , 2011, 192, 760-774.	3.5	81
1378	Exploring the Transcriptome Landscape of Pomegranate Fruit Peel for Natural Product Biosynthetic Gene and SSR Marker Discovery. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 800-813.	4.1	61
1379	Isolation, phylogeny and evolution of the SymRK gene in the legume genus <i>Lupinus</i> L. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 49-61.	1.2	13
1380	Classification and characterization of putative cytochrome P450 genes from <i>Panax ginseng</i> C. A. Meyer. <i>Biochemistry (Moscow)</i> , 2011, 76, 1347-1359.	0.7	23
1381	Muramidases found in the foregut microbiome of the Tammar wallaby can direct cell aggregation and biofilm formation. <i>ISME Journal</i> , 2011, 5, 341-350.	4.4	9
1382	Acoelomorph flatworms are deuterostomes related to <i>Xenoturbella</i> . <i>Nature</i> , 2011, 470, 255-258.	13.7	400
1383	Eutherian mammals use diverse strategies to initiate X-chromosome inactivation during development. <i>Nature</i> , 2011, 472, 370-374.	13.7	394
1384	Investigation of genome structure of a cinnamyl alcohol dehydrogenase locus in a basal angiosperm hardwood species, <i>Liriodendron tulipifera</i> L., reveals low synteny. <i>Journal of Systematics and Evolution</i> , 2011, 49, 396-405.	1.6	2

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1385	Differentially expressed cDNAs in <i>Alternaria alternata</i> treated with 2-propenyl isothiocyanate. <i>Microbiological Research</i> , 2011, 166, 566-577.	2.5	7
1386	454 sequencing of pooled BAC clones on chromosome 3H of barley. <i>BMC Genomics</i> , 2011, 12, 246.	1.2	14
1387	An insight into the sialome of <i>Simulium guianense</i> (DIPTERA:SIMULIIDAE), the main vector of River Blindness Disease in Brazil. <i>BMC Genomics</i> , 2011, 12, 612.	1.2	19
1388	Polyphenism in social insects: insights from a transcriptome-wide analysis of gene expression in the life stages of the key pollinator, <i>Bombus terrestris</i> . <i>BMC Genomics</i> , 2011, 12, 623.	1.2	63
1389	In silicocomparative analysis of SSR markers in plants. <i>BMC Plant Biology</i> , 2011, 11, 15.	1.6	104
1390	Transcriptome mining, functional characterization, and phylogeny of a large terpene synthase gene family in spruce (<i>Picea</i> spp.). <i>BMC Plant Biology</i> , 2011, 11, 43.	1.6	120
1391	Comparative analysis of expressed sequence tags (ESTs) between drought-tolerant and -susceptible genotypes of chickpea under terminal drought stress. <i>BMC Plant Biology</i> , 2011, 11, 70.	1.6	86
1392	Incomplete homogenization of 18 S ribosomal DNA coding regions in <i>Arabidopsis thaliana</i> . <i>BMC Research Notes</i> , 2011, 4, 93.	0.6	21
1393	Denitrifying polyphosphate accumulating organisms population and nitrite reductase gene diversity shift in a DEPHANOX-type activated sludge system fed with municipal wastewater. <i>Journal of Bioscience and Bioengineering</i> , 2011, 111, 185-192.	1.1	28
1394	Red and Green Algal Monophyly and Extensive Gene Sharing Found in a Rich Repertoire of Red Algal Genes. <i>Current Biology</i> , 2011, 21, 328-333.	1.8	101
1395	Post-transcriptional gene silencing of root-knot nematode in transformed soybean roots. <i>Experimental Parasitology</i> , 2011, 127, 90-99.	0.5	85
1396	Deep insights into <i>Dictyocaulus viviparus</i> transcriptomes provides unique prospects for new drug targets and disease intervention. <i>Biotechnology Advances</i> , 2011, 29, 261-271.	6.0	31
1397	Transcript profiling and gene characterization of three fatty acid desaturase genes in high, moderate, and low linolenic acid genotypes of flax (<i>Linum usitatissimum</i>) and their role in linolenic acid accumulation. <i>Genome</i> , 2011, 54, 471-483.	0.9	41
1398	Characterization of barley (<i>Hordeum vulgare</i> L.) NAC transcription factors suggests conserved functions compared to both monocots and dicots. <i>BMC Research Notes</i> , 2011, 4, 302.	0.6	88
1399	EST-Based Approach for Dissecting Root Architecture in Barley Using Mutant Traits of Other Species. , 2011, , 11-72.		3
1400	Involvement of pore-forming molecules in immune defense and development of the Mediterranean mussel (<i>Mytilus galloprovincialis</i>). <i>Developmental and Comparative Immunology</i> , 2011, 35, 1017-1031.	1.0	33
1401	Base-calling for next-generation sequencing platforms. <i>Briefings in Bioinformatics</i> , 2011, 12, 489-497.	3.2	125
1402	Genome-wide survey of alternative splicing in the grass <i>Brachypodium distachyon</i> : a emerging model biosystem for plant functional genomics. <i>Biotechnology Letters</i> , 2011, 33, 629-636.	1.1	23

#	ARTICLE	IF	CITATIONS
1403	Isolation, Phylogeny and Expression Patterns of AP2-Like Genes in Apple (<i>Malus domestica</i> Borkh). <i>Plant Molecular Biology Reporter</i> , 2011, 29, 209-216.	1.0	34
1404	EST Analysis Predicts Putatively Causative Genes Underlying the Pharmaceutical Application of <i>Glycyrrhiza uralensis</i> Fisch. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 814-824.	1.0	6
1405	Development and characterization of microsatellite markers in pomegranate (<i>Punica granatum</i> L.). <i>Molecular Breeding</i> , 2011, 27, 119-128.	1.0	49
1406	In silico gene expression analysis in <i>Codonopsis lanceolata</i> root. <i>Molecular Biology Reports</i> , 2011, 38, 3541-3549.	1.0	5
1407	Development of expressed sequence tag resources for Vanda Mimi Palmer and data mining for EST-SSR. <i>Molecular Biology Reports</i> , 2011, 38, 3903-3909.	1.0	30
1408	Isolation and characterization of an AP2/ERF-RAV transcription factor BnaRAV-1-HY15 in <i>Brassica napus</i> L. HuYou15. <i>Molecular Biology Reports</i> , 2011, 38, 3921-3928.	1.0	37
1409	An assemblage of closteroviruses infects Hawaiian ti (<i>Cordyline fruticosa</i> L.). <i>Virus Genes</i> , 2011, 42, 254-260.	0.7	19
1410	Molecular characterization of a new tospovirus infecting soybean. <i>Virus Genes</i> , 2011, 43, 289-295.	0.7	63
1411	Analysis of ESTs generated from inner bark tissue of an <i>Acacia auriculiformis</i> x <i>Acacia mangium</i> hybrid. <i>Tree Genetics and Genomes</i> , 2011, 7, 143-152.	0.6	18
1412	EST-derived SSR markers in <i>Jatropha curcas</i> L.: development, characterization, polymorphism, and transferability across the species/genera. <i>Tree Genetics and Genomes</i> , 2011, 7, 207-219.	0.6	87
1413	Organization of the chromosome region harboring a FLORICAULA/LEAFY gene in <i>Liriodendron</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 373-384.	0.6	4
1414	Identification and expression profiling of drought-regulated genes in mulberry (<i>Morus</i> sp.) by suppression subtractive hybridization of susceptible and tolerant cultivars. <i>Tree Genetics and Genomes</i> , 2011, 7, 725-738.	0.6	28
1415	Identification of suitable reference genes for normalization of qPCR data in comparative transcriptomics analyses in the Triticeae. <i>Planta</i> , 2011, 233, 163-173.	1.6	120
1416	Heterologous expression of two FAD-dependent oxidases with (S)-tetrahydroprotoberberine oxidase activity from <i>Arge mone mexicana</i> and <i>Berberis wilsoniae</i> in insect cells. <i>Planta</i> , 2011, 233, 1185-1197.	1.6	35
1417	EST analysis of functional genes associated with cell wall biosynthesis and modification in the secondary xylem of the yellow poplar (<i>Liriodendron tulipifera</i>) stem during early stage of tension wood formation. <i>Planta</i> , 2011, 234, 959-977.	1.6	37
1418	Identification of vimentin- and elastin-like transcripts specifically expressed in developing notochord of Atlantic salmon (<i>Salmo salar</i> L.). <i>Cell and Tissue Research</i> , 2011, 346, 191-202.	1.5	9
1419	Identification of a phylogenetically distinct orthobunyavirus from group C. <i>Archives of Virology</i> , 2011, 156, 1173-1184.	0.9	15
1420	Identification and Analysis of Muscle-Related Protein Isoforms Expressed in the White Muscle of the Mandarin Fish (<i>Siniperca chuatsi</i>). <i>Marine Biotechnology</i> , 2011, 13, 151-162.	1.1	27

#	ARTICLE	IF	CITATIONS
1421	A Review of the Major Penaeid Shrimp EST Studies and the Construction of a Shrimp Transcriptome Database Based on the ESTs from Four Penaeid Shrimp. <i>Marine Biotechnology</i> , 2011, 13, 608-621.	1.1	49
1422	Major chimpanzee-specific structural changes in sperm development-associated genes. <i>Functional and Integrative Genomics</i> , 2011, 11, 507-517.	1.4	6
1423	Transcriptome-wide identification and stress properties of the 14-3-3 gene family in cotton (<i>Gossypium</i>) Tj ETQq0 0.0 rgBT /Overlock 10	1.4	44
1424	Complete sequencing and comparative analyses of the pepper (<i>Capsicum annuum</i> L.) plastome revealed high frequency of tandem repeats and large insertion/deletions on pepper plastome. <i>Plant Cell Reports</i> , 2011, 30, 217-229.	2.8	67
1425	Gene identification in black cohosh (<i>Actaea racemosa</i> L.): expressed sequence tag profiling and genetic screening yields candidate genes for production of bioactive secondary metabolites. <i>Plant Cell Reports</i> , 2011, 30, 613-629.	2.8	13
1426	Analysis of expressed sequence tags derived from a compatible <i>Mycosphaerella fijiensis</i> banana interaction. <i>Plant Cell Reports</i> , 2011, 30, 913-928.	2.8	33
1427	Generation and analysis of expressed sequence tags from a normalized cDNA library of young leaf from Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro). <i>Plant Cell Reports</i> , 2011, 30, 2045-2057.	2.8	24
1428	Development of 1,030 genomic SSR markers in switchgrass. <i>Theoretical and Applied Genetics</i> , 2011, 122, 677-686.	1.8	63
1429	Downy mildew (PI 8 and PI 14) and rust (R Adv) resistance genes reside in close proximity to tandemly duplicated clusters of non-TIR-like NBS-LRR-encoding genes on sunflower chromosomes 1 and 13. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1211-1221.	1.8	60
1430	Positive Darwinian Selection Drives the Evolution of the Morphology-Related Gene, EPCAM, in Particularly Species-Rich Lineages of African Cichlid Fishes. <i>Journal of Molecular Evolution</i> , 2011, 73, 1-9.	0.8	9
1431	Isolation and expression analysis of LEA genes in peanut (<i>Arachis hypogaea</i> L.). <i>Journal of Biosciences</i> , 2011, 36, 223-228.	0.5	19
1432	Profiling the Developing <i>Jatropha curcas</i> L. Seed Transcriptome by Pyrosequencing. <i>Bioenergy Research</i> , 2011, 4, 211-221.	2.2	46
1433	A comparative analysis of parallel computing approaches for genome assembly. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2011, 3, 57-63.	2.2	3
1434	Development of fifty-one novel EST-SSR loci for use in rockfish (genus <i>Sebastes</i>). <i>Conservation Genetics Resources</i> , 2011, 3, 335-340.	0.4	1
1435	Isolation of novel microsatellites for the howler monkey bot fly. <i>Conservation Genetics Resources</i> , 2011, 3, 403-407.	0.4	3
1437	Bioinformatic analysis of fruit-specific expressed sequence tag libraries of <i>Diospyros kaki</i> Thunb.: view at the transcriptome at different developmental stages. <i>3 Biotech</i> , 2011, 1, 35-45.	1.1	8
1438	Discovery and expression assessment of the AP2-like genes in <i>Hordeum vulgare</i> . <i>Acta Physiologiae Plantarum</i> , 2011, 33, 1639-1649.	1.0	14
1439	Transcriptomics and molecular evolutionary rate analysis of the bladderwort (<i>Utricularia</i>), a carnivorous plant with a minimal genome. <i>BMC Plant Biology</i> , 2011, 11, 101.	1.6	50

#	ARTICLE	IF	CITATIONS
1440	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 131.	1.6	109
1441	Identification, utilisation and mapping of novel transcriptome-based markers from blackcurrant (<i>Ribes</i>) Tj ETQq1 1 0.784314 10BT /Over	1.6	49
1442	Construction and EST sequencing of full-length, drought stress cDNA libraries for common beans (<i>Phaseolus vulgaris</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 171.	1.6	28
1443	The taming of an impossible child: a standardized all-in approach to the phylogeny of Hymenoptera using public database sequences. <i>BMC Biology</i> , 2011, 9, 55.	1.7	54
1444	mRNA sequencing of <i>Eucalyptus urograndistrees</i> supplemented with flavonoids shows changes on metabolic process and decrease of lignification. <i>BMC Proceedings</i> , 2011, 5, .	1.8	0
1445	An integrated database of <i>Eucalyptus</i> spp. genome project. <i>BMC Proceedings</i> , 2011, 5, .	1.8	2
1446	Comparative transcriptome analysis of tree <i>Eucalyptus</i> species using RNAseq technology: analysis of genes interfering in wood quality aspects. <i>BMC Proceedings</i> , 2011, 5, .	1.8	3
1447	Functional characterization of cellulases identified from the cow rumen fungus <i>Neocallimastix patriciarum</i> W5 by transcriptomic and secretomic analyses. <i>Biotechnology for Biofuels</i> , 2011, 4, 24.	6.2	74
1448	Expressed sequence tags from <i>Atta laevigata</i> and identification of candidate genes for the control of pest leaf-cutting ants. <i>BMC Research Notes</i> , 2011, 4, 203.	0.6	3
1449	Comparison of RNA expression profiles on generations of <i>Porphyra yezoensis</i> (Rhodophyta), based on suppression subtractive hybridization (SSH). <i>BMC Research Notes</i> , 2011, 4, 428.	0.6	9
1450	Generation, analysis and functional annotation of expressed sequence tags from the ectoparasitic mite <i>Psoroptes ovis</i> . <i>Parasites and Vectors</i> , 2011, 4, 145.	1.0	12
1451	Gene discovery in <i>Triatoma infestans</i> . <i>Parasites and Vectors</i> , 2011, 4, 39.	1.0	7
1452	Major prospects for exploring canine vector borne diseases and novel intervention methods using 'omic technologies. <i>Parasites and Vectors</i> , 2011, 4, 53.	1.0	2
1453	Plant centromeric retrotransposons: a structural and cytogenetic perspective. <i>Mobile DNA</i> , 2011, 2, 4.	1.3	186
1454	An automated homology-based approach for identifying transposable elements. <i>BMC Bioinformatics</i> , 2011, 12, 130.	1.2	32
1455	iPhy: an integrated phylogenetic workbench for supermatrix analyses. <i>BMC Bioinformatics</i> , 2011, 12, 30.	1.2	10
1456	iAssembler: a package for de novo assembly of Roche-454/Sanger transcriptome sequences. <i>BMC Bioinformatics</i> , 2011, 12, 453.	1.2	120
1457	Combinatorial analysis and algorithms for quasispecies reconstruction using next-generation sequencing. <i>BMC Bioinformatics</i> , 2011, 12, 5.	1.2	72

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1458	A second-generation anchored genetic linkage map of the tammar wallaby (<i>Macropus eugenii</i>). <i>BMC Genetics</i> , 2011, 12, 72.	2.7	15
1459	Venom gland transcriptomes of two elapid snakes (<i>Bungarus multicinctus</i> and <i>Naja atra</i>) and evolution of toxin genes. <i>BMC Genomics</i> , 2011, 12, 1.	1.2	300
1460	Advancing the STMS genomic resources for defining new locations on the intraspecific genetic linkage map of chickpea (<i>Cicer arietinum</i> L.). <i>BMC Genomics</i> , 2011, 12, 117.	1.2	69
1461	Deep sequencing of the <i>Camellia sinensis</i> transcriptome revealed candidate genes for major metabolic pathways of tea-specific compounds. <i>BMC Genomics</i> , 2011, 12, 131.	1.2	374
1462	A further insight into the sialome of the tropical bont tick, <i>Amblyomma variegatum</i> . <i>BMC Genomics</i> , 2011, 12, 136.	1.2	81
1463	Genome structure of cotton revealed by a genome-wide SSR genetic map constructed from a BC1 population between <i>Gossypium hirsutum</i> and <i>G. barbadense</i> . <i>BMC Genomics</i> , 2011, 12, 15.	1.2	153
1464	Gene discovery in EST sequences from the wheat leaf rust fungus <i>Puccinia triticina</i> sexual spores, asexual spores and haustoria, compared to other rust and corn smut fungi. <i>BMC Genomics</i> , 2011, 12, 161.	1.2	55
1465	Physical mapping and BAC-end sequence analysis provide initial insights into the flax (<i>Linum</i>) Tj ETQq1 1 0.784314 _{rgBT} /Overlock 10 ₆₄	1.2	64
1466	The midgut transcriptome of <i>Phlebotomus</i> (<i>Larrousius</i>) <i>perniciosus</i> , a vector of <i>Leishmania infantum</i> : comparison of sugar fed and blood fed sand flies. <i>BMC Genomics</i> , 2011, 12, 223.	1.2	30
1467	Comprehensive transcriptome analysis of the highly complex <i>Pisum sativum</i> genome using next generation sequencing. <i>BMC Genomics</i> , 2011, 12, 227.	1.2	140
1468	BMP signaling components in embryonic transcriptomes of the hover fly <i>Episyrphus balteatus</i> (Syrphidae). <i>BMC Genomics</i> , 2011, 12, 278.	1.2	22
1469	Identification of SNP and SSR markers in eggplant using RAD tag sequencing. <i>BMC Genomics</i> , 2011, 12, 304.	1.2	193
1470	EuroPineDB: a high-coverage web database for maritime pine transcriptome. <i>BMC Genomics</i> , 2011, 12, 366.	1.2	59
1471	Comparative high-throughput transcriptome sequencing and development of SiESTa, the <i>Silene</i> EST annotation database. <i>BMC Genomics</i> , 2011, 12, 376.	1.2	25
1472	De novo assembly and characterization of the carrot transcriptome reveals novel genes, new markers, and genetic diversity. <i>BMC Genomics</i> , 2011, 12, 389.	1.2	178
1473	Attenuation of virulence in an apicomplexan hemoparasite results in reduced genome diversity at the population level. <i>BMC Genomics</i> , 2011, 12, 410.	1.2	31
1474	Transcriptomic analysis supports similar functional roles for the two thymuses of the tammar wallaby. <i>BMC Genomics</i> , 2011, 12, 420.	1.2	21
1475	Transcriptomic analysis of the interaction between <i>Helianthus annuus</i> and its obligate parasite <i>Plasmopara halstedii</i> shows single nucleotide polymorphisms in CRN sequences. <i>BMC Genomics</i> , 2011, 12, 498.	1.2	32

#	ARTICLE	IF	CITATIONS
1476	The 'PUCE CAFE' Project: the First 15K Coffee Microarray, a New Tool for Discovering Candidate Genes correlated to Agronomic and Quality Traits. <i>BMC Genomics</i> , 2011, 12, 5.	1.2	29
1477	The transcriptome of the novel dinoflagellate <i>Oxyrrhis marina</i> (Alveolata: Dinophyceae): response to salinity examined by 454 sequencing. <i>BMC Genomics</i> , 2011, 12, 519.	1.2	38
1478	Development of genomic resources for the narrow-leaved lupin (<i>Lupinus angustifolius</i>): construction of a bacterial artificial chromosome (BAC) library and BAC-end sequencing. <i>BMC Genomics</i> , 2011, 12, 521.	1.2	53
1479	Transcriptome analysis of orange-spotted grouper (<i>Epinephelus coioides</i>) spleen in response to Singapore grouper iridovirus. <i>BMC Genomics</i> , 2011, 12, 556.	1.2	186
1480	The maternal and early embryonic transcriptome of the milkweed bug <i>Oncopeltus fasciatus</i> . <i>BMC Genomics</i> , 2011, 12, 61.	1.2	110
1481	De novo characterization of the gametophyte transcriptome in bracken fern, <i>Pteridium aquilinum</i> . <i>BMC Genomics</i> , 2011, 12, 99.	1.2	113
1482	In silico secretome analysis approach for next generation sequencing transcriptomic data. <i>BMC Genomics</i> , 2011, 12, S14.	1.2	32
1483	Benefits of random-priming: Exhaustive survey of a cDNA library from lung tissue of a SARS patient. <i>Journal of Medical Virology</i> , 2011, 83, 574-586.	2.5	0
1484	Voltage sensitive phosphoinositide phosphatases of <i>Xenopus</i> : Their tissue distribution and voltage dependence. <i>Journal of Cellular Physiology</i> , 2011, 226, 2740-2746.	2.0	37
1485	Overview of the transcriptome profiles identified in hagfish, shark, and bichir: current issues arising from some nonmodel vertebrate taxa. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2011, 316B, 526-546.	0.6	31
1486	Development of a microarray for <i>Enchytraeus albidus</i> (Oligochaeta): preliminary tool with diverse applications. <i>Environmental Toxicology and Chemistry</i> , 2011, 30, 1395-1402.	2.2	17
1487	Identification of molecular motors in the Woods Hole squid, <i>Loligo pealei</i> : An expressed sequence tag approach. <i>Cytoskeleton</i> , 2011, 68, 566-577.	1.0	9
1488	Cloud computing paradigms for pleasingly parallel biomedical applications. <i>Concurrency Computation Practice and Experience</i> , 2011, 23, 2338-2354.	1.4	36
1489	Estrogen-responsive genes in macrophages of the bony fish gilthead seabream: A transcriptomic approach. <i>Developmental and Comparative Immunology</i> , 2011, 35, 840-849.	1.0	26
1490	Proteomic characterisation of <i>Echinococcus granulosus</i> hydatid cyst fluid from sheep, cattle and humans. <i>Journal of Proteomics</i> , 2011, 74, 1560-1572.	1.2	88
1491	Snake venomomics and venom gland transcriptomic analysis of Brazilian coral snakes, <i>Micrurus altirostris</i> and <i>M. corallinus</i> . <i>Journal of Proteomics</i> , 2011, 74, 1795-1809.	1.2	126
1492	Development of molecular assays for the identification of the 11 <i>Eimeria</i> species of the domestic rabbit (<i>Oryctolagus cuniculus</i>). <i>Veterinary Parasitology</i> , 2011, 176, 275-280.	0.7	44
1493	A gustatory receptor involved in host plant recognition for oviposition of a swallowtail butterfly. <i>Nature Communications</i> , 2011, 2, 542.	5.8	83

#	ARTICLE	IF	CITATIONS
1494	Characterization of 15 novel single nucleotide polymorphisms (SNPs) in the <i>Actinidia chinensis</i> species complex (Actinidiaceae). <i>American Journal of Botany</i> , 2011, 98, e100-e102.	0.8	5
1495	Computational Genomic Signatures. <i>Synthesis Lectures on Biomedical Engineering</i> , 2011, 6, 1-129.	0.1	3
1496	Genetic Structure and Demographic History of New World Screwworm Across Its Current Geographic Range. <i>Journal of Medical Entomology</i> , 2011, 48, 280-290.	0.9	20
1497	Deep sequencing of <i>Ptilidium</i> (Ptilidiaceae) suggests evolutionary stasis in liverwort plastid genome structure. <i>Plant Ecology and Evolution</i> , 2011, 144, 29-43.	0.3	37
1498	Mining and Characterization of Sequence Tagged Microsatellites from the Brown Planthopper <i>Nilaparvata lugens</i> . <i>Journal of Insect Science</i> , 2011, 11, 1-11.	0.6	16
1499	<i>Chryseobacterium piperi</i> sp. nov., isolated from a freshwater creek. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2162-2166.	0.8	36
1500	Metavir: a web server dedicated to virome analysis. <i>Bioinformatics</i> , 2011, 27, 3074-3075.	1.8	147
1501	Translational Genomics in Legumes Allowed Placing <i>In Silico</i> 5460 Unigenes on the Pea Functional Map and Identified Candidate Genes in <i>Pisum sativum</i> L. G3: Genes, Genomes, Genetics, 2011, 1, 93-103.	0.8	113
1502	Expansion of Hexose Transporter Genes Was Associated with the Evolution of Aerobic Fermentation in Yeasts. <i>Molecular Biology and Evolution</i> , 2011, 28, 131-142.	3.5	82
1503	Identification, Bioinformatics Analyses, and Expression of Immunoreactive Antigens of <i>Mycoplasma haemofelis</i> . <i>Vaccine Journal</i> , 2011, 18, 1275-1281.	3.2	3
1504	A Linkage Map of the Asian Tiger Mosquito (<i>Aedes albopictus</i>) Based on cDNA Markers. <i>Journal of Heredity</i> , 2011, 102, 102-112.	1.0	6
1505	Critical assessment of assembly strategies for non-model species mRNA-Seq data and application of next-generation sequencing to the comparison of C3 and C4 species. <i>Journal of Experimental Botany</i> , 2011, 62, 3093-3102.	2.4	88
1506	A discovery 70 years in the making: characterization of the Rose rosette virus. <i>Journal of General Virology</i> , 2011, 92, 1727-1732.	1.3	127
1507	SEED: efficient clustering of next-generation sequences. <i>Bioinformatics</i> , 2011, 27, 2502-2509.	1.8	54
1508	Development of SSR and gene-targeted markers for construction of a framework linkage map of <i>Catharanthus roseus</i> . <i>Annals of Botany</i> , 2011, 108, 321-336.	1.4	24
1509	Prospective Genomic Characterization of the German Enterohemorrhagic <i>Escherichia coli</i> O104:H4 Outbreak by Rapid Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2011, 6, e22751.	1.1	684
1510	Characterization and expression patterns of two 70-kDa heat shock protein genes in the intertidal red alga <i>Porphyra yezoensis</i> . <i>Botanica Marina</i> , 2011, 54, 447-455.	0.6	3
1511	Multilocus Sequence Typing Subtypes of Poultry <i>Clostridium perfringens</i> Isolates Demonstrate Disease Niche Partitioning. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1556-1567.	1.8	41

#	ARTICLE	IF	CITATIONS
1512	SalmonDB: a bioinformatics resource for <i>Salmo salar</i> and <i>Oncorhynchus mykiss</i> . Database: the Journal of Biological Databases and Curation, 2011, 2011, bar050-bar050.	1.4	28
1513	Gene Expression Profiling and Identification of Resistance Genes to <i>Aspergillus flavus</i> Infection in Peanut through EST and Microarray Strategies. Toxins, 2011, 3, 737-753.	1.5	67
1514	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. Genome Research, 2011, 21, 634-641.	2.4	105
1515	Detection and Molecular Characterization of Human Group C Rotavirus in Brazil. Intervirology, 2011, 54, 261-267.	1.2	10
1516	KABOOM! A new suffix array based algorithm for clustering expression data. Bioinformatics, 2011, 27, 3348-3355.	1.8	15
1517	Genic Microsatellite Markers in <i>Brassica rapa</i> : Development, Characterization, Mapping, and Their Utility in Other Cultivated and Wild Brassica Relatives. DNA Research, 2011, 18, 305-320.	1.5	77
1518	Analysis of Leaf and Root Transcriptomes of Soil-Grown <i>Avena barbata</i> Plants. Plant and Cell Physiology, 2011, 52, 317-332.	1.5	34
1519	Effective Population Size Is Positively Correlated with Levels of Adaptive Divergence among Annual Sunflowers. Molecular Biology and Evolution, 2011, 28, 1569-1580.	3.5	88
1520	Analysis of the workers head transcriptome of the Asian subterranean termite, <i>Coptotermes gestroi</i> . Bulletin of Entomological Research, 2011, 101, 383-391.	0.5	15
1521	Conserved and Divergent Rhythms of Crassulacean Acid Metabolism-Related and Core Clock Gene Expression in the Cactus <i>Opuntia ficus-indica</i> . Plant Physiology, 2011, 156, 1978-1989.	2.3	53
1522	Environmental Patterns Are Imposed on the Population Structure of <i>Escherichia coli</i> after Fecal Deposition. Applied and Environmental Microbiology, 2011, 77, 211-219.	1.4	70
1523	Activity-Based Metagenomic Screening and Biochemical Characterization of Bovine Ruminal Protozoan Glycoside Hydrolases. Applied and Environmental Microbiology, 2011, 77, 8106-8113.	1.4	52
1524	Whole-Genome Shotgun Sequencing of the Sulfur-Oxidizing Chemoautotroph <i>Tetrathiodibacter kashmirensis</i> . Journal of Bacteriology, 2011, 193, 5553-5554.	1.0	31
1525	Next-Gen sequencing of the transcriptome of triticale. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 181-184.	0.4	5
1526	Genome sequence assembly and annotation. , 2011, , 109-121.		0
1527	Differential gene expression analysis of <i>Paracoccidioides brasiliensis</i> during keratinocyte infection. Journal of Medical Microbiology, 2011, 60, 269-280.	0.7	10
1528	Development and characterization of 21 EST-derived microsatellite markers in <i>Vicia faba</i> (fava) Tj ETQq0 0.0 rgBT /Overlock 10	0.8	34
1529	saskPrimer — An automated pipeline for design of intron-spanning PCR primers in non-model organisms. , 2011, , .		0

#	ARTICLE	IF	CITATIONS
1530	The Plant Cell Wallâ€™Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
1531	Towards a System Level Understanding of Non-Model Organisms Sampled from the Environment: A Network Biology Approach. <i>PLoS Computational Biology</i> , 2011, 7, e1002126.	1.5	83
1532	Characterization of the partial RNA1 and RNA2 3â€™ untranslated region of Tomato ringspot virus isolates from North America. <i>Canadian Journal of Plant Pathology</i> , 2011, 33, 94-99.	0.8	11
1533	Extensive Genomic Variation within Clonal Complexes of <i>Neisseria meningitidis</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 1406-1418.	1.1	36
1534	A White Spruce Gene Catalog for Conifer Genome Analyses. <i>Plant Physiology</i> , 2011, 157, 14-28.	2.3	143
1535	Metagenomic Analysis of Fever, Thrombocytopenia and Leukopenia Syndrome (FTLS) in Henan Province, China: Discovery of a New Bunyavirus. <i>PLoS Pathogens</i> , 2011, 7, e1002369.	2.1	298
1536	The <i>Lymantria dispar</i> IPLB-Ld652Y Cell Line Transcriptome Comprises Diverse Virus-Associated Transcripts. <i>Viruses</i> , 2011, 3, 2339-2350.	1.5	16
1537	RNA-Seq Assembly â€™ Are We There Yet?. <i>Frontiers in Plant Science</i> , 2012, 3, 220.	1.7	112
1538	Complete Genome Sequence of Virulence-Enhancing Siphophage VHS1 from <i>Vibrio harveyi</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 2790-2796.	1.4	30
1539	The Transcriptome Analysis of <i>Strongyloides stercoralis</i> L3i Larvae Reveals Targets for Intervention in a Neglected Disease. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1513.	1.3	29
1540	Mobilizing the Genome of Lepidoptera through Novel Sequence Gains and End Creation by Non-autonomous Lep1 Helitrons. <i>DNA Research</i> , 2012, 19, 11-21.	1.5	17
1541	Nuclear Microsatellite Primers for the Endangered Relict Fir, <i>Abies pinsapo</i> (Pinaceae) and Cross-Amplification in Related Mediterranean Species. <i>International Journal of Molecular Sciences</i> , 2012, 13, 14243-14250.	1.8	18
1542	Biochemical Diversification through Foreign Gene Expression in Bdelloid Rotifers. <i>PLoS Genetics</i> , 2012, 8, e1003035.	1.5	143
1543	Discovery of High-Confidence Single Nucleotide Polymorphisms from Large-Scale De Novo Analysis of Leaf Transcripts of <i>Aegilops tauschii</i> , A Wild Wheat Progenitor. <i>DNA Research</i> , 2012, 19, 487-497.	1.5	29
1544	Rapid De Novo Evolution of X Chromosome Dosage Compensation in <i>Silene latifolia</i> , a Plant with Young Sex Chromosomes. <i>PLoS Biology</i> , 2012, 10, e1001308.	2.6	146
1545	Salivary Gland Transcriptomes and Proteomes of <i>Phlebotomus tobbi</i> and <i>Phlebotomus sergenti</i> , Vectors of Leishmaniasis. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1660.	1.3	66
1546	Development of 161 novel ESTâ€™SSR markers from <i>Lathyrus sativus</i> (Fabaceae). <i>American Journal of Botany</i> , 2012, 99, e379-90.	0.8	21
1547	A Systematically Improved High Quality Genome and Transcriptome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1455.	1.3	400

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1548	Diversity of Seed Storage Proteins of <i>Arachis hypogaea</i> and Related Species. <i>Crop Science</i> , 2012, 52, 1676-1688.	0.8	8
1549	Development and characterization of microsatellite markers for <i>Actaea racemosa</i> (black cohosh). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	0.8	5
1550	Microsatellite markers for the native Texas perennial grass, <i>Panicum hallii</i> (Poaceae). <i>American Journal of Botany</i> , 2012, 99, e114-6.	0.8	9
1551	<i>Elaeis oleifera</i> Genomic-SSR Markers: Exploitation in Oil Palm Germplasm Diversity and Cross-Amplification in Arecaceae. <i>International Journal of Molecular Sciences</i> , 2012, 13, 4069-4088.	1.8	33
1552	Analysis of the Genome of the Sexually Transmitted Insect Virus <i>Helicoverpa zea</i> Nudivirus 2. <i>Viruses</i> , 2012, 4, 28-61.	1.5	31
1553	Absence of HIV-1 Evolution in the Gut-Associated Lymphoid Tissue from Patients on Combination Antiviral Therapy Initiated during Primary Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002506.	2.1	108
1554	Cultivation-Independent Methods Reveal Differences among Bacterial Gut Microbiota in Triatomine Vectors of Chagas Disease. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1631.	1.3	92
1555	Genetic Basis of a Violation of Dollo's Law: Re-Evolution of Rotating Sex Combs in <i>Drosophila bipectinata</i> . <i>Genetics</i> , 2012, 192, 1465-1475.	1.2	13
1556	The spatial genetic differentiation of the legume pod borer, <i>Maruca vitrata</i> F. (Lepidoptera). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.5	12
1557	Identification of putative candidate genes involved in cuticle formation in <i>Prunus avium</i> (sweet). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	1.4	74
1558	Horizontal Transfers of Tc1 Elements between Teleost Fishes and Their Vertebrate Parasites, Lampreys. <i>Genome Biology and Evolution</i> , 2012, 4, 929-936.	1.1	45
1559	Sequences and transcriptional analysis of <i>Coffea arabica</i> var. Caturra and <i>Coffea liberica</i> plant responses to coffee berry borer <i>Hypothenemus hampei</i> (Coleoptera). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	0.8	10
1560	Uncovering Small RNA-Mediated Responses to Cold Stress in a Wheat Thermosensitive Genic Male-Sterile Line by Deep Sequencing. <i>Plant Physiology</i> , 2012, 159, 721-738.	2.3	166
1561	Transcriptome Analysis Using a High-Density Oligomicroarray under Drought Stress in Various Genotypes of Cassava: An Important Tropical Crop. <i>DNA Research</i> , 2012, 19, 335-345.	1.5	101
1562	Universal Amplification, Next-Generation Sequencing, and Assembly of HIV-1 Genomes. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3838-3844.	1.8	119
1563	High-Throughput Transcriptome Sequencing for Snp and Gene Discovery in a Moth. <i>Environmental Entomology</i> , 2012, 41, 997-1007.	0.7	5
1564	The Transcriptome Analysis and Comparison Explorer T-ACE: a platform-independent, graphical tool to process large RNAseq datasets of non-model organisms. <i>Bioinformatics</i> , 2012, 28, 777-783.	1.8	10
1565	An Insight Into the Sialotranscriptome of <i>Triatoma rubida</i> (Hemiptera: Heteroptera). <i>Journal of Medical Entomology</i> , 2012, 49, 563-572.	0.9	29

#	ARTICLE	IF	CITATIONS
1566	Bee algorithms for solving DNA fragment assembly problem with noisy and noiseless data. , 2012, , .		21
1567	Characterization of polymorphic microsatellites for the invasive grass <i>Microstegium vimineum</i> (Poaceae). American Journal of Botany, 2012, 99, e56-8.	0.8	7
1568	Cell Walls of Developing Wheat Starchy Endosperm: Comparison of Composition and RNA-Seq Transcriptome. Plant Physiology, 2012, 158, 612-627.	2.3	110
1569	Hybrid meta-heuristics for DNA fragment assembly problem for noiseless data. , 2012, , .		2
1570	A Framework for Scalable Genome Assembly on Clusters, Clouds, and Grids. IEEE Transactions on Parallel and Distributed Systems, 2012, 23, 2189-2197.	4.0	14
1571	PeroxiBase: a database for large-scale evolutionary analysis of peroxidases. Nucleic Acids Research, 2012, 41, D441-D444.	6.5	141
1572	Identification and development of polymorphic EST-SSR markers by sequence alignment in pepper, <i>Capsicum annuum</i> (Solanaceae). American Journal of Botany, 2012, 99, e59-61.	0.8	25
1573	An Insight into the Sialotranscriptome of <i>Triatoma matogrossensis</i> , a Kissing Bug Associated with Fogo Selvagem in South America. American Journal of Tropical Medicine and Hygiene, 2012, 86, 1005-1014.	0.6	38
1574	Identification of a novel single-stranded, circular DNA virus from bovine stool. Journal of General Virology, 2012, 93, 635-639.	1.3	38
1575	Quality and quantity of data recovered from massively parallel sequencing: Examples in Asparagales and Poaceae. American Journal of Botany, 2012, 99, 330-348.	0.8	115
1576	Molecular genetic and quantitative trait divergence associated with recent homoploid hybrid speciation: a study of <i>Senecio squalidus</i> (Asteraceae). Heredity, 2012, 108, 87-95.	1.2	47
1577	The Mitogen-Activated Protein Kinase BcSak1 of <i>Botrytis cinerea</i> Is Required for Pathogenic Development and Has Broad Regulatory Functions Beyond Stress Response. Molecular Plant-Microbe Interactions, 2012, 25, 802-816.	1.4	77
1578	miRNEST database: an integrative approach in microRNA search and annotation. Nucleic Acids Research, 2012, 40, D198-D204.	6.5	52
1579	Comprehensive Functional Analyses of Expressed Sequence Tags in Common Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	1.5	46
1580	Case Studies of the Spatial Heterogeneity of DNA Viruses in the Cystic Fibrosis Lung. American Journal of Respiratory Cell and Molecular Biology, 2012, 46, 127-131.	1.4	102
1581	AP2/ERF Transcription Factor in Rice: Genome-Wide Canvas and Syntenic Relationships between Monocots and Eudicots. Evolutionary Bioinformatics, 2012, 8, EBO.S9369.	0.6	162
1582	Distribution of Genes and Repetitive Elements in the <i>Diabrotica virgifera virgifera</i> Genome Estimated Using BAC Sequencing. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-9.	3.0	20
1583	PASSIOMA: Exploring Expressed Sequence Tags during Flower Development in <i>Passiflora</i> spp.. Comparative and Functional Genomics, 2012, 2012, 1-11.	2.0	18

#	ARTICLE	IF	CITATIONS
1584	A Next-Generation Sequencing Approach to Study the Transcriptomic Changes during the Differentiation of <i>Physarum</i> at the Single-Cell Level. <i>Gene Regulation and Systems Biology</i> , 2012, 6, GRSB.S10224.	2.3	7
1585	<i>Pseudoplusia includens</i> Dengue Virus Genome Organization and Expression Strategy. <i>Journal of Virology</i> , 2012, 86, 13127-13128.	1.5	6
1586	Regulation of the Photorespiratory <i>GLDPA</i> Gene in <i>C4</i> <i>Flaveria</i> : An Intricate Interplay of Transcriptional and Posttranscriptional Processes. <i>Plant Cell</i> , 2012, 24, 137-151.	3.1	40
1587	Genome sequencing of the lizard parasite <i>Leishmania tarentolae</i> reveals loss of genes associated to the intracellular stage of human pathogenic species. <i>Nucleic Acids Research</i> , 2012, 40, 1131-1147.	6.5	135
1588	Expression Dynamics of the <i>Medicago truncatula</i> Transcriptome during the Symbiotic Interaction with <i>Sinorhizobium meliloti</i> : Which Role for Nitric Oxide? <i>Plant Physiology</i> , 2012, 161, 425-439.	2.3	87
1589	454-Pyrosequencing of the Transcriptome in Leaf and Flower Buds of Japanese Apricot (<i>Prunus mume</i>) Tj ETQq1 1 0.784314 rgBT /Overl 239-250.	0.8	29
1590	Microsatellite development for an endangered riparian inhabitant, <i>Lilaeopsis schaffneriana</i> subsp. <i>recurva</i> (Apiaceae). <i>American Journal of Botany</i> , 2012, 99, e164-6.	0.8	3
1591	The Transcriptome of <i>Bathymodiolus azoricus</i> Gill Reveals Expression of Genes from Endosymbionts and Free-Living Deep-Sea Bacteria. <i>Marine Drugs</i> , 2012, 10, 1765-1783.	2.2	21
1592	Single Nucleotide Polymorphism Discovery in Cultivated Tomato via Sequencing by Synthesis. <i>Plant Genome</i> , 2012, 5, .	1.6	81
1593	Distribution and drivers of ectomycorrhizal fungal communities across the North American Arctic. <i>Ecosphere</i> , 2012, 3, 1-25.	1.0	84
1594	An Integrated Badnavirus Is Prevalent in Fig Germplasm. <i>Phytopathology</i> , 2012, 102, 1182-1189.	1.1	72
1595	DSAPSO: DNA sequence assembly using continuous Particle Swarm Optimization with Smallest Position Value rule. , 2012, , .		5
1596	Novel Bacterial Community Associated with 500-Year-Old Unpreserved Archaeological Wood from King Henry VIII's Tudor Warship the Mary Rose. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8822-8828.	1.4	13
1597	Extensive variation in surface lipoprotein gene content and genomic changes associated with virulence during evolution of a novel North American house finch epizootic strain of <i>Mycoplasma gallisepticum</i> . <i>Microbiology (United Kingdom)</i> , 2012, 158, 2073-2088.	0.7	43
1598	Next-Generation sequencing-based transcriptomic and proteomic analysis of the common reed, <i>Phragmites australis</i> (Poaceae), reveals genes involved in invasiveness and rhizome specificity. <i>American Journal of Botany</i> , 2012, 99, 232-247.	0.8	49
1599	The genome of flax (<i>Linum usitatissimum</i>) assembled <i>de novo</i> from short shotgun sequence reads. <i>Plant Journal</i> , 2012, 72, 461-473.	2.8	415
1600	Large-scale transcriptome characterization and mass discovery of SNPs in globe artichoke and its related taxa. <i>Plant Biotechnology Journal</i> , 2012, 10, 956-969.	4.1	33
1601	Gene expression profiling of the plant pathogenic basidiomycetous fungus <i>Rhizoctonia solani</i> AG 4 reveals putative virulence factors. <i>Mycologia</i> , 2012, 104, 1020-1035.	0.8	22

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1602	Single nucleotide polymorphisms in <i>Cryptomeria japonica</i> : their discovery and validation for genome mapping and diversity studies. <i>Tree Genetics and Genomes</i> , 2012, 8, 1213-1222.	0.6	21
1603	Sequencing papaya X and Y ^h chromosomes reveals molecular basis of incipient sex chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13710-13715.	3.3	264
1604	<i>Porphyra</i> (Bangiophyceae) Transcriptomes Provide Insights Into Red Algal Development And Metabolism. <i>Journal of Phycology</i> , 2012, 48, 1328-1342.	1.0	56
1605	Computational tools for viral metagenomics and their application in clinical research. <i>Virology</i> , 2012, 434, 162-174.	1.1	59
1606	Wheat <i>CBF</i> gene family: identification of polymorphisms in the CBF coding sequence. <i>Genome</i> , 2012, 55, 865-881.	0.9	16
1607	Polymorphisms in genes encoding mt-tRNA in female breast cancer in Poland. <i>Mitochondrial DNA</i> , 2012, 23, 106-111.	0.6	24
1608	Molecular Phylogenetic Analysis, Trichothecene Chemotype Patterns, and Variation in Aggressiveness of <i>Fusarium</i> Isolates Causing Head Blight in Wheat. <i>Plant Disease</i> , 2012, 96, 1016-1025.	0.7	41
1609	Application of High-Throughput Sequencing in Medicinal Plant Transcriptome Studies. <i>Drug Development Research</i> , 2012, 73, 487-498.	1.4	21
1610	Gene copy number and differential gene expression in haploid and diploid males of the stingless bee, <i>Melipona quadrifasciata</i> . <i>Insectes Sociaux</i> , 2012, 59, 587-598.	0.7	5
1611	A PCR-based marker for a locus conferring the aroma in Myanmar rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 887-896.	1.8	29
1612	Consensus mapping of major resistance genes and independent QTL for quantitative resistance to sunflower downy mildew. <i>Theoretical and Applied Genetics</i> , 2012, 125, 909-920.	1.8	48
1613	Differential gene expression in <i>Ulva prolifera</i> under low light and low temperature conditions. <i>Current Genetics</i> , 2012, 58, 235-244.	0.8	10
1614	Transcriptome profiling and in silico analysis of somatic embryos in Japanese larch (<i>Larix leptolepis</i>). <i>Plant Cell Reports</i> , 2012, 31, 1637-1657.	2.8	44
1615	Construction and analysis of EST libraries of the trans-polyisoprene producing plant, <i>Eucommia ulmoides</i> Oliver. <i>Planta</i> , 2012, 236, 1405-1417.	1.6	33
1616	Additive multiple k-mer transcriptome of the keelworm <i>Pomatoceros lamarckii</i> (Annelida; Serpulidae) reveals annelid trochophore transcription factor cassette. <i>Development Genes and Evolution</i> , 2012, 222, 325-339.	0.4	11
1617	Analyses of diversity among fungicidal <i>Anabaena</i> strains. <i>Journal of Applied Phycology</i> , 2012, 24, 1395-1405.	1.5	4
1618	Identification of genes that were differentially expressed and associated with fiber yield and quality using cDNA-AFLP and a backcross inbred line population. <i>Molecular Breeding</i> , 2012, 30, 975-985.	1.0	7
1619	SNP discovery, gene diversity, and linkage disequilibrium in wild populations of <i>Populus tremuloides</i> . <i>Tree Genetics and Genomes</i> , 2012, 8, 821-829.	0.6	86

#	ARTICLE	IF	CITATIONS
1620	Multiple plant hormones and cell wall metabolism regulate apple fruit maturation patterns and texture attributes. <i>Tree Genetics and Genomes</i> , 2012, 8, 1389-1406.	0.6	28
1621	Analysis of expressed sequence tags from mulberry (<i>Morus indica</i>) roots and implications for comparative transcriptomics and marker identification. <i>Tree Genetics and Genomes</i> , 2012, 8, 1437-1450.	0.6	16
1622	Constructing and random sequencing analysis of normalized cDNA library of testis tissue from oriental river prawn (<i>Macrobrachium nipponense</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 268-276.	0.4	27
1623	Enterohepatic <i>Helicobacter</i> spp. in colonic biopsies of dogs: molecular, histopathological and immunohistochemical investigations. <i>Veterinary Microbiology</i> , 2012, 159, 107-114.	0.8	21
1624	Analysis of the genome of leporid herpesvirus 4. <i>Virology</i> , 2012, 433, 183-191.	1.1	5
1625	Population structure of Blackberry yellow vein associated virus, an emerging crinivirus. <i>Virus Research</i> , 2012, 169, 272-275.	1.1	22
1626	RCDA: A highly sensitive and specific alternatively spliced transcript assembly tool featuring upstream consecutive exon structures. <i>Genomics</i> , 2012, 100, 357-362.	1.3	1
1627	Development of new microsatellite markers derived from expressed sequence tags for the great scallop (<i>Pecten maximus</i>). <i>Conservation Genetics Resources</i> , 2012, 4, 931-934.	0.4	6
1628	Development of EST database and transcriptome analysis in the leaves of <i>Brassica rapa</i> using a newly developed pipeline. <i>Genes and Genomics</i> , 2012, 34, 671-679.	0.5	4
1629	<i>Enterococcus plantarum</i> sp. nov., isolated from plants. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 1499-1505.	0.8	29
1630	A Multiclass Classification Tool Using Cloud Computing Architecture. , 2012, , .		4
1631	A Hybrid PSO-Based Algorithm for Solving DNA Fragment Assembly Problem. , 2012, , .		2
1632	Gene cloning, molecular modeling, and phylogenetics of serine protease P32 and serine carboxypeptidase SCP1 from nematophagous fungi <i>Pochonia rubescens</i> and <i>Pochonia chlamydosporia</i> . <i>Canadian Journal of Microbiology</i> , 2012, 58, 815-827.	0.8	25
1633	Use of Comparative Genomics to Develop EST-SSRs for Red Drum (<i>Sciaenops ocellatus</i>). <i>Marine Biotechnology</i> , 2012, 14, 672-680.	1.1	4
1634	Comparative transcriptome analysis of <i>Paracoccidioides brasiliensis</i> during <i>in vitro</i> adhesion to type I collagen and fibronectin: identification of potential adhesins. <i>Research in Microbiology</i> , 2012, 163, 182-191.	1.0	19
1635	Isolation and expression analysis of CiNIP5, a citrus boron transport gene involved in tolerance to boron deficiency. <i>Scientia Horticulturae</i> , 2012, 142, 149-154.	1.7	25
1636	SEQassembly: A Practical Tools Program for Coding Sequences Splicing. <i>Physics Procedia</i> , 2012, 33, 3-7.	1.2	0
1637	Rabies virus distribution in tissues and molecular characterization of strains from naturally infected non-hematophagous bats. <i>Virus Research</i> , 2012, 165, 119-125.	1.1	33

#	ARTICLE	IF	CITATIONS
1638	Dating cryptodiran nodes: Origin and diversification of the turtle superfamily Testudinoidea. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 496-507.	1.2	63
1639	VpWRKY3, a biotic and abiotic stress-related transcription factor from the Chinese wild <i>Vitis pseudoreticulata</i> . <i>Plant Cell Reports</i> , 2012, 31, 2109-2120.	2.8	68
1640	Rapid development of molecular resources for a freshwater mussel, <i>Villosa liouana</i> (Bivalvia:Unionidae), using an RNA-seq-based approach. <i>Freshwater Science</i> , 2012, 31, 695-708.	0.9	31
1641	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	3.5	210
1642	A root-knot nematode-secreted protein is injected into giant cells and targeted to the nuclei. <i>New Phytologist</i> , 2012, 194, 924-931.	3.5	85
1643	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. <i>American Journal of Botany</i> , 2012, 99, 209-218.	0.8	80
1644	Strategies for transcriptome analysis in nonmodel plants. <i>American Journal of Botany</i> , 2012, 99, 267-276.	0.8	112
1645	High incidence of seed transmission of Papaya ringspot virus and Watermelon mosaic virus, two viruses newly identified in <i>Robinia pseudoacacia</i> . <i>European Journal of Plant Pathology</i> , 2012, 134, 227-230.	0.8	20
1646	Phylogenetic characterization and the expression of recombinant C-reactive protein from the Asian seabass (<i>Lateolabrax japonicus</i>). <i>Aquaculture</i> , 2012, 338-341, 13-22.	1.7	5
1647	The sialotranscriptome of <i>Antricola delacruzi</i> female ticks is compatible with non-hematophagous behavior and an alternative source of food. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 332-342.	1.2	52
1648	Transcriptome and full-length cDNA resources for the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major insect pest of pine forests. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 525-536.	1.2	93
1649	De novo sequencing and analysis of the termite mushroom (<i>Termitomyces albuminosus</i>) transcriptome to discover putative genes involved in bioactive component biosynthesis. <i>Journal of Bioscience and Bioengineering</i> , 2012, 114, 228-231.	1.1	17
1650	Biochemical, physicochemical and molecular characterization of a genuine 2-Cys-peroxiredoxin purified from cowpea [<i>Vigna unguiculata</i> (L.) Walpers] leaves. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2012, 1820, 1128-1140.	1.1	2
1651	Differential expression and intrachromosomal evolution of the sghC1q genes in zebrafish (<i>Danio rerio</i>). <i>Journal of Molecular Evolution</i> , 2012, 74, 107-114.	1.0	11
1652	Gene expression analysis of clams <i>Ruditapes philippinarum</i> and <i>Ruditapes decussatus</i> following bacterial infection yields molecular insights into pathogen resistance and immunity. <i>Developmental and Comparative Immunology</i> , 2012, 36, 140-149.	1.0	51
1653	Transcriptomic signatures of attachment, NF- κ B suppression and IFN stimulation in the catfish gill following columnaris bacterial infection. <i>Developmental and Comparative Immunology</i> , 2012, 38, 169-180.	1.0	163
1654	Identification of a novel metal binding protein, segon, in plasma of the eastern oyster, <i>Crassostrea virginica</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2012, 163, 74-85.	0.7	22
1655	Gene transcription response to weathering of K-bearing minerals by <i>Aspergillus fumigatus</i> . <i>Chemical Geology</i> , 2012, 306-307, 1-9.	1.4	48

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1656	RNA-seq analysis of mucosal immune responses reveals signatures of intestinal barrier disruption and pathogen entry following <i>Edwardsiella ictaluri</i> infection in channel catfish, <i>Ictalurus punctatus</i> . <i>Fish and Shellfish Immunology</i> , 2012, 32, 816-827.	1.6	210
1657	A novel hepcidin-like in turbot (<i>Scophthalmus maximus</i> L.) highly expressed after pathogen challenge but not after iron overload. <i>Fish and Shellfish Immunology</i> , 2012, 32, 879-889.	1.6	50
1658	A new type of Kazal proteinase inhibitor related to shrimp <i>Penaeus</i> (<i>Litopenaeus</i>) <i>vannamei</i> immunity. <i>Fish and Shellfish Immunology</i> , 2012, 33, 134-137.	1.6	8
1659	The oomycete <i>Pythium oligandrum</i> expresses putative effectors during mycoparasitism of <i>Phytophthora infestans</i> and is amenable to transformation. <i>Fungal Biology</i> , 2012, 116, 24-41.	1.1	74
1660	EST-based identification of immune-relevant genes from spleen of Indian catfish, <i>Clarias batrachus</i> (Linnaeus, 1758). <i>Gene</i> , 2012, 502, 53-59.	1.0	8
1661	Smelt was the likely beneficiary of an antifreeze gene laterally transferred between fishes. <i>BMC Evolutionary Biology</i> , 2012, 12, 190.	3.2	30
1662	The mammary gland-specific marsupial ELP and eutherian CTI share a common ancestral gene. <i>BMC Evolutionary Biology</i> , 2012, 12, 80.	3.2	12
1663	Ancient gene transfer from algae to animals: Mechanisms and evolutionary significance. <i>BMC Evolutionary Biology</i> , 2012, 12, 83.	3.2	33
1664	Identification and expression analysis of methyl jasmonate responsive ESTs in paclitaxel producing <i>Taxus cuspidata</i> suspension culture cells. <i>BMC Genomics</i> , 2012, 13, 148.	1.2	37
1665	Evolution of vertebrate interferon inducible transmembrane proteins. <i>BMC Genomics</i> , 2012, 13, 155.	1.2	92
1666	Characterization of host microRNAs that respond to DNA virus infection in a crustacean. <i>BMC Genomics</i> , 2012, 13, 159.	1.2	103
1667	Development and application of a 6.5 million feature Affymetrix Genechip® for massively parallel discovery of single position polymorphisms in lettuce (<i>Lactuca</i> spp.). <i>BMC Genomics</i> , 2012, 13, 185.	1.2	36
1668	A high-resolution map of the Nile tilapia genome: a resource for studying cichlids and other percomorphs. <i>BMC Genomics</i> , 2012, 13, 222.	1.2	104
1669	Gene expression and proteomic analysis of the formation of <i>Phakopsora pachyrhizi</i> appressoria. <i>BMC Genomics</i> , 2012, 13, 269.	1.2	15
1670	Developing the anemone <i>Aiptasia</i> as a tractable model for cnidarian-dinoflagellate symbiosis: the transcriptome of aposymbiotic <i>A. pallida</i> . <i>BMC Genomics</i> , 2012, 13, 271.	1.2	99
1671	Comparative transcriptome analysis between planarian <i>Dugesia japonica</i> and other platyhelminth species. <i>BMC Genomics</i> , 2012, 13, 289.	1.2	34
1672	Oomycete transcriptomics database: A resource for oomycete transcriptomes. <i>BMC Genomics</i> , 2012, 13, 303.	1.2	7
1673	An unbiased approach to identify genes involved in development in a turtle with temperature-dependent sex determination. <i>BMC Genomics</i> , 2012, 13, 308.	1.2	8

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1674	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. <i>BMC Genomics</i> , 2012, 13, 354.	1.2	47
1675	Profiling the resting venom gland of the scorpion <i>Tityus stigmurus</i> through a transcriptomic survey. <i>BMC Genomics</i> , 2012, 13, 362.	1.2	74
1676	Comparative transcript profiling of gene expression between seedless Ponkan mandarin and its seedy wild type during floral organ development by suppression subtractive hybridization and cDNA microarray. <i>BMC Genomics</i> , 2012, 13, 397.	1.2	19
1677	Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. <i>BMC Genomics</i> , 2012, 13, 492.	1.2	51
1678	Transcriptome analyses of early cucumber fruit growth identifies distinct gene modules associated with phases of development. <i>BMC Genomics</i> , 2012, 13, 518.	1.2	98
1679	Fine mapping of complex traits in non-model species: using next generation sequencing and advanced intercross lines in Japanese quail. <i>BMC Genomics</i> , 2012, 13, 551.	1.2	20
1680	Sequencing of the core MHC region of black grouse (<i>Tetrao tetrix</i>) and comparative genomics of the galliform MHC. <i>BMC Genomics</i> , 2012, 13, 553.	1.2	29
1681	De novo assembly of the pepper transcriptome (<i>Capsicum annum</i>): a benchmark for in silico discovery of SNPs, SSRs and candidate genes. <i>BMC Genomics</i> , 2012, 13, 571.	1.2	109
1682	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, <i>Botryococcus braunii</i> race B (Showa)*. <i>BMC Genomics</i> , 2012, 13, 576.	1.2	52
1683	Large-scale sequencing based on full-length-enriched cDNA libraries in pigs: contribution to annotation of the pig genome draft sequence. <i>BMC Genomics</i> , 2012, 13, 581.	1.2	15
1684	Toward understanding the genetic basis of adaptation to high-elevation life in poikilothermic species: A comparative transcriptomic analysis of two ranid frogs, <i>Rana chensinensis</i> and <i>R. kukunoris</i> . <i>BMC Genomics</i> , 2012, 13, 588.	1.2	55
1685	Small RNA and transcriptome deep sequencing proffers insight into floral gene regulation in <i>Rosa</i> cultivars. <i>BMC Genomics</i> , 2012, 13, 657.	1.2	49
1686	Cutoffs and k-mers: implications from a transcriptome study in allopolyploid plants. <i>BMC Genomics</i> , 2012, 13, 92.	1.2	52
1687	Transcriptome analysis reveals the time of the fourth round of genome duplication in common carp (<i>Cyprinus carpio</i>). <i>BMC Genomics</i> , 2012, 13, 96.	1.2	101
1688	Reprogramming of gene expression during compression wood formation in pine: Coordinated modulation of S-adenosylmethionine, lignin and lignan related genes. <i>BMC Plant Biology</i> , 2012, 12, 100.	1.6	55
1689	A putative role for amino acid permeases in sink-source communication of barley tissues uncovered by RNA-seq. <i>BMC Plant Biology</i> , 2012, 12, 154.	1.6	46
1690	Chromosome arm-specific BAC end sequences permit comparative analysis of homoeologous chromosomes and genomes of polyploid wheat. <i>BMC Plant Biology</i> , 2012, 12, 64.	1.6	22
1691	In silico polymorphism analysis for the development of simple sequence repeat and transposon markers and construction of linkage map in cultivated peanut. <i>BMC Plant Biology</i> , 2012, 12, 80.	1.6	135

#	ARTICLE	IF	CITATIONS
1692	Molecular interactions between the olive and the fruit fly <i>Bactrocera oleae</i> . <i>BMC Plant Biology</i> , 2012, 12, 86.	1.6	65
1693	Arapan-S: a fast and highly accurate whole-genome assembly software for viruses and small genomes. <i>BMC Research Notes</i> , 2012, 5, 243.	0.6	6
1694	Assessment of the genetic relationship between <i>Dictyocaulus</i> species from <i>Bos taurus</i> and <i>Cervus elaphus</i> using complete mitochondrial genomic datasets. <i>Parasites and Vectors</i> , 2012, 5, 241.	1.0	36
1695	Characterization of a Virus Infecting <i>Citrus volkameriana</i> with Citrus Leprosis-Like Symptoms. <i>Phytopathology</i> , 2012, 102, 122-127.	1.1	64
1696	Modelling the global distribution of fungal species: new insights into microbial cosmopolitanism. <i>Molecular Ecology</i> , 2012, 21, 5599-5612.	2.0	61
1697	Characterization of an A-type cyclin-dependent kinase gene from <i>Dendrobium candidum</i> . <i>Biologia (Poland)</i> , 2012, 67, 360-368.	0.8	7
1698	Essential Role of IL-4 and IL-4R α Interaction in Adaptive Immunity of Zebrafish: Insight into the Origin of Th2-like Regulatory Mechanism in Ancient Vertebrates. <i>Journal of Immunology</i> , 2012, 188, 5571-5584.	0.4	91
1700	A Transcriptomic View of the Proteome Variability of Newborn and Adult <i>Bothrops jararaca</i> Snake Venoms. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1554.	1.3	61
1701	Proteomic Techniques for Plant-Fungal Interactions. <i>Methods in Molecular Biology</i> , 2012, 835, 75-96.	0.4	4
1702	Phylogenetic Analysis and Expression Patterns of the MAPK Gene Family in Wheat (<i>Triticum aestivum</i>) Tj ETQq1 1 0,784314 r _g BT /Overl 1.7 P7	1.7	17
1703	Review of General Algorithmic Features for Genome Assemblers for Next Generation Sequencers. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 58-73.	3.0	37
1704	Identification of genes differentially expressed in grapevine associated with resistance to <i>Elsinoe ampelina</i> through suppressive subtraction hybridization. <i>Plant Physiology and Biochemistry</i> , 2012, 58, 253-268.	2.8	30
1705	Mitochondrial genome of <i>Angiostrongylus vasorum</i> : Comparison with congeners and implications for studying the population genetics and epidemiology of this parasite. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1884-1891.	1.0	34
1706	Allele Identification in Assembled Genomic Sequence Datasets. <i>Methods in Molecular Biology</i> , 2012, 888, 197-211.	0.4	2
1707	Genome-wide genetic changes during modern breeding of maize. <i>Nature Genetics</i> , 2012, 44, 812-815.	9.4	352
1708	Next-Generation Sequencing Technologies and Fragment Assembly Algorithms. <i>Methods in Molecular Biology</i> , 2012, 855, 155-174.	0.4	24
1709	Identification and Phylogenetic Analysis of <i>Tityus pachyurus</i> and <i>Tityus obscurus</i> Novel Putative Na ⁺ -Channel Scorpion Toxins. <i>PLoS ONE</i> , 2012, 7, e30478.	1.1	70
1710	Mining microsatellite markers from public expressed sequence tag sequences for genetic diversity analysis in pomegranate. <i>Journal of Genetics</i> , 2012, 91, 353-358.	0.4	22

#	ARTICLE	IF	CITATIONS
1711	Shifting the bioinformatics computing paradigm: A case study in parallelizing genome annotation using MAKER and Work Queue. , 2012, , .		3
1712	Venomics Profiling of <i>Thamnodynastes strigatus</i> Unveils Matrix Metalloproteinases and Other Novel Proteins Recruited to the Toxin Arsenal of Rear-Fanged Snakes. Journal of Proteome Research, 2012, 11, 1152-1162.	1.8	61
1713	Identification of differentially expressed genes in potato associated with tuber dormancy release. Molecular Biology Reports, 2012, 39, 11277-11287.	1.0	22
1714	An analysis of the transcriptome of <i>Teladorsagia circumcincta</i> : its biological and biotechnological implications. BMC Genomics, 2012, 13, S10.	1.2	18
1715	Deciphering the complex leaf transcriptome of the allotetraploid species <i>Nicotiana tabacum</i> : a phylogenomic perspective. BMC Genomics, 2012, 13, 406.	1.2	39
1716	DNAGear- a free software for spa type identification in <i>Staphylococcus aureus</i> . BMC Research Notes, 2012, 5, 642.	0.6	24
1717	Broad Phylogenomic Sampling and the Sister Lineage of Land Plants. PLoS ONE, 2012, 7, e29696.	1.1	234
1718	CAPRG: Sequence Assembling Pipeline for Next Generation Sequencing of Non-Model Organisms. PLoS ONE, 2012, 7, e30370.	1.1	4
1719	Evaluating Characteristics of De Novo Assembly Software on 454 Transcriptome Data: A Simulation Approach. PLoS ONE, 2012, 7, e31410.	1.1	72
1720	High Through-Put Sequencing of the <i>Parhyale hawaiiensis</i> mRNAs and microRNAs to Aid Comparative Developmental Studies. PLoS ONE, 2012, 7, e33784.	1.1	35
1721	Phylogenetic Incongruence in <i>E. coli</i> O104: Understanding the Evolutionary Relationships of Emerging Pathogens in the Face of Homologous Recombination. PLoS ONE, 2012, 7, e33971.	1.1	22
1722	Characterization of Common Carp Transcriptome: Sequencing, De Novo Assembly, Annotation and Comparative Genomics. PLoS ONE, 2012, 7, e35152.	1.1	121
1723	Transcriptome Sequencing and Comparative Analysis of <i>Saccharina japonica</i> (Laminariales.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T	1.1	93
1724	Host Gene Expression Signatures Discriminate between Ferrets Infected with Genetically Similar H1N1 Strains. PLoS ONE, 2012, 7, e40743.	1.1	12
1725	SNP Discovery Using Next Generation Transcriptomic Sequencing in Atlantic Herring (<i>Clupea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	1.1	53
1726	Pathogen Webs in Collapsing Honey Bee Colonies. PLoS ONE, 2012, 7, e43562.	1.1	387
1727	SNP Discovery with EST and NextGen Sequencing in Switchgrass (<i>Panicum virgatum</i> L.). PLoS ONE, 2012, 7, e44112.	1.1	16
1728	An Insight into the Sialotranscriptome of the Cat Flea, <i>Ctenocephalides felis</i> . PLoS ONE, 2012, 7, e44612.	1.1	34

#	ARTICLE	IF	CITATIONS
1729	Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of Salmonella Paratyphi A. PLoS ONE, 2012, 7, e45346.	1.1	26
1730	Identification of SNPs in RNA-seq data of two cultivars of Glycine max (soybean) differing in drought resistance. Genetics and Molecular Biology, 2012, 35, 331-334.	0.6	40
1731	An Efficient Genome Fragment Assembling Using GA with Neighborhood Aware Fitness Function. Applied Computational Intelligence and Soft Computing, 2012, 2012, 1-11.	1.6	3
1732	Why Assembling Plant Genome Sequences Is So Challenging. Biology, 2012, 1, 439-459.	1.3	123
1733	The Population Genomics of Sunflowers and Genomic Determinants of Protein Evolution Revealed by RNAseq. Biology, 2012, 1, 575-596.	1.3	34
1734	Molecular characterization of the polyphenol oxidase gene in lulo (Solanum quitoense Lam.) var. Castilla. Brazilian Journal of Plant Physiology, 2012, 24, 261-272.	0.5	3
1735	Cloud Technologies for Microsoft Computational Biology Tools. International Journal of Advanced Information Technology, 2012, 2, 1-19.	1.0	0
1736	The mitochondrial genome of the white-rot fungus Flammulina velutipes. Journal of General and Applied Microbiology, 2012, 58, 331-337.	0.4	17
1737	Thirty-four Musa (Musaceae) expressed sequence tag-derived microsatellite markers transferred to Musella lasiocarpa. Genetics and Molecular Research, 2012, 11, 2094-2098.	0.3	4
1738	Genetic diversity of tyrosine hydroxylase (TH) and dopamine b-hydroxylase (DBH) genes in cattle breeds. Genetics and Molecular Biology, 2012, 35, 435-440.	0.6	8
1739	A web-based bioinformatics interface applied to the GENOSOJA project: databases and pipelines. Genetics and Molecular Biology, 2012, 35, 203-211.	0.6	13
1740	Transcript profiling of expressed sequence tags from semimembranosus muscle of commercial and naturalized pig breeds. Genetics and Molecular Research, 2012, 11, 3315-3328.	0.3	4
1741	Identification of metal-tolerant organisms isolated from the Plankenburg River, Western Cape, South Africa. Water S A, 2012, 38, .	0.2	10
1742	Genome Comparison of Barley and Maize Smut Fungi Reveals Targeted Loss of RNA Silencing Components and Species-Specific Presence of Transposable Elements. Plant Cell, 2012, 24, 1733-1745.	3.1	159
1743	Plant genome sequencing. , 2012, , 83-97.		3
1744	The <i>TvPirin</i> Gene Is Necessary for Haustorium Development in the Parasitic Plant <i>Triphysaria versicolor</i> . Plant Physiology, 2012, 158, 1046-1053.	2.3	31
1745	Global Assembly of Expressed Sequence Tags. Methods in Molecular Biology, 2012, 883, 193-199.	0.4	1
1746	Evolution of coding and non-coding genes in HOX clusters of a marsupial. BMC Genomics, 2012, 13, 251.	1.2	47

#	ARTICLE	IF	CITATIONS
1747	Suppressive subtractive hybridization libraries prepared from the digestive gland of the oyster <i>Crassostrea brasiliana</i> exposed to a diesel fuel water-accommodated fraction. <i>Environmental Toxicology and Chemistry</i> , 2012, 31, 1249-1253.	2.2	16
1748	Transcriptional profiling of genes involved in embryogenic, non-embryogenic calluses and somatic embryogenesis of Valencia sweet orange by SSH-based microarray. <i>Planta</i> , 2012, 236, 1107-1124.	1.6	40
1749	Large Scale In Silico Identification of MYB Family Genes from Wheat Expressed Sequence Tags. <i>Molecular Biotechnology</i> , 2012, 52, 184-192.	1.3	15
1750	Comparison of the two major classes of assembly algorithms: overlap-layout-consensus and de-bruijn-graph. <i>Briefings in Functional Genomics</i> , 2012, 11, 25-37.	1.3	195
1751	Phylogenomic analyses support the position of turtles as the sister group of birds and crocodiles (Archosauria). <i>BMC Biology</i> , 2012, 10, 65.	1.7	296
1752	Designing a transcriptome next-generation sequencing project for a nonmodel plant species. <i>American Journal of Botany</i> , 2012, 99, 257-266.	0.8	192
1753	A COMPLEX OF GENES INVOLVED IN ADAPTATION OF <i>Leptinotarsa decemlineata</i> LARVAE TO INDUCED POTATO DEFENSE. <i>Archives of Insect Biochemistry and Physiology</i> , 2012, 79, 153-181.	0.6	41
1754	Landscape of Somatic Retrotransposition in Human Cancers. <i>Science</i> , 2012, 337, 967-971.	6.0	631
1755	A <i>Papaver somniferum</i> 10-Gene Cluster for Synthesis of the Anticancer Alkaloid Noscapine. <i>Science</i> , 2012, 336, 1704-1708.	6.0	301
1756	Temporal and Fluoride Control of Secondary Metabolism Regulates Cellular Organofluorine Biosynthesis. <i>ACS Chemical Biology</i> , 2012, 7, 1576-1585.	1.6	18
1757	Characterization of active miniature inverted-repeat transposable elements in the peanut genome. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1429-1438.	1.8	76
1758	EST-derived genic molecular markers: development and utilization for generating an advanced transcript map of chickpea. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1449-1462.	1.8	74
1759	Dispersal via stream corridors structures populations of the endangered St. Francis™ satyr butterfly (<i>Neonympha mitchellii francisci</i>). <i>Journal of Insect Conservation</i> , 2012, 16, 263-273.	0.8	7
1760	Development of genomic simple sequence repeat markers for linseed using next-generation sequencing technology. <i>Molecular Breeding</i> , 2012, 30, 597-606.	1.0	32
1761	Exploiting BAC-end sequences for the mining, characterization and utility of new short sequences repeat (SSR) markers in Citrus. <i>Molecular Biology Reports</i> , 2012, 39, 5373-5386.	1.0	41
1762	Development of EST derived SSRs and SNPs as a genomic resource in Indian catfish, <i>Clarias batrachus</i> . <i>Molecular Biology Reports</i> , 2012, 39, 5921-5931.	1.0	13
1763	Analysis of 2,297 expressed sequence tags (ESTs) from a cDNA library of flax (<i>Linum usitatissimum</i> L.) bark tissue. <i>Molecular Biology Reports</i> , 2012, 39, 6289-6296.	1.0	24
1764	Analysis of expressed sequence tags from grapevine flower and fruit and development of simple sequence repeat markers. <i>Molecular Biology Reports</i> , 2012, 39, 6825-6834.	1.0	11

#	ARTICLE	IF	CITATIONS
1765	Generation, functional analysis and utility of <i>Citrus grandis</i> EST from a flower-derived cDNA library. <i>Molecular Biology Reports</i> , 2012, 39, 7221-7235.	1.0	14
1766	Differential gene expression of rice roots inoculated with the diazotroph <i>Herbaspirillum seropedicae</i> . <i>Plant and Soil</i> , 2012, 356, 113-125.	1.8	61
1767	Mining of Candidate Maize Genes for Nitrogen Use Efficiency by Integrating Gene Expression and QTL Data. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 297-308.	1.0	49
1768	A gymnosperm homolog of SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE-1 (SERK1) is expressed during somatic embryogenesis. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 109, 41-50.	1.2	50
1769	Bioprospecting and indexing the microalgal diversity of different ecological habitats of India. <i>World Journal of Microbiology and Biotechnology</i> , 2012, 28, 1657-1667.	1.7	27
1770	Sugarcane genes differentially expressed in response to <i>Puccinia melanocephala</i> infection: identification and transcript profiling. <i>Plant Cell Reports</i> , 2012, 31, 955-969.	2.8	26
1771	WUSCHEL-related genes are expressed during somatic embryogenesis of the basal angiosperm <i>Ocotea catharinensis</i> Mez. (Lauraceae). <i>Trees - Structure and Function</i> , 2012, 26, 493-501.	0.9	14
1772	Novel circovirus in European catfish (<i>Silurus glanis</i>). <i>Archives of Virology</i> , 2012, 157, 1173-1176.	0.9	41
1773	ZOOSPOROGENESIS, MORPHOLOGY, ULTRASTRUCTURE, PIGMENT COMPOSITION, AND PHYLOGENETIC POSITION OF <i>TRACHYDISCUS MINUTUS</i> (EUSTIGMATOPHYCEAE, HETEROKONTOPHYTA). <i>Journal of Phycology</i> , 2012, 48, 231-242.	1.0	45
1774	Molecular characterization of novel <i>Ta</i> NAC genes in wheat and overexpression of <i>Ta</i> NAC2a confers drought tolerance in tobacco. <i>Physiologia Plantarum</i> , 2012, 144, 210-224.	2.6	127
1775	Development of EST-derived SSR markers in pea (<i>Pisum sativum</i>) and their potential utility for genetic mapping and transferability. <i>Plant Breeding</i> , 2012, 131, 118-124.	1.0	36
1776	Development and application of single nucleotide polymorphism markers in the polyploid <i>Brassica napus</i> by 454 sequencing of expressed sequence tags. <i>Plant Breeding</i> , 2012, 131, 293-299.	1.0	21
1777	An arctic community of symbiotic fungi assembled by long-distance dispersers: phylogenetic diversity of ectomycorrhizal basidiomycetes in Svalbard based on soil and sporocarp DNA. <i>Journal of Biogeography</i> , 2012, 39, 74-88.	1.4	143
1778	Maternal control of seed oil content in <i>Brassica napus</i> : the role of silique wall photosynthesis. <i>Plant Journal</i> , 2012, 69, 432-444.	2.8	132
1779	Genetic diversity and comparative analysis of gene expression between <i>Heterorhabditis bacteriophora</i> Az29 and Az36 isolates: Uncovering candidate genes involved in insect pathogenicity. <i>Experimental Parasitology</i> , 2012, 130, 116-125.	0.5	13
1780	A comparative transcriptome analysis reveals expression profiles conserved across three <i>Eimeria</i> spp. of domestic fowl and associated with multiple developmental stages. <i>International Journal for Parasitology</i> , 2012, 42, 39-48.	1.3	30
1781	CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus</i> (<i>Boophilus</i>) microplus. <i>International Journal for Parasitology</i> , 2012, 42, 161-169.	1.3	55
1782	de novo analysis and functional classification of the transcriptome of the root lesion nematode, <i>Pratylenchus thornei</i> , after 454 GS FLX sequencing. <i>International Journal for Parasitology</i> , 2012, 42, 225-237.	1.3	40

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1783	Trichoderma harzianum expressed sequence tags for identification of genes with putative roles in mycoparasitism against Fusarium solani. Biological Control, 2012, 61, 134-140.	1.4	38
1784	Key strongylid nematodes of animals – Impact of next-generation transcriptomics on systems biology and biotechnology. Biotechnology Advances, 2012, 30, 469-488.	6.0	37
1785	MAJOR DEVELOPMENTAL REGULATORS AND THEIR EXPRESSION IN TWO CLOSELY RELATED SPECIES OF <i>PORPHYRA</i> (RHODOPHYTA). Journal of Phycology, 2012, 48, 883-896.	1.0	19
1786	ANALYSIS OF <i>ALEXANDRIUM TAMARENSE</i> (DINOPHYCEAE) GENES REVEALS THE COMPLEX EVOLUTIONARY HISTORY OF A MICROBIAL EUKARYOTE. Journal of Phycology, 2012, 48, 1130-1142.	1.0	29
1787	Rapid microsatellite marker development for African mahogany (<i>Khaya senegalensis</i> , Meliaceae) using next-generation sequencing and assessment of its intra-specific genetic diversity. Molecular Ecology Resources, 2012, 12, 344-353.	2.2	34
1788	Reference-free transcriptome assembly in non-model animals from next-generation sequencing data. Molecular Ecology Resources, 2012, 12, 834-845.	2.2	142
1789	Expression and activity of glutathione S-transferases and catalase in the shrimp <i>Litopenaeus vannamei</i> inoculated with a toxic <i>Microcystis aeruginosa</i> strain. Marine Environmental Research, 2012, 75, 54-61.	1.1	49
1790	Genes under positive selection in a model plant pathogenic fungus, <i>Botrytis</i> . Infection, Genetics and Evolution, 2012, 12, 987-996.	1.0	40
1791	Soil fungal community structure along a soil health gradient in pea fields examined using deep amplicon sequencing. Soil Biology and Biochemistry, 2012, 46, 26-32.	4.2	170
1792	Expressed sequence tag based identification and expression analysis of some cold inducible elements in seabuckthorn (<i>Hippophae rhamnoides</i> L.). Plant Physiology and Biochemistry, 2012, 51, 123-128.	2.8	25
1793	Coleoptera and microbe biomass in Antarctic Dry Valley paleosols adjacent to the Inland Ice: Implications for Mars. Planetary and Space Science, 2012, 60, 386-398.	0.9	8
1794	Comparison of transcript profiles in different life stages of the nematode <i>Globodera pallida</i> under different host potato genotypes. Molecular Plant Pathology, 2012, 13, 1120-1134.	2.0	14
1795	Characterization and genomic annotation of polymorphic EST-SSR loci in <i>Litopenaeus vannamei</i> shrimp. Aquaculture Research, 2012, 43, 1567-1570.	0.9	8
1796	Crossing the divide: gene flow produces intergeneric hybrid in feral transgenic creeping bentgrass population. Molecular Ecology, 2012, 21, 4672-4680.	2.0	31
1797	Bioinformatics meets parasitology. Parasite Immunology, 2012, 34, 265-275.	0.7	23
1798	Generation of an expressed sequence tag (EST) library from salt-stressed roots of <i>Jatropha curcas</i> for identification of abiotic stress-responsive genes. Plant Biology, 2012, 14, 428-437.	1.8	21
1799	Isolation and characterization of pathogen defence-related class I chitinase from the actinorhizal tree <i>Asuarina equisetifolia</i> . Forest Pathology, 2012, 42, 467-480.	0.5	18
1800	A functional screen for recovery of 4-phosphopantetheinyl transferase and associated natural product biosynthesis genes from metagenome libraries. Environmental Microbiology, 2012, 14, 1198-1209.	1.8	50

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1801	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. <i>Environmental Microbiology</i> , 2012, 14, 1308-1324.	1.8	124
1802	Identification of functionally active aerobic methanotrophs in sediments from an arctic lake using stable isotope probing. <i>Environmental Microbiology</i> , 2012, 14, 1403-1419.	1.8	73
1803	<i>Acinetobacter</i> , <i>Aeromonas</i> and <i>Trichococcus</i> populations dominate the microbial community within urban sewer infrastructure. <i>Environmental Microbiology</i> , 2012, 14, 2538-2552.	1.8	153
1804	Morphology and phylogeny of a new woodruffiid ciliate, <i>Etoschophrya inornata</i> sp. n. (Ciliophora, Colpodea, Platyophryida), with an account on evolution of platyophryids. <i>Zoologica Scripta</i> , 2012, 41, 400-416.	0.7	17
1805	Characterization of the fungicidal activity of <i>Calothrix elenkinii</i> using chemical methods and microscopy. <i>Applied Biochemistry and Microbiology</i> , 2012, 48, 51-57.	0.3	38
1806	SNP mining in <i>C. clementina</i> BAC end sequences; transferability in the Citrus genus (Rutaceae), phylogenetic inferences and perspectives for genetic mapping. <i>BMC Genomics</i> , 2012, 13, 13.	1.2	118
1807	Sexual and asexual oogenesis require the expression of unique and shared sets of genes in the insect <i>Acyrtosiphon pisum</i> . <i>BMC Genomics</i> , 2012, 13, 76.	1.2	36
1808	SpiroESTdb: a transcriptome database and online tool for sparganum expressed sequences tags. <i>BMC Research Notes</i> , 2012, 5, 130.	0.6	5
1809	SNP markers retrieval for a non-model species: a practical approach. <i>BMC Research Notes</i> , 2012, 5, 79.	0.6	25
1810	Host Identity Impacts Rhizosphere Fungal Communities Associated with Three Alpine Plant Species. <i>Microbial Ecology</i> , 2012, 63, 682-693.	1.4	72
1811	Development and characterization of genomic and expressed SSRs for levant cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50	1.8	35
1812	Sequence-based novel genomic microsatellite markers for robust genotyping purposes in foxtail millet [<i>Setaria italica</i> (L.) P. Beau.]. <i>Plant Cell Reports</i> , 2012, 31, 323-337.	2.8	78
1813	Expressed sequence-tag analysis of ovaries of <i>Brachiaria brizantha</i> reveals genes associated with the early steps of embryo sac differentiation of apomictic plants. <i>Plant Cell Reports</i> , 2012, 31, 403-416.	2.8	28
1814	Unbiased genomic distribution of genes related to cell morphogenesis in cotton by chromosome mapping. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 108, 529-534.	1.2	7
1815	Comparative full genome analysis of four infectious laryngotracheitis virus (Gallid herpesvirus-1) virulent isolates from the United States. <i>Virus Genes</i> , 2012, 44, 273-285.	0.7	39
1816	A computational study of the dynamics of LTR retrotransposons in the <i>Populus trichocarpa</i> genome. <i>Tree Genetics and Genomes</i> , 2012, 8, 61-75.	0.6	43
1817	Identification and mapping of conserved ortholog set (COS) II sequences of cacao and their conversion to SNP markers for marker-assisted selection in <i>Theobroma cacao</i> and comparative genomics studies. <i>Tree Genetics and Genomes</i> , 2012, 8, 97-111.	0.6	25
1818	Transcriptome analysis of an invasive weed <i>Mikania micrantha</i> . <i>Biologia Plantarum</i> , 2012, 56, 111-116.	1.9	18

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1819	The complete mitochondrial genome of two recently derived species of the fish genus <i>Nannoperca</i> (Perciformes, Percichthyidae). <i>Molecular Biology Reports</i> , 2012, 39, 2767-2772.	1.0	50
1820	Generation and analysis of expressed sequence tags from the bone marrow of Chinese Sika deer. <i>Molecular Biology Reports</i> , 2012, 39, 2981-2990.	1.0	4
1821	Matita, a new retroelement from peanut: characterization and evolutionary context in the light of the <i>Arachis</i> genome divergence. <i>Molecular Genetics and Genomics</i> , 2012, 287, 21-38.	1.0	43
1822	Genomic Resources for Sea Lice: Analysis of ESTs and Mitochondrial Genomes. <i>Marine Biotechnology</i> , 2012, 14, 155-166.	1.1	39
1823	Gene Expression Profiling of Atlantic Cod (<i>Gadus morhua</i>) Embryogenesis Using Microarray. <i>Marine Biotechnology</i> , 2012, 14, 167-176.	1.1	26
1824	The Mining of Pearl Formation Genes in Pearl Oyster <i>Pinctada fucata</i> by cDNA Suppression Subtractive Hybridization. <i>Marine Biotechnology</i> , 2012, 14, 177-188.	1.1	15
1825	RNA sequencing reveals sexually dimorphic gene expression before gonadal differentiation in chicken and allows comprehensive annotation of the W-chromosome. <i>Genome Biology</i> , 2013, 14, R26.	13.9	98
1826	A de novo assembly of the newt transcriptome combined with proteomic validation identifies new protein families expressed during tissue regeneration. <i>Genome Biology</i> , 2013, 14, R16.	13.9	104
1827	Deep transcriptome-sequencing and proteome analysis of the hydrothermal vent annelid <i>Alvinella pompejana</i> identifies the CvP-bias as a robust measure of eukaryotic thermostability. <i>Biology Direct</i> , 2013, 8, 2.	1.9	47
1828	Mining for hemicellulases in the fungus-growing termite <i>Pseudacanthotermes militaris</i> using functional metagenomics. <i>Biotechnology for Biofuels</i> , 2013, 6, 78.	6.2	65
1829	Transcriptome exploration of the sex pheromone gland of <i>Lutzomyia longipalpis</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td	1.0	19
1830	High Variation in Single Nucleotide Polymorphisms (SNPs) and Insertions/Deletions (Indels) in the Highly Invasive <i>Bemisia tabaci</i> (Gennadius) (Hemiptera: Aleyrodidae) Middle East-Asia Minor 1 (MEAM1). <i>Neotropical Entomology</i> , 2013, 42, 521-526.	0.5	7
1831	Development of simple sequence repeat markers and diversity analysis in alfalfa (<i>Medicago sativa</i> L.). <i>Molecular Biology Reports</i> , 2013, 40, 3291-3298.	1.0	40
1832	Comparative analysis of differentially expressed genes in Sika deer antler at different stages. <i>Molecular Biology Reports</i> , 2013, 40, 1665-1676.	1.0	29
1833	Identification of oxidative stress-responsive C2H2 zinc fingers associated with Al tolerance in near-isogenic wheat lines. <i>Plant and Soil</i> , 2013, 366, 199-212.	1.8	9
1834	De Novo Characterization of Leaf Transcriptome Using 454 Sequencing and Development of EST-SSR Markers in Tea (<i>Camellia sinensis</i>). <i>Plant Molecular Biology Reporter</i> , 2013, 31, 524-538.	1.0	57
1835	Molecular characterization of a cellulose synthase gene (<i>AaxmCesA1</i>) isolated from an <i>Acacia auriculiformis</i> x <i>Acacia mangium</i> hybrid. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 303-313.	1.0	4
1836	Proteomic characterization of larval and adult developmental stages in <i>Echinococcus granulosus</i> reveals novel insight into host-parasite interactions. <i>Journal of Proteomics</i> , 2013, 84, 158-175.	1.2	90

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1837	Transcriptome analysis of female reproductive tissues of <i>A. nastrepha obliqua</i> and molecular evolution of eggshell proteins in the <i>fraterculus</i> group. <i>Insect Molecular Biology</i> , 2013, 22, 551-561.	1.0	8
1838	Next-generation sequencing and phylogenetic signal of complete mitochondrial genomes for resolving the evolutionary history of leaf-nosed bats (Phyllostomidae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 728-739.	1.2	55
1839	Transcriptome analysis of venom glands from a single fishing spider <i>Dolomedes mizhoanus</i> . <i>Toxicon</i> , 2013, 73, 23-32.	0.8	24
1840	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. <i>Statistics in Biosciences</i> , 2013, 5, 3-25.	0.6	15
1841	Microsatellite loci for genetic analysis of the arctic gadids <i>Boreogadus saida</i> and <i>Arctogadus glacialis</i> . <i>Conservation Genetics Resources</i> , 2013, 5, 445-448.	0.4	12
1842	New polymorphic microsatellite markers for Chinese shrimp (<i>Fenneropenaeus chinensis</i>) from sequence database. <i>Conservation Genetics Resources</i> , 2013, 5, 461-463.	0.4	0
1843	Development of polymorphic EST-SSR markers in <i>Macrobrachium rosenbergii</i> by data mining. <i>Conservation Genetics Resources</i> , 2013, 5, 133-136.	0.4	10
1844	Nine original microsatellite loci in prickly sculpin (<i>Cottus asper</i>) and their applicability to other closely related <i>Cottus</i> species. <i>Conservation Genetics Resources</i> , 2013, 5, 279-282.	0.4	2
1845	Optimal assembly for high throughput shotgun sequencing. <i>BMC Bioinformatics</i> , 2013, 14, S18.	1.2	63
1846	Phylogenomics of stronglylocentrotid sea urchins. <i>BMC Evolutionary Biology</i> , 2013, 13, 88.	3.2	42
1847	KONAGAbase: a genomic and transcriptomic database for the diamondback moth, <i>Plutella xylostella</i> . <i>BMC Genomics</i> , 2013, 14, 464.	1.2	47
1848	Transcriptome analysis reveals unique C4-like photosynthesis and oil body formation in an arachidonic acid-rich microalga <i>Myrmecea incisa</i> Reisingl H4301. <i>BMC Genomics</i> , 2013, 14, 396.	1.2	30
1849	Optimizing de novo assembly of short-read RNA-seq data for phylogenomics. <i>BMC Genomics</i> , 2013, 14, 328.	1.2	189
1850	Identification of differentially expressed genes from <i>Trichoderma harzianum</i> during growth on cell wall of <i>Fusarium solania</i> a tool for biotechnological application. <i>BMC Genomics</i> , 2013, 14, 177.	1.2	68
1851	Characterization of expressed sequence tags from developing fibers of <i>Gossypium barbadense</i> and evaluation of insertion-deletion variation in tetraploid cultivated cotton species. <i>BMC Genomics</i> , 2013, 14, 170.	1.2	8
1852	Pearl millet [<i>Pennisetum glaucum</i> (L.) R. Br.] consensus linkage map constructed using four RIL mapping populations and newly developed EST-SSRs. <i>BMC Genomics</i> , 2013, 14, 159.	1.2	94
1853	Why so many unknown genes? Partitioning orphans from a representative transcriptome of the lone star tick <i>Amblyomma americanum</i> . <i>BMC Genomics</i> , 2013, 14, 135.	1.2	42
1854	Transcriptome of the dead: characterisation of immune genes and marker development from necropsy samples in a free-ranging marine mammal. <i>BMC Genomics</i> , 2013, 14, 52.	1.2	27

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1855	Genome reannotation of the lizard <i>Anolis carolinensis</i> based on 14 adult and embryonic deep transcriptomes. <i>BMC Genomics</i> , 2013, 14, 49.	1.2	55
1856	Identification of the <i>Hevea brasiliensis</i> AP2/ERF superfamily by RNA sequencing. <i>BMC Genomics</i> , 2013, 14, 30.	1.2	73
1857	Transcriptomic profiling of the salt-stress response in the wild recretohalophyte <i>Reaumuria trigyna</i> . <i>BMC Genomics</i> , 2013, 14, 29.	1.2	147
1858	Transcriptome resources and functional characterization of monoterpene synthases for two host species of the mountain pine beetle, lodgepole pine (<i>Pinus contorta</i>) and jack pine (<i>Pinus banksiana</i>). <i>BMC Plant Biology</i> , 2013, 13, 80.	1.6	57
1859	High-density linkage mapping in a pine tree reveals a genomic region associated with inbreeding depression and provides clues to the extent and distribution of meiotic recombination. <i>BMC Biology</i> , 2013, 11, 50.	1.7	63
1860	The "fossilized" mitochondrial genome of <i>Liriodendron tulipifera</i> : ancestral gene content and order, ancestral editing sites, and extraordinarily low mutation rate. <i>BMC Biology</i> , 2013, 11, 29.	1.7	199
1861	Polyadenylation of 18S rRNA in algae ¹ . <i>Journal of Phycology</i> , 2013, 49, 570-579.	1.0	6
1862	Identification of duplicated and stress-inducible <i>Aox2b</i> gene co-expressed with <i>Aox1</i> in species of the <i>Medicago</i> genus reveals a regulation linked to gene rearrangement in leguminous genomes. <i>Journal of Plant Physiology</i> , 2013, 170, 1609-1619.	1.6	29
1863	Evidence of a conserved functional role for DNA methylation in termites. <i>Insect Molecular Biology</i> , 2013, 22, 143-154.	1.0	36
1864	Computational Methods for Identification of DNA Transposons. <i>Methods in Molecular Biology</i> , 2013, 1057, 289-304.	0.4	2
1865	Transcriptome analysis of <i>Anopheles stephensi</i> embryo using expressed sequence tags. <i>Journal of Biosciences</i> , 2013, 38, 301-309.	0.5	2
1866	Computational identification and analysis of single-nucleotide polymorphisms and insertions/deletions in expressed sequence tag data of <i>Eucalyptus</i> . <i>Journal of Genetics</i> , 2013, 92, 34-38.	0.4	3
1867	Genetic relationship of a cucumber germplasm collection revealed by newly developed EST-SSR markers. <i>Journal of Genetics</i> , 2013, 92, 28-32.	0.4	9
1868	Novel polymorphic microsatellite markers for population genetics of the endangered Caribbean star coral, <i>Montastraea faveolata</i> . <i>Marine Biodiversity</i> , 2013, 43, 167-172.	0.3	47
1869	<i>Kudoa azevedoi</i> n. sp. (Myxozoa, Multivalvulida) from the oocytes of the Atlantic horse mackerel <i>Trachurus trachurus</i> (Perciformes, Carangidae) in Tunisian coasts. <i>Parasitology Research</i> , 2013, 112, 1737-1747.	0.6	35
1870	cDNA-AFLP analysis revealed genes potentially implicated in <i>Catharanthus roseus</i> flowers during wheat blue dwarf phytoplasma infection. <i>Physiological and Molecular Plant Pathology</i> , 2013, 84, 1-9.	1.3	8
1871	De Novo Sequencing and Global Transcriptome Analysis of <i>Nannochloropsis</i> sp. (Eustigmatophyceae) Following Nitrogen Starvation. <i>Bioenergy Research</i> , 2013, 6, 494-505.	2.2	37
1872	Gene expression profiling of three different stressors in the water flea <i>Daphnia magna</i> . <i>Ecotoxicology</i> , 2013, 22, 900-914.	1.1	21

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1873	Phylogenomics supports Panpulmonata: Opisthobranch paraphyly and key evolutionary steps in a major radiation of gastropod molluscs. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 764-771.	1.2	59
1874	<i>Pseudomonas prosekii</i> sp. nov., a Novel Psychrotrophic Bacterium from Antarctica. <i>Current Microbiology</i> , 2013, 67, 637-646.	1.0	38
1875	The PmNAC1 gene is induced by auxin and expressed in differentiating vascular cells in callus cultures of <i>Passiflora</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 115, 275-283.	1.2	8
1876	A <i>Passiflora</i> homolog of a D-type cyclin gene is differentially expressed in response to sucrose, auxin, and cytokinin. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 115, 233-242.	1.2	12
1877	Sequencing of Sitka spruce (<i>Picea sitchensis</i>) cDNA libraries constructed from autumn buds and foliage reveals autumn-specific spruce transcripts. <i>Tree Genetics and Genomes</i> , 2013, 9, 683-691.	0.6	6
1878	Critical role of bioinformatics in translating huge amounts of next-generation sequencing data into personalized medicine. <i>Science China Life Sciences</i> , 2013, 56, 110-118.	2.3	31
1879	Epidemiology of Soybean vein necrosis-associated virus. <i>Phytopathology</i> , 2013, 103, 966-971.	1.1	52
1880	Rhizosphere microbial community and Zn uptake by willow (<i>Salix purpurea</i> L.) depend on soil sulfur concentrations in metalliferous peat soils. <i>Applied Soil Ecology</i> , 2013, 67, 53-60.	2.1	19
1881	RNA-Seq for Transcriptome Analysis in Non-model Plants. <i>Methods in Molecular Biology</i> , 2013, 1069, 43-58.	0.4	56
1882	Genetic variation of six desaturase genes in flax and their impact on fatty acid composition. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2627-2641.	1.8	53
1883	Complete genome sequence of a novel potato virus S strain infecting <i>Solanum phureja</i> in Colombia. <i>Archives of Virology</i> , 2013, 158, 2205-2208.	0.9	23
1884	Complete genome sequence of ϕ CP51, a temperate bacteriophage of <i>Clostridium perfringens</i> . <i>Archives of Virology</i> , 2013, 158, 2015-2017.	0.9	21
1885	Population structure of blackberry chlorotic ringspot virus in the United States. <i>Archives of Virology</i> , 2013, 158, 667-672.	0.9	8
1886	Identification of genes associated with fruit ripening in <i>Ziziphus jujuba</i> using suppression subtractive hybridization approach. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 1997-2008.	1.0	2
1887	Transcriptome responses in the rectal gland of fed and fasted spiny dogfish shark (<i>Squalus acanthias</i>) determined by suppression subtractive hybridization. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 334-343.	0.4	8
1888	Identification of transcription factors potentially involved in the juvenile to adult phase transition in <i>Citrus</i> . <i>Annals of Botany</i> , 2013, 112, 1371-1381.	1.4	11
1889	Comparison of the diversity, composition, and host recurrence of xylariaceous endophytes in subtropical, cool temperate, and subboreal regions in Japan. <i>Population Ecology</i> , 2014, 56, 289-300.	0.7	20
1890	Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. <i>Nature Genetics</i> , 2013, 45, 937-941.	9.4	203

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1891	The mitochondrial genome of <i>Aelurostrongylus abstrusus</i> diagnostic, epidemiological and systematic implications. <i>Gene</i> , 2013, 516, 294-300.	1.0	17
1892	Predominance of bovine viral diarrhea virus 1b and 1d subtypes during eight years of survey in Poland. <i>Veterinary Microbiology</i> , 2013, 166, 639-644.	0.8	32
1893	Cloning and characterization of NBS-LRR encoding resistance gene candidates from Tomato Leaf Curl New Delhi Virus resistant genotype of <i>Luffa cylindrica</i> Roem. <i>Physiological and Molecular Plant Pathology</i> , 2013, 81, 107-117.	1.3	16
1894	Shotgun Label-Free Quantitative Proteomics of Water-Deficit-Stressed Midmature Peanut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBJ /Overl	1.8	31
1895	Multi-locus typing scheme for <i>Babesia bovis</i> and <i>Babesia bigemina</i> reveals high levels of genetic variability in strains from Northern Argentina. <i>Infection, Genetics and Evolution</i> , 2013, 14, 214-222.	1.0	12
1896	The repetitive component of the A genome of peanut (<i>Arachis hypogaea</i>) and its role in remodelling intergenic sequence space since its evolutionary divergence from the B genome. <i>Annals of Botany</i> , 2013, 112, 545-559.	1.4	30
1897	Chiton phylogeny (Mollusca : Polyplacophora) and the placement of the enigmatic species <i>Chorioplax grayi</i> (H. Adams & Angas). <i>Invertebrate Systematics</i> , 2013, 27, 603.	0.5	32
1898	Evolutionary relationship of <i>Panax ginseng</i> and <i>P. quinquefolius</i> inferred from sequencing and comparative analysis of expressed sequence tags. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1377-1387.	0.8	45
1899	NMDA receptor expression and C terminus structure in the rotifer <i>Brachionus plicatilis</i> and long-term potentiation across the Metazoa. <i>Invertebrate Neuroscience</i> , 2013, 13, 125-134.	1.8	2
1900	Sulfur oxidizers dominate carbon fixation at a biogeochemical hot spot in the dark ocean. <i>ISME Journal</i> , 2013, 7, 2349-2360.	4.4	62
1901	The mitochondrial genome of <i>Protostrongylus rufescens</i> implications for population and systematic studies. <i>Parasites and Vectors</i> , 2013, 6, 263.	1.0	18
1902	Long-term performance and operational strategies of a poultry slaughterhouse waste stabilization pond system in a tropical climate. <i>Resources, Conservation and Recycling</i> , 2013, 71, 7-14.	5.3	24
1903	Horizontal Transfer of Entire Genomes via Mitochondrial Fusion in the Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1468-1473.	6.0	322
1904	The Assembly of Sequencing Data. <i>SpringerBriefs in Systems Biology</i> , 2013, , 41-54.	0.1	0
1905	Isolation and characterization of antimicrobial metabolite producing endophytic <i>Phomopsis</i> sp. from <i>Ficus pumila</i> Linn. (Moraceae). <i>International Journal of Chemical and Analytical Science</i> , 2013, 4, 156-160.	0.5	19
1906	Conservation of globin genes in the living fossil <i>Latimeria chalumnae</i> and reconstruction of the evolution of the vertebrate globin family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1801-1812.	1.1	26
1907	Disentangling homeologous contigs in allo-tetraploid assembly: application to durum wheat. <i>BMC Bioinformatics</i> , 2013, 14, S15.	1.2	13
1908	Coupling Deep Transcriptome Analysis with Untargeted Metabolic Profiling in <i>Ophiorrhiza pumila</i> to Further the Understanding of the Biosynthesis of the Anti-Cancer Alkaloid Camptothecin and Anthraquinones. <i>Plant and Cell Physiology</i> , 2013, 54, 686-696.	1.5	88

#	ARTICLE	IF	CITATIONS
1909	Identification of cold-responsive genes in energycane for their use in genetic diversity analysis and future functional marker development. <i>Plant Science</i> , 2013, 211, 122-131.	1.7	42
1910	Identification of differentially expressed genes in American cockroach ovaries and testes by suppression subtractive hybridization and the prediction of its miRNAs. <i>Molecular Genetics and Genomics</i> , 2013, 288, 627-638.	1.0	8
1911	Transcriptome profiling of <i>Gossypium barbadense</i> inoculated with <i>Verticillium dahliae</i> provides a resource for cotton improvement. <i>BMC Genomics</i> , 2013, 14, 637.	1.2	93
1912	Identification of genes expressed in the sex pheromone gland of the black cutworm <i>Agrotis ipsilon</i> with putative roles in sex pheromone biosynthesis and transport. <i>BMC Genomics</i> , 2013, 14, 636.	1.2	111
1913	The ovarian transcriptome of the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> , feeding upon a bovine host infected with <i>Babesia bovis</i> . <i>Parasites and Vectors</i> , 2013, 6, 276.	1.0	31
1914	Transcriptome deep-sequencing and clustering of expressed isoforms from <i>Favia corals</i> . <i>BMC Genomics</i> , 2013, 14, 546.	1.2	22
1915	Horizontally transferred genes in the genome of Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>BMC Evolutionary Biology</i> , 2013, 13, 165.	3.2	17
1916	Bulk segregant RNA-seq reveals expression and positional candidate genes and allele-specific expression for disease resistance against enteric septicemia of catfish. <i>BMC Genomics</i> , 2013, 14, 929.	1.2	79
1917	The neuropeptide complement of the marine annelid <i>Platynereis dumerilii</i> . <i>BMC Genomics</i> , 2013, 14, 906.	1.2	139
1918	Complex gene expression in the dragline silk producing glands of the Western black widow (<i>Latrodectus hesperus</i>). <i>BMC Genomics</i> , 2013, 14, 846.	1.2	25
1919	A BAC based physical map and genome survey of the rice false smut fungus <i>Villosiclava virens</i> . <i>BMC Genomics</i> , 2013, 14, 883.	1.2	10
1920	The planarian regeneration transcriptome reveals a shared but temporally shifted regulatory program between opposing head and tail scenarios. <i>BMC Genomics</i> , 2013, 14, 797.	1.2	50
1921	A whole transcriptomal linkage analysis of gene co-regulation in insecticide resistant house flies, <i>Musca domestica</i> . <i>BMC Genomics</i> , 2013, 14, 803.	1.2	37
1922	High-throughput sequencing identification of novel and conserved miRNAs in the <i>Brassica oleracea</i> leaves. <i>BMC Genomics</i> , 2013, 14, 801.	1.2	42
1923	Transcriptome generation and analysis from spleen of Indian catfish, <i>Clarias batrachus</i> (Linnaeus.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.0	2
1924	Mining of haplotype-based expressed sequence tag single nucleotide polymorphisms in citrus. <i>BMC Genomics</i> , 2013, 14, 746.	1.2	28
1925	RNA-Seq analysis reveals genes associated with resistance to Taura syndrome virus (TSV) in the Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Developmental and Comparative Immunology</i> , 2013, 41, 523-533.	1.0	62
1926	Information Theory of DNA Shotgun Sequencing. <i>IEEE Transactions on Information Theory</i> , 2013, 59, 6273-6289.	1.5	77

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1927	Venom proteomic and venomous glands transcriptomic analysis of the Egyptian scorpion <i>Scorpio maurus palmatus</i> (Arachnida: Scorpionidae). <i>Toxicon</i> , 2013, 74, 193-207.	0.8	77
1928	Characterization of <i>Citrus sinensis</i> transcription factors closely associated with the non-host response to <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> . <i>Journal of Plant Physiology</i> , 2013, 170, 934-942.	1.6	16
1929	Description of <i>Pseudomonas jessenii</i> subsp. <i>pseudopotida</i> subsp. nov., amended description of <i>Pseudomonas jessenii</i> and description of <i>Pseudomonas jessenii</i> subsp. <i>jessenii</i> subsp. nov.. <i>Folia Microbiologica</i> , 2013, 58, 631-639.	1.1	8
1930	GAGM: Genome assembly on GPU using mate pairs. , 2013, , .		5
1931	De novo assembly methods for next generation sequencing data. <i>Tsinghua Science and Technology</i> , 2013, 18, 500-514.	4.1	15
1932	Development and utilization of novel <sc>SSR</sc>s in foxtail millet [<i>Setaria italica</i> (L.) P. Beauv.]. <i>Plant Breeding</i> , 2013, 132, 367-374.	1.0	25
1933	GGAKE: GPU Based Genome Assembly Using K-Mer Extension. , 2013, , .		3
1934	Development and Testing of New Gene-Homologous EST-SSRs for <i>Eucalyptus gomphocephala</i> (Myrtaceae). <i>Applications in Plant Sciences</i> , 2013, 1, 1300004.	0.8	12
1935	Resilience of Arctic mycorrhizal fungal communities after wildfire facilitated by resprouting shrubs. <i>Ecoscience</i> , 2013, 20, 296-310.	0.6	32
1936	Development and Characterization of Microsatellite Loci for Smooth Cordgrass, <i>Spartina alterniflora</i> (Poaceae). <i>Applications in Plant Sciences</i> , 2013, 1, 1200211.	0.8	7
1937	Macedovicin, the second food-grade lantibiotic produced by <i>Streptococcus macedonicus</i> ACA-DC 198. <i>Food Microbiology</i> , 2013, 33, 124-130.	2.1	23
1938	Transcriptome Analysis in the Saccharinae. , 2013, , 121-139.		2
1939	Applications of next-generation sequencing to phylogeography and phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 526-538.	1.2	531
1940	Isolation and characterization of indigenous endophytic bacteria associated with leaves of switchgrass (<i>Panicum virgatum</i> L.) cultivars. <i>Journal of Applied Microbiology</i> , 2013, 114, 836-853.	1.4	152
1941	Evolution of Saxitoxin Synthesis in Cyanobacteria and Dinoflagellates. <i>Molecular Biology and Evolution</i> , 2013, 30, 70-78.	3.5	152
1942	Molecular evolutionary and population genomic analysis of the nine-spined stickleback using a modified restriction-associated DNA tag approach. <i>Molecular Ecology</i> , 2013, 22, 565-582.	2.0	85
1943	Gene expression analysis by ESTs sequencing of the Brazilian frog <i>Phyllomedusa nordestina</i> skin glands. <i>Toxicon</i> , 2013, 61, 139-150.	0.8	6
1944	Molecular epidemiology of betanodavirus—Sequence analysis strategies and quasispecies influence outbreak source attribution. <i>Virology</i> , 2013, 436, 15-23.	1.1	6

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1945	Identification of reproduction-related genes and SSR-markers through expressed sequence tags analysis of a monsoon breeding carp rohu, <i>Labeo rohita</i> (Hamilton). <i>Gene</i> , 2013, 524, 1-14.	1.0	17
1946	Fish-borne trematodes in cultured Nile tilapia (<i>Oreochromis niloticus</i>) and wild-caught fish from Thailand. <i>Veterinary Parasitology</i> , 2013, 198, 230-234.	0.7	15
1947	Molecular characterization and population structure of blackberry vein banding associated virus, new ampelovirus associated with yellow vein disease. <i>Virus Research</i> , 2013, 178, 234-240.	1.1	24
1948	Characterisation of genes transcriptionally upregulated in the liver of sand goby (<i>Pomatoschistus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook transcripts. <i>Chemosphere</i> , 2013, 90, 2722-2729.	4.2	12
1949	The P6 protein of Cauliflower mosaic virus interacts with CHUP1, a plant protein which moves chloroplasts on actin microfilaments. <i>Virology</i> , 2013, 443, 363-374.	1.1	46
1950	Robust cuticular penetration resistance in the common bed bug (<i>Cimex lectularius</i> L.) correlates with increased steady-state transcript levels of CPR-type cuticle protein genes. <i>Pesticide Biochemistry and Physiology</i> , 2013, 106, 190-197.	1.6	99
1951	Basal polarization of the mucosal compartment in <i>Flavobacterium columnare</i> susceptible and resistant channel catfish (<i>Ictalurus punctatus</i>). <i>Molecular Immunology</i> , 2013, 56, 317-327.	1.0	100
1952	Adaptin evolution in kinetoplastids and emergence of the variant surface glycoprotein coat in African trypanosomatids. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 123-128.	1.2	44
1953	The Maternal Transcriptome of the Crustacean <i>Parhyale hawaiiensis</i> Is Inherited Asymmetrically to Invariant Cell Lineages of the Ectoderm and Mesoderm. <i>PLoS ONE</i> , 2013, 8, e56049.	1.1	23
1954	High mortality of juvenile gilthead sea bream (<i>Sparus aurata</i>) from photobacteriosis is associated with alternative macrophage activation and anti-inflammatory response: Results of gene expression profiling of early responses in the head kidney. <i>Fish and Shellfish Immunology</i> , 2013, 34, 1269-1278.	1.6	22
1955	Fungal communities in soils along a vegetative ecotone. <i>Mycologia</i> , 2013, 105, 61-70.	0.8	13
1956	A narrowly endemic photosynthetic orchid is non-specific in its mycorrhizal associations. <i>Molecular Ecology</i> , 2013, 22, 2341-2354.	2.0	58
1957	A dynamic history of gene duplications and losses characterizes the evolution of the SPARC family in eumetazoans. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20122963.	1.2	18
1958	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	13.7	714
1959	Diploidization and genome size change in allopolyploids is associated with differential dynamics of low- and high-copy sequences. <i>Plant Journal</i> , 2013, 74, 829-839.	2.8	112
1960	The <i>Montastraea faveolata</i> microbiome: ecological and temporal influences on a Caribbean reef-building coral in decline. <i>Environmental Microbiology</i> , 2013, 15, 2082-2094.	1.8	80
1961	De novo transcriptomic analyses for non-model organisms: an evaluation of methods across a multi-species data set. <i>Molecular Ecology Resources</i> , 2013, 13, 403-416.	2.2	71
1962	Predicting polymorphic EST-SSR s in silico. <i>Molecular Ecology Resources</i> , 2013, 13, 538-545.	2.2	20

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1963	Whole-exome targeted sequencing of the uncharacterized pine genome. <i>Plant Journal</i> , 2013, 75, 146-156.	2.8	160
1964	Transcriptome analysis based on next-generation sequencing of non-model plants producing specialized metabolites of biotechnological interest. <i>Journal of Biotechnology</i> , 2013, 166, 122-134.	1.9	196
1965	Microsatellite markers from expressed sequence tags (ESTs) of seaweeds in differentiating various <i>Gracilaria</i> species. <i>Journal of Applied Phycology</i> , 2013, 25, 839-846.	1.5	10
1966	Radically different phylogeographies and patterns of genetic variation in two European brown frogs, genus <i>Rana</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 657-670.	1.2	56
1967	New <i>scn</i> SNPs for population genetic analysis reveal possible cryptic speciation of eastern Australian sea mullet (<i>Mugil cephalus</i>). <i>Molecular Ecology Resources</i> , 2013, 13, 715-725.	2.2	35
1968	Combinational effect of mutational bias and translational selection for translation efficiency in tomato (<i>Solanum lycopersicum</i>) cv. Micro-Tom. <i>Genomics</i> , 2013, 101, 290-295.	1.3	7
1969	Gut transcriptome of replete adult female cattle ticks, <i>Rhipicephalus (Boophilus) microplus</i> , feeding upon a <i>Babesia bovis</i> -infected bovine host. <i>Parasitology Research</i> , 2013, 112, 3075-3090.	0.6	37
1970	Tracking the molecular epidemiology of Brazilian Infectious bursal disease virus (IBDV) isolates. <i>Infection, Genetics and Evolution</i> , 2013, 13, 18-26.	1.0	24
1971	Partial venom gland transcriptome of a <i>Drosophila</i> parasitoid wasp, <i>Leptopilina heterotoma</i> , reveals novel and shared bioactive profiles with stinging Hymenoptera. <i>Gene</i> , 2013, 526, 195-204.	1.0	54
1972	ptr-MIR169 is a posttranscriptional repressor of PtrHAP2 during vegetative bud dormancy period of aspen (<i>Populus tremuloides</i>) trees. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 512-518.	1.0	30
1973	Identification and expression levels of pig miRNAs in skeletal muscle. <i>Livestock Science</i> , 2013, 154, 45-54.	0.6	6
1974	Sequence-based SNP genotyping in durum wheat. <i>Plant Biotechnology Journal</i> , 2013, 11, 809-817.	4.1	63
1975	Identification of genes related to agarwood formation: transcriptome analysis of healthy and wounded tissues of <i>Aquilaria sinensis</i> . <i>BMC Genomics</i> , 2013, 14, 227.	1.2	109
1976	Expressed sequence tags and molecular cloning and characterization of gene encoding pinoresinol/lariciresinol reductase from <i>Podophyllum hexandrum</i> . <i>Protoplasma</i> , 2013, 250, 1239-1249.	1.0	30
1977	Characterization of the <i>Pinus massoniana</i> Transcriptional Response to <i>Bursaphelenchus xylophilus</i> Infection Using Suppression Subtractive Hybridization. <i>International Journal of Molecular Sciences</i> , 2013, 14, 11356-11375.	1.8	25
1978	A Practical Approach to Reconstruct Evolutionary History of Animal Sialyltransferases and Gain Insights into the Sequence-Function Relationships of Golgi-Glycosyltransferases. <i>Methods in Molecular Biology</i> , 2013, 1022, 73-97.	0.4	9
1979	Combining gene expression and genetic analyses to identify candidate genes involved in cold responses in pea. <i>Journal of Plant Physiology</i> , 2013, 170, 1148-1157.	1.6	18
1980	Fungal networks in yield-invigorating and -debilitating soils induced by prolonged potato monoculture. <i>Soil Biology and Biochemistry</i> , 2013, 65, 186-194.	4.2	197

#	ARTICLE	IF	CITATIONS
1981	Genomic patterns of introgression in rainbow and westslope cutthroat trout illuminated by overlapping paired-end RAD sequencing. <i>Molecular Ecology</i> , 2013, 22, 3002-3013.	2.0	162
1982	The characterization of the <i>Plebotomus papatasi</i> transcriptome. <i>Insect Molecular Biology</i> , 2013, 22, 211-232.	1.0	20
1983	Identification of potential miRNAs and their targets in <i>Vriesea carinata</i> (Poales, Bromeliaceae). <i>Plant Science</i> , 2013, 210, 214-223.	1.7	33
1984	BAC-end sequences analysis provides first insights into coffee (<i>Coffea canephora</i> P.) genome composition and evolution. <i>Plant Molecular Biology</i> , 2013, 83, 177-189.	2.0	15
1985	Genetic characterization of Blueberry necrotic ring blotch virus, a novel RNA virus with unique genetic features. <i>Journal of General Virology</i> , 2013, 94, 1426-1434.	1.3	54
1986	Direct approaches to exploit many-core architecture in bioinformatics. <i>Future Generation Computer Systems</i> , 2013, 29, 15-26.	4.9	11
1987	<i>Spraguea lophii</i> (Microsporidia) parasite of the teleost fish, <i>Lophius piscatorius</i> from Tunisian coasts: Evidence for an extensive chromosome length polymorphism. <i>Parasitology International</i> , 2013, 62, 66-74.	0.6	9
1988	Analyses of mitochondrial amino acid sequence datasets support the proposal that specimens of <i>Hypodontus macropi</i> from three species of macropodid hosts represent distinct species. <i>BMC Evolutionary Biology</i> , 2013, 13, 259.	3.2	17
1989	Development and Characterization of cDNA Resources for the Common Marmoset: One of the Experimental Primate Models. <i>DNA Research</i> , 2013, 20, 255-262.	1.5	12
1990	Apratoxin H and Apratoxin A Sulfoxide from the Red Sea Cyanobacterium <i>Moorea producens</i> . <i>Journal of Natural Products</i> , 2013, 76, 1781-1788.	1.5	88
1991	CathaCyc, a Metabolic Pathway Database Built from <i>Catharanthus roseus</i> RNA-Seq Data. <i>Plant and Cell Physiology</i> , 2013, 54, 673-685.	1.5	116
1992	Transport of inorganic phosphate in <i>Leishmania infantum</i> and compensatory regulation at low inorganic phosphate concentration. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 2683-2689.	1.1	20
1993	Alveolate Mitochondrial Metabolic Evolution: Dinoflagellates Force Reassessment of the Role of Parasitism as a Driver of Change in Apicomplexans. <i>Molecular Biology and Evolution</i> , 2013, 30, 123-139.	3.5	65
1994	In silico identification and validation of microsatellite markers from onion EST sequences. <i>Journal of Horticultural Science and Biotechnology</i> , 2013, 88, 664-670.	0.9	0
1995	New Volvovirus Isolates from <i>Acheta domesticus</i> (Japan) and <i>Gryllus assimilis</i> (United States). <i>Genome Announcements</i> , 2013, 1, .	0.8	6
1996	<i>Junonia coenia</i> Densovirus (JcDNV) Genome Structure. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1997	Comparative Genomic Analysis of <i>Acheta domesticus</i> Densovirus Isolates from Different Outbreaks in Europe, North America, and Japan. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1998	<i>Acheta domesticus</i> Volvovirus, a Novel Single-Stranded Circular DNA Virus of the House Cricket. <i>Genome Announcements</i> , 2013, 1, e0007913.	0.8	17

#	ARTICLE	IF	CITATIONS
1999	A Novel Ambisense Densovirus, Acheta domesticus Mini Ambidensovirus, from Crickets. Genome Announcements, 2013, 1, .	0.8	11
2000	Discovery of EST-Derived Microsatellite Primers in the Legume Lens culinaris (Fabaceae). Applications in Plant Sciences, 2013, 1, 1200539.	0.8	21
2001	Characterization of the rat developmental liver transcriptome. Physiological Genomics, 2013, 45, 301-311.	1.0	21
2002	Early Disruption of Maternalâ€Zygotic Interaction and Activation of Defense-Like Responses in Arabidopsis Interspecific Crosses. Plant Cell, 2013, 25, 2037-2055.	3.1	41
2003	Parallelizing the execution of sequential scripts. , 2013, , .		14
2004	Reference-Free Population Genomics from Next-Generation Transcriptome Data and the Vertebrateâ€Invertebrate Gap. PLoS Genetics, 2013, 9, e1003457.	1.5	157
2005	Fragment Merger: An Online Tool to Merge Overlapping Long Sequence Fragments. Viruses, 2013, 5, 824-833.	1.5	28
2006	Development and Validation of Single Nucleotide Polymorphisms (SNPs) Markers from Two Transcriptome 454-Runs of Turbot (Scophthalmus maximus) Using High-Throughput Genotyping. International Journal of Molecular Sciences, 2013, 14, 5694-5711.	1.8	33
2007	Fine Analysis of Genetic Diversity of the tpr Gene Family among Treponemal Species, Subspecies and Strains. PLoS Neglected Tropical Diseases, 2013, 7, e2222.	1.3	84
2008	Differential expression of several xyloglucan endotransglucosylase/hydrolase genes regulates flower opening and petal abscission in roses. AoB PLANTS, 2013, 5, plt030-plt030.	1.2	15
2009	Genome Microscale Heterogeneity among Wild Potatoes Revealed by Diversity Arrays Technology Marker Sequences. International Journal of Genomics, 2013, 2013, 1-9.	0.8	14
2010	De Novo Transcriptome Sequencing Reveals Important Molecular Networks and Metabolic Pathways of the Plant, Chlorophytum borivilianum. PLoS ONE, 2013, 8, e83336.	1.1	65
2011	In Silico Expressed Sequence Tag Analysis in Identification of Probable Diabetic Genes as Virtual Therapeutic Targets. BioMed Research International, 2013, 2013, 1-9.	0.9	5
2012	bex-db: Bioinformatics workbench for comprehensive analysis of barley-expressed genes. Breeding Science, 2013, 63, 430-434.	0.9	5
2013	The Oxytricha trifallax Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. PLoS Biology, 2013, 11, e1001473.	2.6	198
2014	The Genome and Development-Dependent Transcriptomes of Pyronema confluens: A Window into Fungal Evolution. PLoS Genetics, 2013, 9, e1003820.	1.5	85
2015	Unique nucleocytoplasmic dsDNA and +ssRNA viruses are associated with the dinoflagellate endosymbionts of corals. ISME Journal, 2013, 7, 13-27.	4.4	84
2016	Functional Transcriptomics of Wild-Caught Lutzomyia intermedia Salivary Glands: Identification of a Protective Salivary Protein against Leishmania braziliensis Infection. PLoS Neglected Tropical Diseases, 2013, 7, e2242.	1.3	60

#	ARTICLE	IF	CITATIONS
2017	Transcriptional Analysis of Drought-Induced Genes in the Roots of a Tolerant Genotype of the Common Bean (<i>Phaseolus vulgaris</i> L.). <i>International Journal of Molecular Sciences</i> , 2013, 14, 7155-7179.	1.8	45
2018	Cognitive impairments associated with CFS and POTS. <i>Frontiers in Physiology</i> , 2013, 4, 113.	1.3	28
2019	Epiphycan from salmon nasal cartilage is a novel type of large leucine-rich proteoglycan. <i>Glycobiology</i> , 2013, 23, 993-1003.	1.3	9
2020	Genome-Wide Landscape of Alternative Splicing Events in <i>Brachypodium distachyon</i> . <i>DNA Research</i> , 2013, 20, 163-171.	1.5	69
2021	4-Coumarate: CoA Ligase Partitions Metabolites for Eugenol Biosynthesis. <i>Plant and Cell Physiology</i> , 2013, 54, 1238-1252.	1.5	64
2022	Characterization of the Genome of the Dairy <i>Lactobacillus helveticus</i> Bacteriophage Î AQ113. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4712-4718.	1.4	24
2023	Computational Translation of Nonmammalian Species Data to Mammalian Species to Meet REACH and Next Generation Risk Assessment Needs. , 2013, , 113-136.		1
2024	Evaluation of Codon Biology in Citrus and <i>Poncirus trifoliata</i> Based on Genomic Features and Frame Corrected Expressed Sequence Tags. <i>DNA Research</i> , 2013, 20, 135-150.	1.5	28
2025	Ecosystem-level consequences of symbiont partnerships in an N-fixing shrub from interior Alaskan floodplains. <i>Ecological Monographs</i> , 2013, 83, 177-194.	2.4	23
2026	Synergistic Effects of Amiodarone and Fluconazole on <i>Candida tropicalis</i> Resistant to Fluconazole. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1691-1700.	1.4	48
2027	Next-Generation Anchor Based Phylogeny (NexABP): Constructing phylogeny from Next-generation sequencing data. <i>Scientific Reports</i> , 2013, 3, 2634.	1.6	10
2028	Transcriptomic Analysis of Cadmium Stress Response in the Heavy Metal Hyperaccumulator <i>Sedum alfredii</i> Hance. <i>PLoS ONE</i> , 2013, 8, e64643.	1.1	100
2029	Evolution of the Eye Transcriptome under Constant Darkness in <i>Sinocyclocheilus</i> Cavefish. <i>Molecular Biology and Evolution</i> , 2013, 30, 1527-1543.	3.5	83
2030	Selecting One of Several Mating Types through Gene Segment Joining and Deletion in <i>Tetrahymena thermophila</i> . <i>PLoS Biology</i> , 2013, 11, e1001518.	2.6	81
2031	Homologous Recombination Drives Both Sequence Diversity and Gene Content Variation in <i>Neisseria meningitidis</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1611-1627.	1.1	34
2032	Separating homeologs by phasing in the tetraploid wheat transcriptome. <i>Genome Biology</i> , 2013, 14, R66.	3.8	126
2033	Use or abuse of bioinformatic tools: a response to Samach. <i>Annals of Botany</i> , 2013, 111, 335-336.	1.4	0
2034	<i>Chryseobacterium angstadtii</i> sp. nov., isolated from a newt tank. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 4777-4783.	0.8	21

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2035	Role of a gamma-aminobutyric acid (<sc>GABA</sc>) receptor mutation in the evolution and spread of <i>Drosophila virgifera virgifera</i> resistance to cyclodiene insecticides. <i>Insect Molecular Biology</i> , 2013, 22, 473-484.	1.0	20
2036	A Statistical Method without Training Step for the Classification of Coding Frame in Transcriptome Sequences. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S10053.	1.0	8
2037	The Aquaporin Channel Repertoire of the Tardigrade <i>Milnesium tardigradum</i>. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S11497.	1.0	23
2038	De Novo Assembly and Functional Annotation of the Olive (<i>Olea europaea</i>) Transcriptome. <i>DNA Research</i> , 2013, 20, 93-108.	1.5	84
2039	RNA-Seq Analysis of Allele-Specific Expression, Hybrid Effects, and Regulatory Divergence in Hybrids Compared with Their Parents from Natural Populations. <i>Genome Biology and Evolution</i> , 2013, 5, 1309-1323.	1.1	131
2040	Development of genomic microsatellites in <i>Gleditsia triacanthos</i> (Fabaceae) using Illumina sequencing. <i>Applications in Plant Sciences</i> , 2013, 1, 1300050.	0.8	10
2041	An RNA-Seq Transcriptome Analysis of Orthophosphate-Deficient White Lupin Reveals Novel Insights into Phosphorus Acclimation in Plants. <i>Plant Physiology</i> , 2013, 161, 705-724.	2.3	184
2042	Orthology-guided assembly in highly heterozygous crops: creating a reference transcriptome to uncover genetic diversity in <i>Lolium perenne</i>. <i>Plant Biotechnology Journal</i> , 2013, 11, 605-617.	4.1	23
2043	Linking Genomics and Ecology to Investigate the Complex Evolution of an Invasive <i>Drosophila</i> Pest. <i>Genome Biology and Evolution</i> , 2013, 5, 745-757.	1.1	138
2044	A High performance cloud computing platform for mRNA analysis. , 2013, 2013, 1510-3.		0
2045	Transcriptome sequencing as a platform to elucidate molecular components of the diapause response in the Asian tiger mosquito <i>Aedes albopictus</i>. <i>Physiological Entomology</i> , 2013, 38, 173-181.	0.6	26
2046	Analysis and identification of IS1548 insertion targets in <i>Streptococcus agalactiae</i> . <i>FEMS Microbiology Letters</i> , 2013, 340, 65-72.	0.7	7
2047	Organic carbon transformations in high-Arctic peat soils: key functions and microorganisms. <i>ISME Journal</i> , 2013, 7, 299-311.	4.4	292
2048	Methylotrophic methanogenic Thermoplasmata implicated in reduced methane emissions from bovine rumen. <i>Nature Communications</i> , 2013, 4, 1428.	5.8	328
2049	Virus-induced gene silencing of <i>Arabidopsis thaliana</i> gene homologues in wheat identifies genes conferring improved drought tolerance. <i>Journal of Experimental Botany</i> , 2013, 64, 1381-1392.	2.4	87
2050	Transcriptome Analysis to Identify Putative Floral-Specific Genes and Flowering Regulatory-Related Genes of Sweet Potato. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2169-2174.	0.6	33
2051	Allele Identification for Transcriptome-Based Population Genomics in the Invasive Plant <i>Centaurea solstitialis</i>. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 359-367.	0.8	65
2052	Identification of New Aquaporin Genes and Single Nucleotide Polymorphism in Bread Wheat. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S12568.	0.6	17

#	ARTICLE	IF	CITATIONS
2053	De Novo Transcriptome Sequencing in <i>Trigonella foenum-graecum</i> L. to Identify Genes Involved in the Biosynthesis of Diosgenin. <i>Plant Genome</i> , 2013, 6, plantgenome2012.08.0021.	1.6	39
2054	Transcriptional profile of <i>Paracoccidioides</i> induced by oenothien B, a potential antifungal agent from the Brazilian Cerrado plant <i>Eugenia uniflora</i> . <i>BMC Microbiology</i> , 2013, 13, 227.	1.3	22
2055	The transcriptome of the invasive eel swimbladder nematode parasite <i>Anguillicola crassus</i> . <i>BMC Genomics</i> , 2013, 14, 87.	1.2	8
2056	Development of highly polymorphic EST-SSR markers and segregation in F1 hybrid population of <i>Vitis vinifera</i> L. <i>Genetics and Molecular Research</i> , 2013, 12, 3871-3878.	0.3	8
2057	Molecular evidence for the polyphyly of <i>Bostryx</i> (Gastropoda: Bulimulidae) and genetic diversity of <i>Bostryx aguilari</i> . <i>Zoologia</i> , 2013, 30, 80-87.	0.5	2
2058	Candidate Chemosensory Genes in the Stemborer <i>Sesamia nonagrioides</i> . <i>International Journal of Biological Sciences</i> , 2013, 9, 481-495.	2.6	47
2059	Genetic diversity of <i>Burkholderia</i> (Proteobacteria) species from the Caatinga and Atlantic rainforest biomes in Bahia, Brazil. <i>Genetics and Molecular Research</i> , 2013, 12, 655-664.	0.3	3
2060	Canine distemper virus infection in a lesser grison (<i>Galictis cuja</i>): first report and virus phylogeny. <i>Pesquisa Veterinaria Brasileira</i> , 2013, 33, 247-250.	0.5	14
2061	A directed approach for the identification of transcripts harbouring the spliced leader sequence and the effect of trans-splicing knockdown in <i>Schistosoma mansoni</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2013, 108, 707-717.	0.8	10
2062	A proposed model for the flowering signaling pathway of sugarcane under photoperiodic control. <i>Genetics and Molecular Research</i> , 2013, 12, 1347-1359.	0.3	16
2063	Alteration of digestive tract microbiome in neonatal Holstein bull calves by bacitracin methylene disalicylate treatment and scours. <i>Journal of Animal Science</i> , 2013, 91, 4984-4990.	0.2	17
2064	De Novo Sequencing of <i>Astyanax mexicanus</i> Surface Fish and <i>Pachytrichia</i> Cavefish Transcriptomes Reveals Enrichment of Mutations in Cavefish Putative Eye Genes. <i>PLoS ONE</i> , 2013, 8, e53553.	1.1	93
2065	Comparative Analysis of the Transcriptome in Tissues Secreting Purple and White Nacre in the Pearl Mussel <i>Hyriopsis cumingii</i> . <i>PLoS ONE</i> , 2013, 8, e53617.	1.1	83
2066	Molecular Analysis and Genomic Organization of Major DNA Satellites in Banana (<i>Musa spp.</i>). <i>PLoS ONE</i> , 2013, 8, e54808.	1.1	49
2067	The Role of Reactive Oxygen Species in <i>Anopheles aquasalis</i> Response to <i>Plasmodium vivax</i> Infection. <i>PLoS ONE</i> , 2013, 8, e57014.	1.1	68
2068	Insight into Hypoxia Tolerance in Cowpea Bruchid: Metabolic Repression and Heat Shock Protein Regulation via Hypoxia-Inducible Factor 1. <i>PLoS ONE</i> , 2013, 8, e57267.	1.1	20
2069	The Complete Chloroplast Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . <i>PLoS ONE</i> , 2013, 8, e57607.	1.1	297
2070	A Comparison of the Olfactory Gene Repertoires of Adults and Larvae in the Noctuid Moth <i>Spodoptera littoralis</i> . <i>PLoS ONE</i> , 2013, 8, e60263.	1.1	109

#	ARTICLE	IF	CITATIONS
2071	Suppression Subtractive Hybridization Analysis of Genes Regulated by Application of Exogenous Abscisic Acid in Pepper Plant (<i>Capsicum annuum</i> L.) Leaves under Chilling Stress. <i>PLoS ONE</i> , 2013, 8, e66667.	1.1	38
2072	Long-Term Nitrogen Amendment Alters the Diversity and Assemblage of Soil Bacterial Communities in Tallgrass Prairie. <i>PLoS ONE</i> , 2013, 8, e67884.	1.1	86
2073	TCW: Transcriptome Computational Workbench. <i>PLoS ONE</i> , 2013, 8, e69401.	1.1	17
2074	Evidence for a Hydrogenosomal-Type Anaerobic ATP Generation Pathway in <i>Acanthamoeba castellanii</i> . <i>PLoS ONE</i> , 2013, 8, e69532.	1.1	34
2075	Comparison of the Nodule vs. Root Transcriptome of the Actinorhizal Plant <i>Datisca glomerata</i> : Actinorhizal Nodules Contain a Specific Class of Defensins. <i>PLoS ONE</i> , 2013, 8, e72442.	1.1	82
2076	Characterisation and Analysis of the <i>Aegilops sharonensis</i> Transcriptome, a Wild Relative of Wheat in the <i>Sitopsis</i> Section. <i>PLoS ONE</i> , 2013, 8, e72782.	1.1	11
2077	Genome-Wide Discovery and Information Resource Development of DNA Polymorphisms in Cassava. <i>PLoS ONE</i> , 2013, 8, e74056.	1.1	12
2078	Short-Term Feed Deprivation Alters Immune Status of Surface Mucosa in Channel Catfish (<i>Ictalurus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 45	1.1	45
2079	Signatures of Rapid Evolution in Urban and Rural Transcriptomes of White-Footed Mice (<i>Peromyscus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 68	1.1	68
2080	Microsatellite Development and First Population Size Estimates for the Groundwater Isopod <i>Proasellus walteri</i> . <i>PLoS ONE</i> , 2013, 8, e76213.	1.1	4
2081	Transcriptome-Mining for Single-Copy Nuclear Markers in Ferns. <i>PLoS ONE</i> , 2013, 8, e76957.	1.1	69
2082	Identification of <i>Pyrus</i> Single Nucleotide Polymorphisms (SNPs) and Evaluation for Genetic Mapping in European Pear and Interspecific <i>Pyrus</i> Hybrids. <i>PLoS ONE</i> , 2013, 8, e77022.	1.1	64
2083	<i>Phytophthora</i> Have Distinct Endogenous Small RNA Populations That Include Short Interfering and microRNAs. <i>PLoS ONE</i> , 2013, 8, e77181.	1.1	88
2084	Expressed Sequence Tags for Bovine Muscle Satellite Cells, Myotube Formed-Cells and Adipocyte-Like Cells. <i>PLoS ONE</i> , 2013, 8, e79780.	1.1	13
2085	Profiling mRNAs of Two <i>Cuscuta</i> Species Reveals Possible Candidate Transcripts Shared by Parasitic Plants. <i>PLoS ONE</i> , 2013, 8, e81389.	1.1	22
2086	Putative Sugar Transporters of the Mustard Leaf Beetle <i>Phaedon cochleariae</i> : Their Phylogeny and Role for Nutrient Supply in Larval Defensive Glands. <i>PLoS ONE</i> , 2013, 8, e84461.	1.1	16
2087	Acclimation to different depths by the marine angiosperm <i>Posidonia oceanica</i> : transcriptomic and proteomic profiles. <i>Frontiers in Plant Science</i> , 2013, 4, 195.	1.7	38
2088	MATCHCLIP: locate precise breakpoints for copy number variation using CIGAR string by matching soft clipped reads. <i>Frontiers in Genetics</i> , 2013, 4, 157.	1.1	16

#	ARTICLE	IF	CITATIONS
2089	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. <i>Frontiers in Microbiology</i> , 2013, 4, 106.	1.5	112
2090	First Insights into the Large Genome of <i>Epimedium sagittatum</i> (Sieb. et Zucc) Maxim, a Chinese Traditional Medicinal Plant. <i>International Journal of Molecular Sciences</i> , 2013, 14, 13559-13576.	1.8	6
2091	Development and characterization of novel expressed sequence tag-derived simple sequence repeat markers in <i>Hevea brasiliensis</i> (rubber tree). <i>Genetics and Molecular Research</i> , 2013, 12, 5905-5910.	0.3	8
2092	Molecular Markers Highlight Variation within and among Kentucky Bluegrass Varieties and Accessions. <i>Crop Science</i> , 2013, 53, 2245-2254.	0.8	10
2093	Bioinformatics tools for development of fast and cost effective simple sequence repeat (SSR), and single nucleotide polymorphisms (SNP) markers from expressed sequence tags (ESTs). <i>African Journal of Biotechnology</i> , 2013, 12, 4713-4721.	0.3	2
2094	Genes that encodes NAGT, MIF1 and MIF2 are not virulence factors for kala-azar caused by <i>Leishmania infantum</i> . <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2014, 47, 593-598.	0.4	1
2095	Selection and Validation of Reference Genes for Gene Expression Analysis in Switchgrass (<i>Panicum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	120
2096	Combining Transcriptome Assemblies from Multiple De Novo Assemblers in the Allo-Tetraploid Plant <i>Nicotiana benthamiana</i> . <i>PLoS ONE</i> , 2014, 9, e91776.	1.1	167
2097	The Effects of Mary Rose Conservation Treatment on Iron Oxidation Processes and Microbial Communities Contributing to Acid Production in Marine Archaeological Timbers. <i>PLoS ONE</i> , 2014, 9, e84169.	1.1	25
2098	Identifying MicroRNAs and Transcript Targets in <i>Jatropha</i> Seeds. <i>PLoS ONE</i> , 2014, 9, e83727.	1.1	35
2099	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. <i>PLoS ONE</i> , 2014, 9, e85568.	1.1	57
2100	Transcriptomic Profiling of Differential Responses to Drought in Two Freshwater Mussel Species, the Giant Floater <i>Pyganodon grandis</i> and the Pondhorn <i>Unio merus tetralasmus</i> . <i>PLoS ONE</i> , 2014, 9, e89481.	1.1	24
2101	Comparative Genome Analysis of <i>Lactobacillus rhamnosus</i> Clinical Isolates from Initial Stages of Dental Pulp Infection: Identification of a New Exopolysaccharide Cluster. <i>PLoS ONE</i> , 2014, 9, e90643.	1.1	30
2102	Scanning of Transposable Elements and Analyzing Expression of Transposase Genes of Sweet Potato [<i>Ipomoea batatas</i>]. <i>PLoS ONE</i> , 2014, 9, e90895.	1.1	11
2103	Antifungal Activity of Naphthoquinoidal Compounds In Vitro against Fluconazole-Resistant Strains of Different <i>Candida</i> Species: A Special Emphasis on Mechanisms of Action on <i>Candida tropicalis</i> . <i>PLoS ONE</i> , 2014, 9, e93698.	1.1	49
2104	Comparative Transcriptome Analysis of Four Prymnesiophyte Algae. <i>PLoS ONE</i> , 2014, 9, e97801.	1.1	34
2105	Knockdown of the <i>Rhipicephalus microplus</i> Cytochrome c Oxidase Subunit III Gene Is Associated with a Failure of <i>Anaplasma marginale</i> Transmission. <i>PLoS ONE</i> , 2014, 9, e98614.	1.1	18
2106	IIS “Integrated Interactome System: A Web-Based Platform for the Annotation, Analysis and Visualization of Protein-Metabolite-Gene-Drug Interactions by Integrating a Variety of Data Sources and Tools. <i>PLoS ONE</i> , 2014, 9, e100385.	1.1	58

#	ARTICLE	IF	CITATIONS
2107	Transcriptomic Analysis of <i>Prunus domestica</i> Undergoing Hypersensitive Response to Plum Pox Virus Infection. PLoS ONE, 2014, 9, e100477.	1.1	38
2108	Gene Discovery through Transcriptome Sequencing for the Invasive Mussel <i>Limnoperna fortunei</i> . PLoS ONE, 2014, 9, e102973.	1.1	50
2109	Metagenomic Survey for Viruses in Western Arctic Caribou, Alaska, through Iterative Assembly of Taxonomic Units. PLoS ONE, 2014, 9, e105227.	1.1	21
2110	Genome Re-Sequencing of Semi-Wild Soybean Reveals a Complex Soja Population Structure and Deep Introgression. PLoS ONE, 2014, 9, e108479.	1.1	26
2111	A Transcriptome for the Study of Early Processes of Retinal Regeneration in the Adult Newt, <i>Cynops pyrrhogaster</i> . PLoS ONE, 2014, 9, e109831.	1.1	37
2112	Genome-Scale Transcriptome Analysis of the Alpine "Glasshouse" Plant <i>Rheum nobile</i> (Polygonaceae) with Special Translucent Bracts. PLoS ONE, 2014, 9, e110712.	1.1	8
2113	Transcriptomic Analysis of the Mussel <i>Elliptio complanata</i> Identifies Candidate Stress-Response Genes and an Abundance of Novel or Noncoding Transcripts. PLoS ONE, 2014, 9, e112420.	1.1	13
2114	Comparative Transcriptomic Analysis of the Response to Cold Acclimation in <i>Eucalyptus dunnii</i> . PLoS ONE, 2014, 9, e113091.	1.1	18
2115	The Odorant Receptor Co-Receptor from the Bed Bug, <i>Cimex lectularius</i> L. PLoS ONE, 2014, 9, e113692.	1.1	20
2116	High-Throughput Sequencing of MicroRNA Transcriptome and Expression Assay in the Sturgeon, <i>Acipenser schrenckii</i> . PLoS ONE, 2014, 9, e115251.	1.1	19
2117	Isolation and Expression Analysis of Novel Silicon Absorption Gene from Roots of Mangrove (<i>Rhizophora apiculata</i>) via Suppression Subtractive Hybridization. BioMed Research International, 2014, 2014, 1-11.	0.9	18
2118	<p>Pelagia benovici sp. nov. (Cnidaria,) Tj ETQq1 1 0.784314 rgBT /Ov</p><p>Sea</p>. Zootaxa, 2014, 3794, 455.	0.2	46
2119	Characterisation of divergent flavivirus NS3 and NS5 protein sequences detected in <i>Rhipicephalus microplus</i> ticks from Brazil. Memórias Do Instituto Oswaldo Cruz, 2014, 109, 38-50.	0.8	59
2120	Isolation and characterization of novel EST-SSRs in the showy dendrobium, <i>Dendrobium nobile</i> (Orchidaceae). Genetics and Molecular Research, 2014, 13, 986-991.	0.3	8
2121	Characterization of EST-derived and non-EST simple sequence repeats in an F1 hybrid population of <i>Vitis vinifera</i> L.. Genetics and Molecular Research, 2014, 13, 2220-2230.	0.3	4
2122	Description of microsporidia in simuliids: molecular and morphological characterization of microsporidia in the larvae of <i>Simulium pertinax</i> Kollar (Diptera: Simuliidae). Revista Da Sociedade Brasileira De Medicina Tropical, 2014, 47, 624-631.	0.4	3
2123	Isolation, <i>in vitro</i> propagation, genetic analysis, and immunogenic characterization of an <i>Ehrlichia canis</i> strain from southeastern Brazil. Journal of Veterinary Science, 2014, 15, 241.	0.5	5
2124	DNA Fragment Assembly Using Multi-Objective Genetic Algorithms. International Journal of Applied Evolutionary Computation, 2014, 5, 84-108.	0.7	5

#	ARTICLE	IF	CITATIONS
2125	Sixteen cytosolic glutamine synthetase genes identified in the <i>Brassica napus</i> L. genome are differentially regulated depending on nitrogen regimes and leaf senescence. <i>Journal of Experimental Botany</i> , 2014, 65, 3927-3947.	2.4	43
2126	Characterization of <i>Bacillus altitudinis</i> as a New Causative Agent of Bacterial Soft Rot. <i>Journal of Phytopathology</i> , 2014, 162, 712-722.	0.5	21
2128	The Peculiar Landscape of Repetitive Sequences in the Olive (<i>Olea europaea</i> L.) Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 776-791.	1.1	77
2129	Heterologous hybridisation to a <i>Pinus</i> microarray: profiling of gene expression in <i>Pinus radiata</i> saplings exposed to ethephon. <i>New Zealand Journal of Forestry Science</i> , 2014, 44, .	0.8	5
2130	Cold stress alters transcription in meiotic anthers of cold tolerant chickpea (<i>Cicer arietinum</i> L.). <i>BMC Research Notes</i> , 2014, 7, 717.	0.6	40
2131	Patterns of microsatellite evolution inferred from the <i>Helianthus annuus</i> (Asteraceae) transcriptome. <i>Journal of Genetics</i> , 2014, 93, 431-442.	0.4	10
2132	Analysis of the transcriptional responses in inflorescence buds of <i>Jatropha curcas</i> exposed to cytokinin treatment. <i>BMC Plant Biology</i> , 2014, 14, 318.	1.6	52
2133	Identification, cross-taxon transferability and application of full-length cDNA SSR markers in <i>Phyllostachys pubescens</i> . <i>SpringerPlus</i> , 2014, 3, 486.	1.2	10
2134	Evaluation of de novo transcriptome assemblies from RNA-Seq data. <i>Genome Biology</i> , 2014, 15, 553.	3.8	256
2135	Allelic diversity in the transcriptomes of contrasting rust-infected genotypes of <i>Lathyrus sativus</i> , a lasting resource for smart breeding. <i>BMC Plant Biology</i> , 2014, 14, 376.	1.6	37
2136	Subtractive transcriptomes of fruit and leaf reveal differential representation of transcripts in <i>Azadirachta indica</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 1331-1351.	0.6	27
2137	Reconstructing an ancestral genotype of two hexachlorocyclohexane-degrading <i>Sphingobium</i> species using metagenomic sequence data. <i>ISME Journal</i> , 2014, 8, 398-408.	4.4	53
2138	Identification of three proteins involved in fertilization and parthenogenetic development of a brown alga, <i>Scytosiphon lomentaria</i> . <i>Planta</i> , 2014, 240, 1253-1267.	1.6	11
2139	The mitochondrial genome of the American lotus borer, <i>Ostrinia penitalis</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.6	3
2140	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	5.8	131
2141	Development of a SNP marker assay for the Lr67 gene of wheat using a genotyping by sequencing approach. <i>Molecular Breeding</i> , 2014, 34, 2109-2118.	1.0	52
2142	Evidence for selection on a CONSTANS-like gene between two red oak species. <i>Annals of Botany</i> , 2014, 113, 967-975.	1.4	43
2143	Spaced seed data structures. , 2014, , .		1

#	ARTICLE	IF	CITATIONS
2144	Extensive Copy-Number Variation of Young Genes across Stickleback Populations. <i>PLoS Genetics</i> , 2014, 10, e1004830.	1.5	70
2145	Assembly of viral genomes from metagenomes. <i>Frontiers in Microbiology</i> , 2014, 5, 714.	1.5	44
2146	De novo assembly of <i>Aureococcus anophagefferens</i> transcriptomes reveals diverse responses to the low nutrient and low light conditions present during blooms. <i>Frontiers in Microbiology</i> , 2014, 5, 375.	1.5	52
2147	Evolution and targeting of Omp85 homologs in the chloroplast outer envelope membrane. <i>Frontiers in Plant Science</i> , 2014, 5, 535.	1.7	40
2148	Transcriptome Sequencing and Developmental Regulation of Gene Expression in <i>Anopheles aquasalis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3005.	1.3	9
2149	Genome of the Avirulent Human-Infective Trypanosome "Trypanosoma rangeli". <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3176.	1.3	72
2150	The Transcriptomes of the Crucian Carp Complex (<i>Carassius auratus</i>) Provide Insights into the Distinction between Unisexual Triploids and Sexual Diploids. <i>International Journal of Molecular Sciences</i> , 2014, 15, 9386-9406.	1.8	12
2151	Genome Sequencing and Comparative Genomics of the Broad Host-Range Pathogen <i>Rhizoctonia solani</i> AG8. <i>PLoS Genetics</i> , 2014, 10, e1004281.	1.5	145
2152	Generation and Analysis of Expressed Sequence Tags (ESTs) from Halophyte <i>Atriplex canescens</i> to Explore Salt-Responsive Related Genes. <i>International Journal of Molecular Sciences</i> , 2014, 15, 11172-11189.	1.8	22
2153	A consensus approach to vertebrate de novo transcriptome assembly from RNA-seq data: assembly of the duck (<i>Anas platyrhynchos</i>) transcriptome. <i>Frontiers in Genetics</i> , 2014, 5, 190.	1.1	33
2154	Phylogeny and phylogeography of functional genes shared among seven terrestrial subsurface metagenomes reveal N-cycling and microbial evolutionary relationships. <i>Frontiers in Microbiology</i> , 2014, 5, 531.	1.5	87
2155	WHIRLY1 is a major organizer of chloroplast nucleoids. <i>Frontiers in Plant Science</i> , 2014, 5, 432.	1.7	48
2156	Genetic mapping of legume orthologs reveals high conservation of synteny between lentil species and the sequenced genomes of <i>Medicago</i> and chickpea. <i>Frontiers in Plant Science</i> , 2014, 5, 676.	1.7	38
2157	Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower (<i>Helianthus annuus</i> L.) Genome. <i>Biology</i> , 2014, 3, 295-319.	1.3	16
2158	Complete Mitochondrial Genome Sequence of <i>Lichtheimia ramosa</i> (syn. <i>Lichtheimia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5Q 182 Td (h	0.8	8
2159	Exploring the Genome of Cheese Starter Lactic Acid Bacterium <i>Lactococcus lactis</i> subsp. <i>lactis</i> CECT 4433. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
2161	Insights into the Preservation of the Homomorphic Sex-Determining Chromosome of <i>Aedes aegypti</i> from the Discovery of a Male-Biased Gene Tightly Linked to the M-Locus. <i>Genome Biology and Evolution</i> , 2014, 6, 179-191.	1.1	40
2162	Characterization of the caleosin gene family in the Triticeae. <i>BMC Genomics</i> , 2014, 15, 239.	1.2	21

#	ARTICLE	IF	CITATIONS
2163	A Comparison of a Campus Cluster and Open Science Grid Platforms for Protein-Guided Assembly Using Pegasus Workflow Management System. , 2014, .		1
2164	A pipeline for the de novo assembly of the <i>Themira biloba</i> (Sepsidae: Diptera) transcriptome using a multiple k-mer length approach. <i>BMC Genomics</i> , 2014, 15, 188.	1.2	14
2165	Gene Prediction and Annotation in <i>Penstemon</i> (Plantaginaceae): A Workflow for Marker Development from Extremely Low-Coverage Genome Sequencing. <i>Applications in Plant Sciences</i> , 2014, 2, 1400044.	0.8	15
2166	Draft Genome Sequence of New <i>Bacillus cereus</i> Strain tsu1. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
2167	A Circo-Like Virus Isolated from <i>Penaeus monodon</i> Shrimps. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
2168	Genome Sequence of <i>Streptococcus phocae</i> subsp. <i>salmonis</i> Strain C-4 T , Isolated from Atlantic Salmon (<i>Salmo salar</i>). <i>Genome Announcements</i> , 2014, 2, .	0.8	4
2169	Exploring the Genome of a Butyric Acid Producer, <i>Clostridium butyricum</i> INCQS635. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
2170	Microbial population in an aerated thermophilic reactor that treats recycled cardboard plant wastewater. <i>Journal of Water Process Engineering</i> , 2014, 4, 74-81.	2.6	6
2171	Analysis of BAC-end sequences in common bean (<i>Phaseolus vulgaris</i> L.) towards the development and characterization of long motifs SSRs. <i>Plant Molecular Biology</i> , 2014, 86, 455-470.	2.0	14
2172	Exploring <i>Picea glauca</i> aquaporins in the context of needle water uptake and xylem refilling. <i>New Phytologist</i> , 2014, 203, 388-400.	3.5	104
2173	Missing Genes, Multiple ORFs, and C-to-U Type RNA Editing in <i>Acrasis kona</i> (Heterolobosea, Excavata) Mitochondrial DNA. <i>Genome Biology and Evolution</i> , 2014, 6, 2240-2257.	1.1	26
2174	Positive selection drives accelerated evolution of mosquito salivary genes associated with blood-feeding. <i>Insect Molecular Biology</i> , 2014, 23, 122-131.	1.0	30
2175	Phenotypic and genotypic characterization of H ₂ S-positive and H ₂ S-negative strains of <i>Shewanella baltica</i> isolated from spoiled whiting (<i>Merlangius merlangus</i>). <i>Letters in Applied Microbiology</i> , 2014, 59, 542-548.	1.0	9
2176	The Regulation of Copper Stress Response Genes in the Polychaete <i>Nereis diversicolor</i> during prolonged Extreme Copper Contamination. <i>Environmental Science & Technology</i> , 2014, 48, 13085-13092.	4.6	11
2177	Molecular interactions between sugar beet and <i>Polymyxa betae</i> during its life cycle. <i>Annals of Applied Biology</i> , 2014, 164, 244-256.	1.3	10
2178	Symbiotic adaptations in the fungal cultivar of leaf-cutting ants. <i>Nature Communications</i> , 2014, 5, 5675.	5.8	84
2179	Parallel signatures of selection in temporally isolated lineages of pink salmon. <i>Molecular Ecology</i> , 2014, 23, 2473-2485.	2.0	22
2180	Multiplexing with three-primer PCR for rapid and economical microsatellite validation. <i>Hereditas</i> , 2014, 151, 43-54.	0.5	22

#	ARTICLE	IF	CITATIONS
2181	Alternative reproductive tactics and sex-biased gene expression: the study of the bulb mite transcriptome. <i>Ecology and Evolution</i> , 2014, 4, 623-632.	0.8	50
2182	Molecular identification of the economically important freshwater mussels (<i>Mollusca</i>) via <i>Bivalvia</i> of Thailand: developing species-specific markers from AFLPs. <i>Animal Genetics</i> , 2014, 45, 235-239.	0.6	6
2183	Fuelling genetic and metabolic exploration of <i>C₃</i> bioenergy crops through the first reference transcriptome of <i>Azadirachta indica</i> . <i>Plant Biotechnology Journal</i> , 2014, 12, 554-567.	4.1	37
2184	Are <i>Niemann-Pick</i> type <i>C</i> proteins key players in cnidarian-dinoflagellate endosymbioses?. <i>Molecular Ecology</i> , 2014, 23, 4527-4540.	2.0	27
2185	Heterochromatin and molecular characterization of DsmarMITE transposable element in the beetle <i>Dichotomius schiffleri</i> (Coleoptera: Scarabaeidae). <i>Genetica</i> , 2014, 142, 575-581.	0.5	7
2186	Draft Genome Sequence of <i>Nitrospira</i> sp. Strain A-D6, an Arsenic-Resistant Gammaproteobacterium Isolated from a Salt Flat. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
2187	The haustorial transcriptomes of <i>Uromyces appendiculatus</i> and <i>Puccinia pachyrhizi</i> and their candidate effector families. <i>Molecular Plant Pathology</i> , 2014, 15, 379-393.	2.0	67
2188	Divergent transcriptional patterns are related to differences in hypoxia tolerance between the intertidal and the subtidal sculpins. <i>Molecular Ecology</i> , 2014, 23, 6091-6103.	2.0	22
2189	The mitochondrial genome of <i>Parascaris univalens</i> - implications for a "forgotten" parasite. <i>Parasites and Vectors</i> , 2014, 7, 428.	1.0	30
2190	A way for accelerating DNA sequences reconstruction problem based on CUDA. , 2014, , .		0
2191	The Transcriptome of <i>Nacobbus aberrans</i> Reveals Insights into the Evolution of Sedentary Endoparasitism in Plant-Parasitic Nematodes. <i>Genome Biology and Evolution</i> , 2014, 6, 2181-2194.	1.1	39
2192	Compartment-specific transcriptomics in a reef-building coral exposed to elevated temperatures. <i>Molecular Ecology</i> , 2014, 23, 5816-5830.	2.0	73
2193	Comparative and Evolutionary Analysis of Major Peanut Allergen Gene Families. <i>Genome Biology and Evolution</i> , 2014, 6, 2468-2488.	1.1	15
2194	Construction of Full-Length cDNA Library and Development of EST-Derived Simple Sequence Repeat (EST-SSR) Markers in <i>Senecio scandens</i> . <i>Biochemical Genetics</i> , 2014, 52, 494-508.	0.8	5
2195	RNA-Seq profile of flavescence dorée phytoplasma in grapevine. <i>BMC Genomics</i> , 2014, 15, 1088.	1.2	34
2196	Construction of a dairy microbial genome catalog opens new perspectives for the metagenomic analysis of dairy fermented products. <i>BMC Genomics</i> , 2014, 15, 1101.	1.2	64
2197	Transcriptome of the inflorescence meristems of the biofuel plant <i>Jatropha curcas</i> treated with cytokinin. <i>BMC Genomics</i> , 2014, 15, 974.	1.2	49
2198	The temporal foliar transcriptome of the perennial C3 desert plant <i>Rhazya stricta</i> in its natural environment. <i>BMC Plant Biology</i> , 2014, 14, 2.	1.6	27

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2199	Next generation sequencing and de novo transcriptomics to study gene evolution. <i>Plant Methods</i> , 2014, 10, 34.	1.9	23
2200	Nonclinical and Clinical <i>Enterococcus faecium</i> Strains, but Not <i>Enterococcus faecalis</i> Strains, Have Distinct Structural and Functional Genomic Features. <i>Applied and Environmental Microbiology</i> , 2014, 80, 154-165.	1.4	58
2201	Polymorphism Identification and Improved Genome Annotation of <i>Brassica rapa</i> Through Deep RNA Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2065-2078.	0.8	29
2202	The Draft Assembly of the Radically Organized <i>Stylonychia lemnae</i> Macronuclear Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 1707-1723.	1.1	58
2203	<i>Arabidopsis</i> ANGULATA10 is required for thylakoid biogenesis and mesophyll development. <i>Journal of Experimental Botany</i> , 2014, 65, 2391-2404.	2.4	13
2204	Ectopic Expression of a Loblolly Pine Class II 4-Coumarate:CoA Ligase Alters Soluble Phenylpropanoid Metabolism but not Lignin Biosynthesis in <i>Populus</i> . <i>Plant and Cell Physiology</i> , 2014, 55, 1669-1678.	1.5	19
2205	Expressed Sequence Tag-Simple Sequence Repeat (EST-SSR) Marker Resources for Diversity Analysis of Mango (<i>Mangifera indica</i> L.). <i>Diversity</i> , 2014, 6, 72-87.	0.7	30
2206	Paf receptor expression in the marsupial embryo and endometrium during embryonic diapause. <i>Reproduction</i> , 2014, 147, 21-31.	1.1	9
2207	Transcriptome sequencing and analysis of the zoonotic parasite <i>Spirometra erinacei</i> spargana (plerocercoids). <i>Parasites and Vectors</i> , 2014, 7, 368.	1.0	15
2208	Identification of differentially expressed genes in female <i>Drosophila antonietae</i> and <i>Drosophila meridionalis</i> response to host cactus odor. <i>BMC Evolutionary Biology</i> , 2014, 14, 191.	3.2	7
2209	The genomic landscape of polymorphic human nuclear mitochondrial insertions. <i>Nucleic Acids Research</i> , 2014, 42, 12640-12649.	6.5	168
2210	iPathCons and iPathDB: an improved insect pathway construction tool and the database. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	14
2211	Developing nuclear DNA phylogenetic markers in the angiosperm genus <i>Leucadendron</i> (Proteaceae): A next-generation sequencing transcriptomic approach. <i>Molecular Phylogenetics and Evolution</i> , 2014, 70, 37-46.	1.2	31
2212	Isolation and characterization of chitin-degrading micro-organisms from the faeces of Goeldi's monkey, <i>Callimico goeldii</i> . <i>Journal of Applied Microbiology</i> , 2014, 116, 52-59.	1.4	10
2213	Microbial community structure and functioning in marine sediments associated with diffuse hydrothermal venting assessed by integrated meta-omics. <i>Environmental Microbiology</i> , 2014, 16, 2699-2710.	1.8	109
2214	An improved trajectory-based hybrid metaheuristic applied to the noisy DNA Fragment Assembly Problem. <i>Information Sciences</i> , 2014, 277, 273-283.	4.0	10
2215	Evolution of the tyrosinase gene family in bivalve molluscs: Independent expansion of the mantle gene repertoire. <i>Acta Biomaterialia</i> , 2014, 10, 3855-3865.	4.1	86
2216	Generation and Analysis of Expressed Sequence Tags (ESTs) from Muscle Full-Length cDNA Library of Wujin Pig. <i>Journal of Integrative Agriculture</i> , 2014, 13, 378-386.	1.7	1

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2217	Insights into the transcriptome of the marine copepod <i>Calanus helgolandicus</i> feeding on the oxylipin-producing diatom <i>Skeletonema marinoi</i> . <i>Harmful Algae</i> , 2014, 31, 153-162.	2.2	31
2218	Survey of Canadian retail pork chops and pork livers for detection of hepatitis E virus, norovirus, and rotavirus using real time RT-PCR. <i>International Journal of Food Microbiology</i> , 2014, 185, 33-40.	2.1	44
2219	Proteomic characterization of the venom and transcriptomic analysis of the venomous gland from the Mexican centipede <i>Scolopendra viridis</i> . <i>Journal of Proteomics</i> , 2014, 111, 224-237.	1.2	24
2220	<i>Bionectria ochroleuca</i> NOTL33"an endophytic fungus from <i>Nothapodytes foetida</i> producing antimicrobial and free radical scavenging metabolites. <i>Annals of Microbiology</i> , 2014, 64, 275-285.	1.1	29
2221	An assay for quantitative virulence in <i>Rhynchosporium commune</i> reveals an association between effector genotype and virulence. <i>Plant Pathology</i> , 2014, 63, 405-414.	1.2	30
2222	Biomaterial Proteins from <i>Mytilus edulis</i> Mantle Tissue Transcriptome. <i>Marine Biotechnology</i> , 2014, 16, 34-45.	1.1	55
2223	Characterization of fifteen SNP markers by mining EST in sea cucumber, <i>Apostichopus japonicus</i> . <i>Journal of Genetics</i> , 2014, 93, 49-53.	0.4	1
2224	Transcriptome Analysis Reveals a Rich Gene Set Related to Innate Immunity in the Eastern Oyster (<i>Crassostrea virginica</i>). <i>Marine Biotechnology</i> , 2014, 16, 17-33.	1.1	135
2225	Microbial communities analysis assessed by pyrosequencing" a new approach applied to conservation state studies of mural paintings. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 887-895.	1.9	39
2226	Characterization of mutations in regulatory genes of Tyl cluster leading to overexpression of tylosin in mutant $\hat{1}^3$ -1 of <i>Streptomyces fradiae</i> NRRL-2702. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 785-793.	1.7	4
2227	Generation of expressed sequence tags under cadmium stress for gene discovery and development of molecular markers in chickpea. <i>Protoplasma</i> , 2014, 251, 955-972.	1.0	3
2228	Gene cloning, expression and characterisation of a new $\hat{1}^2$ -agarase, AgWH50C, producing neoagarobiose from <i>Agarivorans gilvus</i> WH0801. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 1691-1698.	1.7	30
2229	Association of jacalin-related lectins with wheat responses to stresses revealed by transcriptional profiling. <i>Plant Molecular Biology</i> , 2014, 84, 95-110.	2.0	72
2230	Sequence capture using PCR-generated probes: a cost-effective method of targeted high-throughput sequencing for nonmodel organisms. <i>Molecular Ecology Resources</i> , 2014, 14, 1000-1010.	2.2	89
2231	Acquisition of Germ Plasm Accelerates Vertebrate Evolution. <i>Science</i> , 2014, 344, 200-203.	6.0	48
2232	Identification and expression analysis of ethylene biosynthesis and signaling genes provides insights into the early and late coffee cultivars ripening pathway. <i>Planta</i> , 2014, 239, 951-963.	1.6	14
2233	FGF Signaling Emerged Concomitantly with the Origin of Eumetazoans. <i>Molecular Biology and Evolution</i> , 2014, 31, 310-318.	3.5	23
2234	Structural and molecular characterization of <i>Kudoa quraishii</i> n. sp. from the trunk muscle of the Indian mackerel <i>Rastrelliger kanagartha</i> (Perciforme, Scombridae) in Saudi Arabia coasts. <i>Parasitology Research</i> , 2014, 113, 1361-1370.	0.6	14

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2235	Reconstitution of a 10-gene pathway for synthesis of the plant alkaloid dihydrosanguinarine in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2014, 5, 3283.	5.8	149
2236	An investigation of genetic population structure in blue crabs, <i>Callinectes sapidus</i> , using nuclear gene sequences. <i>Marine Biology</i> , 2014, 161, 871-886.	0.7	28
2237	Development and characterization of genomic SSR markers in <i>Cynodon transvaalensis</i> Burt-Davy. <i>Molecular Genetics and Genomics</i> , 2014, 289, 523-531.	1.0	17
2238	PmTCP1 encodes a putative TCP transcription factor and is differentially expressed during in vitro organogenesis in <i>Passiflora</i> . <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2014, 50, 36-44.	0.9	3
2239	Comparative analysis of differential gene expression in kidney tissues of moribund and surviving crucian carp (<i>Carassius auratus gibelio</i>) in response to cyprinid herpesvirus 2 infection. <i>Archives of Virology</i> , 2014, 159, 1961-1974.	0.9	62
2240	Previously Undescribed Plasmids Recovered from Activated Sludge Confer Tetracycline Resistance and Phenotypic Changes to <i>Acinetobacter oleivorans</i> DR1. <i>Microbial Ecology</i> , 2014, 67, 369-379.	1.4	12
2241	Analysis of <i>Jatropha curcas</i> transcriptome for oil enhancement and genic markers. <i>Physiology and Molecular Biology of Plants</i> , 2014, 20, 139-142.	1.4	19
2242	Genetic variability and relationships among six grass carp <i>Ctenopharyngodon idella</i> populations in China estimated using EST-SNP Markers. <i>Fisheries Science</i> , 2014, 80, 475-481.	0.7	9
2243	Characterization of the glutathione S-transferase gene family through ESTs and expression analyses within common and pigmented cultivars of <i>Citrus sinensis</i> (L.) Osbeck. <i>BMC Plant Biology</i> , 2014, 14, 39.	1.6	45
2244	Combining metabolomics and transcriptomics to characterize tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . <i>BMC Genomics</i> , 2014, 15, 73.	1.2	165
2245	Comparative de novo transcriptome analysis and metabolic pathway studies of <i>Citrus paradisi</i> flavedo from naive stage to ripened stage. <i>Molecular Biology Reports</i> , 2014, 41, 3071-3080.	1.0	9
2246	Oil palm (<i>Elaeis guineensis</i> Jacq.) linkage map, and quantitative trait locus analysis for sex ratio and related traits. <i>Molecular Breeding</i> , 2014, 33, 415-424.	1.0	29
2247	Genomics of <i>C</i> opositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. <i>Molecular Ecology Resources</i> , 2014, 14, 166-177.	2.2	45
2248	The complete genome sequence for putative <i>H</i> and <i>S</i> oxidizer <i>Candidatus</i> <i>Sulfuricurvum</i> sp., assembled <i>de novo</i> from an aquifer-derived metagenome. <i>Environmental Microbiology</i> , 2014, 16, 3443-3462.	1.8	69
2249	First insights into the transcriptome and development of new genomic tools of a widespread circum-Mediterranean tree species, <i>Pinus halepensis</i> Mill. <i>Molecular Ecology Resources</i> , 2014, 14, 846-856.	2.2	61
2250	Characterization of novel wheat NBS domain-containing sequences and their utilization, in silico, for genome-scale R-gene mining. <i>Molecular Genetics and Genomics</i> , 2014, 289, 599-613.	1.0	7
2251	Deep sequencing of the mantle transcriptome of the great scallop <i>Pecten maximus</i> . <i>Marine Genomics</i> , 2014, 15, 3-4.	0.4	39
2252	Origins and functional evolution of Y chromosomes across mammals. <i>Nature</i> , 2014, 508, 488-493.	13.7	448

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2253	Accuracy of allele frequency estimation using pooled <i>scRNA</i> Seq. <i>Molecular Ecology Resources</i> , 2014, 14, 381-392.	2.2	54
2254	The extensive set of accessory <i>Pseudomonas aeruginosa</i> genomic components. <i>FEMS Microbiology Letters</i> , 2014, 356, 235-241.	0.7	55
2255	Dynamics and functions of bacterial communities in bark, charcoal and sand filters treating greywater. <i>Water Research</i> , 2014, 54, 21-32.	5.3	40
2256	Genome-wide identification of members in the YTH domain-containing RNA-binding protein family in apple and expression analysis of their responsiveness to senescence and abiotic stresses. <i>Gene</i> , 2014, 538, 292-305.	1.0	38
2257	A <i>de novo</i> transcriptome of <i>E</i> uropean pollen beetle populations and its analysis, with special reference to insecticide action and resistance. <i>Insect Molecular Biology</i> , 2014, 23, 511-526.	1.0	29
2258	Flower development in <i>Coffea arabica</i> L.: new insights into MADS-box genes. <i>Plant Reproduction</i> , 2014, 27, 79-94.	1.3	31
2259	Multistep involvement of glutathione with salicylic acid and ethylene to combat environmental stress. <i>Journal of Plant Physiology</i> , 2014, 171, 940-950.	1.6	54
2260	Characterization of EST-SSR markers in durum wheat EST library and functional analysis of SSR-containing EST fragments. <i>Molecular Genetics and Genomics</i> , 2014, 289, 625-640.	1.0	17
2261	Phylogenomic analysis of echinoderm class relationships supports Asterozoa. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140479.	1.2	102
2262	Genome-wide marker development for the wheat D genome based on single nucleotide polymorphisms identified from transcripts in the wild wheat progenitor <i>Aegilops tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 261-271.	1.8	43
2263	Mitochondrial genomes of <i>Anisakis simplex</i> and <i>Contraecaecum osculatum</i> (sensu stricto) – Comparisons with selected nematodes. <i>Infection, Genetics and Evolution</i> , 2014, 21, 452-462.	1.0	25
2264	Development and application of genomic tools to the restoration of green abalone in southern California. <i>Conservation Genetics</i> , 2014, 15, 109-121.	0.8	30
2265	Nutritional impacts on gene expression in the surface mucosa of blue catfish (<i>Ictalurus furcatus</i>). <i>Developmental and Comparative Immunology</i> , 2014, 44, 226-234.	1.0	31
2266	Molecular characterization of metalloproteases from <i>Bothrops alternatus</i> snake venom. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2014, 12, 74-83.	0.4	6
2267	A Y-chromosome-encoded small RNA acts as a sex determinant in persimmons. <i>Science</i> , 2014, 346, 646-650.	6.0	330
2268	Towards an integrative model of C4 photosynthetic subtypes: insights from comparative transcriptome analysis of NAD-ME, NADP-ME, and PEP-CK C4 species. <i>Journal of Experimental Botany</i> , 2014, 65, 3579-3593.	2.4	102
2269	Genotyping by sequencing transcriptomes in an evolutionary pre-breeding durum wheat population. <i>Molecular Breeding</i> , 2014, 34, 1531-1548.	1.0	20
2270	<i>QDD</i> version 3.1: a user-friendly computer program for microsatellite selection and primer design revisited: experimental validation of variables determining genotyping success rate. <i>Molecular Ecology Resources</i> , 2014, 14, 1302-1313.	2.2	170

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2271	Identification of Puffer Fish of the Genus <i>Lagocephalus</i> : <i>L. lunaris</i> , <i>L. spadiceus</i> and <i>L. inermis</i> , Using Multiplex PCR. <i>Food Biotechnology</i> , 2014, 28, 216-231.	0.6	11
2272	A fault-tolerant method for HLA typing with PacBio data. <i>BMC Bioinformatics</i> , 2014, 15, 296.	1.2	18
2273	Transcriptome analysis of mistletoe (<i>Viscum album</i>) haustorium development. <i>Horticulture Environment and Biotechnology</i> , 2014, 55, 352-361.	0.7	10
2274	Transcriptome Sequencing Uncovers the <i>Avr5</i> Avirulence Gene of the Tomato Leaf Mold Pathogen <i>Cladosporium fulvum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 846-857.	1.4	59
2275	Analysis of <i>ATP6</i> sequence diversity in the <i>Triticum</i> " <i>Aegilops</i> species group reveals the crucial role of rearrangement in mitochondrial genome evolution. <i>Genome</i> , 2014, 57, 279-288.	0.9	2
2276	Crustacean Intersexuality Is Feminization without Demasculinization: Implications for Environmental Toxicology. <i>Environmental Science & Technology</i> , 2014, 48, 13520-13529.	4.6	22
2277	A cDNA Resource for Gene Expression Studies of a Hemichordate, <i>Ptychodera flava</i> . <i>Zoological Science</i> , 2014, 31, 414.	0.3	10
2278	A Multi-Layered Screening Method to Identify Plant Regulatory Genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 293-303.	1.9	2
2279	Standalone EST microsatellite mining and analysis tool (SEMAT): for automated EST-SSR analysis in plants. <i>Tree Genetics and Genomes</i> , 2014, 10, 1755-1757.	0.6	4
2280	CottonGen: a genomics, genetics and breeding database for cotton research. <i>Nucleic Acids Research</i> , 2014, 42, D1229-D1236.	6.5	304
2281	In-silico identification of miRNAs and their regulating target functions in <i>Ocimum basilicum</i> . <i>Gene</i> , 2014, 552, 277-282.	1.0	21
2282	Complete genome sequence of the Gram-negative probiotic <i>Escherichia coli</i> strain Nissle 1917. <i>Journal of Biotechnology</i> , 2014, 187, 106-107.	1.9	76
2283	A reappraisal of the <i>Pleurotus eryngii</i> complex " New species and taxonomic combinations based on the application of a polyphasic approach, and an identification key to <i>Pleurotus</i> taxa associated with Apiaceae plants. <i>Fungal Biology</i> , 2014, 118, 814-834.	1.1	44
2284	Compartment Proteomics Analysis of White Perch (<i>Morone americana</i>) Ovary Using Support Vector Machines. <i>Journal of Proteome Research</i> , 2014, 13, 1515-1526.	1.8	20
2285	Tools, resources and databases for SNPs and indels in sequences: a review. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 264.	0.1	14
2286	Development of a targeted metagenomic approach to study a genomic region involved in light harvesting in marine <i>Synechococcus</i> . <i>FEMS Microbiology Ecology</i> , 2014, 88, 231-249.	1.3	21
2287	Differential retention and divergent resolution of duplicate genes following whole-genome duplication. <i>Genome Research</i> , 2014, 24, 1665-1675.	2.4	111
2288	Global Genomic Diversity of <i>Oryza sativa</i> Varieties Revealed by Comparative Physical Mapping. <i>Genetics</i> , 2014, 196, 937-949.	1.2	10

#	ARTICLE	IF	CITATIONS
2289	Transcriptome sequencing revealed the genes and pathways involved in salinity stress of Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Physiological Genomics</i> , 2014, 46, 177-190.	1.0	107
2290	Development of an improved live attenuated antigenic marker CSF vaccine strain candidate with an increased genetic stability. <i>Virology</i> , 2014, 471-473, 13-18.	1.1	17
2291	ShrimpGPAT: a gene and protein annotation tool for knowledge sharing and gene discovery in shrimp. <i>BMC Genomics</i> , 2014, 15, 506.	1.2	7
2292	Profiling microRNAs in <i>Eucalyptus grandis</i> reveals no mutual relationship between alterations in miR156 and miR172 expression and adventitious root induction during development. <i>BMC Genomics</i> , 2014, 15, 524.	1.2	38
2293	The genome sequence of the biocontrol fungus <i>Metarhizium anisopliae</i> and comparative genomics of <i>Metarhizium</i> species. <i>BMC Genomics</i> , 2014, 15, 660.	1.2	59
2294	The <i>Babesia bovis</i> gene and promoter model: an update from full-length EST analysis. <i>BMC Genomics</i> , 2014, 15, 678.	1.2	8
2295	Genome-wide transcriptome analysis of genes involved in flavonoid biosynthesis between red and white strains of <i>Magnolia sprengeri</i> pamp. <i>BMC Genomics</i> , 2014, 15, 706.	1.2	40
2296	ClonorESTdb: a comprehensive database for <i>Clonorchis sinensis</i> EST sequences. <i>BMC Research Notes</i> , 2014, 7, 388.	0.6	14
2297	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
2298	Comparative in silico analysis of EST-SSRs in angiosperm and gymnosperm tree genera. <i>BMC Plant Biology</i> , 2014, 14, 220.	1.6	29
2299	Single genome analysis reveals genetic characteristics of Neuroadaptation across HIV-1 envelope. <i>Retrovirology</i> , 2014, 11, 65.	0.9	20
2300	A systems biology approach reveals a link between systemic cytokines and skeletal muscle energy metabolism in a rodent smoking model and human COPD. <i>Genome Medicine</i> , 2014, 6, 59.	3.6	20
2301	Transcriptome Analysis of the Entomopathogenic Oomycete <i>Lagenidium giganteum</i> Reveals Putative Virulence Factors. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6427-6436.	1.4	14
2302	Molecular cloning and characterization of two novel fructose-specific transporters from the osmotolerant and fructophilic yeast <i>Candida magnoliae</i> JH110. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3569-3578.	1.7	11
2303	Plant systems biology: insights, advances and challenges. <i>Planta</i> , 2014, 240, 33-54.	1.6	66
2304	Characterization of an apple TT2-type R2R3 MYB transcription factor functionally similar to the poplar proanthocyanidin regulator PtMYB134. <i>Planta</i> , 2014, 240, 497-511.	1.6	61
2305	Molecular characterization of <i>Sarcocystis</i> species from Polish roe deer based on ssu rRNA and cox1 sequence analysis. <i>Parasitology Research</i> , 2014, 113, 3029-3039.	0.6	20
2306	Characterisation of the mitochondrial genome of <i>Parafilaroides normani</i> (lungworm) of <i>Arctocephalus pusillus doriferus</i> (Australian fur seal). <i>Parasitology Research</i> , 2014, 113, 3049-3055.	0.6	9

#	ARTICLE	IF	CITATIONS
2307	Glutamate-gated chloride channel subunit cDNA sequencing of <i>Cochliomyia hominivorax</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	2
2308	Lysis of Antarctic algal strains by bacterial pathogen. <i>Antonie Van Leeuwenhoek</i> , 2014, 105, 997-1005.	0.7	7
2309	Genome-Tagged Amplification (GTA): a PCR-based method to prepare sample-tagged amplicons from hundreds of individuals for next generation sequencing. <i>Molecular Breeding</i> , 2014, 34, 977-988.	1.0	7
2310	Down-regulating annexin gene GhAnn2 inhibits cotton fiber elongation and decreases Ca ²⁺ influx at the cell apex. <i>Plant Molecular Biology</i> , 2014, 85, 613-625.	2.0	58
2311	Presence, viral load and characterization of Torque teno sus viruses in liver and pork chop samples at retail. <i>International Journal of Food Microbiology</i> , 2014, 178, 60-64.	2.1	10
2312	Construction of a cDNA library and identification of genes from Liaoning cashmere goat. <i>Livestock Science</i> , 2014, 164, 26-34.	0.6	6
2313	Computational identification and characterization of conserved miRNAs and their target genes in garlic (<i>Allium sativum</i> L.) expressed sequence tags. <i>Gene</i> , 2014, 537, 333-342.	1.0	43
2314	Deep Proteomics of the <i>Xenopus laevis</i> Egg using an mRNA-Derived Reference Database. <i>Current Biology</i> , 2014, 24, 1467-1475.	1.8	234
2315	Disproportional Plastome-Wide Increase of Substitution Rates and Relaxed Purifying Selection in Genes of Carnivorous Lentibulariaceae. <i>Molecular Biology and Evolution</i> , 2014, 31, 529-545.	3.5	92
2316	Rewiring Host Lipid Metabolism by Large Viruses Determines the Fate of <i>Emiliania huxleyi</i> , a Bloom-Forming Alga in the Ocean. <i>Plant Cell</i> , 2014, 26, 2689-2707.	3.1	132
2317	Rediscovering Medicinal Plants' Potential with OMICS: Microsatellite Survey in Expressed Sequence Tags of Eleven Traditional Plants with Potent Antidiabetic Properties. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 298-309.	1.0	20
2318	Genome-wide characterization and selection of expressed sequence tag simple sequence repeat primers for optimized marker distribution and reliability in peach. <i>Tree Genetics and Genomes</i> , 2014, 10, 1271-1279.	0.6	10
2319	Differential expression analysis of transcripts related to oil metabolism in maturing seeds of <i>Jatropha curcas</i> L.. <i>Physiology and Molecular Biology of Plants</i> , 2014, 20, 181-190.	1.4	8
2320	Fatty acid composition and desaturase gene expression in flax (<i>Linum usitatissimum</i> L.). <i>Journal of Applied Genetics</i> , 2014, 55, 423-432.	1.0	17
2321	De novo transcriptome assembly reveals sex-specific selection acting on evolving neo-sex chromosomes in <i>Drosophila miranda</i> . <i>BMC Genomics</i> , 2014, 15, 241.	1.2	11
2322	Transcriptional profile of <i>Paracoccidioides</i> spp. in response to itraconazole. <i>BMC Genomics</i> , 2014, 15, 254.	1.2	11
2323	A survey of plant and algal genomes and transcriptomes reveals new insights into the evolution and function of the cellulose synthase superfamily. <i>BMC Genomics</i> , 2014, 15, 260.	1.2	63
2324	Patterns of homoeologous gene expression shown by RNA sequencing in hexaploid bread wheat. <i>BMC Genomics</i> , 2014, 15, 276.	1.2	97

#	ARTICLE	IF	CITATIONS
2325	The Mediterranean scorpion <i>Mesobuthus gibbosus</i> (Scorpiones, Buthidae): transcriptome analysis and organization of the genome encoding chlorotoxin-like peptides. <i>BMC Genomics</i> , 2014, 15, 295.	1.2	24
2326	De novo genome assembly of the soil-borne fungus and tomato pathogen <i>Pyrenochaeta lycopersici</i> . <i>BMC Genomics</i> , 2014, 15, 313.	1.2	39
2327	Dramatic expansion of the black widow toxin arsenal uncovered by multi-tissue transcriptomics and venom proteomics. <i>BMC Genomics</i> , 2014, 15, 366.	1.2	93
2328	Evolution of gene structure in the conifer <i>Picea glauca</i> : a comparative analysis of the impact of intron size. <i>BMC Plant Biology</i> , 2014, 14, 95.	1.6	46
2329	STINGRAY: system for integrated genomic resources and analysis. <i>BMC Research Notes</i> , 2014, 7, 132.	0.6	5
2330	Enigmatic Orthology Relationships between Hox Clusters of the African Butterfly Fish and Other Teleosts Following Ancient Whole-Genome Duplication. <i>Molecular Biology and Evolution</i> , 2014, 31, 2592-2611.	3.5	37
2331	Virus-host interactions in persistently FMDV-infected cells derived from bovine pharynx. <i>Virology</i> , 2014, 468-470, 185-196.	1.1	18
2332	Temporally Isolated Lineages of Pink Salmon Reveal Unique Signatures of Selection on Distinct Pools of Standing Genetic Variation. <i>Journal of Heredity</i> , 2014, 105, 835-845.	1.0	30
2333	Grouping and characterization of putative glycosyltransferase genes from <i>Panax ginseng</i> Meyer. <i>Gene</i> , 2014, 536, 186-192.	1.0	29
2334	Molecular cloning and characterization of a cytochrome P450 taxoid 9Å-hydroxylase in <i>Ginkgo biloba</i> cells. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 938-943.	1.0	22
2335	Exploring genetic variability within lentil (<i>Lens culinaris</i> Medik.) and across related legumes using a newly developed set of microsatellite markers. <i>Molecular Biology Reports</i> , 2014, 41, 5607-5625.	1.0	51
2336	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	6.0	436
2337	Molecular characterization, immune responsive expression and functional analysis of QM, a putative tumor suppressor gene from the Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2014, 37, 1-10.	1.6	12
2338	Molecular characterization and expression profiles of olfactory receptor genes in the parasitic wasp, <i>Microplitis mediator</i> (Hymenoptera: Braconidae). <i>Journal of Insect Physiology</i> , 2014, 60, 118-126.	0.9	16
2339	A Chinese jujube (<i>Ziziphus jujuba</i> Mill.) fruit-expressed sequence tag (EST) library: Annotation and EST-SSR characterization. <i>Scientia Horticulturae</i> , 2014, 165, 99-105.	1.7	23
2340	Transcript expression profiling for adventitious roots of <i>Panax ginseng</i> Meyer. <i>Gene</i> , 2014, 546, 89-96.	1.0	34
2341	Modified COLD-PCR for detection of minor microorganisms in wine samples during the fermentation. <i>Food Microbiology</i> , 2014, 39, 74-80.	2.1	8
2342	A classification scheme for alternative oxidases reveals the taxonomic distribution and evolutionary history of the enzyme in angiosperms. <i>Mitochondrion</i> , 2014, 19, 172-183.	1.6	55

#	ARTICLE	IF	CITATIONS
2343	MetaCAA: A clustering-aided methodology for efficient assembly of metagenomic datasets. <i>Genomics</i> , 2014, 103, 161-168.	1.3	18
2344	Accessing transcriptomic data for ecologically important genes in the goose barnacle (<i>Pollicipes</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 2	0.4	2
2345	Genome-wide analysis reveals the expansion of Cytochrome P450 genes associated with xenobiotic metabolism in rice striped stem borer, <i>Chilo suppressalis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 756-760.	1.0	44
2346	Improving transcriptome construction in non-model organisms: integrating manual and automated gene definition in <i>Emiliana huxleyi</i> . <i>BMC Genomics</i> , 2014, 15, 148.	1.2	31
2347	Expanding the repertoire of microsatellite markers for polymorphism studies in Indian accessions of mung bean (<i>Vigna radiata</i> L. Wilczek). <i>Molecular Biology Reports</i> , 2014, 41, 5669-5680.	1.0	14
2348	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6672-6677.	3.3	146
2349	Identification of early <i>Al</i> -responsive genes in rice bean (<i>Vigna umbellata</i>) roots provides new clues to molecular mechanisms of <i>Al</i> toxicity and tolerance. <i>Plant, Cell and Environment</i> , 2014, 37, 1586-1597.	2.8	53
2350	Nuclear pore complex evolution: a trypanosome Mlp analogue functions in chromosomal segregation but lacks transcriptional barrier activity. <i>Molecular Biology of the Cell</i> , 2014, 25, 1421-1436.	0.9	26
2351	Whole Genome Sequencing as a Diagnostic Test: Challenges and Opportunities. <i>Clinical Chemistry</i> , 2014, 60, 724-733.	1.5	64
2352	Interaction of structural core protein of classical swine fever virus with endoplasmic reticulum-associated degradation pathway protein OS9. <i>Virology</i> , 2014, 460-461, 173-179.	1.1	14
2353	Site-related differences in gene expression and bacterial densities in the mussel <i>Bathymodiolus azoricus</i> from the Menez Gwen and Lucky Strike deep-sea hydrothermal vent sites. <i>Fish and Shellfish Immunology</i> , 2014, 39, 343-353.	1.6	21
2354	Salinity-dependent copper accumulation in the guppy <i>Poecilia vivipara</i> is associated with CTR1 and ATP7B transcriptional regulation. <i>Aquatic Toxicology</i> , 2014, 152, 300-307.	1.9	30
2355	Large-Scale Development of Gene-Associated Single-Nucleotide Polymorphism Markers for Molluscan Population Genomic, Comparative Genomic, and Genome-Wide Association Studies. <i>DNA Research</i> , 2014, 21, 183-193.	1.5	15
2356	Development of polymorphic EST-SSR markers by sequence alignment in <i>Frankliniella occidentalis</i> (Pergande). <i>Journal of Asia-Pacific Entomology</i> , 2014, 17, 581-585.	0.4	3
2357	Tallgrass prairie soil fungal communities are resilient to climate change. <i>Fungal Ecology</i> , 2014, 10, 44-57.	0.7	41
2358	Microbial community composition is consistent across anaerobic digesters processing wheat-based fuel ethanol waste streams. <i>Bioresource Technology</i> , 2014, 157, 127-133.	4.8	19
2359	Morphologic and molecular description of <i>Metopus fuscus</i> Kahl from North America and new rDNA sequences from seven metopids (Armophorea, Metopidae). <i>European Journal of Protistology</i> , 2014, 50, 213-230.	0.5	28
2360	Whole-Body Acoel Regeneration Is Controlled by Wnt and Bmp-Admp Signaling. <i>Current Biology</i> , 2014, 24, 1107-1113.	1.8	155

#	ARTICLE	IF	CITATIONS
2361	The mitochondrial respiratory chain of the secondary green alga <i>Euglena gracilis</i> shares many additional subunits with parasitic Trypanosomatidae. <i>Mitochondrion</i> , 2014, 19, 338-349.	1.6	59
2362	Transcriptome and gene expression analysis during flower blooming in <i>Rosa chinensis</i> "Pallida"™. <i>Gene</i> , 2014, 540, 96-103.	1.0	31
2363	A first comprehensive census of fungi in soil reveals both hyperdiversity and fine-scale niche partitioning. <i>Ecological Monographs</i> , 2014, 84, 3-20.	2.4	293
2364	Mitochondrial D-loop mutations can be detected in sporadic malignant tumours in dogs. <i>Bulletin of the Veterinary Institute in Pulawy = Biuletyn Instytutu Weterynarii W Pulawach</i> , 2014, 58, 631-637.	0.4	10
2365	Evaluating Distributed Platforms for Protein-Guided Scientific Workflow. , 2014, , .		0
2366	Identification and Characterization of EST-SSR Markers in Cluster Bean (<i>Cyamopsis</i> spp.). <i>Crop Science</i> , 2014, 54, 1097-1102.	0.8	26
2367	Scaling up genome annotation using MAKER and work queue. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 447.	0.1	11
2368	Concise and Broadly Applicable Method for Determining the Genomic Sequences of North-American Type Porcine Reproductive and Respiratory Syndrome Viruses in Various Clusters. <i>Journal of Veterinary Medical Science</i> , 2014, 76, 1249-1255.	0.3	3
2369	Expression analysis of individual homoeologous wheat genome- and rye genome-specific transcripts in a 2BS.2RL wheat-rye translocation. <i>Genes and Genetic Systems</i> , 2014, 89, 159-168.	0.2	3
2370	Transcriptional dynamics of the developing sweet cherry (<i>Prunus avium</i> L.) fruit: sequencing, annotation and expression profiling of exocarp-associated genes. <i>Horticulture Research</i> , 2014, 1, 11.	2.9	82
2371	Characterization of a Genogroup I Sapovirus Isolated from Chimpanzees in the Republic of Congo. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
2372	Sequencing and comparative genomics analysis in <i>Senecio scandens</i> Buch.-Ham. Ex D. Don, based on full-length cDNA library. <i>Biotechnology and Biotechnological Equipment</i> , 2014, 28, 805-812.	0.5	1
2373	Pathosphere.org: pathogen detection and characterization through a web-based, open-source informatics platform. <i>BMC Bioinformatics</i> , 2015, 16, 416.	1.2	16
2374	Two forward genetic screens for vein density mutants in sorghum converge on a cytochrome P450 gene in the brassinosteroid pathway. <i>Plant Journal</i> , 2015, 84, 257-266.	2.8	36
2375	Deciphering the molecular adaptation of the king scallop (<i>Pecten maximus</i>) to heat stress using transcriptomics and proteomics. <i>BMC Genomics</i> , 2015, 16, 988.	1.2	41
2376	Gene map of large yellow croaker (<i>Larimichthys crocea</i>) provides insights into teleost genome evolution and conserved regions associated with growth. <i>Scientific Reports</i> , 2015, 5, 18661.	1.6	35
2377	Phenome-ing Microbes. <i>Springer Protocols</i> , 2015, , 83-96.	0.1	1
2378	Developing single nucleotide polymorphism markers for the identification of pineapple (<i>Ananas</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 2.9 27	2.9	27

#	ARTICLE	IF	CITATIONS
2379	Identification and comparative expression analysis of odorant binding protein genes in the tobacco cutworm <i>Spodoptera litura</i> . <i>Scientific Reports</i> , 2015, 5, 13800.	1.6	75
2380	Sequencing of plant genomes – a review. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 361-376.	0.8	20
2381	De Novo Assembly and Characterization of Four Anthozoan (Phylum Cnidaria) Transcriptomes. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2441-2452.	0.8	74
2382	Development of EST-SSR Markers in <i>Barringtonia racemosa</i> (Lecythidaceae) and Cross-Amplification in Related Species. <i>Applications in Plant Sciences</i> , 2015, 3, 1500080.	0.8	2
2383	Phylotranscriptomic Analysis Based on Coalescence was Less Influenced by the Evolving Rates and the Number of Genes: A Case Study in Ericales. <i>Evolutionary Bioinformatics</i> , 2015, 11s1, EBO.S22448.	0.6	8
2384	Subtype-independent near full-length HIV genome sequencing and assembly to be used in large molecular epidemiological studies and clinical management. <i>Journal of the International AIDS Society</i> , 2015, 18, 20035.	1.2	33
2385	Transcriptome sequencing of three <i>Pseudo-nitzschia</i> species reveals comparable gene sets and the presence of Nitric Oxide Synthase genes in diatoms. <i>Scientific Reports</i> , 2015, 5, 12329.	1.6	58
2386	Insights into transcriptional changes that accompany organelle sequestration from the stolen nucleus of <i>Mesodinium rubrum</i> . <i>BMC Genomics</i> , 2015, 16, 805.	1.2	30
2387	Transcriptome analysis of 20 taxonomically related benzylisoquinoline alkaloid-producing plants. <i>BMC Plant Biology</i> , 2015, 15, 227.	1.6	70
2388	Mango (<i>Mangifera indica</i> L.) germplasm diversity based on single nucleotide polymorphisms derived from the transcriptome. <i>BMC Plant Biology</i> , 2015, 15, 277.	1.6	41
2389	De novo transcriptome analysis of <i>Medicago falcata</i> reveals novel insights about the mechanisms underlying abiotic stress-responsive pathway. <i>BMC Genomics</i> , 2015, 16, 818.	1.2	48
2390	Developing expressed sequence tag libraries and the discovery of simple sequence repeat markers for two species of raspberry (<i>Rubus</i> L.). <i>BMC Plant Biology</i> , 2015, 15, 258.	1.6	13
2391	The <i>Haemonchus contortus</i> kinome - a resource for fundamental molecular investigations and drug discovery. <i>Parasites and Vectors</i> , 2015, 8, 623.	1.0	14
2392	Discovery and characterization of Alu repeat sequences via precise local read assembly. <i>Nucleic Acids Research</i> , 2015, 43, gkv1089.	6.5	31
2393	A novel sister clade to the enterobacteria microviruses (family) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (<i>M</i>). <i>Microbiology</i> , 2015, 17, 3708-3721.	1.8	37
2394	Negligible nuclear introgression despite complete mitochondrial capture between two species of chipmunks. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1961-1972.	1.1	88
2395	Diversity of nitrogen assimilation pathways among microbial photosynthetic eukaryotes. <i>Journal of Phycology</i> , 2015, 51, 490-506.	1.0	27
2396	Revival of the genus <i>Tropicoperdix</i> – Blyth 1859 (Phasianidae, Aves) using multilocus sequence data. <i>Zoological Journal of the Linnean Society</i> , 2015, 175, 429-438.	1.0	10

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2397	Complete Genome Sequence of a Highly Pathogenic Avian Influenza Virus (H5N2) Associated with an Outbreak in Commercial Chickens, Iowa, USA, 2015. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
2398	De novo sequencing and analysis of <i>Lophophora williamsii</i> transcriptome, and searching for putative genes involved in mescaline biosynthesis. <i>BMC Genomics</i> , 2015, 16, 657.	1.2	17
2399	Gonadal transcriptomics elucidate patterns of adaptive evolution within marine rockfishes (<i>Sebastes</i>). <i>BMC Genomics</i> , 2015, 16, 656.	1.2	8
2400	Pathogen-regulated genes in wheat isogenic lines differing in resistance to brown rust <i>Puccinia triticina</i> . <i>BMC Genomics</i> , 2015, 16, 742.	1.2	27
2401	Asymmetric somatic hybridization induces point mutations and indels in wheat. <i>BMC Genomics</i> , 2015, 16, 807.	1.2	16
2402	Global identification and analysis of long non-coding RNAs in diploid strawberry <i>Fragaria vesca</i> during flower and fruit development. <i>BMC Genomics</i> , 2015, 16, 815.	1.2	106
2403	De novo transcriptome sequencing in <i>Bixa orellana</i> to identify genes involved in methylerythritol phosphate, carotenoid and bixin biosynthesis. <i>BMC Genomics</i> , 2015, 16, 877.	1.2	45
2404	In silico characterization and Molecular modeling of double-strand break repair protein MRE11 from <i>Phoenix dactylifera v deglet nour</i> . <i>Theoretical Biology and Medical Modelling</i> , 2015, 12, 23.	2.1	16
2405	<i>Phlebotomus papatasi</i> SP15: mRNA expression variability and amino acid sequence polymorphisms of field populations. <i>Parasites and Vectors</i> , 2015, 8, 298.	1.0	17
2406	The complete mitochondrial genome of <i>Anoplocephala perfoliata</i> , the first representative for the family <i>Anoplocephalidae</i> . <i>Parasites and Vectors</i> , 2015, 8, 549.	1.0	16
2407	Differential sialotranscriptomes of unfed and fed <i>Rhipicephalus haemaphysaloides</i> , with particular regard to differentially expressed genes of cysteine proteases. <i>Parasites and Vectors</i> , 2015, 8, 597.	1.0	39
2408	Draft Genome Sequence of an Alphaproteobacterium Associated with the Mediterranean Sponge <i>Oscarella lobularis</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	11
2409	Effects of the 2010 coral bleaching on phylogenetic clades and diversity of zooxanthellae (<i>Symbiodinium</i> spp.) in soft corals of the genus <i>Sinularia</i> . <i>Plankton and Benthos Research</i> , 2015, 10, 11-17.	0.2	2
2410	Analysis of Effects of Berberine on the Photosynthesis of <i>Microcystis aeruginosa</i> at Gene Transcriptional Level. <i>Clean - Soil, Air, Water</i> , 2015, 43, 44-50.	0.7	5
2411	Molecular cloning and characterization of the gonadotropin subunits GPI^{\pm} , FSH^{\pm} , and LH^{\pm} genes in the stinging catfish <i>Heteropneustes fossilis</i> : Phylogeny, seasonal expression and pituitary localization. <i>Journal of Experimental Zoology</i> , 2015, 323, n/a-n/a.	1.2	3
2412	An investigation of the genetic basis of increased susceptibility to neutralization by anti-fusion glycoprotein antibody arising on passage of human respiratory syncytial virus in cell culture. <i>Journal of Medical Virology</i> , 2015, 87, 130-140.	2.5	1
2413	Molecular epidemiology of influenza A virus infection among hospitalized children in vietnam during post-epidemic period. <i>Journal of Medical Virology</i> , 2015, 87, 904-912.	2.5	3
2414	Ectomycorrhizal fungi mediate indirect effects of a bark beetle outbreak on secondary chemistry and establishment of pine seedlings. <i>New Phytologist</i> , 2015, 208, 904-914.	3.5	50

#	ARTICLE	IF	CITATIONS
2415	<i>De novo</i> transcriptome assembly and identification of genes associated with feed conversion ratio and breast muscle yield in domestic ducks. <i>Animal Genetics</i> , 2015, 46, 636-645.	0.6	20
2416	Identification and Expression Analysis of Putative Chemosensory Receptor Genes in <i>Microplitis mediator</i> by Antennal Transcriptome Screening. <i>International Journal of Biological Sciences</i> , 2015, 11, 737-751.	2.6	59
2417	Insights into the dynamics of hind leg development in honey bee (<i>Apis mellifera</i> L.) queen and worker larvae - A morphology/differential gene expression analysis. <i>Genetics and Molecular Biology</i> , 2015, 38, 263-277.	0.6	8
2418	De novo assembly and characterization of the root transcriptome and development of simple sequence repeat markers in <i>Paphiopedilum concolor</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 6189-6201.	0.3	9
2419	Characterization of nuclear microsatellite markers for <i>Rumex bucephalophorus</i> (Polygonaceae) using 454 sequencing. <i>Applications in Plant Sciences</i> , 2015, 3, 1500088.	0.8	3
2420	Identification of genes involved in spontaneous leaf color variation in <i>Pseudosasa japonica</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 11827-11840.	0.3	22
2421	Differentially expressed genes in the pituitary of the Amazonian fish <i>Arapaima gigas</i> . <i>International Journal of Fisheries and Aquaculture</i> , 2015, 7, 132-141.	1.1	5
2422	A Long-Read Transcriptome Assembly of Cotton (<i>Gossypium hirsutum</i> L.) and Intraspecific Single Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0068.	1.6	12
2423	Metagenomic Analysis of Upwelling-Affected Brazilian Coastal Seawater Reveals Sequence Domains of Type I PKS and Modular NRPS. <i>International Journal of Molecular Sciences</i> , 2015, 16, 28285-28295.	1.8	11
2424	Ectomycorrhizal Fungal Communities and Enzymatic Activities Vary across an Ecotone between a Forest and Field. <i>Journal of Fungi (Basel, Switzerland)</i> , 2015, 1, 185-210.	1.5	15
2425	Gene expression in the mixotrophic prymnesiophyte, <i>Prymnesium parvum</i> , responds to prey availability. <i>Frontiers in Microbiology</i> , 2015, 6, 319.	1.5	37
2426	Changes in gene expression of <i>Prymnesium parvum</i> induced by nitrogen and phosphorus limitation. <i>Frontiers in Microbiology</i> , 2015, 6, 631.	1.5	46
2427	Recovering full-length viral genomes from metagenomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1069.	1.5	29
2428	In planta Identification of Putative Pathogenicity Factors from the Chickpea Pathogen <i>Ascochyta rabiei</i> by De novo Transcriptome Sequencing Using RNA-Seq and Massive Analysis of cDNA Ends. <i>Frontiers in Microbiology</i> , 2015, 6, 1329.	1.5	22
2429	Development and Characterization of Polymorphic Genic-SSR Markers in <i>Larix kaempferi</i> . <i>Molecules</i> , 2015, 20, 6060-6067.	1.7	17
2430	Transcriptome Analysis of Scorpion Species Belonging to the <i>Vaejovis</i> Genus. <i>PLoS ONE</i> , 2015, 10, e0117188.	1.1	56
2431	A New Set of ESTs from Chickpea (<i>Cicer arietinum</i> L.) Embryo Reveals Two Novel F-Box Genes, CarF-box_PP2 and CarF-box_LysM, with Potential Roles in Seed Development. <i>PLoS ONE</i> , 2015, 10, e0121100.	1.1	8
2432	Binary Gene Expression Patterning of the Molt Cycle: The Case of Chitin Metabolism. <i>PLoS ONE</i> , 2015, 10, e0122602.	1.1	25

#	ARTICLE	IF	CITATIONS
2433	First Detection of an Enterovirus C99 in a Captive Chimpanzee with Acute Flaccid Paralysis, from the Tchimpounga Chimpanzee Rehabilitation Center, Republic of Congo. PLoS ONE, 2015, 10, e0136700.	1.1	30
2434	Incongruent Nuclear and Mitochondrial Genetic Structure of New World Screwworm Fly Populations Due to Positive Selection of Mutations Associated with Dimethyl- and Diethyl-Organophosphates Resistance. PLoS ONE, 2015, 10, e0128441.	1.1	8
2435	In-Depth Transcriptome Sequencing of Mexican Lime Trees Infected with Candidatus Phytoplasma aurantifolia. PLoS ONE, 2015, 10, e0130425.	1.1	39
2436	Collembolan Transcriptomes Highlight Molecular Evolution of Hexapods and Provide Clues on the Adaptation to Terrestrial Life. PLoS ONE, 2015, 10, e0130600.	1.1	25
2437	Transcriptome Profile of the Response of Paracoccidioides spp. to a Camphene Thiosemicarbazide Derivative. PLoS ONE, 2015, 10, e0130703.	1.1	23
2438	An Insight into the Sialome of the Lone Star Tick, Amblyomma americanum, with a Glimpse on Its Time Dependent Gene Expression. PLoS ONE, 2015, 10, e0131292.	1.1	110
2439	Transcriptome Analysis of Beta macrocarpa and Identification of Differentially Expressed Transcripts in Response to Beet Necrotic Yellow Vein Virus Infection. PLoS ONE, 2015, 10, e0132277.	1.1	11
2440	The Evolution of the Secreted Regulatory Protein Progranulin. PLoS ONE, 2015, 10, e0133749.	1.1	53
2441	Development of Transcriptomic Markers for Population Analysis Using Restriction Site Associated RNA Sequencing (RARseq). PLoS ONE, 2015, 10, e0134855.	1.1	7
2442	Molecular phenotypes associated with anomalous stamen development in Alternanthera philoxeroides. Frontiers in Plant Science, 2015, 6, 242.	1.7	11
2443	Dynamic transcriptional profiling provides insights into tuberous root development in Rehmannia glutinosa. Frontiers in Plant Science, 2015, 6, 396.	1.7	27
2444	ReprOlive: a database with linked data for the olive tree (Olea europaea L.) reproductive transcriptome. Frontiers in Plant Science, 2015, 6, 625.	1.7	58
2445	The origin and evolution of phototropins. Frontiers in Plant Science, 2015, 6, 637.	1.7	68
2446	Transcriptomics profiling of Indian mustard (Brassica juncea) under arsenate stress identifies key candidate genes and regulatory pathways. Frontiers in Plant Science, 2015, 6, 646.	1.7	46
2447	A method for the further assembly of targeted unigenes in a transcriptome after assembly by Trinity. Frontiers in Plant Science, 2015, 6, 843.	1.7	6
2448	The IDA Peptide Controls Abscission in Arabidopsis and Citrus. Frontiers in Plant Science, 2015, 6, 1003.	1.7	57
2449	Bioinformatics-Aided Venomics. Toxins, 2015, 7, 2159-2187.	1.5	38
2450	Role of Bioinformatic Tools and Databases in Cotton Research. Agronomy, 2015, , 303-337.	0.2	2

#	ARTICLE	IF	CITATIONS
2451	De Novo Assembly and Transcriptome Characterization of Canine Retina Using High-Throughput Sequencing. <i>Genetics Research International</i> , 2015, 2015, 1-11.	2.0	3
2452	Spaced Seed Data Structures for De Novo Assembly. <i>International Journal of Genomics</i> , 2015, 2015, 1-8.	0.8	6
2453	Genome-Wide Identification of Genes Probably Relevant to the Uniqueness of Tea Plant (<i>Camellia</i>). <i>Trends in Plant Science</i> , 2015, 10, 1-10.	0.8	4
2454	Expressed Sequence Tags Analysis and Design of Simple Sequence Repeats Markers from a Full-Length cDNA Library in <i>Perilla frutescens</i> (L.). <i>International Journal of Genomics</i> , 2015, 2015, 1-7.	0.8	5
2455	Analysis of expressed sequence tags from cDNA library of <i>Fusarium culmorum</i> infected barley (<i>Hordeum vulgare</i> L.) roots. <i>Bioinformatics</i> , 2015, 11, 34-38.	0.2	4
2456	Identification and functional annotation of expressed sequence tags based SSR markers of <i>Stevia rebaudiana</i> . <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 439-450.	0.8	12
2457	Chitinolytic <i>Streptomyces vinaceus</i> drappus S5MW2 isolated from Chilika lake, India enhances plant growth and biocontrol efficacy through chitin supplementation against <i>Rhizoctonia solani</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2015, 31, 1217-1225.	1.7	58
2458	The Ty1-copia LTR retroelement family PARTC is highly conserved in conifers over 200MY of evolution. <i>Gene</i> , 2015, 568, 89-99.	1.0	24
2459	Deep developmental transcriptome sequencing uncovers numerous new genes and enhances gene annotation in the sponge <i>Amphimedon queenslandica</i> . <i>BMC Genomics</i> , 2015, 16, 387.	1.2	91
2460	Construction of EST-SSR Databases for Effective Cultivar Identification and Their Applicability to Complement for Lettuce (<i>Lactuca sativa</i> L.) Distinctness Test. <i>American Journal of Plant Sciences</i> , 2015, 06, 113-125.	0.3	17
2461	Proteomic-based biotyping reveals hidden diversity within a microalgae culture collection: An example using <i>Dunaliella</i> . <i>Scientific Reports</i> , 2015, 5, 10036.	1.6	23
2462	Differences in learning and memory of host plant features between specialist and generalist phytophagous insects. <i>Animal Behaviour</i> , 2015, 106, 1-10.	0.8	24
2463	Next-Generation Sequencing and Assembly of Plant Genomes. , 2015, , 53-64.		1
2464	Are European lobsters (<i>Homarus gammarus</i>) susceptible to infection by a temperate <i>Hematodinium</i> sp.?. <i>Journal of Invertebrate Pathology</i> , 2015, 127, 6-10.	1.5	4
2465	De novo sequencing, assembly and analysis of salivary gland transcriptome of <i>Haemaphysalis flava</i> and identification of sialoprotein genes. <i>Infection, Genetics and Evolution</i> , 2015, 32, 135-142.	1.0	46
2466	Complete genome sequence and intracellular protein localization of Datura yellow vein nucleorhabdovirus. <i>Virus Research</i> , 2015, 205, 7-11.	1.1	24
2467	Comparative transcriptomics uncovers alternative splicing changes and signatures of selection from maize improvement. <i>BMC Genomics</i> , 2015, 16, 363.	1.2	33
2468	The effects of reference genes in qRT-PCR assays for determining the immune response of bovine cells (MDBK) infected with the Bovine Viral Diarrhea Virus 1 (BVDV-1). <i>Gene</i> , 2015, 569, 95-103.	1.0	10

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2469	Enrichment of an intraspecific genetic map of upland cotton by developing markers using parental RAD sequencing. <i>DNA Research</i> , 2015, 22, 147-160.	1.5	50
2470	De Novo Assembly and Annotation of the Asian Tiger Mosquito (<i>Aedes albopictus</i>) Repeatome with dnaPipeTE from Raw Genomic Reads and Comparative Analysis with the Yellow Fever Mosquito (<i>Aedes</i>) Tj ETQq1 1 1017843141rgBT/O...	1.1	14
2471	Low Variation in a Y-Chromosomal Growth Hormone Pseudogene Relative to its Functional Autosomal Progenitor Gene in Chinook Salmon. <i>Transactions of the American Fisheries Society</i> , 2015, 144, 1029-1039.	0.6	3
2472	The genomes of many yam species contain transcriptionally active endogenous geminiviral sequences that may be functionally expressed. <i>Virus Evolution</i> , 2015, 1, vev002.	2.2	30
2473	Gut microbiota richness promotes its stability upon increased dietary fibre intake in healthy adults. <i>Environmental Microbiology</i> , 2015, 17, 4954-4964.	1.8	279
2474	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. <i>Genome Biology and Evolution</i> , 2015, 7, evv172.	1.1	22
2475	Deep sequencing of the Mexican avocado transcriptome, an ancient angiosperm with a high content of fatty acids. <i>BMC Genomics</i> , 2015, 16, 599.	1.2	69
2476	De novo assembly and functional annotation of <i>Myrciaria dubia</i> fruit transcriptome reveals multiple metabolic pathways for L-ascorbic acid biosynthesis. <i>BMC Genomics</i> , 2015, 16, 997.	1.2	25
2477	Genome-wide cataloging and analysis of alternatively spliced genes in cereal crops. <i>BMC Genomics</i> , 2015, 16, 721.	1.2	53
2478	A draft genome sequence of an invasive mosquito: an Italian <i>Aedes albopictus</i> . <i>Pathogens and Global Health</i> , 2015, 109, 207-220.	1.0	35
2479	High-Performance Multiclass Classification Framework Using Cloud Computing Architecture. <i>Journal of Medical and Biological Engineering</i> , 2015, 35, 795-802.	1.0	2
2480	Encephalitozoon hellem Infection in a Captive Juvenile Freshwater Crocodile (<i>Crocodylus johnstoni</i>). <i>Journal of Comparative Pathology</i> , 2015, 153, 352-356.	0.1	4
2481	Genomic characterization of <i>Sinorhizobium meliloti</i> AK21, a wild isolate from the Aral Sea Region. <i>SpringerPlus</i> , 2015, 4, 259.	1.2	5
2482	Characterization and comparison of EST-SSRs in <i>Salix</i> , <i>Populus</i> , and <i>Eucalyptus</i> . <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	11
2483	Understanding the Biochemical Basis of Temperature-Induced Lipid Pathway Adjustments in Plants. <i>Plant Cell</i> , 2015, 27, 86-103.	3.1	161
2484	Next-generation sequencing workflow for assembly of nonmodel mitogenomes exemplified with North Pacific albatrosses (<i>Phoebastria</i> spp.). <i>Molecular Ecology Resources</i> , 2015, 15, 893-902.	2.2	18
2485	A survey of genome sequence assembly techniques and algorithms using high-performance computing. <i>Journal of Supercomputing</i> , 2015, 71, 293-339.	2.4	4
2486	A highly thermostable lichenase from <i>Bacillus</i> sp. UEB-S: Biochemical and molecular characterization. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2015, 115, 8-12.	1.8	4

#	ARTICLE	IF	CITATIONS
2487	Resolving phylogenetic relationships of the recently radiated carnivorous plant genus <i>Sarracenia</i> using target enrichment. <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 76-87.	1.2	108
2488	Development of a Multilocus Sequence Typing scheme for the study of <i>Anaplasma marginale</i> population structure over space and time. <i>Infection, Genetics and Evolution</i> , 2015, 30, 186-194.	1.0	13
2489	Analysis of an antennal cDNA library and the expression patterns of two olfactory genes in <i>Frankliniella occidentalis</i> (Thysanoptera: Thripidae). <i>Applied Entomology and Zoology</i> , 2015, 50, 109-116.	0.6	3
2490	Plant Growth-promoting Fungus <i>Penicillium oxalicum</i> Enhances Plant Growth and Induces Resistance in Pearl Millet Against Downy Mildew Disease. <i>Journal of Phytopathology</i> , 2015, 163, 743-754.	0.5	56
2491	RNA-Seq analysis of rye-grass transcriptomic response to an herbicide inhibiting acetolactate-synthase identifies transcripts linked to non-target-site-based resistance. <i>Plant Molecular Biology</i> , 2015, 87, 473-487.	2.0	115
2492	Shoot transcriptome of the giant reed, <i>Arundo donax</i> . <i>Data in Brief</i> , 2015, 3, 1-6.	0.5	17
2493	Genomic-derived microsatellite markers for diversity analysis in <i>Jatropha curcas</i> . <i>Trees - Structure and Function</i> , 2015, 29, 849-858.	0.9	5
2494	DIME: A Novel Framework for De Novo Metagenomic Sequence Assembly. <i>Journal of Computational Biology</i> , 2015, 22, 159-177.	0.8	15
2495	Gene expression defines natural changes in mammalian lifespan. <i>Aging Cell</i> , 2015, 14, 352-365.	3.0	142
2496	Nature-inspired novel Cuckoo Search Algorithm for genome sequence assembly. <i>Sadhana - Academy Proceedings in Engineering Sciences</i> , 2015, 40, 1-14.	0.8	14
2497	An ensemble strategy that significantly improves de novo assembly of microbial genomes from metagenomic next-generation sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, e46-e46.	6.5	213
2498	Cloning, expression and in silico studies of a serine protease from a marine actinomycete (<i>Nocardiopsis</i> sp. NCIM 5124). <i>Process Biochemistry</i> , 2015, 50, 378-387.	1.8	13
2499	De novo transcriptome assembly for a non-model species, the blood-sucking bug <i>Triatoma brasiliensis</i> , a vector of Chagas disease. <i>Genetica</i> , 2015, 143, 225-239.	0.5	31
2500	Phylogenetic diversity and biological activity of culturable Actinobacteria isolated from freshwater fish gut microbiota. <i>Microbiological Research</i> , 2015, 175, 6-15.	2.5	69
2501	Comparing viral metagenomics methods using a highly multiplexed human viral pathogens reagent. <i>Journal of Virological Methods</i> , 2015, 213, 139-146.	1.0	124
2502	Symbiont type influences trophic plasticity of a model cnidarian-dinoflagellate symbiosis. <i>Journal of Experimental Biology</i> , 2015, 218, 858-863.	0.8	64
2503	Identification of genes differentially expressed in husk tomato (<i>Physalis philadelphica</i>) in response to whitefly (<i>Trialeurodes vaporariorum</i>) infestation. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	1.0	14
2504	Complete genome sequence of nine isolates of canna yellow streak virus reveals its relationship to the sugarcane mosaic virus (SCMV) subgroup of potyviruses. <i>Archives of Virology</i> , 2015, 160, 837-844.	0.9	11

#	ARTICLE	IF	CITATIONS
2505	Identification of Low Temperature Stress Regulated Transcript Sequences and Gene Families in Italian Cypress. <i>Molecular Biotechnology</i> , 2015, 57, 407-418.	1.3	5
2506	Hybrid Dysfunction and Physiological Compensation in Gene Expression. <i>Molecular Biology and Evolution</i> , 2015, 32, 613-622.	3.5	67
2507	Sequence-characterized amplified regions that differentiate New World screwworms from other potential wound-inhabiting flies. <i>Journal of Veterinary Diagnostic Investigation</i> , 2015, 27, 25-30.	0.5	3
2508	E-Microsatellite Markers for <i>Centella asiatica</i> (Gotu Kola) Genome: Validation and Cross-Transferability in Apiaceae Family for Plant Omics Research and Development. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 52-65.	1.0	9
2509	Effects of population density and body size on disease ecology of the European lobster in a temperate marine conservation zone. <i>ICES Journal of Marine Science</i> , 2015, 72, i128-i138.	1.2	21
2510	Isolation and characterization of onion degrading bacteria from onion waste produced in South Buenos Aires province, Argentina. <i>World Journal of Microbiology and Biotechnology</i> , 2015, 31, 487-497.	1.7	6
2511	New polymorphic microsatellite markers for the pelagic fish <i>Normanichthys crockeri</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 493-495.	0.4	0
2512	Different Continuous Cropping Spans Significantly Affect Microbial Community Membership and Structure in a Vanilla-Grown Soil as Revealed by Deep Pyrosequencing. <i>Microbial Ecology</i> , 2015, 70, 209-218.	1.4	205
2513	Development, characterization and cross-species transferability of genomic SSR markers in berseem (<i>Trifolium alexandrinum</i> L.), an important multi-cut annual forage legume. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	9
2514	Isolation, characterization and functional annotation of the salt tolerance genes through screening the high-quality cDNA library of the halophytic green alga <i>Dunaliella salina</i> (Chlorophyta). <i>Annals of Microbiology</i> , 2015, 65, 1293-1302.	1.1	9
2515	Optimal assembly strategies of transcriptome related to ploidies of eukaryotic organisms. <i>BMC Genomics</i> , 2015, 16, 65.	1.2	30
2516	Candidate gene markers associated with cold tolerance in vegetative stage of rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2015, 203, 385-398.	0.6	10
2517	Dark-induced senescence of barley leaves involves activation of plastid transglutaminases. <i>Amino Acids</i> , 2015, 47, 825-838.	1.2	24
2518	Production of bioactive ginsenosides Rh2 and Rg3 by metabolically engineered yeasts. <i>Metabolic Engineering</i> , 2015, 29, 97-105.	3.6	162
2519	De novo assembly and characterization of transcriptomes of early-stage fruit from two genotypes of <i>Annona squamosa</i> L. with contrast in seed number. <i>BMC Genomics</i> , 2015, 16, 86.	1.2	14
2520	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. <i>Genome Medicine</i> , 2015, 7, 6.	3.6	6
2521	Characterization of <i>Pseudomonas monteilii</i> CCM 3423 and its physiological potential for biodegradation of selected organic pollutants. <i>Folia Microbiologica</i> , 2015, 60, 411-416.	1.1	10
2522	A Metagenomics and Case-Control Study To Identify Viruses Associated with Bovine Respiratory Disease. <i>Journal of Virology</i> , 2015, 89, 5340-5349.	1.5	181

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2523	Phenotype and transcriptome analysis reveals chloroplast development and pigment biosynthesis together influenced the leaf color formation in mutants of <i>Anthurium andraeanum</i> "Sonata"™. <i>Frontiers in Plant Science</i> , 2015, 6, 139.	1.7	99
2524	African Swine Fever Virus Georgia 2007 with a Deletion of Virulence-Associated Gene <i>gGL</i> (B119L), when Administered at Low Doses, Leads to Virus Attenuation in Swine and Induces an Effective Protection against Homologous Challenge. <i>Journal of Virology</i> , 2015, 89, 8556-8566.	1.5	141
2525	Analysis of IS6110 insertion sites provide a glimpse into genome evolution of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2015, 5, 12567.	1.6	47
2526	A gyrovirus infecting a sea bird. <i>Archives of Virology</i> , 2015, 160, 2105-2109.	0.9	25
2527	Comprehensive identification and profiling of host miRNAs in response to Singapore grouper iridovirus (SGIV) infection in grouper (<i>Epinephelus coioides</i>). <i>Developmental and Comparative Immunology</i> , 2015, 52, 226-235.	1.0	37
2528	Analysis of a suppressive subtractive hybridization library of <i>Alternaria alternata</i> resistant to 2-propenyl isothiocyanate. <i>Electronic Journal of Biotechnology</i> , 2015, 18, 320-326.	1.2	4
2529	Sequence-independent characterization of viruses based on the pattern of viral small RNAs produced by the host. <i>Nucleic Acids Research</i> , 2015, 43, 6191-6206.	6.5	104
2530	Using the second law of thermodynamics for enrichment and isolation of microorganisms to produce fuel alcohols or hydrocarbons. <i>Journal of Theoretical Biology</i> , 2015, 382, 356-362.	0.8	5
2531	The Transcriptome Sequence of <i>Dientamoeba fragilis</i> Offers New Biological Insights on its Metabolism, Kinome, Degradome and Potential Mechanisms of Pathogenicity. <i>Protist</i> , 2015, 166, 389-408.	0.6	18
2532	Floral Transcriptome Analyses of Four <i>Paphiopedilum</i> Orchids with Distinct Flowering Behaviors and Development of Simple Sequence Repeat Markers. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1928-1952.	1.0	8
2533	Miniaturized mitogenome of the parasitic plant <i>Viscum scurruloideum</i> is extremely divergent and dynamic and has lost all <i>nad</i> genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3515-24.	3.3	254
2534	Towards a more holistic research approach to plant conservation: the case of rare plants on oceanic islands. <i>AoB PLANTS</i> , 2015, 7, plv066.	1.2	22
2535	Species tree estimation of diploid <i>Helianthus</i> (Asteraceae) using target enrichment. <i>American Journal of Botany</i> , 2015, 102, 910-920.	0.8	61
2536	Chloroplast genome of <i>Aconitum barbatum</i> var. <i>puberulum</i> (Ranunculaceae) derived from CCS reads using the PacBio RS platform. <i>Frontiers in Plant Science</i> , 2015, 6, 42.	1.7	59
2537	Characterization of Cry Proteins in Native Strains of <i>Bacillus thuringiensis</i> and Activity Against <i>Anastrepha ludens</i> ¹ . <i>Southwestern Entomologist</i> , 2015, 40, 15-24.	0.1	9
2538	Global Transcriptional Dynamics of Diapause Induction in Non-Blood-Fed and Blood-Fed <i>Aedes albopictus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003724.	1.3	89
2539	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , 2015, 102, 1089-1107.	0.8	157
2540	Characterization of 12 Novel Microsatellite Markers of <i>Sogatella furcifera</i> (Hemiptera: Delphacidae) Identified From Next-Generation Sequence Data. <i>Journal of Insect Science</i> , 2015, 15, 94.	0.6	2

#	ARTICLE	IF	CITATIONS
2541	Capturing prokaryotic dark matter genomes. <i>Research in Microbiology</i> , 2015, 166, 814-830.	1.0	16
2542	Preferential Amplification of Pathogenic Sequences. <i>Scientific Reports</i> , 2015, 5, 11047.	1.6	7
2543	Evolutionary analysis of the female-specific avian W chromosome. <i>Nature Communications</i> , 2015, 6, 7330.	5.8	121
2544	Analysis of plant gene expression during passion fruit <i>Xanthomonas axonopodis</i> interaction implicates lipoxxygenase 2 in host defence. <i>Annals of Applied Biology</i> , 2015, 167, 135-155.	1.3	33
2545	Viral assemblage composition in Yellowstone acidic hot springs assessed by network analysis. <i>ISME Journal</i> , 2015, 9, 2162-2177.	4.4	48
2546	Epithelial Cadherin Determines Resistance to Infectious Pancreatic Necrosis Virus in Atlantic Salmon. <i>Genetics</i> , 2015, 200, 1313-1326.	1.2	170
2547	In Search of Pathogens: Transcriptome-Based Identification of Viral Sequences from the Pine Processionary Moth (<i>Thaumetopoea pityocampa</i>). <i>Viruses</i> , 2015, 7, 456-479.	1.5	17
2548	Saccharina genomes provide novel insight into kelp biology. <i>Nature Communications</i> , 2015, 6, 6986.	5.8	222
2549	Phylogenomic analysis of <i>Emiliania huxleyi</i> provides evidence for haptophyte stramenopile association and a chimeric haptophyte nuclear genome. <i>Marine Genomics</i> , 2015, 21, 31-42.	0.4	8
2550	Genome-wide analysis of the AP2/ERF gene family in <i>Salix arbutifolia</i> . <i>FEBS Open Bio</i> , 2015, 5, 132-137.	1.0	59
2551	Transcriptional profile of the human pathogenic fungus <i>Paracoccidioides lutzii</i> in response to sulfamethoxazole. <i>Medical Mycology</i> , 2015, 53, 477-492.	0.3	9
2552	Lectin genes and their mature proteins: Still an exciting matter, as revealed by biochemistry and bioinformatics analyses of newly reported proteins. <i>Biochemical Systematics and Ecology</i> , 2015, 60, 46-55.	0.6	0
2553	Analyzing serial cDNA libraries revealed reactive oxygen species and gibberellins signaling pathways in the salt response of Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Cell Reports</i> , 2015, 34, 1005-1023.	2.8	26
2554	Allele Mining in Solanum Germplasm: Cloning and Characterization of RB-Homologous Gene Fragments from Late Blight Resistant Wild Potato Species. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1584-1598.	1.0	27
2555	Identification of the trehalose-6-phosphate synthase gene family in winter wheat and expression analysis under conditions of freezing stress. <i>Journal of Genetics</i> , 2015, 94, 55-65.	0.4	58
2556	Delineating bacterial community structure of polluted soil samples collected from cancer prone belt of Punjab, India. <i>3 Biotech</i> , 2015, 5, 727-734.	1.1	11
2557	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015, 16, 112.	1.2	49
2558	Genome diversification within a clonal population of pandemic <i>Vibrio parahaemolyticus</i> seems to depend on the life circumstances of each individual bacteria. <i>BMC Genomics</i> , 2015, 16, 176.	1.2	18

#	ARTICLE	IF	CITATIONS
2559	Columnar apple primary roots share some features of the columnar-specific gene expression profile of aerial plant parts as evidenced by RNA-Seq analysis. <i>BMC Plant Biology</i> , 2015, 15, 34.	1.6	17
2560	Molecular detection and phylogenetic analysis of bovine astrovirus in Brazil. <i>Archives of Virology</i> , 2015, 160, 1519-1525.	0.9	16
2561	Evaluating the performance of anchored hybrid enrichment at the tips of the tree of life: a phylogenetic analysis of Australian <i>Eugongylus</i> group scincid lizards. <i>BMC Evolutionary Biology</i> , 2015, 15, 62.	3.2	57
2562	Identification and characterization of expressed retrotransposons in the genome of the <i>Paracoccidioides</i> species complex. <i>BMC Genomics</i> , 2015, 16, 376.	1.2	2
2563	African Swine Fever Virus Georgia Isolate Harboring Deletions of MGF360 and MGF505 Genes Is Attenuated in Swine and Confers Protection against Challenge with Virulent Parental Virus. <i>Journal of Virology</i> , 2015, 89, 6048-6056.	1.5	234
2564	Metatranscriptomic census of active protists in soils. <i>ISME Journal</i> , 2015, 9, 2178-2190.	4.4	274
2565	Next-generation sequencing detects repetitive elements expansion in giant genomes of annual killifish genus <i>Austrolebias</i> (Cyprinodontiformes, Rivulidae). <i>Genetica</i> , 2015, 143, 353-360.	0.5	21
2566	Validation of dbEST-SSRs and transferability of some other solanaceous species SSR in <i>ashwagandha</i> [<i>Withania Somnifera</i> (L.) Dunal]. <i>3 Biotech</i> , 2015, 5, 933-938.	1.1	4
2567	Response to potent anti-HBV agents in chronic hepatitis B and combined effect of HBV reverse transcriptase mutations. <i>Gene</i> , 2015, 567, 22-30.	1.0	1
2568	The Theory and Practice of Genome Sequence Assembly. <i>Annual Review of Genomics and Human Genetics</i> , 2015, 16, 153-172.	2.5	87
2569	De-novo transcriptome analysis of the banana shrimp (<i>Fenneropenaeus merguensis</i>) and identification of genes associated with reproduction and development. <i>Marine Genomics</i> , 2015, 22, 71-78.	0.4	66
2570	Demystifying computer science for molecular ecologists. <i>Molecular Ecology</i> , 2015, 24, 2619-2640.	2.0	6
2571	Grid-Assembly: An oligonucleotide composition-based partitioning strategy to aid metagenomic sequence assembly. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1541004.	0.3	2
2572	Identification and functional characterization of two Bcl-2 family protein genes in Zhikong scallop <i>Chlamys farreri</i> . <i>Fish and Shellfish Immunology</i> , 2015, 44, 147-155.	1.6	10
2573	Pineapple-banana rotation reduced the amount of <i>Fusarium oxysporum</i> more than maize-banana rotation mainly through modulating fungal communities. <i>Soil Biology and Biochemistry</i> , 2015, 86, 77-86.	4.2	97
2574	High throughput profiling of the cotton bollworm <i>Helicoverpa armigera</i> immunotranscriptome during the fungal and bacterial infections. <i>BMC Genomics</i> , 2015, 16, 321.	1.2	100
2575	The <i>Medicago sativa</i> gene index 1.2: a web-accessible gene expression atlas for investigating expression differences between <i>Medicago sativa</i> subspecies. <i>BMC Genomics</i> , 2015, 16, 502.	1.2	54
2576	Transcriptome Analysis of Pig <i>In Vivo</i> , <i>In Vitro</i> Fertilized, and Nuclear Transfer Blastocyst-Stage Embryos Treated with Histone Deacetylase Inhibitors Postfusion and Activation Reveals Changes in the Lysosomal Pathway. <i>Cellular Reprogramming</i> , 2015, 17, 243-258.	0.5	21

#	ARTICLE	IF	CITATIONS
2577	Next-generation sequencing, assembly, and comparative analyses of the latex transcriptomes from two elite <i>Hevea brasiliensis</i> varieties. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	10
2578	Identification of EST-SSRs and molecular diversity analysis in <i>Mentha piperita</i> . <i>Crop Journal</i> , 2015, 3, 335-342.	2.3	31
2579	A high-resolution physical map integrating an anchored chromosome with the BAC physical maps of wheat chromosome 6B. <i>BMC Genomics</i> , 2015, 16, 595.	1.2	18
2580	Differential carbon utilization and asexual reproduction under elevated CO_2 conditions in the model anemone, <i>Euxiptasia pallida</i> , hosting different symbionts. <i>Limnology and Oceanography</i> , 2015, 60, 2108-2120.	1.6	21
2581	First molecular characterization of <i>Sarcocystis tenella</i> in Tatra chamois (<i>Rupicapra rupicapra tatra</i>) in Poland. <i>Parasitology Research</i> , 2015, 114, 3885-3892.	0.6	16
2582	Discovering new biology through RNA-Seq. <i>Plant Physiology</i> , 2015, 169, pp.01081.2015.	2.3	28
2583	<i>Toxocara vitulorum</i> infection in a cohort of beef calves in Iowa. <i>Veterinary Parasitology</i> , 2015, 214, 96-99.	0.7	20
2584	Development of Microsatellite Markers for <i>Carallia brachiata</i> (Rhizophoraceae). <i>Applications in Plant Sciences</i> , 2015, 3, 1400125.	0.8	2
2585	Identification of genes involved in color variation of bamboo culms by suppression subtractive hybridization. <i>Plant Physiology and Biochemistry</i> , 2015, 97, 156-164.	2.8	11
2586	De novo assembly and characterisation of the field pea transcriptome using RNA-Seq. <i>BMC Genomics</i> , 2015, 16, 611.	1.2	49
2587	Spider Transcriptomes Identify Ancient Large-Scale Gene Duplication Event Potentially Important in Silk Gland Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 1856-1870.	1.1	74
2588	ALOMYbase, a resource to investigate non-target-site-based resistance to herbicides inhibiting acetolactate-synthase (ALS) in the major grass weed <i>Alopecurus myosuroides</i> (black-grass). <i>BMC Genomics</i> , 2015, 16, 590.	1.2	66
2589	Genome-wide analysis of alternative splicing events in <i>Hordeum vulgare</i> : Highlighting retention of intron-based splicing and its possible function through network analysis. <i>FEBS Letters</i> , 2015, 589, 3564-3575.	1.3	34
2590	Characterization of the cork oak transcriptome dynamics during acorn development. <i>BMC Plant Biology</i> , 2015, 15, 158.	1.6	22
2591	Molecular characterization of the gene feminizer in the stingless bee <i>Melipona interrupta</i> (Hymenoptera: Apidae) reveals association to sex and caste development. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 66, 24-30.	1.2	23
2592	Morphology, ontogenesis and molecular characterization of <i>Atractos contortus</i> Vávřina, 1950 and <i>Stichotricha aculeata</i> Wrzesniowski, 1866 (Ciliophora, Stichotrichida) with consideration of their systematic positions. <i>European Journal of Protistology</i> , 2015, 51, 351-373.	0.5	14
2593	Taxonomic relationships among non-macrocytidiata taxa of <i>Lactarius</i> subg. <i>Russularia</i> from Europe with special reference to species from Greece. <i>Mycological Progress</i> , 2015, 14, 1.	0.5	4
2594	Genotyping of classical swine fever virus using high-resolution melt analysis. <i>Journal of Virological Methods</i> , 2015, 224, 53-57.	1.0	4

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2595	Decolorization of Kraft liquor effluents and biochemical characterization of laccases from <i>Phlebia brevispora</i> BAFC 633. <i>International Biodeterioration and Biodegradation</i> , 2015, 104, 443-451.	1.9	21
2596	Six enzymes from mayapple that complete the biosynthetic pathway to the etoposide aglycone. <i>Science</i> , 2015, 349, 1224-1228.	6.0	359
2597	Genome-wide analysis of esterase-like genes in the striped rice stem borer, <i>Chilo suppressalis</i> . <i>Genome</i> , 2015, 58, 323-331.	0.9	5
2598	Early genome duplications in conifers and other seed plants. <i>Science Advances</i> , 2015, 1, e1501084.	4.7	236
2599	Genome-wide analysis of the barley MAPK gene family and its expression patterns in relation to <i>Puccinia hordei</i> infection. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	1.0	8
2600	Genomic insights into the evolutionary origin of Myxozoa within Cnidaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14912-14917.	3.3	193
2601	RNA-seq reveals regional differences in transcriptome response to heat stress in the marine snail <i>Cylindroiulus funebris</i> . <i>Molecular Ecology</i> , 2015, 24, 610-627.	2.0	145
2602	Venom-Related Transcripts from <i>Bothrops jararaca</i> Tissues Provide Novel Molecular Insights into the Production and Evolution of Snake Venom. <i>Molecular Biology and Evolution</i> , 2015, 32, 754-766.	3.5	76
2603	Complete genome sequences of two biologically distinct isolates of Asparagus virus 1. <i>Archives of Virology</i> , 2015, 160, 569-572.	0.9	5
2604	Development and characterization of simple sequence repeat (SSR) markers based on a full-length cDNA library of <i>Scutellaria baicalensis</i> . <i>Genomics</i> , 2015, 105, 61-67.	1.3	16
2605	Diversity and efficiency of anthracene-degrading bacteria isolated from a denitrifying activated sludge system treating municipal wastewater. <i>International Biodeterioration and Biodegradation</i> , 2015, 97, 151-158.	1.9	51
2606	Genome sequence of a virus isolate from tamarillo (<i>Solanum betaceum</i>) in Colombia: evidence for a new potyvirus. <i>Archives of Virology</i> , 2015, 160, 557-560.	0.9	10
2607	Development and characterization of microsatellite markers for the toadfish <i>Aphos porosus</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 411-413.	0.4	1
2608	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	6.0	492
2609	Development and characterization of microsatellite markers from an enriched genomic library of <i>Saccharina japonica</i> . <i>Journal of Applied Phycology</i> , 2015, 27, 479-487.	1.5	15
2610	Human Polyomavirus 7-Associated Pruritic Rash and Viremia in Transplant Recipients. <i>Journal of Infectious Diseases</i> , 2015, 211, 1560-1565.	1.9	92
2611	A memetic particle swarm optimization algorithm for solving the DNA fragment assembly problem. <i>Neural Computing and Applications</i> , 2015, 26, 495-506.	3.2	29
2612	Venom gland transcriptomics for identifying, cataloging, and characterizing venom proteins in snakes. <i>Toxicon</i> , 2015, 93, 1-10.	0.8	70

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2613	Phenotypic polymorphism of <i>Chrysomya albiceps</i> (Wiedemann) (Diptera: Calliphoridae) may lead to species misidentification. <i>Acta Tropica</i> , 2015, 141, 60-72.	0.9	31
2614	Deep sequencing reveals a novel closterovirus associated with wild rose leaf rosette disease. <i>Molecular Plant Pathology</i> , 2015, 16, 449-458.	2.0	31
2615	Identification of a Novel Papillomavirus in a Northern Fulmar (<i>Fulmarus glacialis</i>) With Viral Production in Cartilage. <i>Veterinary Pathology</i> , 2015, 52, 553-561.	0.8	21
2616	Population transcriptomics reveals a potentially positive role of expression diversity in adaptation. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 284-299.	4.1	26
2617	Transcriptomic and proteomic analyses of <i>Amphiura filiformis</i> arm tissue-undergoing regeneration. <i>Journal of Proteomics</i> , 2015, 112, 113-124.	1.2	37
2618	Remnants of the Legume Ancestral Genome Preserved in Gene-Rich Regions: Insights from <i>Lupinus angustifolius</i> Physical, Genetic, and Comparative Mapping. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 84-101.	1.0	18
2619	Differences in Physiological Characteristics and Gene Expression Levels in Fruits between Japanese Persimmon (<i>Diospyros kaki</i> Thunb.) "Hiratanenashi"™ and Its Small Fruit Mutant "Totsutanenashi"™. <i>Horticulture Journal</i> , 2016, 85, 306-314.	0.3	8
2620	Bioinformatics Tools and Genomic Resources Available in Understanding the Structure and Function of <i>Gossypium</i> . , 2016, , .		4
2621	Orthology Guided Transcriptome Assembly of Italian Ryegrass and Meadow Fescue for Single-Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0017.	1.6	9
2622	Hemizyosity Enhances Purifying Selection: Lack of Fast-Z Evolution in Two Satyrine Butterflies. <i>Genome Biology and Evolution</i> , 2016, 8, 3108-3119.	1.1	31
2623	Complete Genome Sequence of a Novel Aquarivirus That Infects the Endangered Fountain Darter, <i>Etheostoma fonticola</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	4
2624	Intravarietal polymorphisms reveal possible common ancestor of native <i>Schinus terebinthifolius</i> Raddi populations in Brazil. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	1
2625	SEX-DETECTOR: A Probabilistic Approach to Study Sex Chromosomes in Non-Model Organisms. <i>Genome Biology and Evolution</i> , 2016, 8, 2530-2543.	1.1	64
2626	Generation and Characterisation of a Reference Transcriptome for Lentil (<i>Lens culinaris</i> Medik.). <i>International Journal of Molecular Sciences</i> , 2016, 17, 1887.	1.8	49
2627	Molecular Identification of <i>Trichoderma</i> spp. in Garlic and Onion Fields and In Vitro Antagonism Trials on <i>Sclerotium cepivorum</i> . <i>Revista Brasileira De Ciencia Do Solo</i> , 2016, 40, .	0.5	2
2628	Novel point mutations in the ERG11 gene in clinical isolates of azole resistant <i>Candida</i> species. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 192-199.	0.8	31
2629	Spoilage potential of <i>Paenibacillus</i> sp. in Brazilian raw milk. <i>Ciencia Rural</i> , 2016, 46, 637-640.	0.3	1
2630	Viral type characterization and clinical aspects of canine parvovirus in naturally infected dogs in São Paulo State, Brazil. <i>Pesquisa Veterinaria Brasileira</i> , 2016, 36, 1181-1185.	0.5	3

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2631	Draft genome of the <i>Leptospira interrogans</i> strains, Acegua, RCA, Prea, and Capivara, obtained from wildlife maintenance hosts and infected domestic animals. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 280-283.	0.8	15
2632	In-Silico Prediction and Functional Analysis of Salt Stress Responsive Genes in Rice (<i>Oryza sativa</i>). <i>Rice Research Open Access</i> , 2016, 4, .	0.4	7
2633	Complete Mitochondrial Genome of <i>Anoplocephala magna</i> Solidifying the Species. <i>Korean Journal of Parasitology</i> , 2016, 54, 369-373.	0.5	5
2634	Functional complementation of <i>Leishmania (Leishmania) amazonensis</i> AP endonuclease gene (<i>lamap</i>) in <i>Escherichia coli</i> mutant strains challenged with DNA damage agents. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 349-354.	0.8	2
2635	Cytochrome c Oxidase Sequences of Zambian Wildlife Helps to Identify Species of Origin of Meat. <i>International Journal of Zoology</i> , 2016, 2016, 1-6.	0.3	5
2636	Development and characterization of novel EST-SSR markers and their application for genetic diversity analysis of Jerusalem artichoke (<i>Helianthus tuberosus</i> L.). <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	4
2637	Transcriptomic Profiling Using Next Generation Sequencing - Advances, Advantages, and Challenges. , 0, , .		8
2638	Gene expression analysis reveals important pathways for drought response in leaves and roots of a wheat cultivar adapted to rainfed cropping in the Cerrado biome. <i>Genetics and Molecular Biology</i> , 2016, 39, 629-645.	0.6	22
2639	17 β -HSD type 12-like is responsible for maturation-inducing hormone synthesis during oocyte maturation in masu salmon ¹ ² . <i>Endocrinology</i> , 2017, 158, en.2016-1349.	1.4	11
2640	Colubrid Venom Composition: An -Omics Perspective. <i>Toxins</i> , 2016, 8, 230.	1.5	61
2641	Microsomal Omega-3 Fatty Acid Desaturase Genes in Low Linolenic Acid Soybean Line RG10 and Validation of Major Linolenic Acid QTL. <i>Frontiers in Genetics</i> , 2016, 7, 38.	1.1	13
2642	Transcriptome and Proteome Studies Reveal Candidate Attachment Genes during the Development of the Barnacle <i>Amphibalanus Amphitrite</i> . <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	12
2643	Draft Genomes Shed Light on the Dual Bacterial Symbiosis that Dominates the Microbiome of the Coral Reef Sponge <i>Amphimedon queenslandica</i> . <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	60
2644	De novo Assembly, Characterization and Functional Annotation of Southern Hake (<i>Merluccius</i>) Tj ETQq1 1 0.784314,rgBT /Oyerlock 10 1.2 2		
2645	MALDI-TOF Mass Spectrometry Discriminates Known Species and Marine Environmental Isolates of <i>Pseudoalteromonas</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 104.	1.5	23
2646	GenSeed-HMM: A Tool for Progressive Assembly Using Profile HMMs as Seeds and its Application in <i>Alpavirinae</i> Viral Discovery from Metagenomic Data. <i>Frontiers in Microbiology</i> , 2016, 7, 269.	1.5	30
2647	Genomic Insights into a New <i>Citrobacter koseri</i> Strain Revealed Gene Exchanges with the Virulence-Associated <i>Yersinia pestis</i> pPCP1 Plasmid. <i>Frontiers in Microbiology</i> , 2016, 7, 340.	1.5	13
2648	Associations between Ectomycorrhizal Fungi and Bacterial Needle Endophytes in <i>Pinus radiata</i> : Implications for Biotic Selection of Microbial Communities. <i>Frontiers in Microbiology</i> , 2016, 7, 399.	1.5	21

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2649	Transcriptome Analysis of <i>Scrippsiella trochoidea</i> CCMP 3099 Reveals Physiological Changes Related to Nitrate Depletion. <i>Frontiers in Microbiology</i> , 2016, 7, 639.	1.5	33
2650	Complete Sequence of pEC012, a Multidrug-Resistant IncI1 ST71 Plasmid Carrying blaCTX-M-65, rmtB, fosA3, floR, and oqxAB in an Avian <i>Escherichia coli</i> ST117 Strain. <i>Frontiers in Microbiology</i> , 2016, 7, 1117.	1.5	12
2651	Evidence for the presence of African swine fever virus in an endemic region of Western Kenya in the absence of any reported outbreak. <i>BMC Veterinary Research</i> , 2016, 12, 192.	0.7	30
2652	Population Genetics of the Rubber-Producing Russian Dandelion (<i>Taraxacum kok-saghyz</i>). <i>PLoS ONE</i> , 2016, 11, e0146417.	1.1	22
2653	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016, 12, e1005954.	1.5	105
2654	Novel Pectate Lyase Genes of <i>Heterodera glycines</i> Play Key Roles in the Early Stage of Parasitism. <i>PLoS ONE</i> , 2016, 11, e0149959.	1.1	11
2655	Genomic Characterization of Phenylalanine Ammonia Lyase Gene in Buckwheat. <i>PLoS ONE</i> , 2016, 11, e0151187.	1.1	18
2656	MOXD2, a Gene Possibly Associated with Olfaction, Is Frequently Inactivated in Birds. <i>PLoS ONE</i> , 2016, 11, e0152431.	1.1	2
2657	De novo Analysis of the Epiphytic Transcriptome of the Cucurbit Powdery Mildew Fungus <i>Podosphaera xanthii</i> and Identification of Candidate Secreted Effector Proteins. <i>PLoS ONE</i> , 2016, 11, e0163379.	1.1	29
2658	CandiSSR: An Efficient Pipeline used for Identifying Candidate Polymorphic SSRs Based on Multiple Assembled Sequences. <i>Frontiers in Plant Science</i> , 2015, 6, 1171.	1.7	72
2659	Transcriptome Analysis of <i>Gerbera hybrida</i> Including in silico Confirmation of Defense Genes Found. <i>Frontiers in Plant Science</i> , 2016, 7, 247.	1.7	23
2660	Suppression Subtractive Hybridization and NGS Reveal Differential Transcriptome Expression Profiles in Wayfaring Tree (<i>Viburnum lantana</i> L.) Treated with Ozone. <i>Frontiers in Plant Science</i> , 2016, 7, 713.	1.7	12
2661	Insights into the Indian Peanut Genotypes for ahFAD2 Gene Polymorphism Regulating Its Oleic and Linoleic Acid Fluxes. <i>Frontiers in Plant Science</i> , 2016, 7, 1271.	1.7	30
2662	DArT Markers Effectively Target Gene Space in the Rye Genome. <i>Frontiers in Plant Science</i> , 2016, 07, 1600.	1.7	33
2663	The tRNA-Derived Small RNAs Regulate Gene Expression through Triggering Sequence-Specific Degradation of Target Transcripts in the Oomycete Pathogen <i>Phytophthora sojae</i> . <i>Frontiers in Plant Science</i> , 2016, 07, 1938.	1.7	45
2664	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016, 5, .	2.8	237
2665	Latitude delineates patterns of biogeography in terrestrial <i>Streptomyces</i> . <i>Environmental Microbiology</i> , 2016, 18, 4931-4945.	1.8	35
2666	An evaluation of transcriptome-based exon capture for frog phylogenomics across multiple scales of divergence (Class: Amphibia, Order: Anura). <i>Molecular Ecology Resources</i> , 2016, 16, 1069-1083.	2.2	92

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2667	Hybridization and divergence in multi-species oak (<i>Quercus</i>) communities. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 99-114.	0.8	24
2668	Para-allopatry in hybridizing fire-bellied toads (<i>Bombina bombina</i> and <i>B. variegata</i>): Inference from transcriptome-wide coalescence analyses. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1803-1818.	1.1	25
2669	Microsatellite markers and cytoplasmic sequences reveal contrasting pattern of spatial genetic structure in the red algae species complex <i>Mazzaella laminarioides</i> . <i>Journal of Phycology</i> , 2016, 52, 806-816.	1.0	3
2670	Population genomics of sexual and asexual lineages in fissiparous ribbon worms (Lineus, Nemertea): hybridization, polyploidy and the Meselson effect. <i>Molecular Ecology</i> , 2016, 25, 3356-3369.	2.0	58
2671	Genomewide scan for adaptive differentiation along altitudinal gradient in the Andrew's toad <i>Bufo andrewsi</i> . <i>Molecular Ecology</i> , 2016, 25, 3884-3900.	2.0	38
2672	Local interspecies introgression is the main cause of extreme levels of intraspecific differentiation in mussels. <i>Molecular Ecology</i> , 2016, 25, 269-286.	2.0	97
2673	Population genomic evidence for adaptive differentiation in the Baltic Sea herring. <i>Molecular Ecology</i> , 2016, 25, 2833-2852.	2.0	80
2674	Genome-wide analysis of chitinase genes and their varied functions in larval moult, pupation and eclosion in the rice striped stem borer, <i>Chilo suppressalis</i> . <i>Insect Molecular Biology</i> , 2016, 25, 401-412.	1.0	42
2675	Monitoring the freshness of fish: development of a qPCR method applied to MAP chilled whiting. <i>Journal of the Science of Food and Agriculture</i> , 2016, 96, 2080-2089.	1.7	3
2676	Exon capture phylogenomics: efficacy across scales of divergence. <i>Molecular Ecology Resources</i> , 2016, 16, 1059-1068.	2.2	132
2677	Phylogenomics at the tips: inferring lineages and their demographic history in a tropical lizard, <i>Carlia amax</i> . <i>Molecular Ecology</i> , 2016, 25, 1367-1380.	2.0	46
2678	Gene expression analysis and SNP/InDel discovery to investigate yield heterosis of two rubber tree F1 hybrids. <i>Scientific Reports</i> , 2016, 6, 24984.	1.6	30
2679	Integrative analysis of transcriptomics and proteomics of skeletal muscles of the Chinese indigenous Shaziling pig compared with the Yorkshire breed. <i>BMC Genetics</i> , 2016, 17, 80.	2.7	58
2680	Transcriptome analysis confers a complex disease resistance network in wild rice <i>Oryza meyeriana</i> against <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Scientific Reports</i> , 2016, 6, 38215.	1.6	26
2681	The Amaranth Genome: Genome, Transcriptome, and Physical Map Assembly. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0062.	1.6	115
2682	Recurrence of Chromosome Rearrangements and Reuse of DNA Breakpoints in the Evolution of the Triticeae Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3837-3847.	0.8	28
2683	Venom gland transcriptome analyses of two freshwater stingrays (Myliobatiformes): Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 102 Td (Potar	1.6	24
2684	Linear regression with an unknown permutation: Statistical and computational limits. , 2016, , .		23

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2685	Bifunctional CYP81AA proteins catalyse identical hydroxylations but alternative regioselective phenol couplings in plant xanthone biosynthesis. <i>Nature Communications</i> , 2016, 7, 11472.	5.8	46
2686	In Silico identification of SNP diversity in cultivated and wild tomato species: insight from molecular simulations. <i>Scientific Reports</i> , 2016, 6, 38715.	1.6	21
2687	The testes transcriptome of the New World Screwworm, <i>Cochliomyia hominivorax</i> . <i>Data in Brief</i> , 2016, 9, 1141-1146.	0.5	1
2688	Wheat methionine sulfoxide reductase genes and their response to abiotic stress. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	6
2689	Analysis of Annotation and Differential Expression Methods used in RNA-seq Studies in Crustacean Systems. <i>Integrative and Comparative Biology</i> , 2016, 56, 1067-1079.	0.9	20
2690	The two chromosomes of the mitochondrial genome of a sugarcane cultivar: assembly and recombination analysis using long PacBio reads. <i>Scientific Reports</i> , 2016, 6, 31533.	1.6	55
2691	Proteomic comparison reveals the contribution of chloroplast to salt tolerance of a wheat introgression line. <i>Scientific Reports</i> , 2016, 6, 32384.	1.6	18
2692	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. <i>Genome Biology</i> , 2016, 17, 260.	3.8	141
2693	Genetics and Genomics of <i>Cucurbita</i> spp.. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 211-227.	0.3	4
2694	A memetic gravitation search algorithm for solving DNA fragment assembly problems. <i>Journal of Intelligent and Fuzzy Systems</i> , 2016, 30, 2245-2255.	0.8	10
2695	Medicinal plant transcriptomes: the new gateways for accelerated understanding of plant secondary metabolism. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 256-269.	0.4	21
2696	Metatranscriptomics workflow analysis from environmental sample of fungi. <i>AIP Conference Proceedings</i> , 2016, , .	0.3	0
2697	Challenges in the analysis of viral metagenomes. <i>Virus Evolution</i> , 2016, 2, vew022.	2.2	83
2698	High-throughput multiplexed mitogenomics for Metazoa: prospects and limitations. , 0, , 84-100.		0
2699	Molecular analysis of <i>Cercospora beticola</i> isolates for strobilurin resistance from the Central High Plains, USA. <i>European Journal of Plant Pathology</i> , 2016, 146, 817-827.	0.8	6
2700	Data supporting the nuclear phylogenomics of the palm subfamily Arecoideae (Arecaceae). <i>Data in Brief</i> , 2016, 7, 532-536.	0.5	1
2701	A wheat histone variant gene TaH2A.7 enhances drought tolerance and promotes stomatal closure in <i>Arabidopsis</i> . <i>Plant Cell Reports</i> , 2016, 35, 1853-1862.	2.8	27
2702	Microsatellites from <i>Fosterella christophii</i> (Bromeliaceae) by de novo transcriptome sequencing on the Pacific Biosciences RS platform. <i>Applications in Plant Sciences</i> , 2016, 4, 1500084.	0.8	3

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2703	Gene expression characterizes different nutritional strategies among three mixotrophic protists. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw106.	1.3	45
2704	The WRKY Transcription Factor Family in Citrus: Valuable and Useful Candidate Genes for Citrus Breeding. <i>Applied Biochemistry and Biotechnology</i> , 2016, 180, 516-543.	1.4	24
2705	Heterologous production, characterization and dye decolorization ability of a novel thermostable laccase isoenzyme from <i>Trametes trogii</i> BAFC 463. <i>Process Biochemistry</i> , 2016, 51, 895-903.	1.8	57
2706	Effects of drought and salt-stresses on gene expression in <i>Caragana korshinskii</i> seedlings revealed by RNA-seq. <i>BMC Genomics</i> , 2016, 17, 200.	1.2	47
2707	In silico mining of EST-SSRs in <i>Arachis hypogaea</i> L. and their utilization for genetic structure and diversity analysis in cultivars/breeding lines in Odisha, India. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	5
2708	Description of <i>Pseudomonas gregormendelii</i> sp. nov., a Novel Psychrotrophic Bacterium from James Ross Island, Antarctica. <i>Current Microbiology</i> , 2016, 73, 84-90.	1.0	19
2709	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	25
2710	Developing Single Nucleotide Polymorphism (SNP) Markers for the Identification of Coffee Germplasm. <i>Tropical Plant Biology</i> , 2016, 9, 82-95.	1.0	34
2711	Complete mitochondrial genome of the striped scat <i>Selenotoca multifasciata</i> (Perciformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 T	0.7	2
2712	Transcriptome reveals senescing callus tissue of <i>Aquilaria malaccensis</i> , an endangered tropical tree, triggers similar response as wounding with respect to terpenoid biosynthesis. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	15
2713	Cassava (<i>Manihot esculenta</i>) transcriptome analysis in response to infection by the fungus <i>Colletotrichum gloeosporioides</i> using an oligonucleotide-DNA microarray. <i>Journal of Plant Research</i> , 2016, 129, 711-726.	1.2	28
2714	Analysis of Alternative Splicing Landscape in Pineapple (<i>Ananas comosus</i>). <i>Tropical Plant Biology</i> , 2016, 9, 150-160.	1.0	18
2715	Recoding structural glycoprotein E2 in classical swine fever virus (CSFV) produces complete virus attenuation in swine and protects infected animals against disease. <i>Virology</i> , 2016, 494, 178-189.	1.1	20
2716	Analysis of EST-SSRs in silver birch (<i>Betula pendula</i> Roth.). <i>Journal of Forestry Research</i> , 2016, 27, 639-646.	1.7	2
2717	Evolution of a CAM anatomy predates the origins of Crassulacean acid metabolism in the Agavoideae (Asparagaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 102-113.	1.2	95
2718	De novo assembly of <i>Zea nicaraguensis</i> root transcriptome identified 5 261 full-length transcripts. <i>Journal of Integrative Agriculture</i> , 2016, 15, 1207-1217.	1.7	1
2719	Transcriptome discovery in non-model wild fish species for the development of quantitative transcript abundance assays. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 20, 27-40.	0.4	17
2720	A +1 ribosomal frameshifting motif prevalent among plant amalgaviruses. <i>Virology</i> , 2016, 498, 201-208.	1.1	53

#	ARTICLE	IF	CITATIONS
2721	Influences of host plant identity and disturbance on spatial structure and community composition of ectomycorrhizal fungi in a northern Mississippi uplands ecosystem. <i>Fungal Ecology</i> , 2016, 24, 7-14.	0.7	9
2722	Deletion of carotenoid cleavage dioxygenase 4a (CmCCD4a) and global up-regulation of plastid protein-coding genes in a mutant chrysanthemum cultivar producing yellow petals. <i>Scientia Horticulturae</i> , 2016, 212, 49-59.	1.7	12
2723	Branchial transcriptional responses of spotted scat, <i>Scatophagus argus</i> , to acute hypo-osmotic stress. <i>Agri Gene</i> , 2016, 1, 100-108.	1.9	2
2724	Development of a panel of unigene-derived polymorphic EST-SSR markers in lentil using public database information. <i>Crop Journal</i> , 2016, 4, 425-433.	2.3	10
2725	Accurate Estimation of Fungal Diversity and Abundance through Improved Lineage-Specific Primers Optimized for Illumina Amplicon Sequencing. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7217-7226.	1.4	321
2726	Accounting for Uncertainty in Gene Tree Estimation: Summary-Coalescent Species Tree Inference in a Challenging Radiation of Australian Lizards. <i>Systematic Biology</i> , 2017, 66, syw089.	2.7	56
2727	Association of Bartonella Species with Wild and Synanthropic Rodents in Different Brazilian Biomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7154-7164.	1.4	43
2728	Gene transfers from diverse bacteria compensate for reductive genome evolution in the chromatophore of <i>Paulinella chromatophora</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12214-12219.	3.3	127
2729	Phylogenomics of Lophotrochozoa with Consideration of Systematic Error. <i>Systematic Biology</i> , 2017, 66, syw079.	2.7	164
2730	Detection of Strawberry necrotic shock virus using conventional and TaqMan [®] quantitative RT-PCR. <i>Journal of Virological Methods</i> , 2016, 235, 176-181.	1.0	17
2731	Mercury resistance and volatilization by <i>Pseudoxanthomonas</i> sp. SE1 isolated from soil. <i>Environmental Technology and Innovation</i> , 2016, 6, 94-104.	3.0	41
2732	Molecule Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. <i>MSystems</i> , 2016, 1, .	1.7	89
2733	Linkage mapping with paralogs exposes regions of residual tetrasomic inheritance in chum salmon (<i>Oncorhynchus keta</i>). <i>Molecular Ecology Resources</i> , 2016, 16, 17-28.	2.2	60
2734	Barcoding the kingdom Plantae: new PCR primers for ITS regions of plants with improved universality and specificity. <i>Molecular Ecology Resources</i> , 2016, 16, 138-149.	2.2	280
2735	Phylogenomic analyses of species relationships in the genus <i>Sabal</i> (Arecaceae) using targeted sequence capture. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 106-120.	0.7	99
2736	Development of SCAR markers linked to sin-2, the stringless pod trait in pea (<i>Pisum sativum</i> L.). <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	7
2737	Transcriptome analysis of smooth cordgrass (<i>Spartina alterniflora</i> Loisel), a monocot halophyte, reveals candidate genes involved in its adaptation to salinity. <i>BMC Genomics</i> , 2016, 17, 657.	1.2	55
2738	Local Auxin Biosynthesis Mediated by a YUCCA Flavin Monooxygenase Regulates Haustorium Development in the Parasitic Plant <i>Phtheirospermum japonicum</i> . <i>Plant Cell</i> , 2016, 28, 1795-1814.	3.1	102

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2739	Assemble CRISPRs from metagenomic sequencing data. <i>Bioinformatics</i> , 2016, 32, i520-i528.	1.8	10
2740	Identification and Characterization of Sex-Associated Loci in Sockeye Salmon Using Genotyping-by-Sequencing and Comparison with a Sex-Determining Assay Based on the <i>sYGene</i> . <i>Journal of Heredity</i> , 2016, 107, 559-566.	1.0	32
2741	Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics. <i>Science of the Total Environment</i> , 2016, 572, 697-712.	3.9	213
2742	Elucidating modes of activation and herbicide resistance by sequence assembly and molecular modelling of the Acetolactate synthase complex in sugarcane. <i>Journal of Theoretical Biology</i> , 2016, 407, 184-197.	0.8	9
2743	DOMINO: development of informative molecular markers for phylogenetic and genome-wide population genetic studies in non-model organisms. <i>Bioinformatics</i> , 2016, 32, 3753-3759.	1.8	8
2744	Use of expressed sequence tag microsatellite markers for exploring genetic diversity in lentil and related wild species. <i>Journal of Agricultural Science</i> , 2016, 154, 1254-1269.	0.6	7
2745	Chloroplast and Mitochondrial Genomes of Tomato. <i>Compendium of Plant Genomes</i> , 2016, , 111-137.	0.3	0
2746	Assembly and Application to the Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , 139-158.	0.3	0
2747	Transcript, protein and metabolite temporal dynamics in the CAM plant <i>Agave</i> . <i>Nature Plants</i> , 2016, 2, 16178.	4.7	158
2748	Candidate egg case silk genes for the spider <i>Argiope argentata</i> from differential gene expression analyses. <i>Insect Molecular Biology</i> , 2016, 25, 757-768.	1.0	11
2749	Transcriptome Sequencing of Diverse Peanut (<i>Arachis</i>) Wild Species and the Cultivated Species Reveals a Wealth of Untapped Genetic Variability. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3825-3836.	0.8	18
2750	Dietary breadth is positively correlated with venom complexity in cone snails. <i>BMC Genomics</i> , 2016, 17, 401.	1.2	81
2751	A Coronavirus Associated with Runting Stunting Syndrome in Broiler Chickens. <i>Avian Diseases</i> , 2016, 60, 528-534.	0.4	16
2752	Here We Are, But Where Do We Go? A Systematic Review of Crustacean Transcriptomic Studies from 2014-2015. <i>Integrative and Comparative Biology</i> , 2016, 56, 1055-1066.	0.9	21
2753	Isolation and characterization of chitinase from soil fungi, <i>Paecilomyces</i> sp.. <i>Agriculture and Natural Resources</i> , 2016, 50, 232-242.	0.4	12
2754	Improved metagenome assemblies and taxonomic binning using long-read circular consensus sequence data. <i>Scientific Reports</i> , 2016, 6, 25373.	1.6	139
2755	In silico search, characterization and validation of new EST-SSR markers in the genus <i>Prunus</i> . <i>BMC Research Notes</i> , 2016, 9, 336.	0.6	16
2756	Trends in the Evolution of Snake Toxins Underscored by an Integrative Omics Approach to Profile the Venom of the Colubrid <i>Phalotris mertensi</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2266-2287.	1.1	29

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2757	Identification of drought-responsive microRNAs and their targets in <i>Ammopiptanthus mongolicus</i> by using high-throughput sequencing. <i>Scientific Reports</i> , 2016, 6, 34601.	1.6	38
2758	Unmasking <i>Aurelia</i> species in the Mediterranean Sea: an integrative morphometric and molecular approach. <i>Zoological Journal of the Linnean Society</i> , 2016, , .	1.0	43
2759	Hypoxic stress -responsive genes in air breathing catfish, <i>Clarias magur</i> (Hamilton 1822) and their possible physiological adaptive function. <i>Fish and Shellfish Immunology</i> , 2016, 59, 46-56.	1.6	8
2760	Neofunctionalization of zona pellucida proteins enhances freeze-prevention in the eggs of Antarctic notothenioids. <i>Nature Communications</i> , 2016, 7, 12987.	5.8	33
2761	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.	2.4	34
2762	Discovery of parvovirus-related sequences in an unexpected broad range of animals. <i>Scientific Reports</i> , 2016, 6, 30880.	1.6	61
2763	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016, 2, e1600633.	4.7	64
2764	Transcriptomic Resources and Marker Validation for Diploid and Polyploid <i>Veronica</i> (Plantaginaceae) from New Zealand and Europe. <i>Applications in Plant Sciences</i> , 2016, 4, 1600091.	0.8	2
2765	The complete mitochondrial genome sequence of <i>Astyanax paranae</i> (Teleostei: characiformes). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 586-587.	0.2	6
2766	Whole-transcriptome analysis of differentially expressed genes in the ray florets and disc florets of <i>Chrysanthemum morifolium</i> . <i>BMC Genomics</i> , 2016, 17, 398.	1.2	39
2767	Gain-of-function in <i>Arabidopsis</i> (GAINA) for identifying functional genes in <i>Hevea brasiliensis</i> . <i>SpringerPlus</i> , 2016, 5, 1853.	1.2	3
2768	Gene expression in the kidneys of broilers fed ochratoxin A for different time periods. <i>World Mycotoxin Journal</i> , 2016, 9, 257-268.	0.8	3
2769	Retrotransposon Proliferation Coincident with the Evolution of Dioecy in <i>Asparagus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2679-2685.	0.8	22
2770	SNP Marker Discovery in Pima Cotton (<i>Gossypium barbadense</i> L.) Leaf Transcriptomes. <i>Genomics Insights</i> , 2016, 9, GEI.S40377.	3.0	8
2771	Mitogenome of the extinct helmeted musk ox, <i>Bootherium bombifrons</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 862-863.	0.2	3
2772	Comparative mitogenomic and phylogenetic characterization on the complete mitogenomes of <i>Talaromyces</i> (<i>Penicillium</i>) <i>marneffei</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 941-942.	0.2	4
2773	Characterization of the teosinte transcriptome reveals adaptive sequence divergence during maize domestication. <i>Molecular Ecology Resources</i> , 2016, 16, 1465-1477.	2.2	7
2774	Transcriptome-wide patterns of divergence during allopatric evolution. <i>Molecular Ecology</i> , 2016, 25, 1478-1493.	2.0	52

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2775	Transcriptome-derived evidence supports recent polyploidization and a major phylogeographic division in <i>Trituraria submersa</i> (Hydrocharitaceae, Nymphaeales). <i>New Phytologist</i> , 2016, 210, 310-323.	3.5	10
2776	Differences in PfEMP1s recognized by antibodies from patients with uncomplicated or severe malaria. <i>Malaria Journal</i> , 2016, 15, 258.	0.8	23
2777	Recovering complete and draft population genomes from metagenome datasets. <i>Microbiome</i> , 2016, 4, 8.	4.9	254
2778	Development of SSR markers from <i>Musa balbisiana</i> for genetic diversity analysis among Thai bananas. <i>Plant Systematics and Evolution</i> , 2016, 302, 739-761.	0.3	12
2779	Structural organization of fatty acid desaturase loci in linseed lines with contrasting linolenic acid contents. <i>Functional and Integrative Genomics</i> , 2016, 16, 429-439.	1.4	3
2780	Isolation and characterization of genomic microsatellite markers for small cardamom (<i>Elettaria</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 <i>Plants</i> , 2016, 22, 219-229.	1.4	10
2781	Phylogenetic Identification and Enzyme Activities of Indigenous Bacteria from a Landfill Stabilization Pond. <i>Environmental Processes</i> , 2016, 3, 341-352.	1.7	11
2782	Effects of Gene Duplication, Positive Selection, and Shifts in Gene Expression on the Evolution of the Venom Gland Transcriptome in Widow Spiders. <i>Genome Biology and Evolution</i> , 2016, 8, 228-242.	1.1	54
2783	Transcriptome Display During Testicular Differentiation of Channel Catfish (<i>Ictalurus punctatus</i>) as Revealed by RNA-Seq Analysis. <i>Biology of Reproduction</i> , 2016, 95, 19-19.	1.2	35
2784	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. <i>American Journal of Botany</i> , 2016, 103, 1203-1211.	0.8	98
2785	Bioinformatics resources for pollen. <i>Plant Reproduction</i> , 2016, 29, 133-147.	1.3	6
2786	Thermal reactionomes reveal divergent responses to thermal extremes in warm and cool-climate ant species. <i>BMC Genomics</i> , 2016, 17, 171.	1.2	19
2787	Characterization and functional analysis of two inhibitor of apoptosis genes in Zhikong scallop <i>Chlamys farreri</i> . <i>Developmental and Comparative Immunology</i> , 2016, 60, 1-11.	1.0	9
2788	Transcriptome sequencing based annotation and homologous evidence based scaffolding of <i>Anguilla japonica</i> draft genome. <i>BMC Genomics</i> , 2016, 17, 13.	1.2	9
2789	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	1.2	109
2790	Transcriptome analysis and molecular marker discovery in <i>Solanum incanum</i> and <i>S. aethiopicum</i> , two close relatives of the common eggplant (<i>Solanum melongena</i>) with interest for breeding. <i>BMC Genomics</i> , 2016, 17, 300.	1.2	63
2791	Identification and characterization of abundant repetitive sequences in <i>Eragrostis tef</i> cv. Enatite genome. <i>BMC Plant Biology</i> , 2016, 16, 39.	1.6	16
2792	Transcriptome and metabolome analysis in shoot and root of <i>Valeriana fauriei</i> . <i>BMC Genomics</i> , 2016, 17, 303.	1.2	17

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2793	A putative pyruvate transporter TaBASS2 positively regulates salinity tolerance in wheat via modulation of ABI4 expression. <i>BMC Plant Biology</i> , 2016, 16, 109.	1.6	34
2794	Solute carriers (SLCs) identified and characterized from kidney transcriptome of golden mahseer (<i>Tor taylori</i>). <i>Journal of Herpetology</i> , 2016, 50, 1-10.	0.7	10
2795	Picoplankton Bloom in Global South? A High Fraction of Aerobic Anoxygenic Phototrophic Bacteria in Metagenomes from a Coastal Bay (Arraial do Cabo, Brazil). <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 76-87.	1.0	9
2796	Transcriptome sequencing reveals population differentiation in gene expression linked to functional traits and environmental gradients in the South African shrub <i>Protea repens</i> . <i>New Phytologist</i> , 2016, 210, 295-309.	3.5	43
2797	Isolation and characterization of 5S rDNA sequences in catfishes genome (Heptapteridae and <i>Pseudorasbora parva</i>). <i>Journal of Herpetology</i> , 2016, 50, 2711-2720.	0.7	7
2798	Alterations in gene expression during fasting-induced atresia of early secondary ovarian follicles of coho salmon, <i>Oncorhynchus kisutch</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2016, 201, 1-11.	0.8	7
2799	A novel emaravirus is associated with redbud yellow ringspot disease. <i>Virus Research</i> , 2016, 222, 41-47.	1.1	38
2800	Comprehensive analyses of the annexin gene family in wheat. <i>BMC Genomics</i> , 2016, 17, 415.	1.2	68
2801	An integrated linkage map reveals candidate genes underlying adaptive variation in Chinook salmon (<i>Oncorhynchus tshawytscha</i>). <i>Molecular Ecology Resources</i> , 2016, 16, 769-783.	2.2	49
2802	A replicated climate change field experiment reveals rapid evolutionary response in an ecologically important soil invertebrate. <i>Global Change Biology</i> , 2016, 22, 2370-2379.	4.2	15
2803	Pathotypic and Sequence Characterization of Newcastle Disease Viruses from Vaccinated Chickens Reveals Circulation of Genotype II, IV and XIII and in India. <i>Transboundary and Emerging Diseases</i> , 2016, 63, 523-539.	1.3	24
2804	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. <i>Environmental Microbiology</i> , 2016, 18, 2825-2842.	1.8	72
2805	Comparing de novo and reference-based transcriptome assembly strategies by applying them to the blood-sucking bug <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 69, 25-33.	1.2	31
2806	Identification of Differentially Expressed Genes in Sugarcane During Pathogenesis of <i>Colletotrichum falcatum</i> by Suppression Subtractive Hybridization (SSH). <i>Sugar Tech</i> , 2016, 18, 176-183.	0.9	18
2807	De novo transcriptome analyses of host-fungal interactions in oil palm (<i>Elaeis guineensis</i> Jacq.). <i>BMC Genomics</i> , 2016, 17, 66.	1.2	67
2808	De novo assembly and analysis of midgut transcriptome of <i>Haemaphysalis flava</i> and identification of genes involved in blood digestion, feeding and defending from pathogens. <i>Infection, Genetics and Evolution</i> , 2016, 38, 62-72.	1.0	29
2809	Description of <i>Endozoicomonas arenosclerae</i> sp. nov. using a genomic taxonomy approach. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 431-438.	0.7	39
2810	Essential Roles of TIM-1 and TIM-4 Homologs in Adaptive Humoral Immunity in a Zebrafish Model. <i>Journal of Immunology</i> , 2016, 196, 1686-1699.	0.4	34

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2811	Clonality Analysis of Immunoglobulin Gene Rearrangement by Next-Generation Sequencing in Endemic Burkitt Lymphoma Suggests Antigen Drive Activation of BCR as Opposed to Sporadic Burkitt Lymphoma. <i>American Journal of Clinical Pathology</i> , 2016, 145, 116-127.	0.4	35
2812	Comparative Transcriptomic Analyses of Three Species of <i>Placobdella</i> (Rhynchobdellida). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 107</i> 102, 143-150.	0.3	34
2813	De novo Transcriptome Analysis of Apical Meristem of <i>Jatropha</i> spp. Using 454 Pyrosequencing Platform, and Identification of SNP and EST-SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 786-793.	1.0	9
2814	Burden of Norovirus and Rotavirus in Children After Rotavirus Vaccine Introduction, Cochabamba, Bolivia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 212-217.	0.6	49
2815	A wheat superoxide dismutase gene TaSOD2 enhances salt resistance through modulating redox homeostasis by promoting NADPH oxidase activity. <i>Plant Molecular Biology</i> , 2016, 91, 115-130.	2.0	63
2816	Discovery of unfixed endogenous retrovirus insertions in diverse human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2326-34.	3.3	225
2817	Pleurochrysome: A Web Database of Pleurochrysis Transcripts and Orthologs Among Heterogeneous Algae. <i>Plant and Cell Physiology</i> , 2016, 57, e6-e6.	1.5	4
2818	A comprehensive transcriptome of early development in yellowtail kingfish (<i>Seriola lalandi</i>). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 107</i> 2.2 17	2.2	17
2819	Cloning and analysis of gene expression of interleukin-17 homolog in triangle-shell pearl mussel, <i>Hyriopsis cumingii</i> , during pearl sac formation. <i>Fish and Shellfish Immunology</i> , 2016, 52, 151-156.	1.6	12
2820	Understanding intra and inter-archipelago population genetic patterns within a recently evolved insular endemic lineage. <i>Plant Systematics and Evolution</i> , 2016, 302, 367-384.	0.3	20
2821	Porcine parvovirus as a contaminant in cell cultures and laboratory supplies. <i>Biologicals</i> , 2016, 44, 53-59.	0.5	6
2822	Transcriptional response to heat shock in liver of snow trout (<i>Schizothorax richardsonii</i>) a vulnerable Himalayan Cyprinid fish. <i>Functional and Integrative Genomics</i> , 2016, 16, 203-213.	1.4	34
2823	De novo transcriptome assembly of <i>Perkinsus olseni</i> trophozoite stimulated in vitro with Manila clam (<i>Ruditapes philippinarum</i>) plasma. <i>Journal of Invertebrate Pathology</i> , 2016, 135, 22-33.	1.5	14
2824	Studying long 16S rDNA sequences with ultrafast-metagenomic sequence classification using exact alignments (Kraken). <i>Journal of Microbiological Methods</i> , 2016, 122, 38-42.	0.7	34
2825	A passion fruit putative ortholog of the SOMATIC EMBRYOGENESIS RECEPTOR KINASE1 gene is expressed throughout the in vitro de novo shoot organogenesis developmental program. <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 125, 107-117.	1.2	15
2826	De novo transcriptome profiling and characterization of voltage-sensitive sodium channel gene of <i>Tropilaelaps mercedesae</i> parasitizing honey bees. <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 89-93.	0.4	1
2827	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.	6.0	30
2828	Transcriptome analysis of stress tolerance in entomopathogenic nematodes of the genus <i>Steinernema</i> . <i>International Journal for Parasitology</i> , 2016, 46, 83-95.	1.3	14

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2829	Identification of Multiple QTL Hotspots in Sockeye Salmon (<i>Oncorhynchus nerka</i>) Using Genotyping-by-Sequencing and a Dense Linkage Map. <i>Journal of Heredity</i> , 2016, 107, 122-133.	1.0	43
2830	Characterization of gonadal transcriptomes from the turbot (<i>Scophthalmus maximus</i>). <i>Genome</i> , 2016, 59, 1-10.	0.9	19
2831	Nuclear phylogenomics of the palm subfamily Arecoideae (Arecaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 32-42.	1.2	32
2832	Suppression Subtractive Hybridization analysis provides new insights into the tomato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock. <i>Journal of Plant Physiology</i> , 2016, 190, 79-94.	1.6	56
2833	Gene Expression and Chromatin Modifications Associated with Maize Centromeres. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 183-192.	0.8	30
2834	Transcriptome profiling of the cysticercus stage of the laboratory model <i>Taenia crassiceps</i> , strain ORF. <i>Acta Tropica</i> , 2016, 154, 50-62.	0.9	13
2835	Identification and analysis of miRNAs and their targets in ginger using bioinformatics approach. <i>Gene</i> , 2016, 575, 570-576.	1.0	52
2836	Bioremediation potential of a highly mercury resistant bacterial strain <i>Sphingobium</i> SA2 isolated from contaminated soil. <i>Chemosphere</i> , 2016, 144, 330-337.	4.2	71
2837	Molecular marker development from transcript sequences and germplasm evaluation for cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Molecular Genetics and Genomics</i> , 2016, 291, 363-381.	1.0	21
2838	Laboratory-scale bioaugmentation relieves acetate accumulation and stimulates methane production in stalled anaerobic digesters. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 1009-1017.	1.7	45
2839	Development and validation of EST-derived SSR markers and diversity analysis in cluster bean (<i>Cyamopsis tetragonoloba</i>). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2016, 25, 263-269.	0.9	28
2840	Parallelism and Epistasis in Skeletal Evolution Identified through Use of Phylogenomic Mapping Strategies. <i>Molecular Biology and Evolution</i> , 2016, 33, 162-173.	3.5	32
2841	Multiplexed pyrosequencing of nine sea anemone (Cnidaria: Anthozoa: Hexacorallia: Actiniaria) mitochondrial genomes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2826-2832.	0.7	21
2842	Mitochondrial DNA control region of three mackerels, genus <i>Rastrelliger</i> : structure, molecular diversity and phylogenetic relationship. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2395-2400.	0.7	6
2843	An improved problem aware local search algorithm for the DNA fragment assembly problem. <i>Soft Computing</i> , 2017, 21, 1709-1720.	2.1	6
2844	Computational Identification of MicroRNAs and Their Targets from Finger Millet (<i>Eleusine coracana</i>). <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 72-79.	2.2	5
2845	Odorant-binding and chemosensory proteins identified in the antennal transcriptome of <i>Adelphocoris suturalis</i> Jakovlev. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 24, 139-145.	0.4	33
2846	Complete mitochondrial genome of the Neotropic cormorant (<i>Phalacrocorax brasilianus</i>). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 401-402.	0.7	6

#	ARTICLE	IF	CITATIONS
2847	ISEA: Iterative Seed-Extension Algorithm for De Novo Assembly Using Paired-End Information and Insert Size Distribution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 916-925.	1.9	20
2848	A gapless genome sequence of the fungus <i>Botrytis cinerea</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 75-89.	2.0	265
2849	De novo assembly of a tadpole shrimp (<i>Triops newberryi</i>) transcriptome and preliminary differential gene expression analysis. <i>Molecular Ecology Resources</i> , 2017, 17, 161-171.	2.2	28
2850	The clinically approved antiviral drug sofosbuvir inhibits Zika virus replication. <i>Scientific Reports</i> , 2017, 7, 40920.	1.6	167
2851	Identification and characterization of protein 14-3-3 in carcinogenic liver fluke <i>Opisthorchis viverrini</i> . <i>Parasitology International</i> , 2017, 66, 426-431.	0.6	12
2852	Co-option and <i>de novo</i> gene evolution underlie molluscan shell diversity. <i>Molecular Biology and Evolution</i> , 2017, 34, msw294.	3.5	67
2853	Integrating genomic resources of flatfish (Pleuronectiformes) to boost aquaculture production. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 21, 41-55.	0.4	21
2854	Functional <i>PTB</i> phosphate transporters are present in streptophyte algae and early diverging land plants. <i>New Phytologist</i> , 2017, 214, 1158-1171.	3.5	25
2855	Intertypic recombination of human parechovirus 4 isolated from infants with sepsis-like disease. <i>Journal of Clinical Virology</i> , 2017, 88, 1-7.	1.6	10
2856	Positive selection on sperm ion channels in a brooding brittle star: consequence of life-history traits evolution. <i>Molecular Ecology</i> , 2017, 26, 3744-3759.	2.0	20
2857	A polychromatic <i>greenbeard</i> locus determines patterns of cooperation in a social amoeba. <i>Nature Communications</i> , 2017, 8, 14171.	5.8	44
2858	Evidence for positive selection and recombination hotspots in Deformed wing virus (DWV). <i>Scientific Reports</i> , 2017, 7, 41045.	1.6	79
2859	Characterization of two complete <i>Isospora</i> mitochondrial genomes from passerine birds: <i>Isospora serinuse</i> in a domestic canary and <i>Isospora manorinae</i> in a yellow-throated miner. <i>Veterinary Parasitology</i> , 2017, 237, 137-142.	0.7	8
2860	Using Next-Generation Sequencing for DNA Barcoding: Capturing Allelic Variation in <i>ITS2</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 19-29.	0.8	38
2861	Evolutionary plasticity of plasma membrane interaction in DREPP family proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 686-697.	1.4	16
2862	Bacterial community structure and prevalence of <i>Pusillimonas</i> -like bacteria in aged landfill leachate. <i>Environmental Science and Pollution Research</i> , 2017, 24, 6757-6769.	2.7	25
2863	Identification of up-regulated genes provides integrated insight into salt-induced tolerance mechanisms in <i>Sesuvium portulacastrum</i> roots. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	3
2864	Diversity in sequences, post-translational modifications and expected pharmacological activities of toxins from four <i>Conus</i> species revealed by the combination of cutting-edge proteomics, transcriptomics and bioinformatics. <i>Toxicon</i> , 2017, 130, 116-125.	0.8	14

#	ARTICLE	IF	CITATIONS
2865	Chestnut Red Stain: Identification of the fungi associated with the costly discolouration of <i>Castanea sativa</i> . <i>Forest Pathology</i> , 2017, 47, e12335.	0.5	11
2866	Structure and Origin of the <i>White Cap</i> Locus and Its Role in Evolution of Grain Color in Maize. <i>Genetics</i> , 2017, 206, 135-150.	1.2	36
2867	High-throughput sequencing of multiple amplicons for barcoding and integrative taxonomy. <i>Scientific Reports</i> , 2017, 7, 41948.	1.6	101
2868	Life-history, substrate choice and Cytochrome Oxidase I variations in sandy beach peracaridans along the Rio de la Plata estuary. <i>Estuarine, Coastal and Shelf Science</i> , 2017, 187, 152-159.	0.9	11
2869	Amalga-like virus infecting <i>Antonospora locustae</i> , a microsporidian pathogen of grasshoppers, plus related viruses associated with other arthropods. <i>Virus Research</i> , 2017, 233, 95-104.	1.1	18
2870	Comparative Transcriptomics of Malaria Mosquito Testes: Function, Evolution, and Linkage. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1127-1136.	0.8	9
2871	Computational complexity of algorithms for sequence comparison, short-read assembly and genome alignment. <i>BioSystems</i> , 2017, 156-157, 72-85.	0.9	34
2872	Analysis and Profiling of <i>Leishmania major</i> Expressed Sequence Tags. <i>Irbm</i> , 2017, 38, 149-155.	3.7	0
2873	The potential for mycobiont sharing between shrubs and seedlings to facilitate tree establishment after wildfire at Alaska arctic treeline. <i>Molecular Ecology</i> , 2017, 26, 3826-3838.	2.0	32
2874	Development of standard methods for Zika virus propagation, titration, and purification. <i>Journal of Virological Methods</i> , 2017, 246, 65-74.	1.0	58
2875	Large-scale collection of full-length cDNA and transcriptome analysis in <i>Hevea brasiliensis</i> . <i>DNA Research</i> , 2017, 24, dsw056.	1.5	18
2876	Squamate Conserved Loci (Sq<scp>CL</scp>): A unified set of conserved loci for phylogenomics and population genetics of squamate reptiles. <i>Molecular Ecology Resources</i> , 2017, 17, e12-e24.	2.2	36
2877	Obtaining the Most Accurate de novo Transcriptomes for Non-model Organisms: The Case of <i>Castanea sativa</i> . <i>Lecture Notes in Computer Science</i> , 2017, , 489-499.	1.0	0
2878	Transposable elements in the <i>Anopheles funestus</i> transcriptome. <i>Genetica</i> , 2017, 145, 275-293.	0.5	6
2879	The Whole-Genome and Transcriptome of the Manila Clam (<i>Ruditapes philippinarum</i>). <i>Genome Biology and Evolution</i> , 2017, 9, 1487-1498.	1.1	75
2880	From data to knowledge: The future of multi-omics data analysis for the rhizosphere. <i>Rhizosphere</i> , 2017, 3, 222-229.	1.4	30
2881	Molecular profiling and bioactive potential of an endophytic fungus <i>Aspergillus sulphureus</i> isolated from <i>Sida acuta</i> : a medicinal plant. <i>Pharmaceutical Biology</i> , 2017, 55, 1623-1630.	1.3	8
2882	Genome sequences of a capulavirus infecting <i>Plantago lanceolata</i> in the Åland archipelago of Finland. <i>Archives of Virology</i> , 2017, 162, 2041-2045.	0.9	39

#	ARTICLE	IF	CITATIONS
2883	Target enrichment sequencing in cultivated peanut (<i>Arachis hypogaea</i> L.) using probes designed from transcript sequences. <i>Molecular Genetics and Genomics</i> , 2017, 292, 955-965.	1.0	17
2884	Intra and intergeneric transferable gene-derived orthologous microsatellite markers in <i>Eucalyptus</i> and <i>Corymbia</i> species. <i>Journal of Forest Research</i> , 2017, 22, 65-68.	0.7	3
2885	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. <i>Genome Biology and Evolution</i> , 2017, 9, 1130-1147.	1.1	75
2886	An internet-based bioinformatics toolkit for plant biosecurity diagnosis and surveillance of viruses and viroids. <i>BMC Bioinformatics</i> , 2017, 18, 26.	1.2	52
2887	Pan-Genomic Approaches in <i>Lactobacillus reuteri</i> as a Porcine Probiotic: Investigation of Host Adaptation and Antipathogenic Activity. <i>Microbial Ecology</i> , 2017, 74, 709-721.	1.4	15
2888	Dynamics of the Interaction between Cotton Bollworm <i>Helicoverpa armigera</i> and Nucleopolyhedrovirus as Revealed by Integrated Transcriptomic and Proteomic Analyses. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1009-1028.	2.5	40
2889	<i>Tabula rasa</i> in the Patagonian Channels? The phylogeography of <i>Oreobolus obtusangulus</i> (Cyperaceae). <i>Molecular Ecology</i> , 2017, 26, 4027-4044.	2.0	9
2890	Polymorphism in 5' untranslated region of heat shock protein 70 gene as marker of postpartum anoestrus in Murrah buffaloes. <i>Reproduction in Domestic Animals</i> , 2017, 52, 505-512.	0.6	2
2891	The RAG transposon is active through the deuterostome evolution and domesticated in jawed vertebrates. <i>Immunogenetics</i> , 2017, 69, 391-400.	1.2	36
2892	Sequence Assembly. <i>Methods in Molecular Biology</i> , 2017, 1525, 35-45.	0.4	2
2893	A report of cherry rusty mottle-associated virus in South Carolina. <i>Australasian Plant Disease Notes</i> , 2017, 12, 1.	0.4	5
2894	Nanopore sequencing data analysis: state of the art, applications and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, 1256-1272.	3.2	91
2895	Characteristics and Expression Profile of <i>KRT71</i> Screened by Suppression Subtractive Hybridization cDNA Library in Curly Fleece Chinese Tan Sheep. <i>DNA and Cell Biology</i> , 2017, 36, 552-564.	0.9	11
2896	Tomato root microbiota and <i>Phytophthora parasitica</i> -associated disease. <i>Microbiome</i> , 2017, 5, 56.	4.9	65
2897	Identification of the abiotic stress-related transcription in little Neptune grass <i>Cymodocea nodosa</i> with RNA-seq. <i>Marine Genomics</i> , 2017, 34, 47-56.	0.4	16
2898	De novo transcriptome sequencing and comparative analysis of midgut tissues of four non-model insects pertaining to Hemiptera, Coleoptera, Diptera and Lepidoptera. <i>Gene</i> , 2017, 627, 85-93.	1.0	8
2899	Functional metagenomics of oil-impacted mangrove sediments reveals high abundance of hydrolases of biotechnological interest. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 141.	1.7	20
2900	Lineage-specific expansion and loss of tyrosinase genes across platyhelminths and their induction profiles in the carcinogenic oriental liver fluke, <i>Clonorchis sinensis</i> . <i>Parasitology</i> , 2017, 144, 1316-1327.	0.7	4

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2901	History cleans up messes: The impact of time in driving divergence and introgression in a tropical suture zone. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1888-1899.	1.1	17
2902	Silk gene expression of theridiid spiders: implications for male-specific silk use. <i>Zoology</i> , 2017, 122, 107-114.	0.6	20
2903	Tropical specialist vs. climate generalist: Diversification and demographic history of sister species of <i>Carlia</i> skinks from northwestern Australia. <i>Molecular Ecology</i> , 2017, 26, 4045-4058.	2.0	25
2904	A metagenomic approach to discover a novel α -glucosidase from bovine rumens. <i>Pure and Applied Chemistry</i> , 2017, 89, 941-950.	0.9	5
2905	Salicylic acid seed priming instigates defense mechanism by inducing PR-Proteins in <i>Solanum melongena</i> L. upon infection with <i>Verticillium dahliae</i> Kleb.. <i>Plant Physiology and Biochemistry</i> , 2017, 117, 12-23.	2.8	37
2906	Genome Size in North American Fireflies: Substantial Variation Likely Driven by Neutral Processes. <i>Genome Biology and Evolution</i> , 2017, 9, 1499-1512.	1.1	41
2907	SSR Marker Development, Linkage Mapping, and QTL Analysis for Establishment Rate in Common Bermudagrass. <i>Plant Genome</i> , 2017, 10, plantgenome2016.07.0074.	1.6	20
2908	Spontaneous Mutation at Amino Acid 544 of the Ebola Virus Glycoprotein Potentiates Virus Entry and Selection in Tissue Culture. <i>Journal of Virology</i> , 2017, 91, .	1.5	24
2909	Whipworm kinomes reflect a unique biology and adaptation to the host animal. <i>International Journal for Parasitology</i> , 2017, 47, 857-866.	1.3	10
2910	Deciphering genes associated with root wilt disease of coconut and development of its transcriptomic database (CnTDB). <i>Physiological and Molecular Plant Pathology</i> , 2017, 100, 255-263.	1.3	12
2911	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention. <i>Plant Journal</i> , 2017, 91, 3-21.	2.8	95
2912	Characterization and expression analysis of serpinB3, the first clade B serine protease inhibitor in Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Developmental and Comparative Immunology</i> , 2017, 72, 103-111.	1.0	6
2913	Identification of cvSI-3 and evidence for the wide distribution and active evolution of the I84 family of protease inhibitors in mollusks. <i>Fish and Shellfish Immunology</i> , 2017, 62, 332-340.	1.6	11
2914	A physiologically-oriented transcriptomic analysis of the midgut of <i>Tenebrio molitor</i> . <i>Journal of Insect Physiology</i> , 2017, 99, 58-66.	0.9	17
2915	Genetic basis of benzimidazole resistance in <i>Teladorsagia circumcincta</i> in Ireland. <i>Irish Veterinary Journal</i> , 2017, 70, 8.	0.8	20
2916	Embryo arrest and reactivation: potential candidates controlling embryonic diapause in the tammar wallaby and mink. <i>Biology of Reproduction</i> , 2017, 96, 877-894.	1.2	21
2917	Patterns of cross-contamination in a multispecies population genomic project: detection, quantification, impact, and solutions. <i>BMC Biology</i> , 2017, 15, 25.	1.7	100
2918	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain PAB 2.2 Isolated from Abrolhos Bank (Brazil). <i>Genome Announcements</i> , 2017, 5, .	0.8	0

#	ARTICLE	IF	CITATIONS
2919	Genomic evidence for convergent evolution of a key trait underlying divergence in island birds. <i>Molecular Ecology</i> , 2017, 26, 3760-3774.	2.0	20
2920	New polymorphic microsatellite markers derived from hemocyte cDNA library of Manila clam <i>Ruditapes philippinarum</i> challenged by the protozoan parasite <i>Perkinsus olseni</i> . <i>Ocean Science Journal</i> , 2017, 52, 139-146.	0.6	0
2921	A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. <i>Current Biology</i> , 2017, 27, 958-967.	1.8	423
2922	Revealing large metagenomic regions through long DNA fragment hybridization capture. <i>Microbiome</i> , 2017, 5, 33.	4.9	8
2923	Changes in renal gene expression associated with induced ochratoxicosis in chickens: activation and deactivation of transcripts after varying durations of exposure. <i>Poultry Science</i> , 2017, 96, 1855-1865.	1.5	6
2924	The ANGULATA 7 gene encodes a DnaJ-like zinc finger domain protein involved in chloroplast function and leaf development in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2017, 89, 870-884.	2.8	25
2925	In Silico Mining of Conserved miRNAs of Indian Catfish <i>Clarias batrachus</i> (Linnaeus, 1758) from the Contigs, ESTs, and BAC End Sequences. <i>Applied Biochemistry and Biotechnology</i> , 2017, 182, 956-966.	1.4	3
2926	miRNA mediated gene regulatory network analysis of <i>Cichorium intybus</i> (chicory). <i>Agri Gene</i> , 2017, 3, 37-45.	1.9	6
2927	Transcriptomic analysis of <i>Casuarina equisetifolia</i> L. in responses to cold stress. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	15
2928	In silico identification of alternative oxidase 2 (AOX2) in monocots: A new evolutionary scenario. <i>Journal of Plant Physiology</i> , 2017, 210, 58-63.	1.6	18
2929	Analysis of <i>de novo</i> sequencing and transcriptome assembly and lignocellulolytic enzymes gene expression of <i>Coriopsis gallica</i> HTC. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 460-468.	0.6	3
2930	Expression of metallothionein in the liver and kidneys of the red deer (<i>Cervus elaphus</i> L.) from an industrial metal smelting area of Poland. <i>Ecotoxicology and Environmental Safety</i> , 2017, 137, 121-129.	2.9	11
2931	Whole genome sequencing of mouse lymphoma L5178Y-3.7.2C (TK +/â”) reveals millions of mutations and genetic markers. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2017, 814, 1-6.	0.9	5
2932	Races of the Celery Pathogen <i>Fusarium oxysporum</i> f. sp. <i>apii</i> Are Polyphyletic. <i>Phytopathology</i> , 2017, 107, 463-473.	1.1	44
2933	Genome-Wide Analysis of Soybean LATERAL ORGAN BOUNDARIES Domain-Containing Genes: A Functional Investigation of <i>GmLBD12</i> . <i>Plant Genome</i> , 2017, 10, plantgenome2016.07.0058.	1.6	26
2934	Transcriptomic analysis of juvenile wood formation during the growing season in <i>Pinus canariensis</i> . <i>Holzforschung</i> , 2017, 71, 919-937.	0.9	11
2935	Spatial organization of silybin biosynthesis in milk thistle [<i>Silybum marianum</i> (L.) Gaertn]. <i>Plant Journal</i> , 2017, 92, 995-1004.	2.8	41
2936	Comparison of a South African and Canadian Isolate of the Nucleopolyhedrosis Virus Infecting the Insect <i>Trichoplusia ni</i> . <i>African Entomology</i> , 2017, 25, 341-360.	0.6	0

#	ARTICLE	IF	CITATIONS
2937	Soybean Functional Genomics: Bridging the Genotype-to-Phenotype Gap. Compendium of Plant Genomes, 2017, , 151-170.	0.3	6
2938	Study of microRNA mediated gene regulation in <i>Striga hermonthica</i> through in-silico approach. <i>Agri Gene</i> , 2017, 6, 47-53.	1.9	1
2939	RNA-seq Analysis in Plant-Fungus Interactions. , 2017, , 1-25.		0
2940	A Metagenomic Analysis of Bacterial Microbiota in the Digestive Tract of Triatomines. <i>Bioinformatics and Biology Insights</i> , 2017, 11, 117793221773342.	1.0	14
2941	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	1.6	24
2942	Reference transcriptome assembly and annotation for perennial ryegrass. <i>Genome</i> , 2017, 60, 1086-1088.	0.9	7
2943	Development of transcriptome based web genomic resources of yellow mosaic disease in <i>Vigna mungo</i> . <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 767-777.	1.4	11
2944	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
2945	Deep sequencing reveals the first fabavirus infecting peach. <i>Scientific Reports</i> , 2017, 7, 11329.	1.6	23
2946	A Driving Bioinformatics Approach to Explore Co-regulation of AOX Gene Family Members During Growth and Development. <i>Methods in Molecular Biology</i> , 2017, 1670, 219-224.	0.4	2
2947	Transcriptional response of the harmful raphidophyte <i>Heterosigma akashiwo</i> to nitrate and phosphate stress. <i>Harmful Algae</i> , 2017, 68, 258-270.	2.2	32
2948	Comparative genomics of <i>Lactobacillus salivarius</i> strains focusing on their host adaptation. <i>Microbiological Research</i> , 2017, 205, 48-58.	2.5	36
2949	Analysis of the first <i>Taraxacum kok-saghyz</i> transcriptome reveals potential rubber yield related SNPs. <i>Scientific Reports</i> , 2017, 7, 9939.	1.6	50
2950	Characterization of Fungi Associated With Wood Decay of Tree Species and Grapevine in Greece. <i>Plant Disease</i> , 2017, 101, 1929-1940.	0.7	17
2951	A multiplex PCR assay for the identification of five commercially important Portunid crabs: <i>Portunus pelagicus</i> , <i>P. gladiator</i> , <i>P. sanguinolentus</i> , <i>Charybdis natator</i> , and <i>C. feriatius</i> . <i>Food Biotechnology</i> , 2017, 31, 177-192.	0.6	4
2952	Integrated Venomics and Venom Gland Transcriptome Analysis of Juvenile and Adult Mexican Rattlesnakes <i>Crotalus simus</i> , <i>C. tzabcan</i> , and <i>C. culminatus</i> Revealed miRNA-modulated Ontogenetic Shifts. <i>Journal of Proteome Research</i> , 2017, 16, 3370-3390.	1.8	82
2953	Draft whole genome sequence of groundnut stem rot fungus <i>Athelia rolfsii</i> revealing genetic architect of its pathogenicity and virulence. <i>Scientific Reports</i> , 2017, 7, 5299.	1.6	17
2954	Population structure and cryptic species in the cosmopolitan rotifer <i>Euchlanis dilatata</i> . <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 757-777.	1.0	18

#	ARTICLE	IF	CITATIONS
2955	Genome-wide identification of the radiation sensitivity protein-23 (RAD23) family members in apple (<i>Malus domestica</i> Borkh.) and expression analysis of their stress responsiveness. <i>Journal of Integrative Agriculture</i> , 2017, 16, 820-827.	1.7	6
2956	De novo transcriptome assembly and its annotation for the aposematic wood tiger moth (<i>Parasemia</i>) Tj ETQq1 1 0,784314 rgBT /Overl 1.3 7		
2957	Range instability leads to cytonuclear discordance in a morphologically cryptic ground squirrel species complex. <i>Molecular Ecology</i> , 2017, 26, 4743-4755.	2.0	23
2958	Construction and characterization of a bacterial artificial chromosome library for <i>Camellia sinensis</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	6
2959	Functional characterization of Aquaporin-like genes in the human bed bug <i>Cimex lectularius</i> . <i>Scientific Reports</i> , 2017, 7, 3214.	1.6	18
2960	Population-wide sampling of retrotransposon insertion polymorphisms using deep sequencing and efficient detection. <i>GigaScience</i> , 2017, 6, 1-11.	3.3	11
2961	Development of Microsatellite Markers for <i>Eurya acuminatissima</i> (Theaceae). <i>Applications in Plant Sciences</i> , 2017, 5, 1700037.	0.8	0
2962	Overexpression of GhDof1 improved salt and cold tolerance and seed oil content in <i>Gossypium hirsutum</i> . <i>Journal of Plant Physiology</i> , 2017, 218, 222-234.	1.6	67
2963	Differential expression patterns of MIKCC-type MADS-box genes in the endangered fern <i>Vandenboschia speciosa</i> . <i>Plant Gene</i> , 2017, 12, 50-56.	1.4	6
2964	An update on bioinformatics resources for plant genomics research. <i>Current Plant Biology</i> , 2017, 11-12, 33-40.	2.3	7
2965	Genome Analysis. <i>Compendium of Plant Genomes</i> , 2017, , 3-19.	0.3	0
2966	Azole sensitivity in <i>Leptosphaeria</i> pathogens of oilseed rape: the role of lanosterol 14 α -demethylase. <i>Scientific Reports</i> , 2017, 7, 15849.	1.6	11
2967	The deep conservation of the Lepidoptera Z chromosome suggests a non-canonical origin of the W. <i>Nature Communications</i> , 2017, 8, 1486.	5.8	87
2968	Establishment of a de novo Reference Transcriptome of <i>Histomonas meleagridis</i> Reveals Basic Insights About Biological Functions and Potential Pathogenic Mechanisms of the Parasite. <i>Protist</i> , 2017, 168, 663-685.	0.6	28
2969	Development, characterization and cross-amplification of microsatellite markers for <i>Chrysolaena obovata</i> , an important Asteraceae from Brazilian Cerrado. <i>Journal of Genetics</i> , 2017, 96, 47-53.	0.4	6
2970	Transcriptome profiling and expression analysis of immune responsive genes in the liver of Golden mahseer (<i>Tor putitora</i>) challenged with <i>Aeromonas hydrophila</i> . <i>Fish and Shellfish Immunology</i> , 2017, 67, 655-666.	1.6	36
2971	A rapid and cost-effective approach for the development of polymorphic microsatellites in non-model species using paired-end RAD sequencing. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1165-1174.	1.0	5
2972	SCPP Genes and Their Relatives in Gar: Rapid Expansion of Mineralization Genes in Osteichthyans. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 645-665.	0.6	25

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2973	Comparative landscape of alternative splicing in fruit plants. <i>Current Plant Biology</i> , 2017, 9-10, 29-36.	2.3	16
2974	Phylogenomic analyses of 539 highly informative loci dates a fully resolved time tree for the major clades of living turtles (Testudines). <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 7-15.	1.2	62
2975	Virulent strain of African swine fever virus eclipses its attenuated derivative after challenge. <i>Archives of Virology</i> , 2017, 162, 3081-3088.	0.9	10
2976	New species in the papaya ringspot virus cluster: Insights into the evolution of the PRSV lineage. <i>Virus Research</i> , 2017, 241, 88-94.	1.1	22
2977	Systematic comparison of lncRNAs with protein coding mRNAs in population expression and their response to environmental change. <i>BMC Plant Biology</i> , 2017, 17, 42.	1.6	36
2978	Mining a differential sialotranscriptome of <i>Rhipicephalus microplus</i> guides antigen discovery to formulate a vaccine that reduces tick infestations. <i>Parasites and Vectors</i> , 2017, 10, 206.	1.0	46
2979	Analysis of early events in barley (<i>Hordeum vulgare</i> L.) roots in response to <i>Fusarium culmorum</i> infection. <i>European Journal of Plant Pathology</i> , 2017, 148, 343-355.	0.8	7
2980	Full-Length Mitochondrial-DNA Sequencing on the PacBio RSII. <i>Methods in Molecular Biology</i> , 2017, 1492, 179-184.	0.4	8
2981	Identification and functional characterizations of serpin8, a potential prophenoloxidase-activating protease inhibitor in Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2017, 60, 492-501.	1.6	15
2982	Full-length sequence assembly reveals circular RNAs with diverse non-GT/AG splicing signals in rice. <i>RNA Biology</i> , 2017, 14, 1055-1063.	1.5	113
2983	Novel hydrolytic extremely halotolerant alkaliphiles from mature landfill leachate with key involvement in maturation process. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2017, 52, 64-73.	0.9	23
2984	Molecular characterization of a novel ssRNA ourmia-like virus from the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Archives of Virology</i> , 2017, 162, 891-895.	0.9	33
2985	Genomic islands of divergence linked to ecotypic variation in sockeye salmon. <i>Molecular Ecology</i> , 2017, 26, 554-570.	2.0	62
2986	Genomic skimming for identification of medium/highly abundant transposable elements in <i>Arundo donax</i> and <i>Arundo plinii</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 157-171.	1.0	4
2987	The sequence capture by hybridization: a new approach for revealing the potential of monoaromatic hydrocarbons bioattenuation in a deep oligotrophic aquifer. <i>Microbial Biotechnology</i> , 2017, 10, 469-479.	2.0	17
2988	Molecular characterization and genetic diversity of bovine Kobuvirus, Brazil. <i>Virus Genes</i> , 2017, 53, 105-110.	0.7	14
2989	Genetic elaborations of glandular and non-glandular trichomes in <i>Mentha arvensis</i> genotypes: assessing genotypic and phenotypic correlations along with gene expressions. <i>Protoplasma</i> , 2017, 254, 1045-1061.	1.0	14
2990	A large set of 26 new reference transcriptomes dedicated to comparative population genomics in crops and wild relatives. <i>Molecular Ecology Resources</i> , 2017, 17, 565-580.	2.2	53

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2991	Differential expression of genes during the interaction between <i>Colletotrichum lindemuthianum</i> and <i>Phaseolus vulgaris</i> . <i>European Journal of Plant Pathology</i> , 2017, 147, 653-670.	0.8	6
2992	Authentication of <i>Myristica fragrans</i> Houtt. using DNA barcoding. <i>Food Control</i> , 2017, 73, 1010-1015.	2.8	34
2993	Comparative transcriptomics reveal host-specific nucleotide variation in entomophthoralean fungi. <i>Molecular Ecology</i> , 2017, 26, 2092-2110.	2.0	33
2994	Transcriptomic profile of Manila clam (<i>Ruditapes philippinarum</i>) haemocytes in response to <i>Perkinsus olseni</i> infection. <i>Aquaculture</i> , 2017, 467, 170-181.	1.7	15
2995	Zinc supply impacts on the relative expression of a metallothionein-like gene in <i>Coffea arabica</i> plants. <i>Plant and Soil</i> , 2017, 411, 179-191.	1.8	15
2996	Transcriptome and physiological analysis of a lutein-producing alga <i>Desmodesmus</i> sp. reveals the molecular mechanisms for high lutein productivity. <i>Algal Research</i> , 2017, 21, 103-119.	2.4	19
2997	Chloroplast phylogenomic analyses maternal relationships among sections in the genus <i>Populus</i> . <i>Biochemical Systematics and Ecology</i> , 2017, 70, 132-140.	0.6	5
2998	Seeksv: an accurate tool for somatic structural variation and virus integration detection. <i>Bioinformatics</i> , 2017, 33, 184-191.	1.8	64
2999	Mercury remediation potential of a mercury resistant strain <i>Sphingopyxis</i> sp. SE2 isolated from contaminated soil. <i>Journal of Environmental Sciences</i> , 2017, 51, 128-137.	3.2	33
3000	Molecular Identification of Four Members of the <i>Anopheles dirus</i> Complex Using the Mitochondrial Cytochrome C Oxidase Subunit I Gene. <i>Journal of the American Mosquito Control Association</i> , 2017, 33, 263-269.	0.2	4
3001	Phylogeny of Anophelinae using mitochondrial protein coding genes. <i>Royal Society Open Science</i> , 2017, 4, 170758.	1.1	83
3002	Primers for <i>Castilleja</i> and their utility across <i>Orobanchaceae</i> : II. Single-copy nuclear loci. <i>Applications in Plant Sciences</i> , 2017, 5, 1700038.	0.8	11
3003	Patterns of genomic variation in Coho salmon following reintroduction to the interior Columbia River. <i>Ecology and Evolution</i> , 2017, 7, 10350-10360.	0.8	11
3004	Cloning and sequence analysis of chalcone synthase gene in <i>Curcuma alismatifolia</i> . <i>Acta Horticulturae</i> , 2017, , 299-304.	0.1	2
3005	Cleaning and disinfection programs against <i>Campylobacter jejuni</i> for broiler chickens: productive performance, microbiological assessment and characterization. <i>Poultry Science</i> , 2017, 96, 3188-3198.	1.5	22
3006	Estimation of phylogenetic divergence times in <i>Panagrolaimidae</i> and other nematodes using relaxed molecular clocks calibrated with insect and crustacean fossils. <i>Nematology</i> , 2017, 19, 899-913.	0.2	6
3007	Probabilistic estimation of overlap graphs for large sequence datasets. , 2017, , .		0
3009	Identification and Characterization of Odorant Binding Proteins in the Forelegs of <i>Adelphocoris lineolatus</i> (Goeze). <i>Frontiers in Physiology</i> , 2017, 8, 735.	1.3	55

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3010	Comparative Analysis of Transcriptomes in Rhizophoraceae Provides Insights into the Origin and Adaptive Evolution of Mangrove Plants in Intertidal Environments. <i>Frontiers in Plant Science</i> , 2017, 8, 795.	1.7	39
3011	De novo Assembly of the <i>Camellia nitidissima</i> Transcriptome Reveals Key Genes of Flower Pigment Biosynthesis. <i>Frontiers in Plant Science</i> , 2017, 8, 1545.	1.7	43
3012	Rice Seed Germination Underwater: Morpho-Physiological Responses and the Bases of Differential Expression of Alcoholic Fermentation Enzymes. <i>Frontiers in Plant Science</i> , 2017, 8, 1857.	1.7	32
3013	Abiotic Stress Responsive miRNA-Target Network and Related Markers (SNP, SSR) in <i>Brassica juncea</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1943.	1.7	39
3014	A genome-wide transcriptome map of pistachio (<i>Pistacia vera</i> L.) provides novel insights into salinity-related genes and marker discovery. <i>BMC Genomics</i> , 2017, 18, 627.	1.2	33
3015	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2017, 18, 578.	1.2	54
3016	Reliable Detection of Herpes Simplex Virus Sequence Variation by High-Throughput Resequencing. <i>Viruses</i> , 2017, 9, 226.	1.5	9
3017	Evolutionary Conserved Cysteines Function as cis-Acting Regulators of Arabidopsis PIN-FORMED 2 Distribution. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2274.	1.8	28
3018	Exploration for the Salinity Tolerance-Related Genes from Xero-Halophyte <i>Atriplex canescens</i> Exploiting Yeast Functional Screening System. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2444.	1.8	15
3019	Complete Chloroplast Genome of <i>Pinus massoniana</i> (Pinaceae): Gene Rearrangements, Loss of <i>ndh</i> Genes, and Short Inverted Repeats Contraction, Expansion. <i>Molecules</i> , 2017, 22, 1528.	1.7	33
3020	Generation and Characterisation of a Reference Transcriptome for <i>Phalaris</i> (<i>Phalaris aquatica</i> L.). <i>Agronomy</i> , 2017, 7, 14.	1.3	8
3021	Characterisation of Faba Bean (<i>Vicia faba</i> L.) Transcriptome Using RNA-Seq: Sequencing, De Novo Assembly, Annotation, and Expression Analysis. <i>Agronomy</i> , 2017, 7, 53.	1.3	10
3022	Expression Profiling in <i>Pinus pinaster</i> in Response to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2017, 8, 279.	0.9	22
3023	Identification and Characterization of TALE Homeobox Genes in the Endangered Fern <i>Vandenboschia speciosa</i> . <i>Genes</i> , 2017, 8, 275.	1.0	12
3024	The Transcriptomes of <i>Xiphinema index</i> and <i>Longidorus elongatus</i> Suggest Independent Acquisition of Some Plant Parasitism Genes by Horizontal Gene Transfer in Early-Branching Nematodes. <i>Genes</i> , 2017, 8, 287.	1.0	19
3025	The Distinct Transcriptional Response of the Midgut of <i>Amblyomma sculptum</i> and <i>Amblyomma aureolatum</i> Ticks to <i>Rickettsia rickettsii</i> Correlates to Their Differences in Susceptibility to Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 129.	1.8	23
3026	Integrative Taxonomy of Amazon Reefs' <i>Arenosclera</i> spp.: A New Clade in the Haplosclerida (Demospongiae). <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	10
3027	Phenotypic Microdiversity and Phylogenetic Signal Analysis of Traits Related to Social Interaction in <i>Bacillus</i> spp. from Sediment Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 29.	1.5	21

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3028	Conserved Transcriptional Responses to Nutrient Stress in Bloom-Forming Algae. <i>Frontiers in Microbiology</i> , 2017, 8, 1279.	1.5	31
3029	pH Stress-Induced Cooperation between <i>Rhodococcus ruber</i> YYL and <i>Bacillus cereus</i> MLY1 in Biodegradation of Tetrahydrofuran. <i>Frontiers in Microbiology</i> , 2017, 8, 2297.	1.5	25
3030	Characterization of Antimicrobial-Producing Beneficial Bacteria Isolated from Huanglongbing Escape Citrus Trees. <i>Frontiers in Microbiology</i> , 2017, 8, 2415.	1.5	48
3031	Diverse CO ₂ -Induced Responses in Physiology and Gene Expression among Eukaryotic Phytoplankton. <i>Frontiers in Microbiology</i> , 2017, 8, 2547.	1.5	27
3032	Preparing and Analyzing Expressed Sequence Tags (ESTs) Library for the Mammary Tissue of Local Turkish Kivircik Sheep. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.	0.8	0
3033	Down-regulation of aminopeptidase N and ABC transporter subfamily G transcripts in Cry1Ab and Cry1Ac resistant Asian corn borer, <i>Ostrinia furnacalis</i> (Lepidoptera: Crambidae). <i>International Journal of Biological Sciences</i> , 2017, 13, 835-851.	2.6	43
3034	EUCANEXT: an integrated database for the exploration of genomic and transcriptomic data from Eucalyptus species. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	12
3035	De novo transcriptome analysis shows differential expression of genes in salivary glands of edible bird's nest producing swiftlets. <i>BMC Genomics</i> , 2017, 18, 504.	1.2	9
3036	African Non-Human Primates Host Diverse Enteroviruses. <i>PLoS ONE</i> , 2017, 12, e0169067.	1.1	29
3037	Genetic Analysis of <i>Vibrio parahaemolyticus</i> O3:K6 Strains That Have Been Isolated in Mexico Since 1998. <i>PLoS ONE</i> , 2017, 12, e0169722.	1.1	12
3038	Genetic Polymorphisms and Phenotypic Profiles of Sulfadiazine-Resistant and Sensitive <i>Toxoplasma gondii</i> Isolates Obtained from Newborns with Congenital Toxoplasmosis in Minas Gerais, Brazil. <i>PLoS ONE</i> , 2017, 12, e0170689.	1.1	20
3039	Bruchid egg induced transcript dynamics in developing seeds of black gram (<i>Vigna mungo</i>). <i>PLoS ONE</i> , 2017, 12, e0176337.	1.1	6
3040	Crude oil impairs immune function and increases susceptibility to pathogenic bacteria in southern flounder. <i>PLoS ONE</i> , 2017, 12, e0176559.	1.1	38
3041	De novo transcriptome of the mayfly <i>Cloeon viridulum</i> and transcriptional signatures of <i>Prometabola</i> . <i>PLoS ONE</i> , 2017, 12, e0179083.	1.1	13
3042	Mitogenome sequence accuracy using different elucidation methods. <i>PLoS ONE</i> , 2017, 12, e0179971.	1.1	15
3043	Differential expression of small RNA pathway genes associated with the <i>Biomphalaria glabrata</i> / <i>Schistosoma mansoni</i> interaction. <i>PLoS ONE</i> , 2017, 12, e0181483.	1.1	13
3044	Challenges and advances for transcriptome assembly in non-model species. <i>PLoS ONE</i> , 2017, 12, e0185020.	1.1	38
3045	The mitochondrial genome of Muga silkworm (<i>Antheraea assamensis</i>) and its comparative analysis with other lepidopteran insects. <i>PLoS ONE</i> , 2017, 12, e0188077.	1.1	27

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3046	A Spirochaete is suggested as the causative agent of Akoya oyster disease by metagenomic analysis. PLoS ONE, 2017, 12, e0182280.	1.1	38
3047	The sea cucumber genome provides insights into morphological evolution and visceral regeneration. PLoS Biology, 2017, 15, e2003790.	2.6	202
3048	Prohibition of antibiotic growth promoters has affected the genomic profiles of <i>Lactobacillus salivarius</i> inhabiting the swine intestine. PLoS ONE, 2017, 12, e0186671.	1.1	5
3049	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . PLoS Biology, 2017, 15, e2002266.	2.6	170
3050	The complete chloroplast genome of <i>Primulina</i> and two novel strategies for development of high polymorphic loci for population genetic and phylogenetic studies. BMC Evolutionary Biology, 2017, 17, 224.	3.2	18
3051	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and Réunion. Virology Journal, 2017, 14, 146.	1.4	20
3052	Identification of 76 novel B1 metallo- β -lactamases through large-scale screening of genomic and metagenomic data. Microbiome, 2017, 5, 134.	4.9	75
3053	Transcriptome profiling of tobacco (<i>Nicotiana tabacum</i>) pollen and pollen tubes. BMC Genomics, 2017, 18, 581.	1.2	24
3054	Insights from tissue-specific transcriptome sequencing analysis of <i>Triatoma infestans</i> . Memorias Do Instituto Oswaldo Cruz, 2017, 112, 456-457.	0.8	5
3055	Genetic diversity of piroplasmids species in equids from island of São Luís, northeastern Brazil. Brazilian Journal of Veterinary Parasitology, 2017, 26, 331-339.	0.2	18
3056	Isolation and Characterization of Microcystin Degrading Bacteria from Holy Ponds in India. International Journal of Applied Sciences and Biotechnology, 2017, 4, 436-447.	0.4	4
3057	High-Throughput RNA-Seq Data Analysis of the Single Nucleotide Polymorphisms (SNPs) and Zygomorphic Flower Development in Pea (<i>Pisum sativum</i> L.). International Journal of Molecular Sciences, 2017, 18, 2710.	1.8	9
3058	Transcriptome Analysis for Non-Model Organism: Current Status and Best-Practices. , 0, , .		10
3059	Detection of differentially methylated regions of irradiated fig tree selections. Scientia Agricola, 2017, 74, 285-293.	0.6	2
3060	Characterization of a <i>CONSTANS-like</i> Gene from Pigeon Orchid (<i>Dendrobium crumenatum</i>) Tj ETQq0 0 0 rgBT /Overlock 1 252-262.	0.3	10
3061	Association of variation in the sugarcane transcriptome with sugar content. BMC Genomics, 2017, 18, 909.	1.2	41
3062	Approaches for in silico finishing of microbial genome sequences. Genetics and Molecular Biology, 2017, 40, 553-576.	0.6	17
3063	De Novo Assembly of <i>Lucina pectinata</i> Genome using Ion Torrent Reads. , 2017, , .		1

#	ARTICLE	IF	CITATIONS
3064	The vertical distribution of prokaryotes in the surface sediment of Jiaolong cold seep at the northern South China Sea. <i>Extremophiles</i> , 2018, 22, 499-510.	0.9	24
3065	Linear Regression With Shuffled Data: Statistical and Computational Limits of Permutation Recovery. <i>IEEE Transactions on Information Theory</i> , 2018, 64, 3286-3300.	1.5	56
3066	Comparative transcriptome analysis reveals an early gene expression profile that contributes to cold resistance in <i>Hevea brasiliensis</i> (the Para rubber tree). <i>Tree Physiology</i> , 2018, 38, 1409-1423.	1.4	26
3067	An optimized approach for local de novo assembly of overlapping paired-end RAD reads from multiple individuals. <i>Royal Society Open Science</i> , 2018, 5, 171589.	1.1	10
3068	Bacterial isolates exhibiting multidrug resistance, hemolytic activity, and high 16S <i>rRNA</i> gene similarity with well-known pathogens found in camel milk samples of Riyadh region. <i>Apmis</i> , 2018, 126, 215-226.	0.9	3
3069	<i>Miscanthus giganteus</i> : Regeneration system with assessment of genetic and epigenetic stability in long-term in vitro culture. <i>Industrial Crops and Products</i> , 2018, 116, 150-161.	2.5	9
3070	Targeted Sequencing of Venom Genes from Cone Snail Genomes Improves Understanding of Conotoxin Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 1210-1224.	3.5	33
3071	Draft Genome Sequence of <i>Burkholderia gladioli</i> Coa14, a Bacterium with Petroleum Bioremediation Potential Isolated from Coari Lake, Amazonas, Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
3072	Putative resistance-associated genes induced in sugarcane in response to the brown rust fungus, <i>Puccinia melanocephala</i> and their use in genetic diversity analysis of Louisiana sugarcane clones. <i>Plant Gene</i> , 2018, 14, 20-28.	1.4	10
3073	Brassicales phylogeny inferred from 72 plastid genes: A reanalysis of the phylogenetic localization of two paleopolyploid events and origin of novel chemical defenses. <i>American Journal of Botany</i> , 2018, 105, 463-469.	0.8	76
3074	Genome Re-Sequencing of Diverse Sweet Cherry (<i>Prunus avium</i>) Individuals Reveals a Modifier Gene Mutation Conferring Pollen-Part Self-Compatibility. <i>Plant and Cell Physiology</i> , 2018, 59, 1265-1275.	1.5	37
3075	Molecular cloning and characterization of Pif gene from pearl mussel, <i>Hyriopsis cumingii</i> , and the gene expression analysis during pearl formation. <i>3 Biotech</i> , 2018, 8, 214.	1.1	4
3076	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	3.5	30
3077	Mining and comparative survey of EST-SSR markers among members of Euphorbiaceae family. <i>Molecular Biology Reports</i> , 2018, 45, 453-468.	1.0	5
3078	De novo assembly of honey bee RNA viral genomes by tapping into the innate insect antiviral response pathway. <i>Journal of Invertebrate Pathology</i> , 2018, 152, 38-47.	1.5	23
3079	Analysis of differential transcript expression in chickpea during compatible and incompatible interactions with <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> Race 4. <i>3 Biotech</i> , 2018, 8, 111.	1.1	7
3080	SeagrassDB: An open-source transcriptomics landscape for phylogenetically profiled seagrasses and aquatic plants. <i>Scientific Reports</i> , 2018, 8, 2749.	1.6	12
3081	A hybrid crow search algorithm for solving the DNA fragment assembly problem. <i>Expert Systems With Applications</i> , 2018, 102, 44-56.	4.4	37

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3082	Salt Stress-Induced Loss of Iron Oxidoreduction Activities and Reacquisition of That Phenotype Depend on <i>rus</i> Operon Transcription in <i>Acidithiobacillus ferridurans</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	11
3083	Beyond the primary structure of Kazal domains in decapod crustaceans. <i>Journal of Crustacean Biology</i> , 2018, 38, 156-165.	0.3	1
3084	Paralithocins, Antimicrobial Peptides with Unusual Disulfide Connectivity from the Red King Crab, <i>Paralithodes camtschaticus</i> . <i>Journal of Natural Products</i> , 2018, 81, 140-150.	1.5	16
3085	Evidence for contemporary plant mitoviruses. <i>Virology</i> , 2018, 518, 14-24.	1.1	95
3086	Virtual Genome Walking across the 32Gb <i>Ambystoma mexicanum</i> genome; assembling gene models and intronic sequence. <i>Scientific Reports</i> , 2018, 8, 618.	1.6	9
3087	Description of <i>Alteromonas abrolhosensis</i> sp. nov., isolated from sea water of Abrolhos Bank, Brazil. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1131-1138.	0.7	2
3088	Mining <i>Ferula gummosa</i> transcriptome to identify miRNAs involved in the regulation and biosynthesis of terpenes. <i>Gene</i> , 2018, 645, 41-47.	1.0	38
3089	Viral discovery and diversity in trypanosomatid protozoa with a focus on relatives of the human parasite <i>Leishmania</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E506-E515.	3.3	75
3090	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. <i>ISME Journal</i> , 2018, 12, 173-184.	4.4	132
3091	Respiratory disease associated with migrating <i>Ascaris</i> larvae in a beef calf. <i>Veterinary Parasitology: Regional Studies and Reports</i> , 2018, 12, 9-12.	0.3	1
3092	Enrichment of <i>Cryptosporidium parvum</i> from in vitro culture as measured by total RNA and subsequent sequence analysis. <i>Molecular and Biochemical Parasitology</i> , 2018, 220, 5-9.	0.5	3
3093	Identification, characterization and gene expression analyses of important flowering genes related to photoperiodic pathway in bamboo. <i>BMC Genomics</i> , 2018, 19, 190.	1.2	32
3094	The mRNA and miRNA transcriptomic landscape of <i>Panax ginseng</i> under the high ambient temperature. <i>BMC Systems Biology</i> , 2018, 12, 27.	3.0	10
3095	Uncovering the molecular mechanisms of lignocellulose digestion in shipworms. <i>Biotechnology for Biofuels</i> , 2018, 11, 59.	6.2	42
3096	Population-specific transcriptional differences associated with freeze tolerance in a terrestrial worm. <i>Ecology and Evolution</i> , 2018, 8, 3774-3786.	0.8	12
3097	Development of polymorphic <i>EST</i> <i>SSR</i> markers in <i>Itea chinensis</i> (Iteaceae) and cross-amplification in related species. <i>Applications in Plant Sciences</i> , 2018, 6, e1013.	0.8	9
3098	Microsatellite analysis and marker development in garlic: distribution in EST sequence, genetic diversity analysis, and marker transferability across Alliaceae. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1091-1106.	1.0	18
3099	Adhesive gland transcriptomics uncovers a diversity of genes involved in glue formation in marine tube-building polychaetes. <i>Acta Biomaterialia</i> , 2018, 72, 316-328.	4.1	21

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3100	Surgical necrotizing enterocolitis in extremely premature neonates is associated with genetic variations in an intergenic region of chromosome 8. <i>Pediatric Research</i> , 2018, 83, 943-953.	1.1	17
3101	Advances in kinome research of parasitic worms - implications for fundamental research and applied biotechnological outcomes. <i>Biotechnology Advances</i> , 2018, 36, 915-934.	6.0	8
3102	De novo assembly and characterizing of the culm-derived meta-transcriptome from the polyploid sugarcane genome based on coding transcripts. <i>Heliyon</i> , 2018, 4, e00583.	1.4	12
3103	Phylogenetic analysis of cnidarian peroxiredoxins and stress-responsive expression in the estuarine sea anemone <i>Nematostella vectensis</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2018, 221, 32-43.	0.8	8
3104	IDP-denovo: <i>de novo</i> transcriptome assembly and isoform annotation by hybrid sequencing. <i>Bioinformatics</i> , 2018, 34, 2168-2176.	1.8	41
3105	A resource provisioning framework for bioinformatics applications in multi-cloud environments. <i>Future Generation Computer Systems</i> , 2018, 78, 379-391.	4.9	23
3106	Characterization of <i>Tulbaghia violacea</i> (Tulbaghieae, Alliioideae, Amaryllidaceae) from India: a cytogenetic and molecular approach. <i>Nucleus (India)</i> , 2018, 61, 29-34.	0.9	2
3107	The transcriptome, extracellular proteome and active secretome of agroinfiltrated <i>Nicotiana benthamiana</i> uncover a large, diverse protease repertoire. <i>Plant Biotechnology Journal</i> , 2018, 16, 1068-1084.	4.1	54
3108	Temporal dynamics of uncultured viruses: a new dimension in viral diversity. <i>ISME Journal</i> , 2018, 12, 199-211.	4.4	44
3109	The roles of mucus-forming mucins, peritrophins and peritrophins with mucin domains in the insect midgut. <i>Insect Molecular Biology</i> , 2018, 27, 46-60.	1.0	48
3110	First detection of <i>Edwardsiella ictaluri</i> (Proteobacteria: Enterobacteriaceae) in wild Australian catfish. <i>Journal of Fish Diseases</i> , 2018, 41, 199-208.	0.9	8
3111	Transcriptome analysis using de novo RNA-seq to compare ginseng roots cultivated in different environments. <i>Plant Growth Regulation</i> , 2018, 84, 149-157.	1.8	6
3112	De novo transcriptome assembly of the calanoid copepod <i>Neocalanus flemingeri</i> : A new resource for emergence from diapause. <i>Marine Genomics</i> , 2018, 37, 114-119.	0.4	19
3113	Transcriptome-based discovery of pathways and genes related to reproduction of the black tiger shrimp (<i>Penaeus monodon</i>). <i>Marine Genomics</i> , 2018, 37, 69-73.	0.4	31
3114	Nanovirus-alpha satellite complex identified in <i>Vicia cracca</i> in the Rhône delta region of France. <i>Archives of Virology</i> , 2018, 163, 695-700.	0.9	25
3115	The intron landscape of the mtDNA <i>cytb</i> gene among the Ascomycota: introns and intron-encoded open reading frames. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1015-1024.	0.7	40
3116	Pleistocene climatic changes drive diversification across a tropical savanna. <i>Molecular Ecology</i> , 2018, 27, 520-532.	2.0	31
3117	Comparative transcriptome analysis of ATP-binding cassette (ABC) transporter genes in eri-silkworm, <i>Samia cynthia ricini</i> in response to 1-deoxynojirimycin. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 168-178.	0.4	2

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3118	Actin genes and their expression in pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 479-493.	1.0	12
3119	<i>De novo</i> assembly of the zucchini genome reveals a whole-genome duplication associated with the origin of the <i>Cucurbita</i> genus. <i>Plant Biotechnology Journal</i> , 2018, 16, 1161-1171.	4.1	160
3120	Contribution of nitric oxide synthase from coagulase-negative staphylococci to the development of red myoglobin derivatives. <i>International Journal of Food Microbiology</i> , 2018, 266, 310-316.	2.1	15
3121	Metagenomic investigation of bacterial diversity of hot spring soil from Manikaran, Himachal Pradesh, India. <i>Ecological Genetics and Genomics</i> , 2018, 6, 16-21.	0.3	7
3122	The main spoilage-related psychrotrophic bacteria in refrigerated raw milk. <i>Journal of Dairy Science</i> , 2018, 101, 75-83.	1.4	76
3123	Increase in taxonomic assignment efficiency of viral reads in metagenomic studies. <i>Virus Research</i> , 2018, 244, 230-234.	1.1	10
3124	Optimized Yellow Dwarf Virus Multiplex PCR Assay Reveals a Common Occurrence of Barley yellow dwarf virus-PAS in Kansas Winter Wheat. <i>Plant Health Progress</i> , 2018, 19, 37-43.	0.8	8
3125	Genome Sequences of <i>Vibrio maerlii</i> sp. nov. and <i>Vibrio rhodolitus</i> sp. nov., Isolated from Rhodoliths. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
3126	Peculiar features of the plastids of the colourless alga <i>Euglena longa</i> and photosynthetic euglenophytes unveiled by transcriptome analyses. <i>Scientific Reports</i> , 2018, 8, 17012.	1.6	35
3127	Multiple environmental stressors induce complex transcriptomic responses indicative of phenotypic outcomes in Western fence lizard. <i>BMC Genomics</i> , 2018, 19, 877.	1.2	8
3128	Anatomical and Chemical Responses of Eastern White Pine (<i>Pinus strobus</i> L.) to Blue-Stain (<i>Ophiostoma minus</i>) Inoculation. <i>Forests</i> , 2018, 9, 690.	0.9	8
3129	Evidence supporting cryptic species within two sessile microinvertebrates, <i>Limnias melicerta</i> and <i>L. ceratophylli</i> (Rotifera, Gnesiotrocha). <i>PLoS ONE</i> , 2018, 13, e0205203.	1.1	12
3130	Proteolytic and lipolytic potential of <i>Pseudomonas</i> spp. from goat and bovine raw milk. <i>Pesquisa Veterinaria Brasileira</i> , 2018, 38, 1577-1583.	0.5	6
3131	Identification of salt-induced transcripts by suppression subtractive hybridization and their expression analysis under the combination of salt and elevated CO ₂ conditions in <i>Salicornia brachiata</i> . <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	1
3132	MALDI-TOF MS Affords Discrimination of <i>Deinococcus aquaticus</i> Isolates Obtained From Diverse Biofilm Habitats. <i>Frontiers in Microbiology</i> , 2018, 9, 2442.	1.5	7
3133	CmZNF384-like gene in hypoxia-tolerant Indian catfish, <i>Clarias magur</i> (Hamilton 1822) in hypometabolic states associated with acute hypoxia and summer aestivation. <i>Agri Gene</i> , 2018, 10, 1-11.	1.9	4
3134	Growth factor gene IGF1 is associated with bill size in the black-bellied seedcracker <i>Pyrenestes ostrinus</i> . <i>Nature Communications</i> , 2018, 9, 4855.	5.8	24
3135	TransFlow: a modular framework for assembling and assessing accurate de novo transcriptomes in non-model organisms. <i>BMC Bioinformatics</i> , 2018, 19, 416.	1.2	16

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3136	The non-random patterns of genetic variation induced by asymmetric somatic hybridization in wheat. <i>BMC Plant Biology</i> , 2018, 18, 244.	1.6	5
3137	De novo assembly of wheat root transcriptomes and transcriptional signature of longitudinal differentiation. <i>PLoS ONE</i> , 2018, 13, e0205582.	1.1	5
3138	Rapid Expansion of a Highly Germline-Expressed <i>Mariner</i> Element Acquired by Horizontal Transfer in the Fire Ant Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 3262-3278.	1.1	6
3139	A multigene typing system for human adenoviruses reveals a new genotype in a collection of Swedish clinical isolates. <i>PLoS ONE</i> , 2018, 13, e0209038.	1.1	13
3140	Variation in proviral content among human genomes mediated by LTR recombination. <i>Mobile DNA</i> , 2018, 9, 36.	1.3	71
3141	Parallel MapReduce: Maximizing Cloud Resource Utilization and Performance Improvement Using Parallel Execution Strategies. <i>BioMed Research International</i> , 2018, 2018, 1-17.	0.9	2
3142	Comparative transcriptome analyses of oleaginous <i>Botryococcus braunii</i> race A reveal significant differences in gene expression upon cobalt enrichment. <i>Biotechnology for Biofuels</i> , 2018, 11, 333.	6.2	12
3143	Nanopore-based detection and characterization of yam viruses. <i>Scientific Reports</i> , 2018, 8, 17879.	1.6	57
3144	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. <i>Ecology and Evolution</i> , 2018, 8, 11273-11292.	0.8	9
3145	Analysis of Transcriptome and Alternative Splicing Landscape in Pineapple. <i>Plant Genetics and Genomics: Crops and Models</i> , 2018, , 195-213.	0.3	2
3146	De Novo Transcriptome Assembly of Cucurbita Pepo L. Leaf Tissue Infested by Aphis Gossypii. <i>Data</i> , 2018, 3, 36.	1.2	8
3147	Functional Analysis of Four Terpene Synthases in Rose-Scented Pelargonium Cultivars (<i>Pelargonium</i> sp.) <i>Tj ETQq1 1 0.784314 rgBT /Ove</i>	1.7	16
3148	Surveying the genome and constructing a high-density genetic map of napiergrass (<i>Cenchrus</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262</i>	1.6	32
3149	Development and application of SSR markers derived from <i>Bauhinia Strychnifolia</i> a semi-endemic plant in Thailand. <i>Journal of Herbs, Spices and Medicinal Plants</i> , 2018, 24, 386-393.	0.5	4
3150	First genetic linkage map of <i>Lathyrus cicera</i> based on RNA sequencing-derived markers: Key tool for genetic mapping of disease resistance. <i>Horticulture Research</i> , 2018, 5, 45.	2.9	19
3151	A phylogenetic approach to the Philippines endemic centipedes of the genus <i>Scolopendra</i> Linnaeus, 1758 (<i>Scolopendromorpha</i> , <i>Scolopendridae</i>), with the description of a new species. <i>Zootaxa</i> , 2018, 4483, 401.	0.2	0
3152	Gene floR e a resistÃancia ao florfenicol em isolados de <i>Aeromonas</i> spp. autÃctones de organismos aquÃticos. <i>Pesquisa Veterinaria Brasileira</i> , 2018, 38, 357-366.	0.5	0
3153	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	1.2	21

#	ARTICLE	IF	CITATIONS
3154	Tandem repeat sequences expressed in the hemocytes of <i>Litopenaeus vannamei</i> Boone, 1931 (Decapoda: Tj ETQq0,0 rgBT ₀ Overlock		
3155	SSR-Seq: Genotyping of microsatellites using next-generation sequencing reveals higher level of polymorphism as compared to traditional fragment size scoring. <i>Ecology and Evolution</i> , 2018, 8, 10817-10833.	0.8	48
3156	Genome sequencing of <i>Prototheca zopfii</i> genotypes 1 and 2 provides evidence of a severe reduction in organellar genomes. <i>Scientific Reports</i> , 2018, 8, 14637.	1.6	34
3157	Characterization and phylogenetic analysis of the mitochondrial genome of <i>Schizothorax taliensis</i> , a national-protected fish in China. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 650-651.	0.2	3
3158	Genetic diversity in <i>Radix</i> species from the middle and south of Iraq based on simple sequence repeats. <i>African Journal of Biotechnology</i> , 2018, 17, 1119-1128.	0.3	1
3159	The Genetic Basis of Adaptation following Plastic Changes in Coloration in a Novel Environment. <i>Current Biology</i> , 2018, 28, 2970-2977.e7.	1.8	83
3160	Molecular and in silico cloning, identification, and preharvest period expression analysis of a putative cytochrome P450 monooxygenase gene from <i>Camellia sinensis</i> (L.) Kuntze (tea). <i>Turkish Journal of Biology</i> , 2018, 42, 1-11.	2.1	4
3161	Genome Evolution of Bartonellaceae Symbionts of Ants at the Opposite Ends of the Trophic Scale. <i>Genome Biology and Evolution</i> , 2018, 10, 1687-1704.	1.1	26
3162	New insights into <i>Phakopsora pachyrhizi</i> infection based on transcriptome analysis in planta. <i>Genetics and Molecular Biology</i> , 2018, 41, 671-691.	0.6	4
3163	Assessing Field <i>Prunus</i> Genotypes for Drought Responsive Potential by Carbon Isotope Discrimination and Promoter Analysis. <i>Agronomy</i> , 2018, 8, 42.	1.3	4
3164	Genome Wide Identification of Mutational Hotspots in the Apicomplexan Parasite <i>Neospora caninum</i> and the Implications for Virulence. <i>Genome Biology and Evolution</i> , 2018, 10, 2417-2431.	1.1	17
3165	<i>Drosophila</i> parasitoid wasps bears a distinct DNA transposon profile. <i>Mobile DNA</i> , 2018, 9, 23.	1.3	7
3166	Draft genome of <i>Dugesia japonica</i> provides insights into conserved regulatory elements of the brain restriction gene <i>nou-darake</i> in planarians. <i>Zoological Letters</i> , 2018, 4, 24.	0.7	38
3167	Ensamblado de fragmentos de ADN utilizando un novedoso algoritmo de <i>luci</i> en GPU. <i>DYNA (Colombia)</i> , 2018, 85, 108-116.	0.2	3
3168	Genetic diversity of thermophilic spoilage microorganisms of milk from Brazilian dairy farms. <i>Journal of Dairy Science</i> , 2018, 101, 6927-6936.	1.4	22
3169	Viral Metagenomic-Based Screening of Sugarcane from Florida Reveals Occurrence of Six Sugarcane-Infecting Viruses and High Prevalence of <i>Sugarcane yellow leaf virus</i> . <i>Plant Disease</i> , 2018, 102, 2317-2323.	0.7	20
3170	Analysis of genetic diversity in CYTB and control region sequences of <i>Melanochelys trijuga</i> (Schweigger, 1812) from Karnataka. <i>Journal of Asia-Pacific Biodiversity</i> , 2018, 11, 346-352.	0.2	2
3171	Heat stress transcripts, differential expression, and profiling of heat stress tolerant gene <i>TaHsp90</i> in Indian wheat (<i>Triticum aestivum</i> L.) cv C306. <i>PLoS ONE</i> , 2018, 13, e0198293.	1.1	31

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3172	The Little-known Freshwater Metopid Ciliate, <i>Idiometopus turbo</i> (Dragesco and Dragesco-KernÃ©is), Tj ETQq0 0 0 rgBT /Overlock 10 Tf Protist, 2018, 169, 494-506.	0.6	15
3173	Sialome diversity of ticks revealed by RNAseq of single tick salivary glands. PLoS Neglected Tropical Diseases, 2018, 12, e0006410.	1.3	79
3174	Characterization and development of EST-SSR markers to study the genetic diversity and populations analysis of Jerusalem artichoke (<i>Helianthus tuberosus</i> L.). Genes and Genomics, 2018, 40, 1023-1032.	0.5	14
3175	Draft Genome Sequence of the Novel Enterobacter cloacae Strain amazonensis, a Highly Heavy Metal-Resistant Bacterium from a Contaminated Stream in Amazonas, Brazil. Genome Announcements, 2018, 6, .	0.8	2
3176	Draft Genome Sequence of a White Spot Syndrome Virus Isolate Obtained in Ecuador. Genome Announcements, 2018, 6, .	0.8	16
3177	Identification of MicroRNAs and Their Target Genes Associated with Ovarian Development in Black Tiger Shrimp (<i>Penaeus monodon</i>) Using High-Throughput Sequencing. Scientific Reports, 2018, 8, 11602.	1.6	11
3178	New genomic data and analyses challenge the traditional vision of animal epithelium evolution. BMC Genomics, 2018, 19, 393.	1.2	50
3179	Red Clover (<i>Trifolium pratense</i>) and Zigzag Clover (<i>T. medium</i>) â€œ A Picture of Genomic Similarities and Differences. Frontiers in Plant Science, 2018, 9, 724.	1.7	18
3180	Molecular Characterization and Expression Analysis of GhWRI1 in Upland Cotton. Journal of Plant Biology, 2018, 61, 186-197.	0.9	6
3181	Transcriptomics investigation of thyroid hormone disruption in the olfactory system of the Rana [Lithobates] catesbeiana tadpole. Aquatic Toxicology, 2018, 202, 46-56.	1.9	17
3182	A Novel Eukaryotic Denitrification Pathway in Foraminifera. Current Biology, 2018, 28, 2536-2543.e5.	1.8	75
3183	De novo genome and transcriptome resources of the Adzuki bean borer <i>Ostrinia scapularis</i> (Lepidoptera: Crambidae). Data in Brief, 2018, 17, 781-787.	0.5	7
3184	Genomic Attributes of Novel Symbiont <i>Pseudovibrio brasiliensis</i> sp. nov. Isolated From the Sponge <i>Arenosclera brasiliensis</i> . Frontiers in Marine Science, 2018, 5, .	1.2	10
3185	Identifying Group-Specific Sequences for Microbial Communities Using Long k-mer Sequence Signatures. Frontiers in Microbiology, 2018, 9, 872.	1.5	17
3186	Transcriptomic Analysis Reveals Reduced Inorganic Sulfur Compound Oxidation Mechanism in <i>Acidithiobacillus ferroplhilus</i> . Microbiology, 2018, 87, 486-501.	0.5	4
3187	Transcriptome Assembly of the Bast Fiber Crop, Ramie, <i>Boehmeria nivea</i> (L.) Gaud. (Urticaceae). Fibers, 2018, 6, 8.	1.8	3
3188	Transcriptome-Wide Analysis Reveals the Origin of Peloria in Chinese Cymbidium (<i>Cymbidium sinense</i>). Plant and Cell Physiology, 2018, 59, 2064-2074.	1.5	14
3189	Molecular mechanisms of fission in echinoderms: Transcriptome analysis. PLoS ONE, 2018, 13, e0195836.	1.1	28

#	ARTICLE	IF	CITATIONS
3190	Computational Studies of Snake Venom Toxins. <i>Toxins</i> , 2018, 10, 8.	1.5	22
3191	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	13.5	420
3192	GinMicrosatDb: a genome-wide microsatellite markers database for sesame (<i>Sesamum indicum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 929-937.	1.4	6
3193	Exon-Capture-Based Phylogeny and Diversification of the Venomous Gastropods (Neogastropoda), Tj ETQq1 1 0.784314 rgBT /Overlook	3.5	46
3194	PCR-RFLP assay as an option for primary HPV test. <i>Brazilian Journal of Medical and Biological Research</i> , 2018, 51, e7098.	0.7	7
3195	Genomic analysis of MHC-based mate choice in the monogamous California mouse. <i>Behavioral Ecology</i> , 2018, 29, 1167-1180.	1.0	9
3196	Identification of novel microsatellite markers in okra (<i>Abelmoschus esculentus</i> (L.) Moench) through next-generation sequencing and their utilization in analysis of genetic relatedness studies and cross-species transferability. <i>Journal of Genetics</i> , 2018, 97, 39-47.	0.4	13
3197	Complete genome sequence of bacteriophage Deep-Purple, a novel member of the family Siphoviridae infecting <i>Bacillus cereus</i> . <i>Archives of Virology</i> , 2018, 163, 2555-2559.	0.9	6
3198	The aquatic animalsâ€™ transcriptome resource for comparative functional analysis. <i>BMC Genomics</i> , 2018, 19, 103.	1.2	5
3199	Phylogenomics of a rapid radiation: the Australian rainbow skinks. <i>BMC Evolutionary Biology</i> , 2018, 18, 15.	3.2	26
3200	Sequencing Plant Genomes. <i>Progress in Botany Fortschritte Der Botanik</i> , 2018, , 109-193.	0.1	4
3201	Generation of a novel next-generation sequencing-based method for the isolation of new human papillomavirus types. <i>Virology</i> , 2018, 520, 1-10.	1.1	25
3202	Improved strategy for the curation and classification of kinases, with broad applicability to other eukaryotic protein groups. <i>Scientific Reports</i> , 2018, 8, 6808.	1.6	10
3203	Optimization and characterization of extracellular cellulase produced by <i>Bacillus pumilus</i> MGB05 isolated from midgut of muga silkworm (<i>Antheraea assamensis</i> Helfer). <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 1171-1181.	0.4	13
3204	Mitochondrial genomics challenges the theory of clonality in <i>Trypanosoma congolense</i> : Reply to Tibayrenc and Ayala. <i>Molecular Ecology</i> , 2018, 27, 3425-3431.	2.0	14
3205	Characterization of leaf transcriptome, development and utilization of unigenes-derived microsatellite markers in sugarcane (<i>Saccharum sp. hybrid</i>). <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 665-682.	1.4	2
3206	Discovery of <i>Culex pipiens</i> associated tunisia virus: a new ssRNA(+) virus representing a new insect associated virus family. <i>Virus Evolution</i> , 2018, 4, vex040.	2.2	17
3207	RNA-Seq reveals large quantitative differences between the transcriptomes of outbreak and non-outbreak locusts. <i>Scientific Reports</i> , 2018, 8, 9207.	1.6	10

#	ARTICLE	IF	CITATIONS
3208	Identification of drought-inducible regulatory factors in <i>Lablab purpureus</i> by a comparative genomic approach. <i>Crop and Pasture Science</i> , 2018, 69, 632.	0.7	7
3209	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. <i>Science</i> , 2018, 360, 1355-1358.	6.0	234
3210	The <i>Plasmodium falciparum</i> transcriptome in severe malaria reveals altered expression of genes involved in important processes including surface antigen-encoding var genes. <i>PLoS Biology</i> , 2018, 16, e2004328.	2.6	67
3211	Recent polyploidization events in three <i>Saccharum</i> founding species. <i>Plant Biotechnology Journal</i> , 2019, 17, 264-274.	4.1	40
3212	Semi-aquatic spider silks: transcripts, proteins, and silk fibres of the fishing spider, <i>Dolomedes triton</i> (Pisauridae). <i>Insect Molecular Biology</i> , 2019, 28, 35-51.	1.0	9
3213	<i>Genome Informatics</i> , 2019, , 178-194.		0
3214	Selection of Protein-Rich <i>Saccharomyces cerevisiae</i> from Sugarcane Mills in Thailand for Feed and Food Applications. <i>Sugar Tech</i> , 2019, 21, 348-354.	0.9	4
3215	Shuffled Linear Regression with Erroneous Observations. , 2019, , .		11
3216	A homolog of the ALOG family controls corolla tube differentiation in <i>Torenia fournieri</i> . <i>Development (Cambridge)</i> , 2019, 146, .	1.2	7
3217	Field distribution and disease incidence of tomato chlorotic spot virus, an emerging virus threatening tomato production in South Florida. <i>Tropical Plant Pathology</i> , 2019, 44, 430-437.	0.8	5
3218	The complete plastid genome of the brown alga <i>Scytosiphon lomentaria</i> (scytosiphonaceae.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.2	1
3219	New record of <i>Trichodina unionis</i> (Ciliophora, Trichodinidae) from freshwater gastropods in Bangkok, Thailand. <i>Parasite</i> , 2019, 26, 47.	0.8	4
3220	Leishmania DNA detection and species characterization within phlebotomines (Diptera: Psychodidae) from a peridomicile-forest gradient in an Amazonian/Guianan bordering area. <i>PLoS ONE</i> , 2019, 14, e0219626.	1.1	7
3221	Comparative transcriptome analysis of translucent flesh disorder in mangosteen (<i>Garcinia</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	1.1	12
3222	De novo sequencing of tree peony (<i>Paeonia suffruticosa</i>) transcriptome to identify critical genes involved in flowering and floral organ development. <i>BMC Genomics</i> , 2019, 20, 572.	1.2	23
3223	Diverse and variable virus communities in wild plant populations revealed by metagenomic tools. <i>PeerJ</i> , 2019, 7, e6140.	0.9	53
3224	A viral genome wide association study and genotypic resistance testing in patients failing first line antiretroviral therapy in the first large countrywide Ethiopian HIV cohort. <i>BMC Infectious Diseases</i> , 2019, 19, 569.	1.3	6
3225	Phosphorus Mobilizing Enzymes of <i>Alnus</i> -Associated Ectomycorrhizal Fungi in an Alaskan Boreal Floodplain. <i>Forests</i> , 2019, 10, 554.	0.9	19

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3226	Eye Degeneration and Loss of <i>otx5b</i> Expression in the Cavefish <i>Sinocyclocheilus tileihornes</i> . <i>Journal of Molecular Evolution</i> , 2019, 87, 199-208.	0.8	10
3227	Tissue specific alpha-2-Macroglobulin (A2M) splice isoform diversity in Hilsa shad, <i>Tenualosa ilisha</i> (Hamilton, 1822). <i>PLoS ONE</i> , 2019, 14, e0216144.	1.1	6
3228	Pheromone gland transcriptome of the pink bollworm moth, <i>Pectinophora gossypiella</i> : Comparison between a laboratory and field population. <i>PLoS ONE</i> , 2019, 14, e0220187.	1.1	8
3229	Extreme Diversity of Mycoviruses Present in Isolates of <i>Rhizoctonia solani</i> AG2-2 LP From <i>Zoysia japonica</i> From Brazil. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 244.	1.8	78
3230	Whole-genome comparison between reference sequences and oyster <i>Vibrio vulnificus</i> C-genotype strains. <i>PLoS ONE</i> , 2019, 14, e0220385.	1.1	5
3231	AporÃ© virus, a novel mammarenavirus (Bunyvirales: Arenaviridae) related to highly pathogenic virus from South America. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180586.	0.8	7
3232	Isolation of Highly Pathogenic H5N1 Influenza Viruses in 2009â€“2013 in Vietnam. <i>Frontiers in Microbiology</i> , 2019, 10, 1411.	1.5	5
3233	Identification and functional characterization of the <i>Marshallia</i> (Asteraceae) Clade III Cytokinin Response Factor (CRF). <i>Plant Signaling and Behavior</i> , 2019, 14, e1633886.	1.2	5
3234	Improved detection of influenza A virus from blue-winged teals by sequencing directly from swab material. <i>Ecology and Evolution</i> , 2019, 9, 6534-6546.	0.8	18
3235	Algicidal potential of cultivable bacteria from pelagic waters against the toxic dinoflagellate <i>Pyrodinium bahamense</i> (Dinophyceae). <i>Journal of Applied Phycology</i> , 2019, 31, 3721-3735.	1.5	9
3236	Short communication: Effect of bactofugation of raw milk on counts and microbial diversity of psychrotrophs. <i>Journal of Dairy Science</i> , 2019, 102, 7794-7799.	1.4	9
3237	Complete mitochondrial genomes from transcriptomes: assessing pros and cons of data mining for assembling new mitogenomes. <i>Scientific Reports</i> , 2019, 9, 14806.	1.6	14
3238	Antagonistic and plant-growth promoting novel <i>Bacillus</i> species from long-term organic farming soils from Sikkim, India. <i>3 Biotech</i> , 2019, 9, 416.	1.1	30
3239	Gene Expression Profiling Reveals Enhanced Defense Responses in an Invasive Weed Compared to Its Native Congener during Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4916.	1.8	5
3240	New different origins and evolutionary processes of AP2/EREBP transcription factors in <i>Taxus chinensis</i> . <i>BMC Plant Biology</i> , 2019, 19, 413.	1.6	11
3241	Host and geography together drive early adaptive radiation of Hawaiian planthoppers. <i>Molecular Ecology</i> , 2019, 28, 4513-4528.	2.0	6
3242	Development of high-resolution DNA barcodes for <i>Dioscorea</i> species discrimination and phylogenetic analysis. <i>Ecology and Evolution</i> , 2019, 9, 10843-10853.	0.8	15
3243	Transcriptome Profiling of the Salt-Stress Response in the Halophytic Green Alga <i>Dunaliella salina</i> . <i>Plant Molecular Biology Reporter</i> , 2019, 37, 421-435.	1.0	13

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3244	In-silico prediction of novel genes responsive to drought and salinity stress tolerance in bread wheat (<i>Triticum aestivum</i>). PLoS ONE, 2019, 14, e0223962.	1.1	7
3245	Assembly and annotation of the mitochondrial minicircle genome of a differentiation-competent strain of <i>Trypanosoma brucei</i> . Nucleic Acids Research, 2019, 47, 11304-11325.	6.5	42
3246	Generation of a Comprehensive Transcriptome Atlas and Transcriptome Dynamics in Medicinal Cannabis. Scientific Reports, 2019, 9, 16583.	1.6	45
3247	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	13.5	268
3248	Exploring Plasmodium falciparum Var Gene Expression to Assess Host Selection Pressure on Parasites During Infancy. Frontiers in Immunology, 2019, 10, 2328.	2.2	4
3249	Venom Diversity and Evolution in the Most Divergent Cone Snail Genus <i>Profundiconus</i> . Toxins, 2019, 11, 623.	1.5	16
3250	Development and characterization of white spot disease linked microsatellite DNA markers in <i>Penaeus monodon</i> , and their application to determine the population diversity, cluster and structure. Journal of Invertebrate Pathology, 2019, 168, 107275.	1.5	5
3251	Copper oxide nanoparticles as an effective anti-biofilm agent against a copper tolerant marine bacterium, <i>Staphylococcus lentus</i> . Biofouling, 2019, 35, 1007-1025.	0.8	18
3252	Molecular characterization and In Vitro synthesis of infectious RNA of a Turnip vein-clearing virus isolated from <i>Alliaria petiolata</i> in Hungary. PLoS ONE, 2019, 14, e0224398.	1.1	2
3253	Complete mitochondrial genome of the sea star <i>Archaster typicus</i> (Asteroidea: Archasteridae). Mitochondrial DNA Part B: Resources, 2019, 4, 3130-3132.	0.2	8
3254	Stacks 2: Analytical methods for paired-end sequencing improve RADseq-based population genomics. Molecular Ecology, 2019, 28, 4737-4754.	2.0	648
3255	First Report of <i>Erysiphe fallax</i> Causing Powdery Mildew on Phasey Bean (<i>Macroptilium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.8	2
3256	Transcript profiling of chickpea pod wall revealed the expression of floral homeotic gene AGAMOUS-like X2 (CaAGLX2). Molecular Biology Reports, 2019, 46, 5713-5722.	1.0	1
3257	De Novo Transcriptome Assembly of <i>Eucalyptus nitens</i> and the Expression of R2R3-MYB Genes in Response to Cold Acclimation in <i>Eucalyptus</i> Spp.. Plant Molecular Biology Reporter, 2019, 37, 376-388.	1.0	3
3258	Phylogenetic analysis revealed the co-circulation of four dengue virus serotypes in Southern Thailand. PLoS ONE, 2019, 14, e0221179.	1.1	31
3259	Identification of spontaneous mutation for broad-spectrum brown planthopper resistance in a large, long-term fast neutron mutagenized rice population. Rice, 2019, 12, 16.	1.7	20
3260	The alternative reality of plant mitochondrial DNA: One ring does not rule them all. PLoS Genetics, 2019, 15, e1008373.	1.5	184
3261	Development and Application of EST-SSR Markers for DNA Fingerprinting and Genetic Diversity Analysis of the Main Cultivars of Black Locust (<i>Robinia pseudoacacia</i> L.) in China. Forests, 2019, 10, 644.	0.9	8

#	ARTICLE	IF	CITATIONS
3262	Current status in whole genome sequencing and analysis of <i>Ipomoea</i> spp.. <i>Plant Cell Reports</i> , 2019, 38, 1365-1371.	2.8	16
3263	A transcriptome-based phylogenetic study of hard ticks (Ixodidae). <i>Scientific Reports</i> , 2019, 9, 12923.	1.6	30
3264	Genetic diversity among asparagus species and cultivars using SSR markers. <i>Journal of Biodiversity Conservation and Bioresource Management</i> , 2019, 4, 21-32.	0.3	5
3265	The expression of alfalfa MsPP2CA1 gene confers ABA sensitivity and abiotic stress tolerance on <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2019, 143, 176-182.	2.8	6
3266	Variability of P26 and P10 genes in Colombian isolates of Potato yellow vein virus (PYV). <i>Agronomia Colombiana</i> , 2019, 37, 129-143.	0.1	0
3267	Pedigree-based estimation of human mobile element retrotransposition rates. <i>Genome Research</i> , 2019, 29, 1567-1577.	2.4	75
3268	RNAseq analysis reveals drought-responsive molecular pathways with candidate genes and putative molecular markers in root tissue of wheat. <i>Scientific Reports</i> , 2019, 9, 13917.	1.6	60
3269	Using de novo transcriptome assembly and analysis to study RNAi in <i>Phenacoccus solenopsis</i> Tinsley (Hemiptera: Pseudococcidae). <i>Scientific Reports</i> , 2019, 9, 13710.	1.6	17
3270	Evolution of Young Sex Chromosomes in Two Dioecious Sister Plant Species with Distinct Sex Determination Systems. <i>Genome Biology and Evolution</i> , 2019, 11, 350-361.	1.1	40
3271	A selective genome-guided method for environmental Burkholderia isolation. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 345-362.	1.4	7
3272	Dataset from de novo transcriptome assembly of <i>Nephelium lappaceum</i> aril. <i>Data in Brief</i> , 2019, 22, 566-569.	0.5	4
3273	Genomic resources for the Neotropical tree genus <i>Cedrela</i> (Meliaceae) and its relatives. <i>BMC Genomics</i> , 2019, 20, 58.	1.2	15
3274	EST (Expressed Sequence Tag): A Technique for Identification of Plant Secondary Metabolite Genes. , 2019, , 207-225.		1
3275	Molecular mechanisms underpinning transgenerational plasticity in the green sea urchin <i>Psammechinus miliaris</i> . <i>Scientific Reports</i> , 2019, 9, 952.	1.6	25
3276	The Tritryps Comparative Repeatome: Insights on Repetitive Element Evolution in Trypanosomatid Pathogens. <i>Genome Biology and Evolution</i> , 2019, 11, 546-551.	1.1	24
3277	Comparison of fertile and sterile male gametogenesis in <i>Cryptomeria japonica</i> D. Don. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	7
3278	Early Sex-Chromosome Evolution in the Diploid Dioecious Plant <i>Mercurialis annua</i> . <i>Genetics</i> , 2019, 212, 815-835.	1.2	53
3279	MULKSG: MULTiple K Simultaneous Graph Assembly. <i>Lecture Notes in Computer Science</i> , 2019, , 125-136.	1.0	1

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3280	Legacy effects of tree mortality mediated by ectomycorrhizal fungal communities. <i>New Phytologist</i> , 2019, 224, 155-165.	3.5	21
3281	Cicada Endosymbionts Have tRNAs That Are Correctly Processed Despite Having Genomes That Do Not Encode All of the tRNA Processing Machinery. <i>MBio</i> , 2019, 10, .	1.8	8
3282	Genome-Wide Identification and Expression Profiles of Myosin Genes in the Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>Frontiers in Physiology</i> , 2019, 10, 610.	1.3	9
3283	Expanding Alternative Splicing Identification by Integrating Multiple Sources of Transcription Data in Tomato. <i>Frontiers in Plant Science</i> , 2019, 10, 689.	1.7	26
3284	<i>Neospora caninum</i> DNA in feces of crab-eating fox (<i>Cerdocyon thous</i> â€“ Linnaeus, 1776) from northeastern Brazil. <i>Acta Tropica</i> , 2019, 197, 105068.	0.9	7
3285	Transcriptome sequence resource for the cucurbit powdery mildew pathogen <i>Podosphaera xanthii</i> . <i>Scientific Data</i> , 2019, 6, 95.	2.4	10
3286	Population Genomic Signatures of Genetic Structure and Environmental Selection in the Catadromous Roughskin Sculpin <i>Trachidermus fasciatus</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1751-1764.	1.1	18
3287	Peyssonosides Aâ€“B, Unusual Diterpene Glycosides with a Sterically Encumbered Cyclopropane Motif: Structure Elucidation Using an Integrated Spectroscopic and Computational Workflow. <i>Journal of Organic Chemistry</i> , 2019, 84, 8531-8541.	1.7	26
3288	Historical contingency shapes adaptive radiation in Antarctic fishes. <i>Nature Ecology and Evolution</i> , 2019, 3, 1102-1109.	3.4	50
3289	Evidence for long-term prevalence of cucumber vein yellowing virus in Sudan and genetic variation of the virus in Sudan and the Mediterranean Basin. <i>Plant Pathology</i> , 2019, 68, 1268-1275.	1.2	15
3290	Taurine metabolism and effects of inclusion levels in rotifer (<i>Brachionus rotundiformis</i>), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 Td (Ts 353-363.	1.7	4
3291	A new bunya-like virus associated with mass mortality of white-clawed crayfish in the wild. <i>Virology</i> , 2019, 533, 115-124.	1.1	9
3292	Rapid molecular evolution of pain insensitivity in multiple African rodents. <i>Science</i> , 2019, 364, 852-859.	6.0	57
3293	Recombinant production and characterization of a novel esterase from a hypersaline lake, AcÃ±gÃ±l, by metagenomic approach. <i>Extremophiles</i> , 2019, 23, 507-520.	0.9	13
3294	Characterization of Flagellotropic, Chi-Like Salmonella Phages Isolated from Thai Poultry Farms. <i>Viruses</i> , 2019, 11, 520.	1.5	28
3295	The mobilome of <i>Drosophila incompta</i> , a flower-breeding species: comparison of transposable element landscapes among generalist and specialist flies. <i>Chromosome Research</i> , 2019, 27, 203-219.	1.0	9
3296	Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. <i>PLoS Genetics</i> , 2019, 15, e1008119.	1.5	70
3297	Redondoviridae, a Family of Small, Circular DNA Viruses of the Human Oro-Respiratory Tract Associated with Periodontitis and Critical Illness. <i>Cell Host and Microbe</i> , 2019, 25, 719-729.e4.	5.1	83

#	ARTICLE	IF	CITATIONS
3298	How dynamic could be the 45S rDNA cistron? An intriguing variability in a grasshopper species revealed by integration of chromosomal and genomic data. <i>Chromosoma</i> , 2019, 128, 165-175.	1.0	14
3299	Integrated transcriptome analysis of immunological responses in the pearl sac of the triangle sail mussel (<i>Hyriopsis cumingii</i>) after mantle implantation. <i>Fish and Shellfish Immunology</i> , 2019, 90, 385-394.	1.6	19
3300	Pervasive hybridizations in the history of wheat relatives. <i>Science Advances</i> , 2019, 5, eaav9188.	4.7	79
3301	Biocatalyst Potential of Cellulose-Degrading Microorganisms Isolated from Orange Juice Processing Waste. <i>Beverages</i> , 2019, 5, 21.	1.3	6
3302	Comparative effectiveness of bioassay methods in identifying the most virulent entomopathogenic fungal strains to control <i>Bemisia tabaci</i> (Gennadius) (Hemiptera: Aleyrodidae). <i>Egyptian Journal of Biological Pest Control</i> , 2019, 29, .	0.8	11
3303	Mitovirus and Mitochondrial Coding Sequences from Basal Fungus <i>Entomophthora muscae</i> . <i>Viruses</i> , 2019, 11, 351.	1.5	21
3304	Dauer signalling pathway model for <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2019, 12, 187.	1.0	25
3305	Phylogenetic relationship among Indian population of <i>Fusarium oxysporum</i> f. sp. <i>lentis</i> infecting lentil and development of specific SCAR markers for detection. <i>3 Biotech</i> , 2019, 9, 196.	1.1	2
3306	Transcriptome-wide identification of WRKY family genes and their expression under cold acclimation in <i>Eucalyptus globulus</i> . <i>Trees - Structure and Function</i> , 2019, 33, 1313-1327.	0.9	12
3307	Complete mitochondrial genome of <i>Cyprinus carpio</i> triploid. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1072-1073.	0.2	0
3308	A natural antisense transcript of the <i>fem-1</i> gene was found expressed in female gonads during the characterization, expression profile, and cellular localization of the <i>fem-1</i> gene in Pacific white shrimp <i>Penaeus vannamei</i> . <i>Gene</i> , 2019, 706, 19-31.	1.0	19
3309	Draft Genome Sequences of Four <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Gallinarum Strains Isolated from Layer Breeder Flocks in an Outbreak of Fowl Typhoid in Colombia. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
3310	Response of a novel selenium-dependent glutathione peroxidase from thick shell mussel <i>Mytilus coruscus</i> exposed to lipopolysaccharide, copper and benzo[\pm]pyrene. <i>Fish and Shellfish Immunology</i> , 2019, 89, 595-602.	1.6	9
3311	Transcriptome-wide analysis of differentially expressed chemokine receptors, SNPs, and SSRs in the age-related macular degeneration. <i>Human Genomics</i> , 2019, 13, 15.	1.4	26
3312	Massive Changes of Genome Size Driven by Expansions of Non-autonomous Transposable Elements. <i>Current Biology</i> , 2019, 29, 1161-1168.e6.	1.8	71
3313	A complete protocol for whole-genome sequencing of virus from clinical samples: Application to coronavirus OC43. <i>Virology</i> , 2019, 531, 141-148.	1.1	28
3314	Molecular detection of rabies virus strain with N-gene that clustered with China lineage 2 co-circulating with Africa lineages in Monrovia, Liberia: first reported case in Africa. <i>Epidemiology and Infection</i> , 2019, 147, e85.	1.0	11
3315	Algorithms and Fundamental Limits for Unlabeled Detection Using Types. <i>IEEE Transactions on Signal Processing</i> , 2019, 67, 2022-2035.	3.2	16

#	ARTICLE	IF	CITATIONS
3316	Perchlorate-Reducing Bacteria from Hypersaline Soils of the Colombian Caribbean. <i>International Journal of Microbiology</i> , 2019, 2019, 1-13.	0.9	10
3317	Compatibility of entomopathogenic fungi with insecticides and their efficacy for IPM of <i>Bemisia tabaci</i> in cotton. <i>Journal of Pesticide Sciences</i> , 2019, 44, 97-105.	0.8	31
3318	Analysis of Genetic Diversity and Population Structure in <i>Sophora japonica</i> Linn. in China With Newly Developed SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 87-97.	1.0	4
3319	Molecular characterization of a new botybirnavirus that infects <i>Botrytis cinerea</i> . <i>Archives of Virology</i> , 2019, 164, 1479-1483.	0.9	3
3320	Keeping it light: (re)analyzing community-wide datasets without major infrastructure. <i>GigaScience</i> , 2019, 8, .	3.3	2
3321	Lack of Signal for the Impact of Conotoxin Gene Diversity on Speciation Rates in Cone Snails. <i>Systematic Biology</i> , 2019, 68, 781-796.	2.7	16
3322	A novel invertebrate toll-like receptor is involved in TLR mediated signal pathway of thick shell mussel <i>Mytilus coruscus</i> . <i>Developmental and Comparative Immunology</i> , 2019, 97, 11-19.	1.0	18
3323	Antibacterial Oligomeric Polyphenols from the Green Alga <i>Cladophora socialis</i> . <i>Journal of Organic Chemistry</i> , 2019, 84, 5035-5045.	1.7	22
3324	Temperature-induced aerobic scope and Hsp70 expression in the sea cucumber <i>Holothuria scabra</i> . <i>PLoS ONE</i> , 2019, 14, e0214373.	1.1	11
3325	Diversity and Biotechnological Potential of Xylan-Degrading Microorganisms from Orange Juice Processing Waste. <i>Water (Switzerland)</i> , 2019, 11, 274.	1.2	11
3326	Development of microsatellite markers for a monotypic and globally endangered species, <i>Glyptostrobos pensilis</i> (Cupressaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e01217.	0.8	3
3327	Parallel pattern of differentiation at a genomic island shared between clinal and mosaic hybrid zones in a complex of cryptic seahorse lineages. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 817-835.	1.1	28
3328	Metagenomic Analysis Reveals Three Novel and Prevalent Mosquito Viruses from a Single Pool of <i>Aedes vexans nipponii</i> Collected in the Republic of Korea. <i>Viruses</i> , 2019, 11, 222.	1.5	26
3329	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	2.9	17
3330	Isolation of a Novel Beta-2 Human Papillomavirus from Skin. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
3331	Origin and recent expansion of an endogenous gammaretroviral lineage in domestic and wild canids. <i>Retrovirology</i> , 2019, 16, 6.	0.9	16
3332	Tetracycline Gene Transfer in <i>Staphylococcus xylosus</i> in situ During Sausage Fermentation. <i>Frontiers in Microbiology</i> , 2019, 10, 392.	1.5	21
3333	Molecular mechanism of inbreeding effects based on RNA-Seq analysis of the adductor muscle of bay scallop (<i>Argopecten irradians</i>). <i>Acta Oceanologica Sinica</i> , 2019, 38, 44-51.	0.4	2

#	ARTICLE	IF	CITATIONS
3334	The complete mitochondrial genome of <i>Xenocypris yunnanensis</i> (Nichols, 1925), threatened fishes of the world. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 428-429.	0.2	1
3335	Extensive conservation of the proneuropeptide and peptide prohormone complement in mollusks. <i>Scientific Reports</i> , 2019, 9, 4846.	1.6	23
3336	Data on solute carrier transporter genes of a threatened Himalayan fish species “ <i>Schizothorax richardsonii</i> . <i>Data in Brief</i> , 2019, 23, 103712.	0.5	3
3337	A novel invertebrate toll-like receptor with broad recognition spectrum from thick shell mussel <i>Mytilus coruscus</i> . <i>Fish and Shellfish Immunology</i> , 2019, 89, 132-140.	1.6	14
3338	Neofunctionalisation of basic helix~loop~helix proteins occurred when embryophytes colonised the land. <i>New Phytologist</i> , 2019, 223, 993-1008.	3.5	18
3339	Occurrence of tomato leaf curl Bangladesh virus and associated subviral DNA molecules in papaya in Bangladesh: molecular detection and characterization. <i>Archives of Virology</i> , 2019, 164, 1661-1665.	0.9	7
3340	<i>Halomonas coralii</i> sp. nov. Isolated from <i>Mussismilia braziliensis</i> . <i>Current Microbiology</i> , 2019, 76, 678-680.	1.0	2
3341	Transcriptome Analysis Identified Genes for Growth and Omega-3/-6 Ratio in Saline Tilapia. <i>Frontiers in Genetics</i> , 2019, 10, 244.	1.1	20
3342	Culture dependent and independent analysis and appraisal of early stage biofilm-forming bacterial community composition in the Southern coastal seawater of India. <i>Science of the Total Environment</i> , 2019, 666, 308-320.	3.9	33
3343	Complete genome sequence of maize sterile stunt virus. <i>Archives of Virology</i> , 2019, 164, 1221-1223.	0.9	4
3344	Identification of Eilat virus and prevalence of infection among <i>Culex pipiens</i> L. populations, Morocco, 2016. <i>Virology</i> , 2019, 530, 85-88.	1.1	7
3345	Reference assembly and gene expression analysis of <i>Apostichopus japonicus</i> larval development. <i>Scientific Reports</i> , 2019, 9, 1131.	1.6	13
3346	Characterization of <i>mecC</i> gene-carrying coagulase-negative <i>Staphylococcus</i> spp. isolated from various animals. <i>Veterinary Microbiology</i> , 2019, 230, 138-144.	0.8	38
3347	Re-emergence of a coxsackievirus A24 variant causing acute hemorrhagic conjunctivitis in Brazil from 2017 to 2018. <i>Archives of Virology</i> , 2019, 164, 1181-1185.	0.9	15
3348	The complete coding region of the maxicircle as a superior phylogenetic marker for exploring evolutionary relationships between members of the Leishmaniinae. <i>Infection, Genetics and Evolution</i> , 2019, 70, 90-100.	1.0	18
3349	The Two Prevalent Genotypes of an Emerging Infectious Disease, Deformed Wing Virus, Cause Equally Low Pupal Mortality and Equally High Wing Deformities in Host Honey Bees. <i>Viruses</i> , 2019, 11, 114.	1.5	65
3350	Isolation and characterization of hypoxia inducible gene connective tissue growth factor (CTGF) in <i>Labeo rohita</i> . <i>Molecular Biology Reports</i> , 2019, 46, 1683-1691.	1.0	2
3351	A novel approach using microsporidia to estimate the flight route of the common cutworm, <i>Spodoptera litura</i> (Lepidoptera: Noctuidae). <i>Applied Entomology and Zoology</i> , 2019, 54, 185-192.	0.6	2

#	ARTICLE	IF	CITATIONS
3352	G1P[8] Rotavirus in children with severe diarrhea in the post-vaccine introduction era in Brazil: Evidence of reassortments and structural modifications of the antigenic VP7 and VP4 regions. <i>Infection, Genetics and Evolution</i> , 2019, 69, 255-266.	1.0	12
3353	The genome of the soybean cyst nematode (<i>Heterodera glycines</i>) reveals complex patterns of duplications involved in the evolution of parasitism genes. <i>BMC Genomics</i> , 2019, 20, 119.	1.2	55
3354	Genome and pan-genome analysis to classify emerging bacteria. <i>Biology Direct</i> , 2019, 14, 5.	1.9	61
3355	Health Services Data: Big Data Analytics for Deriving Predictive Healthcare Insights. <i>Health Services Research</i> , 2019, , 3-18.	0.2	4
3356	Optimized DNA extraction and library preparation for minute arthropods: Application to target enrichment in chalcid wasps used for biocontrol. <i>Molecular Ecology Resources</i> , 2019, 19, 702-710.	2.2	48
3357	Specific Gene Disruption in the Major Livestock Pests <i>Cochliomyia hominivorax</i> and <i>Lucilia cuprina</i> Using CRISPR/Cas9. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3045-3055.	0.8	32
3358	Aquatic Hemiptera in Southwest Cameroon: Biodiversity of Potential Reservoirs of <i>Mycobacterium ulcerans</i> and Multiple <i>Wolbachia</i> Sequence Types Revealed by Metagenomics. <i>Diversity</i> , 2019, 11, 225.	0.7	2
3359	Isolation of biosurfactant producing bacteria from Potwar oil fields: Effect of non-fossil fuel based carbon sources. <i>Green Processing and Synthesis</i> , 2019, 9, 77-86.	1.3	16
3360	Draft Genome Sequences of Two Textile Azo Dye-Degrading <i>Shewanella</i> sp. Strains Isolated from a Textile Effluent in Peru. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
3361	Endangered but genetically stable " <i>Erythrophleum fordii</i> within <i>Feng Shui</i> woodlands in suburbanized villages. <i>Ecology and Evolution</i> , 2019, 9, 10950-10963.	0.8	4
3362	Secreted metabolite-mediated interactions between rhizosphere bacteria and <i>Trichoderma</i> biocontrol agents. <i>PLoS ONE</i> , 2019, 14, e0227228.	1.1	22
3363	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. <i>Frontiers in Genetics</i> , 2019, 10, 957.	1.1	8
3364	CRISPR elements provide a new framework for the genealogy of the citrus canker pathogen <i>Xanthomonas citri</i> pv. <i>citri</i> . <i>BMC Genomics</i> , 2019, 20, 917.	1.2	16
3365	Development of a Genomic Resource and Identification of Nucleotide Diversity of Yellow Perch by RAD Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 992.	1.1	2
3366	Microbial Composition and Variability of Natural Marine Planktonic and Biofouling Communities From the Bay of Bengal. <i>Frontiers in Microbiology</i> , 2019, 10, 2738.	1.5	18
3367	Nanopore Targeted Sequencing for Rapid Gene Mutations Detection in Acute Myeloid Leukemia. <i>Genes</i> , 2019, 10, 1026.	1.0	26
3368	Bidirectional transfer of Anelloviridae lineages between graft and host during lung transplantation. <i>American Journal of Transplantation</i> , 2019, 19, 1086-1097.	2.6	30
3369	A wheat GTP-binding protein like gene reduces tolerance to low temperature in <i>Arabidopsis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 148-153.	1.0	3

#	ARTICLE	IF	CITATIONS
3370	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648.	6.5	70
3371	The Harderian gland transcriptomes of <i>Caraiba andreae</i> , <i>Cubophis cantherigerus</i> and <i>Tretanorhinus variabilis</i> , three colubroid snakes from Cuba. <i>Genomics</i> , 2019, 111, 1720-1727.	1.3	10
3372	Influence of Recombination and GC-biased Gene Conversion on the Adaptive and Nonadaptive Substitution Rate in Mammals versus Birds. <i>Molecular Biology and Evolution</i> , 2019, 36, 458-471.	3.5	41
3373	Overcoming challenges in variant calling: exploring sequence diversity in candidate genes for plant development in perennial ryegrass (<i>Lolium perenne</i>). <i>DNA Research</i> , 2019, 26, 1-12.	1.5	14
3374	Wound healing mechanism in Mongolian gerbil skin. <i>Histochemistry and Cell Biology</i> , 2019, 151, 229-238.	0.8	7
3375	Development of New SSR (Simple Sequence Repeat) Markers for Lentils (<i>Lens culinaris</i> Medik.) from Genomic Library Enriched with AG and AC Microsatellites. <i>Biochemical Genetics</i> , 2019, 57, 338-353.	0.8	10
3376	Development of potential dbEST-derived microsatellite markers for genetic evaluation of sugarcane and related cereal grasses. <i>Industrial Crops and Products</i> , 2019, 128, 38-47.	2.5	17
3377	Population genomic footprints of environmental pollution pressure in natural populations of the Mediterranean mussel. <i>Marine Genomics</i> , 2019, 45, 11-15.	0.4	5
3378	Pre-exposure with influenza A virus A/WSN/1933(H1N1) resulted in viral shedding reduction from pigs challenged with either swine H1N1 or H3N2 virus. <i>Veterinary Microbiology</i> , 2019, 228, 26-31.	0.8	2
3379	CAARS: comparative assembly and annotation of RNA-Seq data. <i>Bioinformatics</i> , 2019, 35, 2199-2207.	1.8	2
3380	Association mapping of ectomycorrhizal traits in loblolly pine (<i>Pinus taeda</i> L.). <i>Molecular Ecology</i> , 2019, 28, 2088-2099.	2.0	6
3381	Dataset of the first de novo transcriptome assembly of the arillode of <i>Baccaurea motleyana</i> . <i>Data in Brief</i> , 2019, 22, 332-335.	0.5	4
3382	Comparative Transcriptomics Reveals Patterns of Adaptive Evolution Associated with Depth and Age Within Marine Rockfishes (<i>Sebastes</i>). <i>Journal of Heredity</i> , 2019, 110, 340-350.	1.0	12
3383	Application of MALDI Biotyper System for Rapid Identification of Bacteria Isolated from a Fresh Produce Market. <i>Current Microbiology</i> , 2019, 76, 290-296.	1.0	12
3384	Transcriptomic signature reveals mechanism of flower bud distortion in witches' broom disease of soybean (<i>Glycine max</i>). <i>BMC Plant Biology</i> , 2019, 19, 26.	1.6	15
3385	Comparative bioinformatic analysis suggests that specific dauer-like signalling pathway components regulate <i>Toxocara canis</i> development and migration in the mammalian host. <i>Parasites and Vectors</i> , 2019, 12, 32.	1.0	15
3386	Genome-wide identification and comparative analysis of alternative splicing across four legume species. <i>Planta</i> , 2019, 249, 1133-1142.	1.6	16
3387	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. <i>Nucleic Acids Research</i> , 2019, 47, D1137-D1145.	6.5	285

#	ARTICLE	IF	CITATIONS
3388	Revisiting avian "missing" genes from de novo assembled transcripts. BMC Genomics, 2019, 20, 4.	1.2	36
3389	Detection of Fowlpox virus carrying distinct genome segments of Reticuloendotheliosis virus. Virus Research, 2019, 260, 53-59.	1.1	26
3390	Intraspecific phylogeny of Anopheles (Kerteszia) neivai Howard, Dyar & Knab 1913, based on mitochondrial and nuclear ribosomal genes. Infection, Genetics and Evolution, 2019, 67, 183-190.	1.0	2
3391	Hybrid capture data unravel a rapid radiation of pimpliform parasitoid wasps (Hymenoptera: Tj ETQq1 1 0.784314 19 BT / Overlock 10 TF	1.7	43
3392	Detection of a putative novel genotype of Ehrlichia sp. from opossums (Didelphis aurita) from Brazil. Brazilian Journal of Veterinary Parasitology, 2019, 28, 140-144.	0.2	13
3393	A novel putative member of the family <i>Benyviridae</i> is associated with soilborne wheat mosaic disease in Brazil. Plant Pathology, 2019, 68, 588-600.	1.2	18
3394	A novel interleukin-1 receptor-associated kinase-4 from thick shell mussel Mytilus coruscus is involved in inflammatory response. Fish and Shellfish Immunology, 2019, 84, 213-222.	1.6	18
3395	Molecular characteristics and induction profiles of hypoxia-inducible factor-1 and other basic helix-loop-helix and PerArnt-Sim domain-containing proteins identified in a carcinogenic liver fluke Clonorchis sinensis. Parasitology, 2019, 146, 176-186.	0.7	2
3396	Genetic Variation and Differentiation of Hylesia metabus (Lepidoptera: Saturniidae): Moths of Public Health Importance in French Guiana and in Venezuela. Journal of Medical Entomology, 2019, 56, 137-148.	0.9	2
3397	Identification of salt stress response genes using the Artemia transcriptome. Aquaculture, 2019, 500, 305-314.	1.7	31
3398	Screening of broad spectrum natural pesticides against conserved target arginine kinase in cotton pests by molecular modeling. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1022-1042.	2.0	6
3399	Anatomical and hormonal description of rootlet primordium development along white lupin cluster root. Physiologia Plantarum, 2019, 165, 4-16.	2.6	15
3400	Exploitation of Walnut (Juglans regia L.) Expressed Sequence Tags for Development of SSR Markers After In Silico Analysis. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2019, 89, 267-274.	0.4	0
3401	Biodegradation of biodiesel-oil by <i>Cellulosimicrobium</i> sp. Isolated from Colombian Caribbean soils. Environmental Technology (United Kingdom), 2020, 41, 2337-2349.	1.2	4
3402	Alphacoronavirus Detection in Lungs, Liver, and Intestines of Bats from Brazil. Microbial Ecology, 2020, 79, 203-212.	1.4	16
3403	Novel in silico EST-SSR markers and bioinformatic approaches to detect genetic variation among peach (Prunus persica L.) germplasm. Journal of Forestry Research, 2020, 31, 1359-1370.	1.7	3
3404	CAFU: a Galaxy framework for exploring unmapped RNA-Seq data. Briefings in Bioinformatics, 2020, 21, 676-686.	3.2	13
3405	Isolation and Molecular Characterization of Tick-Borne Relapsing Fever Borrelia Infecting Ornithodoros (Pavlovskyella) verrucosus Ticks Collected in Ukraine. Journal of Infectious Diseases, 2020, 221, 804-811.	1.9	8

#	ARTICLE	IF	CITATIONS
3406	Data, time and money: evaluating the best compromise for inferring molecular phylogenies of non-model animal taxa. <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106660.	1.2	13
3407	Genome sequence of <i>Shewanella corallii</i> strain A687 isolated from pufferfish (<i>Spherooides spengleri</i>). <i>Genetics and Molecular Biology</i> , 2020, 43, e20180314.	0.6	2
3408	Hybridization capture-based next generation sequencing reliably detects FLT3 mutations and classifies FLT3-internal tandem duplication allelic ratio in acute myeloid leukemia: a comparative study to standard fragment analysis. <i>Modern Pathology</i> , 2020, 33, 334-343.	2.9	18
3409	Genotyping and De Novo Discovery of Allelic Variants at the Brassicaceae Self-Incompatibility Locus from Short-Read Sequencing Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 1193-1201.	3.5	19
3410	Molecular and functional characterisation of a putative <i>elovl4</i> gene and its expression in response to dietary fatty acid profile in Atlantic bluefin tuna (<i>Thunnus thynnus</i>). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2020, 240, 110372.	0.7	22
3411	<i>Enterovibrio baiacu</i> sp. nov.. <i>Current Microbiology</i> , 2020, 77, 154-157.	1.0	3
3412	Isolation and characterization of hypoxia inducible heme oxygenase 1 (HMOX1) gene in <i>Labeo rohita</i> . <i>Genomics</i> , 2020, 112, 2327-2333.	1.3	10
3413	Contribution of introns to the species diversity associated with the apicomplexan parasite, <i>Neospora caninum</i> . <i>Parasitology Research</i> , 2020, 119, 431-445.	0.6	2
3414	Identification and characterisation of common glow-worm RNA viruses. <i>Virus Genes</i> , 2020, 56, 236-248.	0.7	6
3415	Putative new plant viruses associated with <i>Plasmopara viticola</i> -infected grapevine samples. <i>Annals of Applied Biology</i> , 2020, 176, 180-191.	1.3	50
3416	A Pathogen-Responsive Gene Cluster for Highly Modified Fatty Acids in Tomato. <i>Cell</i> , 2020, 180, 176-187.e19.	13.5	94
3417	The zebrafish NLRP3 inflammasome has functional roles in ASC-dependent interleukin-1 β maturation and gasdermin E-mediated pyroptosis. <i>Journal of Biological Chemistry</i> , 2020, 295, 1120-1141.	1.6	41
3418	Candidate <i>foraging</i> gene orthologs in a lower termite, <i>Reticulitermes flavipes</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 168-177.	0.6	4
3419	Evolution of <i>Carthamus</i> species revealed through sequence analyses of the <i>fad2</i> gene family. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 419-432.	1.4	3
3420	Neoproterozoic origin and multiple transitions to macroscopic growth in green seaweeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2551-2559.	3.3	85
3421	Development of Simple Sequence Repeat Markers from De Novo Assembled Transcriptomes of Pumpkins. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 130-136.	1.0	9
3422	De novo transcriptome datasets of <i>Shorea balangeran</i> leaves and basal stem in waterlogged and dry soil. <i>Data in Brief</i> , 2020, 28, 104998.	0.5	3
3423	The Evolution of Unusually Small Amelogenin Genes in Cetaceans; Pseudogenization, X \rightarrow Y Gene Conversion, and Feeding Strategy. <i>Journal of Molecular Evolution</i> , 2020, 88, 122-135.	0.8	7

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3424	Identification of salt-responsive genes from C4 halophyte <i>Suaeda nudiflora</i> through suppression subtractive hybridization and expression analysis under individual and combined treatment of salt and elevated carbon dioxide conditions. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 163-172.	1.4	4
3425	Exploring the genetic potential of a fosmid metagenomic library from an oil-impacted mangrove sediment for metabolism of aromatic compounds. <i>Ecotoxicology and Environmental Safety</i> , 2020, 189, 109974.	2.9	16
3426	Identification, recombinant protein production, and functional analysis of a M60-like metallopeptidase, secreted by the liver fluke <i>Opisthorchis viverrini</i> . <i>Parasitology International</i> , 2020, 75, 102050.	0.6	7
3427	The genomic architecture of the sex-determining region and sex-related metabolic variation in <i>Ginkgo biloba</i> . <i>Plant Journal</i> , 2020, 104, 1399-1409.	2.8	26
3428	RNaseq Reveals Sensitive, Concentration-Dependent Transcriptional Markers of Copper in <i>Mytilus californianus</i> Larvae and Adults. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
3429	High-Throughput Sequencing for Deciphering the Virome of Alfalfa (<i>Medicago sativa</i> L.). <i>Frontiers in Microbiology</i> , 2020, 11, 553109.	1.5	24
3430	An empirical study on the underutilized medicinal genus <i>Kaempferia</i> from India revealed cytological and genetic variability. <i>Nucleus (India)</i> , 2020, 63, 257-270.	0.9	3
3431	Functional description and development of polymorphic EST-SSR markers in bread wheat and their gene interactions network. <i>Gene Reports</i> , 2020, 21, 100902.	0.4	2
3432	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	1.3	25
3433	Discovery and engineering of colchicine alkaloid biosynthesis. <i>Nature</i> , 2020, 584, 148-153.	13.7	152
3434	Making Decisions by Unlabeled Bits. <i>IEEE Transactions on Signal Processing</i> , 2020, , 1-1.	3.2	5
3435	Characterization and in vitro functional analysis of thioredoxin glutathione reductase from the liver fluke <i>Opisthorchis viverrini</i> . <i>Acta Tropica</i> , 2020, 210, 105621.	0.9	4
3436	Evidence for Dosage Compensation in <i>Coccinia grandis</i> , a Plant with a Highly Heteromorphic XY System. <i>Genes</i> , 2020, 11, 787.	1.0	12
3437	Effect of milk bactofugation on the counts and diversity of thermotolerant bacteria. <i>Journal of Dairy Science</i> , 2020, 103, 8782-8790.	1.4	14
3438	The Allelic Diversity of the Gibberellin Signaling Pathway Genes in <i>Aegilops tauschii</i> Coss. <i>Plants</i> , 2020, 9, 1696.	1.6	4
3439	Molecular characterization of tomato leaf curl Joydebpur virus and tomato leaf curl New Delhi virus associated with severe leaf curl symptoms of papaya in Bangladesh. <i>European Journal of Plant Pathology</i> , 2020, 158, 457-472.	0.8	3
3440	Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the Triploid Bridge in <i>Arundo</i> (Poaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5247.	1.8	5
3441	<i>Stenamoeba dejonckheerei</i> sp. nov., a Free-Living Amoeba Isolated from a Thermal Spring. <i>Pathogens</i> , 2020, 9, 586.	1.2	6

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3442	Genomic Characterization and Expression of Juvenile Hormone Esterase-Like Carboxylesterase Genes in Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 5444.	1.8	6
3443	In silico mining of SSR markers from expressed sequence tags of <i>Clematis chinensis</i> . <i>Gene Reports</i> , 2020, 21, 100810.	0.4	1
3444	Cathepsins L and B in <i>Dysdercus peruvianus</i> , <i>Rhodnius prolixus</i> , and <i>Mahanarva fimbriolata</i> . Looking for enzyme adaptations to digestion. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103488.	1.2	11
3445	Molecular Analysis of the Gibberellin Signaling Pathway Genes in Cultivated Rye (<i>Secale cereale</i> L.). <i>Moscow University Biological Sciences Bulletin</i> , 2020, 75, 125-129.	0.1	0
3446	RNA-sequencing of the <i>Nyssomyia neivai</i> sialome: a sand fly-vector from a Brazilian endemic area for tegumentary leishmaniasis and pemphigus foliaceus. <i>Scientific Reports</i> , 2020, 10, 17664.	1.6	2
3447	Genome/transcriptome analysis of the chigger mite <i>Leptotrombidium pallidum</i> , a major vector for scrub typhus, with a special focus on genes more abundantly expressed in larval stage. <i>Journal of Asia-Pacific Entomology</i> , 2020, 23, 816-824.	0.4	4
3449	Increased viral read counts and metagenomic full genome characterization of porcine astrovirus 4 and Posavirus 1 in sows in a swine farm with unexplained neonatal piglet diarrhea. <i>Virus Genes</i> , 2020, 56, 696-704.	0.7	4
3450	A first phylogenomic hypothesis for Eulophidae (Hymenoptera, Chalcidoidea). <i>Journal of Natural History</i> , 2020, 54, 597-609.	0.2	12
3451	B chromosomes of multiple species have intense evolutionary dynamics and accumulated genes related to important biological processes. <i>BMC Genomics</i> , 2020, 21, 656.	1.2	22
3452	KmerGO: A Tool to Identify Group-Specific Sequences With k-mers. <i>Frontiers in Microbiology</i> , 2020, 11, 2067.	1.5	7
3453	Costus stripe mosaic virus, a tentative new member of the genus Potyvirus. <i>Archives of Virology</i> , 2020, 165, 2541-2548.	0.9	3
3454	Adaptation and molecular evidence for convergence in decapod crustaceans from deep-sea hydrothermal vent environments. <i>Molecular Ecology</i> , 2020, 29, 3954-3969.	2.0	13
3455	Structural characterization of the DRF1 gene of <i>Aegilops speltoides</i> and comparison of its sequence with those of B and other Triticeae genomes. <i>Euphytica</i> , 2020, 216, 1.	0.6	4
3456	GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. <i>Genome Biology</i> , 2020, 21, 241.	3.8	1,538
3457	Afoxolaner as a Treatment for a Novel <i>Sarcoptes scabiei</i> Infestation in a Juvenile Potbelly Pig. <i>Frontiers in Veterinary Science</i> , 2020, 7, 473.	0.9	4
3458	A Novel Taxon of Monosegmented Double-Stranded RNA Viruses Endemic to Triclad Flatworms. <i>Journal of Virology</i> , 2020, 94, .	1.5	8
3459	De novo assembly of transcriptome dataset from leaves of <i>Dryobalanops aromatica</i> (Syn.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td 2020, 13, 405.	0.6	3
3460	Divergence, gene flow, and the origin of leapfrog geographic distributions: The history of colour pattern variation in <i>Phyllobates</i> poison dart frogs. <i>Molecular Ecology</i> , 2020, 29, 3702-3719.	2.0	14

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3461	Dramatic Increase in Content of Diverse Flavonoids Accompanied with Down-Regulation of F-Box Genes in a Chrysanthemum (<i>Chrysanthemum</i> Å— morifolium (Ramat.) Hemsl.) Mutant Cultivar Producing Dark-Purple Ray Florets. <i>Genes</i> , 2020, 11, 865.	1.0	7
3462	Virulence factors and antimicrobial resistance in <i>Staphylococcus aureus</i> isolated from bovine mastitis in Brazil. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 2111-2122.	0.8	14
3463	The Central Role of Salivary Metalloproteases in Host Acquired Resistance to Tick Feeding. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 563349.	1.8	9
3464	A quick and sensitive diagnostic tool for detection of Maize streak virus. <i>Scientific Reports</i> , 2020, 10, 19633.	1.6	11
3465	De-novo transcriptome analysis unveils differentially expressed genes regulating drought and salt stress response in <i>Panicum sumatrense</i> . <i>Scientific Reports</i> , 2020, 10, 21251.	1.6	18
3466	Gene expression data support the hypothesis that <i>Isoetes</i> rootlets are true roots and not modified leaves. <i>Scientific Reports</i> , 2020, 10, 21547.	1.6	9
3467	Sequence Composition of Bacterial Chromosome Clones in a Transgressive Root-Knot Nematode Resistance Chromosome Region in Tetraploid Cotton. <i>Frontiers in Plant Science</i> , 2020, 11, 574486.	1.7	3
3468	Prediction of mitochondrial genome-wide variation through sequencing of mitochondrion-enriched extracts. <i>Scientific Reports</i> , 2020, 10, 19123.	1.6	5
3469	A Second Genome Sequence of an Enterovirus C99 Detected in a Healthy Chimpanzee. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
3470	Complete mitogenome data from a European specimen of <i>Ostrinia scapularis</i> (Walker, 1859) (Lepidoptera, Pyraloidea, Crambidae, Pyraustinae). <i>Data in Brief</i> , 2020, 33, 106427.	0.5	3
3471	Comparative viromes of <i>Culicoides</i> and mosquitoes reveal their consistency and diversity in viral profiles. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
3472	Mitochondrial DNAs provide insight into trypanosome phylogeny and molecular evolution. <i>BMC Evolutionary Biology</i> , 2020, 20, 161.	3.2	25
3473	m6A RNA Methylation in Marine Plants: First Insights and Relevance for Biological Rhythms. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7508.	1.8	10
3474	Tracking the Distribution and Burst of Nuclear Mitochondrial DNA Sequences (NUMTs) in Fig Wasp Genomes. <i>Insects</i> , 2020, 11, 680.	1.0	12
3475	The Transfer of the Ferredoxin Gene From the Chloroplast to the Nuclear Genome Is Ancient Within the Paraphyletic Genus <i>Thalassiosira</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 523689.	1.5	4
3476	Custom Matrix-Assisted Laser Desorption Ionizationâ€“Time of Flight Mass Spectrometric Database for Identification of Environmental Isolates of the Genus <i>Burkholderia</i> and Related Genera. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	6
3477	Silent Infection of B and CD8 + T Lymphocytes by Influenza A Virus in Children with Tonsillar Hypertrophy. <i>Journal of Virology</i> , 2020, 94, .	1.5	5
3478	Identification and in silico expression analysis of three transcription factors in the wild potato. <i>Journal of Crop Improvement</i> , 2020, 34, 676-686.	0.9	0

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3479	Cuppy Y Chromosome Integrity Maintained by Incomplete Recombination Suppression. <i>Genome Biology and Evolution</i> , 2020, 12, 965-977.	1.1	34
3480	Molecular changes in <i>Mesembryanthemum crystallinum</i> guard cells underlying the C3 to CAM transition. <i>Plant Molecular Biology</i> , 2020, 103, 653-667.	2.0	14
3481	Development and characterization of EST α -SSR markers for <i>Camellia reticulata</i> . <i>Applications in Plant Sciences</i> , 2020, 8, e11348.	0.8	7
3482	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. <i>Genome Biology</i> , 2020, 21, 126.	3.8	74
3483	Abiotic-stress tolerance in plants-system biology approach. , 2020, , 577-609.		6
3484	Characterization of the complete chloroplast genome of <i>Paphiopedilum micranthum</i> , an Endangered orchid in China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 115-116.	0.2	0
3485	Endogenous viral elements integrated into the genome of the soybean aphid, <i>Aphis glycines</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 123, 103405.	1.2	13
3486	Ephemeral detection of <i>Bonamia exitiosa</i> (Haplosporida) in adult and larval European flat oysters <i>Ostrea edulis</i> in the Solent, United Kingdom. <i>Journal of Invertebrate Pathology</i> , 2020, 174, 107421.	1.5	3
3487	Secondary origin, hybridization and sexual reproduction in a diploid α -tetraploid contact zone of the facultatively apomictic orchid <i>Zygopetalum mackayi</i> . <i>Plant Biology</i> , 2020, 22, 939-948.	1.8	4
3488	De novo RNA sequencing analysis of <i>Aeluropus littoralis</i> halophyte plant under salinity stress. <i>Scientific Reports</i> , 2020, 10, 9148.	1.6	14
3489	Extracellular synthesis of nanoselenium from fresh water bacteria <i>Bacillus</i> sp., and its validation of antibacterial and cytotoxic potential. <i>Biocatalysis and Agricultural Biotechnology</i> , 2020, 27, 101655.	1.5	23
3490	Phylogenetic relationships of <i>Strongyloides</i> species in carnivore hosts. <i>Parasitology International</i> , 2020, 78, 102151.	0.6	17
3491	Genetic analyses of native <i>Fusarium</i> head blight resistance in two spring wheat populations identifies QTL near the B1, Ppd-D1, Rht-1, Vrn-1, Fhb1, Fhb2, and Fhb5 loci. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2775-2796.	1.8	9
3492	Characterization of StAR protein of <i>Rhinella arenarum</i> (Amphibia, Anura). <i>General and Comparative Endocrinology</i> , 2020, 295, 113535.	0.8	1
3493	Animal fat and glycerol bioconversion to polyhydroxyalkanoate by produced water bacteria. <i>E-Polymers</i> , 2020, 20, 92-102.	1.3	9
3494	Transcriptional analysis of WUSCHEL-related HOMEBOX (WOX) genes in <i>Coffea arabica</i> L.. <i>Biologia (Poland)</i> , 2020, 75, 1483-1495.	0.8	5
3495	Development and transferability of microsatellite markers for a complex of <i>Aspidosperma</i> Mart. & Zucc. (Apocynaceae) species from South American Seasonally Dry Tropical Forests. <i>Revista Brasileira De Botanica</i> , 2020, 43, 139-145.	0.5	1
3496	An Algebraic-Geometric Approach for Linear Regression Without Correspondences. <i>IEEE Transactions on Information Theory</i> , 2020, 66, 5130-5144.	1.5	14

#	ARTICLE	IF	CITATIONS
3497	Antimalarial Peptide and Polyketide Natural Products from the Fijian Marine Cyanobacterium <i>Moorea</i> producens. <i>Marine Drugs</i> , 2020, 18, 167.	2.2	29
3498	Wheat dwarf India Virus and associated betasatellite infecting wheat in Pakistan. <i>Australasian Plant Disease Notes</i> , 2020, 15, 1.	0.4	3
3499	Eight Million Years of Satellite DNA Evolution in Grasshoppers of the Genus <i>Schistocerca</i> Illuminate the Ins and Outs of the Library Hypothesis. <i>Genome Biology and Evolution</i> , 2020, 12, 88-102.	1.1	30
3500	New Viral Sequences Identified in the Flavescence Disease Phytoplasma Vector <i>Scaphoideus titanus</i> . <i>Viruses</i> , 2020, 12, 287.	1.5	14
3501	Central and peripheral clocks in Atlantic bluefin tuna (<i>Thunnus thynnus</i> , L.): Daily rhythmicity of hepatic lipid metabolism and digestive genes. <i>Aquaculture</i> , 2020, 523, 735220.	1.7	12
3502	TeaMiD: a comprehensive database of simple sequence repeat markers of tea. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	19
3503	Comparative Transcriptomic Response of Two <i>Pinus</i> Species to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2020, 11, 204.	0.9	19
3504	The Segment Matters: Probable Reassortment of Tilapia Lake Virus (TiLV) Complicates Phylogenetic Analysis and Inference of Geographical Origin of New Isolate from Bangladesh. <i>Viruses</i> , 2020, 12, 258.	1.5	43
3505	A comprehensive non-redundant reference transcriptome for the Atlantic silverside <i>Menidia menidia</i> . <i>Marine Genomics</i> , 2020, 53, 100738.	0.4	6
3506	Diverse mobilome of <i>Dichotomius (Luederwaldtinia) schiffleri</i> (Coleoptera: Scarabaeidae) reveals long-range horizontal transfer events of DNA transposons. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1339-1353.	1.0	8
3507	Characterization of microRNA genes from Pigeonpea (<i>Cajanus cajan</i> L.) and understanding their involvement in drought stress. <i>Journal of Biotechnology</i> , 2020, 321, 23-34.	1.9	10
3508	Identification and editing of a hybrid lethality gene expands the range of interspecific hybridization potential in <i>Nicotiana</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 2915-2925.	1.8	9
3509	The complete chloroplast genome sequence of <i>Stachys sieboldii</i> Miquel. (Labiatae), a kind of vegetable crop and Chinese medicinal material plant. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1832-1833.	0.2	2
3510	Characterization and phylogenetic analysis of the mitochondrial genome of <i>Hemipterus villosus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1457-1458.	0.2	1
3511	Extraordinarily conserved chromosomal synteny of <i>Citrus</i> species revealed by chromosome-specific painting. <i>Plant Journal</i> , 2020, 103, 2225-2235.	2.8	33
3512	The effect of variant interference on de novo assembly for viral deep sequencing. <i>BMC Genomics</i> , 2020, 21, 421.	1.2	4
3513	Transcriptome profiling of venom gland from wasp species: de novo assembly, functional annotation, and discovery of molecular markers. <i>BMC Genomics</i> , 2020, 21, 427.	1.2	7
3514	Common occurrence of <i>Cryptosporidium hominis</i> in children attending day-care centers in Medellin, Colombia. <i>Parasitology Research</i> , 2020, 119, 2935-2942.	0.6	6

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3515	The complete mitochondrial genome of the green alga <i>Chloroidium</i> sp. UTEX 3077 (Watanabea clade.) <i>Tj ETQq0 0 0 rBT /Overlock 10 T</i>	0.2	0
3516	TypeTE: a tool to genotype mobile element insertions from whole genome resequencing data. <i>Nucleic Acids Research</i> , 2020, 48, e36-e36.	6.5	11
3517	Antifreeze protein complements cryoprotective dehydration in the freeze-avoiding springtail <i>Megaphorura arctica</i> . <i>Scientific Reports</i> , 2020, 10, 3047.	1.6	16
3518	Target Of Rapamycin pathway in the white-rot fungus <i>Phanerochaete chrysosporium</i> . <i>PLoS ONE</i> , 2020, 15, e0224776.	1.1	7
3519	Passion Fruit Green Spot Virus Genome Harbors a New Orphan ORF and Highlights the Flexibility of the 5'â€²-End of the RNA2 Segment Across Cileviruses. <i>Frontiers in Microbiology</i> , 2020, 11, 206.	1.5	41
3520	Transcriptomeâ€based targetâ€enrichment baits for stony corals (Cnidaria: Anthozoa: Scleractinia). <i>Molecular Ecology Resources</i> , 2020, 20, 807-818.	2.2	26
3521	Novel routes towards bioplastics from plants: elucidation of the methylperillate biosynthesis pathway from <i>Salvia dorisiana</i> trichomes. <i>Journal of Experimental Botany</i> , 2020, 71, 3052-3065.	2.4	13
3522	Genome wide identification, characterization and validation of novel miRNA-based SSR markers in pomegranate (<i>Punica granatum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 683-696.	1.4	28
3523	Molecular bases for drought tolerance in common vetch: designing new molecular breeding tools. <i>BMC Plant Biology</i> , 2020, 20, 71.	1.6	20
3524	Interactive effects of iron and light limitation on the molecular physiology of the Southern Ocean diatom <i>Fragilariopsis kerguelensis</i> . <i>Limnology and Oceanography</i> , 2020, 65, 1511-1531.	1.6	16
3525	Genome- and transcriptome-derived microsatellite loci in lumpfish <i>Cyclopterus lumpus</i> : molecular tools for aquaculture, conservation and fisheries management. <i>Scientific Reports</i> , 2020, 10, 559.	1.6	8
3526	Comparison among three methods for obtaining chloroplast genome sequences from the conifer <i>Pinus massoniana</i> . <i>Genomics</i> , 2020, 112, 2459-2466.	1.3	2
3527	Enrichment of Anaerobic Syngas-Converting Communities and Isolation of a Novel Carboxydotrophic <i>Acetobacterium wieringae</i> Strain JM. <i>Frontiers in Microbiology</i> , 2020, 11, 58.	1.5	21
3528	Transcriptome reconstruction and functional analysis of eukaryotic marine plankton communities via high-throughput metagenomics and metatranscriptomics. <i>Genome Research</i> , 2020, 30, 647-659.	2.4	50
3529	Characterization of Potato Virus Y Isolates and Assessment of Nanopore Sequencing to Detect and Genotype Potato Viruses. <i>Viruses</i> , 2020, 12, 478.	1.5	48
3530	Diversity and Genetic Basis for Carbapenem Resistance in a Coastal Marine Environment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	12
3531	Molecular identification and evaluation of the impact of red heat damage causing halophilic microbes on salted hide and skin. <i>International Biodeterioration and Biodegradation</i> , 2020, 150, 104940.	1.9	8
3532	De novo transcriptome assembly and analysis of <i>Phragmites karka</i> , an invasive halophyte, to study the mechanism of salinity stress tolerance. <i>Scientific Reports</i> , 2020, 10, 5192.	1.6	24

#	ARTICLE	IF	CITATIONS
3533	Occurrence and pathogenicity of <i>Enterobacter</i> sp. causing sprout decay and seedling stunting of upland cotton (<i>Gossypium hirsutum</i> L.). <i>Journal of Phytopathology</i> , 2020, 168, 391-398.	0.5	2
3534	Integrating transcriptome, proteome and QTL data to discover functionally important genes for duck eggshell and albumen formation. <i>Genomics</i> , 2020, 112, 3687-3695.	1.3	11
3535	Exploring the Brazilian diversity of <i>Aspergillus</i> sp. strains for lovastatin and itaconic acid production. <i>Fungal Genetics and Biology</i> , 2020, 138, 103367.	0.9	1
3536	Annotation and characterization of <i>Babesia gibsoni</i> apicoplast genome. <i>Parasites and Vectors</i> , 2020, 13, 209.	1.0	1
3537	Prevalence and seasonal variation of <i>Acanthamoeba</i> in domestic tap water in greater Sydney, Australia. <i>Australasian journal of optometry, The</i> , 2020, 103, 782-786.	0.6	11
3538	Regulation of growth-related genes by nutrition in paralarvae of the common octopus (<i>Octopus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	5
3539	Is adaptation limited by mutation? A timescale-dependent effect of genetic diversity on the adaptive substitution rate in animals. <i>PLoS Genetics</i> , 2020, 16, e1008668.	1.5	55
3540	Microbiological and molecular insights on rare Actinobacteria harboring bioactive prospective. <i>Bulletin of the National Research Centre</i> , 2020, 44, .	0.7	38
3541	Reconstruction of plasmids by shotgun sequencing from environmental DNA: which bioinformatic workflow?. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
3542	Conserved Pigment Profiles in Phylogenetically Diverse Symbiotic Bacteria Associated with the Corals <i>Montastraea cavernosa</i> and <i>Mussismilia braziliensis</i> . <i>Microbial Ecology</i> , 2021, 81, 267-277.	1.4	4
3543	A first genomic portrait of the Florida stone crab <i>Menippe mercenaria</i> : Genome size, mitochondrial chromosome, and repetitive elements. <i>Marine Genomics</i> , 2021, 57, 100821.	0.4	7
3544	The sialotranscriptome of the gopher-tortoise tick, <i>Amblyomma tuberculatum</i> . <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101560.	1.1	4
3545	Elucidation of enzymes involved in the biosynthetic pathway of bioactive polyacetylenes in <i>Bidens pilosa</i> using integrated omics approaches. <i>Journal of Experimental Botany</i> , 2021, 72, 525-541.	2.4	4
3546	Evolutionary dynamics of transposable elements and satellite DNAs in polyploid <i>Spartina</i> species. <i>Plant Science</i> , 2021, 302, 110671.	1.7	9
3547	Selection, drift, and constraint in cyprinid luciferases and the diversification of bioluminescent signals in sea fireflies. <i>Molecular Ecology</i> , 2021, 30, 1864-1879.	2.0	14
3548	Expression profiles of neotropical termites reveal microbiota-associated, caste-biased genes and biotechnological targets. <i>Insect Molecular Biology</i> , 2021, 30, 152-164.	1.0	1
3549	Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021, 5, 231-242.	3.4	51
3550	Whole exome sequencing identifies the potential for genetic rescue in iconic and critically endangered Panamanian harlequin frogs. <i>Global Change Biology</i> , 2021, 27, 50-70.	4.2	15

#	ARTICLE	IF	CITATIONS
3551	The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. <i>Current Biology</i> , 2021, 31, 911-922.e4.	1.8	24
3552	Drought responsiveness in black pepper (<i>Piper nigrum</i> L.): Genes associated and development of a genomic resource. <i>Physiologia Plantarum</i> , 2021, 172, 669-683.	2.6	7
3553	Microbial prospection of an Amazonian blackwater lake and whole-genome sequencing of bacteria capable of polyhydroxyalkanoate synthesis. <i>Polymer Journal</i> , 2021, 53, 191-202.	1.3	2
3554	Cercarial trematodes in freshwater snails from Bangkok, Thailand: prevalence, morphological and molecular studies and human parasite perspective. <i>Parasitology</i> , 2021, 148, 366-383.	0.7	18
3555	Dioecy Is Associated with High Genetic Diversity and Adaptation Rates in the Plant Genus <i>Silene</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 805-818.	3.5	31
3556	On the reappearance of the Indian grey wolf in Bangladesh after 70 years: what do we know?. <i>Mammalian Biology</i> , 2021, 101, 163-171.	0.8	3
3557	Genome skimming resolves the giant clam (Bivalvia: Cardiidae: Tridacninae) tree of life. <i>Coral Reefs</i> , 2022, 41, 497-510.	0.9	12
3558	A genomic portrait of <i>Sturnira parvidens</i> : mitochondrial chromosome, repetitive elements, and microsatellite discovery. <i>Journal of Mammalogy</i> , 2022, 103, 82-90.	0.6	4
3561	MITGARD: an automated pipeline for mitochondrial genome assembly in eukaryotic species using RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	15
3562	Omics to Understand Drought Tolerance in Plants: An Update. , 2021, , 69-93.		0
3563	Mitochondrial genome of <i>Rhabdosynochus viridis</i> (Monogenea: Diplectanidae), a parasite of Pacific white snook <i>Centropomus viridis</i> . <i>Journal of Helminthology</i> , 2021, 95, e21.	0.4	2
3564	Comparative transcriptomics and host-specific parasite gene expression profiles inform on drivers of proliferative kidney disease. <i>Scientific Reports</i> , 2021, 11, 2149.	1.6	15
3565	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90.		0
3566	Disparate outer membrane exclusionary properties underlie intrinsic resistance to hydrophobic substances in <i>Pseudomonas</i> spp. isolated from surface waters under triclosan selection. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2021, 56, 257-268.	0.9	3
3567	Development of mPing-based activation tags for crop insertional mutagenesis. <i>Plant Direct</i> , 2021, 5, e00300.	0.8	6
3568	Novel polymorphisms in Stearoyl-CoA Desaturase (SCD) and Fatty Acid Desaturase 2 (FADS2) in channel catfish (<i>Ictalurus punctatus</i> , Rafinesque, 1818). <i>Journal of Applied Ichthyology</i> , 2021, 37, 120-124.	0.3	0
3569	Cultivable Microbiota Associated with Gold Ore from the Rozňava Gold Mine, Hodruša-Hámre, Slovakia. <i>Geomicrobiology Journal</i> , 2021, 38, 415-425.	1.0	6
3570	Antigen receptor repertoires of one of the smallest known vertebrates. <i>Science Advances</i> , 2021, 7, .	4.7	8

#	ARTICLE	IF	CITATIONS
3571	DNA Fragment Assembly Using Quantum-Inspired Genetic Algorithm. , 2021, , 811-828.		1
3572	Molecular Evidence of <i>Rickettsia felis</i> in <i>Phereocera</i> sp.. Brazilian Journal of Veterinary Parasitology, 2021, 30, e015620.	0.2	5
3573	Novel <i>Streptococcus equi</i> subsp. <i>equi</i> identified in isolates circulating in Argentina. Equine Veterinary Journal, 2022, 54, 132-138.	0.9	3
3574	Choosing source of microorganisms and processing technology for next generation beet bioinoculant. Scientific Reports, 2021, 11, 2829.	1.6	8
3575	Characterizing Ectomycorrhizal Fungal Community Structure and Function of Two Varieties of <i>Pinus clausa</i> That Differ in Disturbance History. Forests, 2021, 12, 219.	0.9	2
3576	A first look at the repeatome™ of <i>Benedenia humboldti</i> , a major pathogen in yellowtail aquaculture: Repetitive element characterization, nuclear rRNA operon assembly, and microsatellite discovery. Marine Genomics, 2021, 58, 100848.	0.4	1
3577	Thermal reaction norms of key metabolic enzymes reflect divergent physiological and behavioral adaptations of closely related amphipod species. Scientific Reports, 2021, 11, 4562.	1.6	7
3579	Comparative Transcriptomics and RNA-Seq-Based Bulk Segregant Analysis Reveals Genomic Basis Underlying <i>Cronartium ribicola</i> vcr2 Virulence. Frontiers in Microbiology, 2021, 12, 602812.	1.5	6
3580	Microbial Succession and Identification of Effective Indigenous Pectinolytic Yeasts From Orange Juice Processing Wastewater. Waste and Biomass Valorization, 2021, 12, 4885-4899.	1.8	4
3583	A 16S rRNA Gene and Draft Genome Database for the Murine Oral Bacterial Community. MSystems, 2021, 6, .	1.7	14
3584	Nudivirus Sequences Identified from the Southern and Western Corn Rootworms (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	1.5	9
3585	Comparative transcriptome analysis during developmental stages of direct somatic embryogenesis in <i>Tilia amurensis</i> Rupr. Scientific Reports, 2021, 11, 6359.	1.6	9
3586	Mycoviral diversity and characteristics of a negative-stranded RNA virus LeNSRV1 in the edible mushroom <i>Lentinula edodes</i> . Virology, 2021, 555, 89-101.	1.1	16
3587	Transcriptomic Responses of Four Pelagophytes to Nutrient (N, P) and Light Stress. Frontiers in Marine Science, 2021, 8, .	1.2	3
3588	Ectopic expression of a wheat superoxide dismutase gene TaSOD5 enhances salt and oxidative stress tolerance in <i>Arabidopsis</i> . Biologia Plantarum, 0, 65, 19-26.	1.9	8
3590	Revealing the high variability on nonconserved core and mobile elements of <i>Austropuccinia psidii</i> and other rust mitochondrial genomes. PLoS ONE, 2021, 16, e0248054.	1.1	5
3591	Yield and antiyield genes in common bean (<i>Phaseolus vulgaris</i> L.). , 2021, 3, e91.		3
3593	In Silico Molecular Docking Analysis of β -Pinene: An Antioxidant and Anticancer Drug Obtained from <i>Myrtus communis</i> . International Journal of Cancer Management, 2021, 14, .	0.2	4

#	ARTICLE	IF	CITATIONS
3594	Abundance of Mobilized Colistin Resistance Gene (<i>mcr-1</i>) in Commensal <i>Escherichia coli</i> from Diverse Sources. <i>Microbial Drug Resistance</i> , 2021, 27, 1585-1593.	0.9	6
3595	Fipronil biodegradation and metabolization by <i>Bacillus megaterium</i> strain <i>E1</i> . <i>Journal of Chemical Technology and Biotechnology</i> , 2022, 97, 474-481.	1.6	7
3596	Exploring the Diversity of Fungal DyPs in Mangrove Soils to Produce and Characterize Novel Biocatalysts. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 321.	1.5	5
3597	Common virulence gene expression in adult first-time infected malaria patients and severe cases. <i>ELife</i> , 2021, 10, .	2.8	20
3598	A novel fragmented mitochondrial genome in the protist pathogen <i>Toxoplasma gondii</i> and related tissue coccidia. <i>Genome Research</i> , 2021, 31, 852-865.	2.4	17
3599	Characterisation of turnip mosaic virus isolates reveals high genetic variability and occurrence of pathotype 1 in Brazil. <i>European Journal of Plant Pathology</i> , 2021, 160, 883-900.	0.8	3
3600	Large-Scale Annotation and Evolution Analysis of MiRNA in Insects. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	15
3601	Multispacer Sequence Typing for <i>Mycobacterium bovis</i> Genotyping. <i>Frontiers in Veterinary Science</i> , 2021, 8, 666283.	0.9	1
3602	A Python script to merge Sanger sequences. <i>PeerJ</i> , 2021, 9, e11354.	0.9	0
3603	Genome sequence of <i>Vibrio fluvialis</i> 362.3 isolated from coral <i>Mussismilia braziliensis</i> reveals genes related to marine environment adaptation. <i>Archives of Microbiology</i> , 2021, 203, 3683-3686.	1.0	0
3604	Mitochondrial genome of <i>Scutogyrus longicornis</i> (Monogenea: Dactylogyridea), a parasite of Nile tilapia <i>Oreochromis niloticus</i> . <i>Parasitology International</i> , 2021, 81, 102281.	0.6	11
3605	The Ponto-Caspian parasite <i>Plagioporus cf. skrjabini</i> reaches the River Rhine system in Central Europe: higher infestation in the native than in the introduced Danubian form of the gastropod <i>Theodoxus fluviatilis</i> . <i>Hydrobiologia</i> , 2021, 848, 2569-2578.	1.0	0
3606	Functional annotations of ESTs of <i>Stevia rebaudiana</i> involved in abiotic stress signaling through computational approach. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 2602-2612.	1.8	1
3607	Biological Control of <i>Pythium aphanidermatum</i> , the Causal Agent of Tomato Root Rot by Two <i>Streptomyces</i> Root Symbionts. <i>Agronomy</i> , 2021, 11, 846.	1.3	32
3608	Bacteriophage-Host Association in the Phytoplasma Insect Vector <i>Euscelidius variegatus</i> . <i>Pathogens</i> , 2021, 10, 612.	1.2	9
3609	Physiological and transcriptomic analyses characterized high temperature stress response mechanisms in <i>Sorbus pohuashanensis</i> . <i>Scientific Reports</i> , 2021, 11, 10117.	1.6	7
3610	Disruption of the odorant coreceptor <i>Orco</i> impairs foraging and host finding behaviors in the New World screwworm fly. <i>Scientific Reports</i> , 2021, 11, 11379.	1.6	7
3611	Constructing a de novo transcriptome and a reference proteome for the bivalve <i>Scrobicularia plana</i> : Comparative analysis of different assembly strategies and proteomic analysis. <i>Genomics</i> , 2021, 113, 1543-1553.	1.3	5

#	ARTICLE	IF	CITATIONS
3612	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	2.0	107
3613	Accelerated Evolution of Tissue-Specific Genes Mediates Divergence Amidst Gene Flow in European Green Lizards. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
3614	Target sequence capture in orchids: Developing a kit to sequence hundreds of single-copy loci. <i>Applications in Plant Sciences</i> , 2021, 9, e11416.	0.8	21
3615	The brain transcriptome of the wolf spider, <i>Schizocosa ocreata</i> . <i>BMC Research Notes</i> , 2021, 14, 236.	0.6	0
3616	Potato spindle tuber viroid. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2021, 25, 269-275.	0.4	2
3617	Isolation and Characterization of an Endophytic Fungus <i>Colletotrichum coccodes</i> Producing Tyrosol From <i>Houttuynia cordata</i> Thunb. Using ITS2 RNA Secondary Structure and Molecular Docking Study. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 650247.	2.0	28
3618	Larvicidal Activities against <i>Aedes aegypti</i> of Supernatant and Pellet Fractions from Cultured <i>Bacillus</i> spp. Isolated from Amazonian Microenvironments. <i>Tropical Medicine and Infectious Disease</i> , 2021, 6, 104.	0.9	6
3619	Glycogen Synthase Kinase 3 Gene Is Important in Growth and Molting of the Pacific White Shrimp <i>Litopenaeus vannamei</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
3620	Comparative genomics of the chitinase gene family in lodgepole and jack pines: contrasting responses to biotic threats and landscape level investigation of genetic differentiation. <i>Botany</i> , 2021, 99, 355-378.	0.5	4
3621	Whole-Genome Duplication Facilitated the Evolution of C4 Photosynthesis in <i>Gynandropsis gynandra</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 4715-4731.	3.5	13
3624	SearchHPV: A novel approach to identify and assemble human papillomavirus host genomic integration events in cancer. <i>Cancer</i> , 2021, 127, 3531-3540.	2.0	8
3625	Cis-regulatory evolution spotlights species differences in the adaptive potential of gene expression plasticity. <i>Nature Communications</i> , 2021, 12, 3376.	5.8	25
3626	Chloroplast genome of a pair of <i>Triticum aestivum</i> L. recombinant inbred lines with significant difference in seed size. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1886-1887.	0.2	0
3627	2-kupl: mapping-free variant detection from DNA-seq data of matched samples. <i>BMC Bioinformatics</i> , 2021, 22, 304.	1.2	1
3628	Schistosome W-Linked Genes Inform Temporal Dynamics of Sex Chromosome Evolution and Suggest Candidate for Sex Determination. <i>Molecular Biology and Evolution</i> , 2021, 38, 5345-5358.	3.5	12
3629	Cas9 targeted enrichment of mobile elements using nanopore sequencing. <i>Nature Communications</i> , 2021, 12, 3586.	5.8	33
3631	Family I84 protease inhibitors likely constitute a Mollusca-specific protein family functioning in host defense. <i>Diseases of Aquatic Organisms</i> , 2021, 145, 89-100.	0.5	3
3632	Characterization of a novel strain of <i>Tribonema minus</i> demonstrating high biomass productivity in outdoor raceway ponds. <i>Bioresource Technology</i> , 2021, 331, 125007.	4.8	11

#	ARTICLE	IF	CITATIONS
3633	Metagenome-Assembled Genomes Contribute to Unraveling of the Microbiome of Cocoa Fermentation. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0058421.	1.4	11
3634	De novo transcriptome assembly data for sengon (<i>Falcataria moluccana</i>) trees displaying resistance and susceptibility to boktor stem borers (<i>Xystrocera festiva</i> Pascoe). <i>BMC Research Notes</i> , 2021, 14, 261.	0.6	3
3635	Complexity and Local Specificity of the Virome Associated with Tospovirus-Transmitting Thrips Species. <i>Journal of Virology</i> , 2021, 95, e0059721.	1.5	25
3636	High-precision and cost-efficient sequencing for real-time COVID-19 surveillance. <i>Scientific Reports</i> , 2021, 11, 13669.	1.6	15
3637	TransPI: A balancing act between transcriptome assemblers. <i>Peer Community in Genomics</i> , 0, , .	0.0	0
3638	Identification and Characterization of a Glycoside Hydrolase Family 9 Member from the Digestive Gland of the Snail <i>Achatina fulica</i> . <i>Bioenergy Research</i> , 2022, 15, 466-478.	2.2	2
3639	Metabolic flexibility of aerobic methanotrophs under anoxic conditions in Arctic lake sediments. <i>ISME Journal</i> , 2022, 16, 78-90.	4.4	25
3640	Draft Whole-Genome Sequence of <i>Bacillus paramycooides</i> LB_RP2, a Putative Polyhydroxyalkanoate-Producing Bacterium Isolated from an Amazonian Blackwater River. <i>Microbiology Resource Announcements</i> , 2021, 10, e0043821.	0.3	0
3642	Expression of <i>Melocactus glaucescens</i> SERK1 sheds new light on the mechanism of areolar activation in cacti. <i>Plant Cell, Tissue and Organ Culture</i> , 2021, 147, 437-451.	1.2	2
3643	The Sisal Virome: Uncovering the Viral Diversity of Agave Varieties Reveals New and Organ-Specific Viruses. <i>Microorganisms</i> , 2021, 9, 1704.	1.6	5
3644	Gene expression profiling reveals candidate genes for defining spider silk gland types. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 135, 103594.	1.2	9
3645	First Report of Coffee Leaf Rust Caused by <i>Hemileia vastatrix</i> on Coffee (<i>Coffea arabica</i>) in Hawaii. <i>Plant Disease</i> , 2022, 106, 761.	0.7	14
3646	Metagenomic analysis reveals <i>Culex</i> mosquito virome diversity and Japanese encephalitis genotype V in the Republic of Korea. <i>Molecular Ecology</i> , 2021, 30, 5470-5487.	2.0	19
3647	Dinoflagellate-targeted PCR reveals highly abundant and diverse communities of parasitic dinoflagellates in and near Zhubi Reef, South China Sea. <i>Coral Reefs</i> , 0, , 1.	0.9	3
3648	Combining OSMAC Approach and Untargeted Metabolomics for the Identification of New Glycolipids with Potent Antiviral Activity Produced by a Marine Rhodococcus. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9055.	1.8	14
3649	Duplicated antagonistic EPF peptides optimize grass stomatal initiation. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	6
3650	The coordination of major events in C4 photosynthesis evolution in the genus <i>Flaveria</i> . <i>Scientific Reports</i> , 2021, 11, 15618.	1.6	12
3651	Insights into the Host Specificity of a New Oomycete Root Pathogen, <i>Pythium brassicum</i> P1: Whole Genome Sequencing and Comparative Analysis Reveals Contracted Regulation of Metabolism, Protein Families, and Distinct Pathogenicity Repertoire. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9002.	1.8	3

#	ARTICLE	IF	CITATIONS
3652	Venom of the Annulated Sea Snake <i>Hydrophis cyanocinctus</i> : A Biochemically Simple but Genetically Complex Weapon. <i>Toxins</i> , 2021, 13, 548.	1.5	4
3653	Redondovirus Diversity and Evolution on Global, Individual, and Molecular Scales. <i>Journal of Virology</i> , 2021, 95, e0081721.	1.5	12
3654	HITAC-seq enables high-throughput cost-effective sequencing of plasmids and DNA fragments with identity. <i>Journal of Genetics and Genomics</i> , 2021, 48, 671-680.	1.7	2
3655	Temporal variations in the expression of a diatom nitrate transporter gene in coastal waters off northern Taiwan: The roles of nitrate and bacteria. <i>Continental Shelf Research</i> , 2021, 227, 104506.	0.9	2
3656	Novel Symbiotic Association Between <i>Euwallacea Ambrosia</i> Beetle and <i>Fusarium</i> Fungus on Fig Trees in Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 725210.	1.5	9
3657	Identification, phylogeny and transcript profiling of ERF family genes during temperature stress treatment in Pea (<i>Pisum sativum</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 561-572.	0.9	7
3658	Genetic variation of avirulence genes (<i>AVR-Pi9</i> , <i>AVR-Pik</i> , <i>AVR-Pita1</i>) and genetic diversity of rice blast fungus, <i>Pyricularia oryzae</i> , in Thailand. <i>Plant Pathology</i> , 2022, 71, 322-333.	1.2	4
3659	Up-regulation of apoptotic- and cell survival-related gene pathways following exposures of western corn rootworm to <i>B. thuringiensis</i> crystalline pesticidal proteins in transgenic maize roots. <i>BMC Genomics</i> , 2021, 22, 639.	1.2	4
3660	Modulation of bioelectric cues in the evolution of flying fishes. <i>Current Biology</i> , 2021, 31, 5052-5061.e8.	1.8	16
3661	Long-read metagenomics of multiple displacement amplified DNA of low-biomass human gut phageomes by SACRA preprocessing chimeric reads. <i>DNA Research</i> , 2021, 28, .	1.5	11
3662	Locating and Quantifying Carbon Steel Corrosion Rates Linked to Fungal B20 Biodiesel Degradation. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0117721.	1.4	1
3663	Validation of conventional PCR-like alternative to SARS-CoV-2 detection with target nucleocapsid protein gene in naso-oropharyngeal samples. <i>PLoS ONE</i> , 2021, 16, e0257350.	1.1	3
3664	Occurrence of <i>Metarhizium</i> spp. isolated from forest samples in South India and their potential in biological control of banana stem weevil <i>Odoiporus longicollis</i> Oliver. <i>Egyptian Journal of Biological Pest Control</i> , 2021, 31, .	0.8	5
3665	Development of a new set of genic SSR markers in the genus <i>Gentiana</i> : in silico mining, characterization and validation. <i>3 Biotech</i> , 2021, 11, 430.	1.1	1
3666	Molecular Pathogenesis and Immune Evasion of Vesicular Stomatitis New Jersey Virus Inferred from Genes Expression Changes in Infected Porcine Macrophages. <i>Pathogens</i> , 2021, 10, 1134.	1.2	1
3667	Genomic Analysis of <i>Limosilactobacillus fermentum</i> ATCC 23271, a Potential Probiotic Strain with Anti-Candida Activity. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 794.	1.5	14
3668	A simple screen to detect hybrids between native and introduced <i>Phragmites australis</i> in the United States and Canada. <i>Journal of Great Lakes Research</i> , 2021, 47, 1453-1457.	0.8	5
3669	Dietary DHA and ARA level and ratio affect the occurrence of skeletal anomalies in pikeperch larvae (<i>Sander lucioperca</i>) through a regulation of immunity and stress related gene expression. <i>Aquaculture</i> , 2021, 544, 737060.	1.7	8

#	ARTICLE	IF	CITATIONS
3670	Understanding rice growth-promoting potential of <i>Enterobacter</i> spp. isolated from long-term organic farming soil in India through a supervised learning approach. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100035.	1.4	4
3671	Investigation of <i>Capitella</i> spp. symbionts in the context of varying anthropic pressures: First occurrence of a transient advantageous epibiosis with the giant bacteria <i>Thiomargarita</i> sp. to survive seasonal increases of sulfides in sediments. <i>Science of the Total Environment</i> , 2021, 798, 149149.	3.9	5
3672	Phenotypic traits of individuals in a long-term colony of <i>Anopheles</i> (<i>Nyssorhynchus</i>) <i>aquasalis</i> (Diptera: Culicidae) show variable susceptibility to <i>Plasmodium</i> and suggest cryptic speciation. <i>Acta Tropica</i> , 2021, 224, 106129.	0.9	0
3673	Deciphering the animal genomics using bioinformatics approaches. , 2021, , 281-297.		1
3674	Culturable bacteria associated with <i>Anopheles darlingi</i> and their paratransgenesis potential. <i>Malaria Journal</i> , 2021, 20, 40.	0.8	14
3675	Insights from the cDNA and EST analysis of <i>Antrodia cinnamomea</i> . <i>Bioinformatics</i> , 2021, 17, 109-118.	0.2	0
3676	DNA Fragment Assembly Using Quantum-Inspired Genetic Algorithm. , 2021, , 228-245.		0
3677	Characterization and Expression Analysis of Insulin Growth Factor Binding Proteins (IGFBPs) in Pacific White Shrimp <i>Litopenaeus vannamei</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 1056.	1.8	5
3678	Telomere length de novo assembly of all 7 chromosomes and mitogenome sequencing of the model entomopathogenic fungus, <i>Metarhizium brunneum</i> , by means of a novel assembly pipeline. <i>BMC Genomics</i> , 2021, 22, 87.	1.2	10
3683	Bioinformatics and Triticeae Genomics: Resources and Future Developments. , 2004, , 425-446.		1
3684	DNA Fragment Assembly by Ant Colony and Nearest Neighbour Heuristics. <i>Lecture Notes in Computer Science</i> , 2006, , 1008-1017.	1.0	6
3685	Efficient Selection of Unique and Popular Oligos for Large EST Databases. <i>Lecture Notes in Computer Science</i> , 2003, , 384-401.	1.0	6
3686	The <i>Gossypium</i> Transcriptome. , 2009, , 157-185.		4
3687	Bioinformatic Resources for Soybean Genetic and Genomic Research. , 2008, , 141-159.		1
3688	Genomics of Soybean Seed Development. , 2008, , 163-184.		2
3689	Genome resources for the DT40 community. <i>Sub-Cellular Biochemistry</i> , 2006, 40, 25-37.	1.0	2
3690	Bioinformatic Tools in Crop Improvement. , 2013, , 49-122.		6
3691	From Sequence Mapping to Genome Assemblies. <i>Methods in Molecular Biology</i> , 2015, 1201, 19-50.	0.4	5

#	ARTICLE	IF	CITATIONS
3692	Impact of Next-Generation Technologies on Exploring Socioeconomically Important Parasites and Developing New Interventions. <i>Methods in Molecular Biology</i> , 2015, 1247, 437-474.	0.4	9
3693	Finding and Characterizing Repeats in Plant Genomes. <i>Methods in Molecular Biology</i> , 2016, 1374, 293-337.	0.4	7
3694	Construction of Artificial miRNAs to Prevent Drought Stress in <i>Solanum tuberosum</i> . <i>Methods in Molecular Biology</i> , 2016, 1398, 271-290.	0.4	11
3695	Managing Sequencing Projects in the GAP4 Environment. , 2003, , 327-344.		9
3696	Isolation of Microsatellites from <i>Catharanthus roseus</i> (L.) G. Don Using Enriched Libraries. <i>Methods in Molecular Biology</i> , 2009, 547, 289-302.	0.4	2
3697	Genome Sequencing and Assembly. <i>Methods in Molecular Biology</i> , 2011, 722, 1-9.	0.4	7
3698	The Reyan 7-33-97 Rubber Tree Genome: Insight into Its Structure, Composition and Application. <i>Compendium of Plant Genomes</i> , 2020, , 13-40.	0.3	3
3699	Assembly and Data Quality. , 2017, , 81-103.		2
3700	Ontology-Driven Workflow Management for Biosequence Processing Systems. <i>Lecture Notes in Computer Science</i> , 2004, , 781-790.	1.0	12
3701	New EST Trimming Procedure Applied to SUCEST Sequences. , 2007, , 57-68.		2
3702	SeqTrim " A Validation and Trimming Tool for All Purpose Sequence Reads. <i>Advances in Intelligent and Soft Computing</i> , 2007, , 353-360.	0.2	5
3703	A Web Tool to Discover Full-Length Sequences " Full-Lengther. <i>Advances in Intelligent and Soft Computing</i> , 2007, , 361-368.	0.2	11
3704	Microarray data quality analysis: lessons from the AFGC project. , 2002, , 119-131.		2
3705	Advancements in Microbial Genome Sequencing and Microbial Community Characterization. , 2019, , 87-113.		1
3707	Development and characterization of EST-derived SSR markers in the cereal cyst nematode <i>Heterodera avenae</i> . <i>European Journal of Plant Pathology</i> , 2018, 150, 105-113.	0.8	6
3708	Biofilm inhibitory activity of metallo-protein AHL-lactonase from cell-free lysate of endophytic <i>Enterobacter</i> species isolated from <i>Coscinium fenestratum</i> Gaertn.. <i>Biocatalysis and Agricultural Biotechnology</i> , 2019, 18, 101009.	1.5	18
3709	Systematic assessment of chlorine tolerance mechanism in a potent biofilm-forming marine bacterium <i>Halomonas boliviensis</i> . <i>International Biodeterioration and Biodegradation</i> , 2020, 151, 104967.	1.9	20
3710	The zebrafish NLRP3 inflammasome has functional roles in ASC-dependent interleukin-1 β maturation and gasdermin E-mediated pyroptosis. <i>Journal of Biological Chemistry</i> , 2020, 295, 1120-1141.	1.6	65

#	ARTICLE	IF	CITATIONS
3711	Tick saliva: from pharmacology and biochemistry to transcriptome analysis and functional genomics. , 2008, , 92-107.		8
3712	Evolution and conservation of Characidium sex chromosomes. Heredity, 2017, 119, 237-244.	1.2	15
3713	The Wheat Dwarf India Virus-Betasatellite Complex Has a Wider Host Range Than Previously Reported. Plant Health Progress, 2020, 21, 119-122.	0.8	2
3714	Description of Trichococcus ilyis sp. nov. by combined physiological and in silico genome hybridization analyses. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3957-3963.	0.8	27
3715	Morphologic and molecular characterization of Brachonella pulchra (Kahl, 1927) comb. nov. (Armophorea, Ciliophora) with comments on cyst structure and formation. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3052-3065.	0.8	11
3716	Flavobacterium chryseum sp. nov. and Flavobacterium psychroterrae sp. nov., novel environmental bacteria isolated from Antarctica. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3132-3139.	0.8	12
3717	The discovery of Halictivirus resolves the Sinaivirus phylogeny. Journal of General Virology, 2017, 98, 2864-2875.	1.3	31
3718	Viruses of invasive Argentine ants from the European Main supercolony: characterization, interactions and evolution. Journal of General Virology, 2018, 99, 1129-1140.	1.3	35
3719	A cross-reactive neisserial antigen encoded by the NMB0035 locus shows high sequence conservation but variable surface accessibility. Journal of Medical Microbiology, 2008, 57, 80-87.	0.7	11
3720	Dynamics of acute Montipora white syndrome: bacterial communities of healthy and diseased M. capitata colonies during and after a disease outbreak. Microbiology (United Kingdom), 2018, 164, 1240-1253.	0.7	9
3763	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. Genome Research, 2001, 11, 281-289.	2.4	25
3764	An Efficient-Assembler Whale Optimization Algorithm for DNA Fragment Assembly Problem: Analysis and Validations. IEEE Access, 2020, 8, 222144-222167.	2.6	15
3765	Hepatopancreatic multi-transcript expression patterns in the crayfish Cherax quadricarinatus during the moult cycle. Insect Molecular Biology, 2007, .	1.0	1
3766	New Bioinformatic Strategies to Rapidly Characterize Retroviral Integration Sites of Gene Therapy Vectors. Methods of Information in Medicine, 2007, 46, 542-547.	0.7	16
3768	Comparative chloroplast genomics of the genus Taxodium. BMC Genomics, 2020, 21, 114.	1.2	23
3769	Optimization of xylanase from Pseudomonas mohnii isolated from Simlipal Biosphere Reserve, Odisha, using response surface methodology. Journal of Genetic Engineering and Biotechnology, 2020, 18, 81.	1.5	11
3770	Comparative Developmental Transcriptomics Reveals Rewiring of a Highly Conserved Gene Regulatory Network during a Major Life History Switch in the Sea Urchin Genus Heliocidaris. PLoS Biology, 2016, 14, e1002391.	2.6	78
3771	Evolutionary restoration of fertility in an interspecies hybrid yeast, by whole-genome duplication after a failed mating-type switch. PLoS Biology, 2017, 15, e2002128.	2.6	84

#	ARTICLE	IF	CITATIONS
3772	Spliced integrated retrotransposed element (SpIRE) formation in the human genome. PLoS Biology, 2018, 16, e2003067.	2.6	11
3773	Inter-population Differences in Retrogene Loss and Expression in Humans. PLoS Genetics, 2015, 11, e1005579.	1.5	12
3774	Needles in the EST Haystack: Large-Scale Identification and Analysis of Excretory-Secretory (ES) Proteins in Parasitic Nematodes Using Expressed Sequence Tags (ESTs). PLoS Neglected Tropical Diseases, 2008, 2, e301.	1.3	44
3775	Isolation of Novel Trypanosomatid, <i>Zelonia australiensis</i> sp. nov. (Kinetoplastida: Trypanosomatidae) Provides Support for a Gondwanan Origin of Dixenous Parasitism in the Leishmaniinae. PLoS Neglected Tropical Diseases, 2017, 11, e0005215.	1.3	55
3776	Transcriptome of <i>Pneumocystis carinii</i> during Fulminate Infection: Carbohydrate Metabolism and the Concept of a Compatible Parasite. PLoS ONE, 2007, 2, e423.	1.1	58
3777	Targeted Development of Registries of Biological Parts. PLoS ONE, 2008, 3, e2671.	1.1	63
3778	Polymicrobial Nature of Chronic Diabetic Foot Ulcer Biofilm Infections Determined Using Bacterial Tag Encoded FLX Amplicon Pyrosequencing (bTEFAP). PLoS ONE, 2008, 3, e3326.	1.1	456
3779	Identification and Gene Expression Analysis of a Taxonomically Restricted Cysteine-Rich Protein Family in Reef-Building Corals. PLoS ONE, 2009, 4, e4865.	1.1	62
3780	Proteomic Analysis of Tardigrades: Towards a Better Understanding of Molecular Mechanisms by Anhydrobiotic Organisms. PLoS ONE, 2010, 5, e9502.	1.1	58
3781	Ployploidy Did Not Predate the Evolution of Nodulation in All Legumes. PLoS ONE, 2010, 5, e11630.	1.1	88
3782	Polyploidization Altered Gene Functions in Cotton (<i>Gossypium</i> spp.). PLoS ONE, 2010, 5, e14351.	1.1	20
3783	De Novo Analysis of Transcriptome Dynamics in the Migratory Locust during the Development of Phase Traits. PLoS ONE, 2010, 5, e15633.	1.1	215
3784	New Modularity of DAP-Kinases: Alternative Splicing of the DRP-1 Gene Produces a ZIPK-Like Isoform. PLoS ONE, 2011, 6, e17344.	1.1	17
3785	The ITS1-5.8S-ITS2 Sequence Region in the Musaceae: Structure, Diversity and Use in Molecular Phylogeny. PLoS ONE, 2011, 6, e17863.	1.1	79
3786	Resistance to Hemi-Biotrophic <i>F. graminearum</i> Infection Is Associated with Coordinated and Ordered Expression of Diverse Defense Signaling Pathways. PLoS ONE, 2011, 6, e19008.	1.1	258
3787	Induction of Larval Metamorphosis of the Coral <i>Acropora millepora</i> by Tetrabromopyrrole Isolated from a <i>Pseudoalteromonas</i> Bacterium. PLoS ONE, 2011, 6, e19082.	1.1	184
3788	Evaluating the Fidelity of De Novo Short Read Metagenomic Assembly Using Simulated Data. PLoS ONE, 2011, 6, e19984.	1.1	65
3789	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095.	1.1	59

#	ARTICLE	IF	CITATIONS
3790	Snapshot of the Eukaryotic Gene Expression in Muskoxen Rumen—A Metatranscriptomic Approach. PLoS ONE, 2011, 6, e20521.	1.1	113
3791	Spinning Gland Transcriptomics from Two Main Clades of Spiders (Order: Araneae) - Insights on Their Molecular, Anatomical and Behavioral Evolution. PLoS ONE, 2011, 6, e21634.	1.1	30
3792	A Molecular Insight into Algal-Oomycete Warfare: cDNA Analysis of <i>Ectocarpus siliculosus</i> Infected with the Basal Oomycete <i>Eurychasma dicksonii</i> . PLoS ONE, 2011, 6, e24500.	1.1	33
3793	Predicting the Impact of Alternative Splicing on Plant MADS Domain Protein Function. PLoS ONE, 2012, 7, e30524.	1.1	80
3794	Assessing the Diversity and Specificity of Two Freshwater Viral Communities through Metagenomics. PLoS ONE, 2012, 7, e33641.	1.1	227
3795	Exploring the Switchgrass Transcriptome Using Second-Generation Sequencing Technology. PLoS ONE, 2012, 7, e34225.	1.1	60
3796	Examining the Fish Microbiome: Vertebrate-Derived Bacteria as an Environmental Niche for the Discovery of Unique Marine Natural Products. PLoS ONE, 2012, 7, e35398.	1.1	79
3797	Digital Gene Expression Analysis Based on Integrated De Novo Transcriptome Assembly of Sweet Potato [<i>Ipomoea batatas</i> (L.) Lam.]. PLoS ONE, 2012, 7, e36234.	1.1	156
3798	High-Coverage ITS Primers for the DNA-Based Identification of Ascomycetes and Basidiomycetes in Environmental Samples. PLoS ONE, 2012, 7, e40863.	1.1	895
3799	454 Transcriptome Sequencing Suggests a Role for Two-Component Signalling in Cellularization and Differentiation of Barley Endosperm Transfer Cells. PLoS ONE, 2012, 7, e41867.	1.1	29
3800	Development, Characterization and Experimental Validation of a Cultivated Sunflower (<i>Helianthus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	28
3801	A Complex Set of Sex Pheromones Identified in the Cuttlefish <i>Sepia officinalis</i> . PLoS ONE, 2012, 7, e46531.	1.1	7
3802	Updating the Salivary Gland Transcriptome of <i>Phlebotomus papatasi</i> (Tunisian Strain): The Search for Sand Fly-Secreted Immunogenic Proteins for Humans. PLoS ONE, 2012, 7, e47347.	1.1	59
3803	Venom Proteome of the Box Jellyfish <i>Chironex fleckeri</i> . PLoS ONE, 2012, 7, e47866.	1.1	57
3804	RNA Interference of Endochitinases in the Sugarcane Endophyte <i>Trichoderma virens</i> 223 Reduces Its Fitness as a Biocontrol Agent of Pineapple Disease. PLoS ONE, 2012, 7, e47888.	1.1	36
3805	Identification of MicroRNAs from <i>Eugenia uniflora</i> by High-Throughput Sequencing and Bioinformatics Analysis. PLoS ONE, 2012, 7, e49811.	1.1	38
3806	Suppression Subtractive Hybridization Reveals Transcript Profiling of <i>Chlorella</i> under Heterotrophy to Photoautotrophy Transition. PLoS ONE, 2012, 7, e50414.	1.1	14
3807	The Carcinogenic Liver Fluke, <i>Clonorchis sinensis</i> : New Assembly, Reannotation and Analysis of the Genome and Characterization of Tissue Transcriptomes. PLoS ONE, 2013, 8, e54732.	1.1	77

#	ARTICLE	IF	CITATIONS
3808	Consequences of Normalizing Transcriptomic and Genomic Libraries of Plant Genomes Using a Duplex-Specific Nuclease and Tetramethylammonium Chloride. <i>PLoS ONE</i> , 2013, 8, e55913.	1.1	37
3809	Transcriptome and Proteome Exploration to Provide a Resource for the Study of <i>Agrocybe aegerita</i> . <i>PLoS ONE</i> , 2013, 8, e56686.	1.1	56
3810	Transcriptome Analysis of Pacific White Shrimp (<i>Litopenaeus vannamei</i>) Hepatopancreas in Response to Taura Syndrome Virus (TSV) Experimental Infection. <i>PLoS ONE</i> , 2013, 8, e57515.	1.1	101
3811	Differential Expression Profiles in the Midgut of <i>Triatoma infestans</i> Infected with <i>Trypanosoma cruzi</i> . <i>PLoS ONE</i> , 2013, 8, e61203.	1.1	39
3812	Deep Sequencing Reveals Transcriptome Re-Programming of <i>Taxus</i> \checkmark media Cells to the Elicitation with Methyl Jasmonate. <i>PLoS ONE</i> , 2013, 8, e62865.	1.1	71
3813	Mechanisms of Foot-and-Mouth Disease Virus Tropism Inferred from Differential Tissue Gene Expression. <i>PLoS ONE</i> , 2013, 8, e64119.	1.1	20
3814	Male-Biased Genes in Catfish as Revealed by RNA-Seq Analysis of the Testis Transcriptome. <i>PLoS ONE</i> , 2013, 8, e68452.	1.1	71
3815	ESTs Analysis Reveals Putative Genes Involved in Symbiotic Seed Germination in <i>Dendrobium officinale</i> . <i>PLoS ONE</i> , 2013, 8, e72705.	1.1	53
3816	Functional Metagenomics Reveals Novel Pathways of Prebiotic Breakdown by Human Gut Bacteria. <i>PLoS ONE</i> , 2013, 8, e72766.	1.1	78
3817	Identification and Expression Profiling of Odorant Binding Proteins and Chemosensory Proteins between Two Wingless Morphs and a Winged Morph of the Cotton Aphid <i>Aphis gossypii</i> Glover. <i>PLoS ONE</i> , 2013, 8, e73524.	1.1	86
3818	Transcriptome Profile of the Green Odorous Frog (<i>Odorrana margaretae</i>). <i>PLoS ONE</i> , 2013, 8, e75211.	1.1	33
3819	Large-Scale Collection and Analysis of Full-Length cDNAs from <i>Brachypodium distachyon</i> and Integration with Pooideae Sequence Resources. <i>PLoS ONE</i> , 2013, 8, e75265.	1.1	27
3820	Comparative Analysis of Latex Transcriptome Reveals Putative Molecular Mechanisms Underlying Super Productivity of <i>Hevea brasiliensis</i> . <i>PLoS ONE</i> , 2013, 8, e75307.	1.1	32
3821	Comparing Memory-Efficient Genome Assemblers on Stand-Alone and Cloud Infrastructures. <i>PLoS ONE</i> , 2013, 8, e75505.	1.1	21
3822	Sequence and Expression Characteristics of Long Noncoding RNAs in Honey Bee Caste Development $\hat{\epsilon}$ Potential Novel Regulators for Transgressive Ovary Size. <i>PLoS ONE</i> , 2013, 8, e78915.	1.1	69
3823	Identification of New Sphingomyelinases D in Pathogenic Fungi and Other Pathogenic Organisms. <i>PLoS ONE</i> , 2013, 8, e79240.	1.1	32
3824	Evaluation of Assembly Strategies Using RNA-Seq Data Associated with Grain Development of Wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2013, 8, e83530.	1.1	33
3825	In Silico Analysis of Antibiotic Resistance Genes in the Gut Microflora of Individuals from Diverse Geographies and Age-Groups. <i>PLoS ONE</i> , 2013, 8, e83823.	1.1	74

#	ARTICLE	IF	CITATIONS
3826	Sniffing Out Chemosensory Genes from the Mediterranean Fruit Fly, <i>Ceratitis capitata</i> . PLoS ONE, 2014, 9, e85523.	1.1	37
3827	Analyses of Hypomethylated Oil Palm Gene Space. PLoS ONE, 2014, 9, e86728.	1.1	26
3828	Using Mitogenomic and Nuclear Ribosomal Sequence Data to Investigate the Phylogeny of the <i>Xiphinema americanum</i> Species Complex. PLoS ONE, 2014, 9, e90035.	1.1	21
3829	De Novo Transcriptome Hybrid Assembly and Validation in the European Earwig (Dermaptera, Forficula) <i>Tj ETQq1 1.0,784314 rgBT /Ome</i>	1.1	17
3830	The Mitochondrial Genome of the Leaf-Cutter Ant <i>Atta laevigata</i> : A Mitogenome with a Large Number of Intergenic Spacers. PLoS ONE, 2014, 9, e97117.	1.1	37
3831	Sequence and Expression Analyses of Ethylene Response Factors Highly Expressed in Latex Cells from <i>Hevea brasiliensis</i> . PLoS ONE, 2014, 9, e99367.	1.1	21
3832	Molecular Characterization and Differential Expression of Olfactory Genes in the Antennae of the Black Cutworm Moth <i>Agrotis ipsilon</i> . PLoS ONE, 2014, 9, e103420.	1.1	66
3833	Frequent Loss and Alteration of the <i>MOXD2</i> Gene in Catarrhines and Whales: A Possible Connection with the Evolution of Olfaction. PLoS ONE, 2014, 9, e104085.	1.1	7
3834	Molecular Analysis of the Cold Tolerant Antarctic Nematode, <i>Panagrolaimus davidi</i> . PLoS ONE, 2014, 9, e104526.	1.1	28
3835	Exploring the Genetic Basis of Adaptation to High Elevations in Reptiles: A Comparative Transcriptome Analysis of Two Toad-Headed Agamas (Genus <i>Phrynocephalus</i>). PLoS ONE, 2014, 9, e112218.	1.1	27
3836	Comparisons of De Novo Transcriptome Assemblers in Diploid and Polyploid Species Using Peanut (<i>Arachis spp.</i>) RNA-Seq Data. PLoS ONE, 2014, 9, e115055.	1.1	54
3837	MicroRNA-Like Small RNAs Prediction in the Development of <i>Antrodia cinnamomea</i> . PLoS ONE, 2015, 10, e0123245.	1.1	35
3838	Asparagus Spears as a Model to Study Heteroxylan Biosynthesis during Secondary Wall Development. PLoS ONE, 2015, 10, e0123878.	1.1	17
3839	Analyses of the Complete Genome and Gene Expression of Chloroplast of Sweet Potato [<i>Ipomoea batata</i>]. PLoS ONE, 2015, 10, e0124083.	1.1	42
3840	Whitefly Genome Expression Reveals Host-Symbiont Interaction in Amino Acid Biosynthesis. PLoS ONE, 2015, 10, e0126751.	1.1	28
3841	Whole-Transcriptome Analysis of Differentially Expressed Genes in the Vegetative Buds, Floral Buds and Buds of <i>Chrysanthemum morifolium</i> . PLoS ONE, 2015, 10, e0128009.	1.1	54
3842	Male- and Female-Biased Gene Expression of Olfactory-Related Genes in the Antennae of Asian Corn Borer, <i>Ostrinia furnacalis</i> (Guené) (Lepidoptera: Crambidae). PLoS ONE, 2015, 10, e0128550.	1.1	33
3843	Identification and Evaluation of Reference Genes for Accurate Transcription Normalization in Safflower under Different Experimental Conditions. PLoS ONE, 2015, 10, e0140218.	1.1	13

#	ARTICLE	IF	CITATIONS
3844	Fixing Formalin: A Method to Recover Genomic-Scale DNA Sequence Data from Formalin-Fixed Museum Specimens Using High-Throughput Sequencing. PLoS ONE, 2015, 10, e0141579.	1.1	112
3845	Transcriptome Analysis of <i>Syringa oblata</i> Lindl. Inflorescence Identifies Genes Associated with Pigment Biosynthesis and Scent Metabolism. PLoS ONE, 2015, 10, e0142542.	1.1	34
3846	Gonadal Transcriptome Analysis in Sterile Double Haploid Japanese Flounder. PLoS ONE, 2015, 10, e0143204.	1.1	10
3847	Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. PLoS ONE, 2015, 10, e0145031.	1.1	28
3848	Comparative Analysis of Transcriptomes from Secondary Reproductives of Three Reticulitermes Termite Species. PLoS ONE, 2015, 10, e0145596.	1.1	14
3849	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. PLoS ONE, 2016, 11, e0146062.	1.1	93
3850	Analysis of the Transcriptome of the Infective Stage of the Beet Cyst Nematode, <i>H. schachtii</i> . PLoS ONE, 2016, 11, e0147511.	1.1	19
3851	Profiling Ethylene-Responsive Genes Expressed in the Latex of the Mature Virgin Rubber Trees Using cDNA Microarray. PLoS ONE, 2016, 11, e0152039.	1.1	18
3852	Characterization of Five Novel Mitoviruses in the White Pine Blister Rust Fungus <i>Cronartium ribicola</i> . PLoS ONE, 2016, 11, e0154267.	1.1	17
3853	Dissecting the Root Nodule Transcriptome of Chickpea (<i>Cicer arietinum</i> L.). PLoS ONE, 2016, 11, e0157908.	1.1	20
3854	Next-Generation Sequencing of an 88-Year-Old Specimen of the Poorly Known Species <i>Liagora japonica</i> (Nemaliales, Rhodophyta) Supports the Recognition of <i>Otohimella</i> gen. nov.. PLoS ONE, 2016, 11, e0158944.	1.1	21
3855	The Widespread Prevalence and Functional Significance of Silk-Like Structural Proteins in Metazoan Biological Materials. PLoS ONE, 2016, 11, e0159128.	1.1	19
3856	SNP Identification through Transcriptome Analysis of the European Brown Hare (<i>Lepus europaeus</i>): Cellular Energetics and Mother's Curse. PLoS ONE, 2016, 11, e0159939.	1.1	9
3857	Leaf Transcriptome Sequencing for Identifying Genic-SSR Markers and SNP Heterozygosity in Crossbred Mango Variety "Amrapali" (Mangifera indica L.). PLoS ONE, 2016, 11, e0164325.	1.1	25
3858	Metagenomic-Based Screening and Molecular Characterization of Cowpea-Infecting Viruses in Burkina Faso. PLoS ONE, 2016, 11, e0165188.	1.1	46
3859	Evolution of the Tetrapyrrole Biosynthetic Pathway in Secondary Algae: Conservation, Redundancy and Replacement. PLoS ONE, 2016, 11, e0166338.	1.1	33
3860	Metavisitor, a Suite of Galaxy Tools for Simple and Rapid Detection and Discovery of Viruses in Deep Sequence Data. PLoS ONE, 2017, 12, e0168397.	1.1	8
3861	De novo transcriptome analysis of the excretory tubules of <i>Carausius morosus</i> (Phasmatodea) and possible functions of the midgut "appendices". PLoS ONE, 2017, 12, e0174984.	1.1	9

#	ARTICLE	IF	CITATIONS
3862	A genome-wide analysis of the RNA-guided silencing pathway in coffee reveals insights into its regulatory mechanisms. <i>PLoS ONE</i> , 2017, 12, e0176333.	1.1	16
3863	De novo transcriptomic analysis and development of EST-SSRs for <i>Sorbus pohuashanensis</i> (Hance) Hedl.. <i>PLoS ONE</i> , 2017, 12, e0179219.	1.1	16
3864	A first linkage map and downy mildew resistance QTL discovery for sweet basil (<i>Ocimum basilicum</i>) facilitated by double digestion restriction site associated DNA sequencing (ddRADseq). <i>PLoS ONE</i> , 2017, 12, e0184319.	1.1	20
3865	Characterization of the <i>Lycium barbarum</i> fruit transcriptome and development of EST-SSR markers. <i>PLoS ONE</i> , 2017, 12, e0187738.	1.1	41
3866	Taxonomically-linked growth phenotypes during arsenic stress among arsenic resistant bacteria isolated from soils overlying the Centralia coal seam fire. <i>PLoS ONE</i> , 2018, 13, e0191893.	1.1	16
3867	Prospecting for viral natural enemies of the fire ant <i>Solenopsis invicta</i> in Argentina. <i>PLoS ONE</i> , 2018, 13, e0192377.	1.1	19
3868	Antifreeze protein dispersion in eelpouts and related fishes reveals migration and climate alteration within the last 20 Ma. <i>PLoS ONE</i> , 2020, 15, e0243273.	1.1	6
3869	Intrahepatic Transcriptional Signature Associated with Response to Interferon- γ Treatment in the Woodchuck Model of Chronic Hepatitis B. <i>PLoS Pathogens</i> , 2015, 11, e1005103.	2.1	42
3870	EST analysis of mRNAs expressed during embryogenesis in <i>Gallus gallus</i> . <i>International Journal of Developmental Biology</i> , 2004, 48, 333-337.	0.3	10
3871	A conserved set of maternal genes? Insights from a molluscan transcriptome. <i>International Journal of Developmental Biology</i> , 2014, 58, 501-511.	0.3	28
3873	Investigations of molecular evolutionary mechanisms in partially sequenced heat shock protein70 homologue-coding gene of Oliveleaf yellowing-associated virus isolates from Tunisia. <i>Journal of DNA and RNA Research</i> , 2016, 1, 1-30.	1.0	1
3874	Improving automated de-novo transcriptome definition in non-model organisms by integrating manually defined gene information. <i>EMBnet Journal</i> , 2013, 19, 45.	0.2	1
3875	A comprehensive comparison between reference-based and "de novo" isoform assembly approaches. <i>EMBnet Journal</i> , 2013, 19, 76.	0.2	1
3876	Characterization of a Suite of 40 EST-derived Microsatellite Markers For Use in Sitka Spruce (<i>Picea</i>)	0.4	14
3877	Nuclear microsatellite markers for population genetic studies in sugar maple (<i>Acer saccharum</i>)	0.6	10
3878	Transcriptome resources and genome-wide marker development for Japanese larch (<i>Larix kaempferi</i>). <i>Frontiers of Agricultural Science and Engineering</i> , 2014, 1, 77.	0.9	10
3879	Annotation and validation of genes involved in photosynthesis and starch synthesis from a <i>Manihot</i> full-length cDNA library. <i>Frontiers of Agricultural Science and Engineering</i> , 2016, 3, 308.	0.9	1
3880	Biodiversidad y endemismo de los caracoles terrestres <i>Megalobulimus</i> y <i>Systrophia</i> en la Amazonia occidental. <i>Revista Peruana De Biología</i> , 2012, 19, 059-074.	0.1	19

#	ARTICLE	IF	CITATIONS
3881	Variabilidad genética de aislamientos colombianos del Potato mop-top virus (PMTV).. Agronomy Mesoamerican, 2013, 24, 1.	0.1	4
3882	Induction of programmed cell death in aging <i>Procentrum donghaiense</i> cells as was evidenced preliminarily by the identification of associated transcripts. <i>Acta Biologica Hungarica</i> , 2006, 57, 473-483.	0.7	9
3883	<i>Pseudomonas</i> spp. and other psychrotrophic microorganisms in inspected and non-inspected Brazilian Minas Frescal cheese: proteolytic, lipolytic and AprX production potential. <i>Pesquisa Veterinaria Brasileira</i> , 2019, 39, 807-815.	0.5	7
3884	Trimming and clustering sugarcane ESTs. <i>Genetics and Molecular Biology</i> , 2001, 24, 17-23.	0.6	49
3885	Identification of citrus expressed sequence tags (ESTs) encoding pleiotropic drug resistance (PDR)-like proteins. <i>Genetics and Molecular Biology</i> , 2007, 30, 857-865.	0.6	2
3886	ESTs and putative line-specific (broiler and layer) SNPs identified in genes expressed in <i>Gallus gallus</i> pituitary and hypothalamus. <i>Genetics and Molecular Biology</i> , 2007, 30, 1077-1081.	0.6	1
3887	Identification of methyl jasmonate-responsive genes in sugarcane using cDNA arrays. <i>Brazilian Journal of Plant Physiology</i> , 2005, 17, 173-180.	0.5	17
3888	Lytic bacteriophages as a potential alternative to control <i>Staphylococcus aureus</i> . <i>Pesquisa Agropecuaria Brasileira</i> , 0, 54, .	0.9	7
3889	Population Genetic Analysis of Oceanic Paddle Crab (<i>Varuna litterata</i>) in Thailand. <i>Sains Malaysiana</i> , 2017, 46, 2251-2261.	0.3	5
3890	CHARACTERIZATION OF THREE NOVEL VIRUSES INFECTING RASPBERRY. <i>Acta Horticulturae</i> , 2008, , 317-322.	0.1	2
3891	Effects of chilling accumulation on <i>DORMANCY-ASSOCIATED MADS-box</i> gene expressions in 'Satonishiki'™ sweet cherry. <i>Acta Horticulturae</i> , 2019, , 421-426.	0.1	2
3892	Tools and databases for solving problems in detection and identification of repetitive DNA sequences. <i>Periodicum Biologorum</i> , 2020, 121-122, 7-14.	0.1	5
3893	DEVELOPMENT OF EST-SSR MARKERS TO ASSESS GENETIC DIVERSITY OF BROCCOLI AND ITS RELATED SPECIES. <i>Indonesian Journal of Agricultural Science</i> , 2017, 17, 17.	0.3	8
3894	Differential Gene Expression of Resistant and Susceptible Sweetpotato Plants after Infection with the Causal Agents of Sweet Potato Virus Disease. <i>Journal of the American Society for Horticultural Science</i> , 2009, 134, 658-666.	0.5	27
3895	Transferability of Microsatellite Markers in the <i>Betulaceae</i> . <i>Journal of the American Society for Horticultural Science</i> , 2010, 135, 159-173.	0.5	35
3896	Microsatellite Markers for Raspberry and Blackberry. <i>Journal of the American Society for Horticultural Science</i> , 2010, 135, 271-278.	0.5	45
3897	Transcriptional Profiling of Rapidly Growing Cucumber Fruit by 454-Pyrosequencing Analysis. <i>Journal of the American Society for Horticultural Science</i> , 2010, 135, 291-302.	0.5	56
3898	Reflective Films and Expression of Light-regulated Genes in Field-grown Apple. <i>Journal of the American Society for Horticultural Science</i> , 2014, 139, 487-494.	0.5	5

#	ARTICLE	IF	CITATIONS
3899	Morphological and molecular characterization of <i>Colletotrichum capsici</i> causing leaf-spot of soybean. <i>Tropical Plant Research</i> , 2016, 3, 481-490.	0.4	4
3900	Gene expression profiling and expression analysis of freshwater shrimp (<i>Neocaridina denticulata</i>) Tj ETQq1 1 0.784314 rgBT /Overlock <i>Environmental Biology</i> , 2018, 39, 51-57.	0.2	11
3901	Dna Sequence Assembly Involving an Acyclic Graph Model. <i>Foundations of Computing and Decision Sciences</i> , 2013, 38, 25-34.	0.5	5
3903	Characterization of single nucleotide polymorphisms from expressed sequence tags of Chinese mitten crab <i>Eriocheir sinensis</i> A. <i>Aquatic Biology</i> , 2010, 11, 193-199.	0.5	6
3904	Incongruence of morphological determinations and DNA barcode sequences: a case study in <i>Cinnamomum</i> (Lauraceae). <i>Willdenowia</i> , 2019, 49, 383.	0.5	4
3905	<i>Pseudomonas azotoformans</i> Belonging to <i>Pseudomonas fluorescens</i> Group as Causative Agent of Blue Coloration in Carcasses of Slaughterhouse Rabbits. <i>Animals</i> , 2020, 10, 256.	1.0	12
3906	Characterization of a New Mixture of Mono-Rhamnolipids Produced by <i>Pseudomonas gessardii</i> Isolated from Edmonson Point (Antarctica). <i>Marine Drugs</i> , 2020, 18, 269.	2.2	19
3907	Infection Load and Prevalence of Novel Viruses Identified from the Bank Vole Do Not Associate with Exposure to Environmental Radioactivity. <i>Viruses</i> , 2020, 12, 44.	1.5	6
3908	Characterization of EST-SSR markers in bread wheat EST related to drought tolerance and functional analysis of SSR-containing unigenes. , 0, , 1-12.		3
3909	Genetic Evaluation of EST-SSRs Derived from <i>Gossypium herbaceum</i> . <i>Acta Agronomica Sinica</i> (China), 2009, 34, 2085-2091.	0.1	2
3910	Isolation, Characterization, and Mapping of Genomic Microsatellite Markers for the First Time in Sea-Island Cotton (<i>Gossypium barbadense</i>). <i>Acta Agronomica Sinica</i> (China), 2009, 35, 1013-1020.	0.1	3
3911	Comparative Genomics in Switchgrass Using 61,585 High-Quality Expressed Sequence Tags. <i>Plant Genome</i> , 2008, 1, .	1.6	57
3912	Abiotic Stress-Related Expressed Sequence Tags from the Diploid Strawberry <i>Fragaria vesca</i> f. <i>semperflorens</i> . <i>Plant Genome</i> , 2011, 4, .	1.6	7
3913	Identification and molecular characterization of a receptor-like protein kinase gene from <i>Corchorus capsularis</i> . <i>Turkish Journal of Biology</i> , 0, , .	2.1	4
3914	Isolation and Sequence of the Phosphoenolpyruvate Carboxylase Gene of the Marine Cyanobacterium <i>Synechococcus</i> PCC 7002. <i>Journal of Biological Sciences</i> , 2008, 8, 1261-1270.	0.1	7
3915	Cloning and mRNA Expression Analysis of the Gene Encoding Phenylalanine Ammonia-Lyase of the Ectomycorrhizal Fungus <i>Tricholoma matsutake</i> . <i>Journal of Microbiology and Biotechnology</i> , 2013, 23, 1055-1059.	0.9	9
3916	Bioinformatics Analysis of Distribution of Microsatellite Markers (SSRs) / Single Nucleotide Polymorphism (SNPs) in Expressed Transcripts of <i>Prosopis juliflora</i> : Frequency and Distribution. <i>Journal of Computer Science and Systems Biology</i> , 2008, 01, .	0.0	8
3917	Tandem repetitions in transcriptomes of some Solanaceae species. <i>American Journal of Molecular Biology</i> , 2012, 02, 140-152.	0.1	4

#	ARTICLE	IF	CITATIONS
3918	DNA Barcodes in Fig Cultivars (<i>Ficus carica</i> L.) Using ITS Regions of Ribosomal DNA, the psbA-trnH Spacer and the matK Coding Sequence. <i>American Journal of Plant Sciences</i> , 2015, 06, 95-102.	0.3	17
3919	Efficiency of microsatellite isolation from orchids via next generation sequencing. <i>Open Journal of Genetics</i> , 2012, 02, 167-172.	0.1	6
3920	Identification and characterization of differentially expressed genes during incompatible interaction between the foliar rust <i>Melampsora larici-populina</i> and poplar. <i>Genetics and Molecular Research</i> , 2014, 13, 2082-2093.	0.3	5
3921	In silico characterization of putative members of the coffee (<i>Coffea arabica</i>) ethylene signaling pathway. <i>Genetics and Molecular Research</i> , 2011, 10, 1277-1289.	0.3	6
3922	Identification of genes encoding hypothetical proteins in open-reading frame expressed sequence tags from mammalian stages of <i>Trypanosoma cruzi</i> . <i>Genetics and Molecular Research</i> , 2011, 10, 1589-1630.	0.3	4
3923	ChromaPipe: a pipeline for analysis, quality control and management for a DNA sequencing facility. <i>Genetics and Molecular Research</i> , 2008, 7, 861-871.	0.3	112
3924	Generation of a preliminary bovine gene atlas, using expression clustering to annotate gene function. <i>Genetics and Molecular Research</i> , 2009, 8, 1013-1027.	0.3	2
3925	Diversity of endophytic bacteria in Brazilian sugarcane. <i>Genetics and Molecular Research</i> , 2010, 9, 250-258.	0.3	122
3926	ISOLATION OF TWO VACCINIA VIRUS STRAINS FROM A SINGLE BOVINE VACCINIA OUTBREAK IN RURAL AREA FROM BRAZIL: IMPLICATIONS ON THE EMERGENCE OF ZOONOTIC ORTHOPOXVIRUSES. <i>American Journal of Tropical Medicine and Hygiene</i> , 2006, 75, 486-490.	0.6	90
3927	Metaheuristics for the DNA Fragment Assembly Problem. <i>International Journal of Computational Intelligence Research</i> , 2005, 1, .	0.3	18
3928	DNA Sequence Assembly using Particle Swarm Optimization. <i>International Journal of Computer Applications</i> , 2011, 28, 33-38.	0.2	17
3929	Insilico Analysis for Expressed Sequence Tags from Embryogenic Callus and Flower Buds of Panax ginseng C. A. Meyer. <i>Journal of Ginseng Research</i> , 2011, 35, 21-30.	3.0	12
3930	Human IgG inhibits IgA1 protease-dependent adherence of <i>Haemophilus influenzae</i> strains to human lung epithelial cells. <i>Asian Biomedicine</i> , 2011, 5, 45-56.	0.2	2
3931	Bio301: A Web-Based EST Annotation Pipeline That Facilitates Functional Comparison Studies. , 2012, 2012, 1-5.		4
3932	Platform of Hot Pepper Defense Genomics: Isolation of Pathogen Responsive Genes in Hot Pepper (<i>Capsicum annuum</i> L.) Non-Host Resistance Against Soybean Pustule Pathogen (<i>Xanthomonas</i>) Tj ETQq0 0 0 rgBT Overlock 10 Tf 50 1		
3933	Shifts in soil fungal communities in <i>Tuber melanosporum</i> plantations over a 20-year transition from agriculture fields to oak woodlands. <i>Forest Systems</i> , 2016, 25, 05.	0.1	3
3934	Expressed Sequence Tag Analysis for Identification and Characterization of Sex-Related Genes in the Giant Tiger Shrimp <i>Penaeus monodon</i> . <i>BMB Reports</i> , 2007, 40, 501-510.	1.1	62
3935	Mining for single nucleotide polymorphisms and insertions / deletions in expressed sequence tag libraries of oil palm. <i>Bioinformatics</i> , 2007, 2, 128-131.	0.2	25

#	ARTICLE	IF	CITATIONS
3936	Predicted metal binding sites for phytoremediation. <i>Bioinformatics</i> , 2009, 4, 66-70.	0.2	2
3937	Identification of single nucleotide polymorphism in ginger using expressed sequence tags. <i>Bioinformatics</i> , 2009, 4, 119-122.	0.2	17
3938	Exploiting EST databases for the mining and characterization of short sequence repeat (SSR) markers in <i>Catharanthus roseus</i> L. <i>Bioinformatics</i> , 2011, 5, 378-381.	0.2	11
3939	EuDBase: An online resource for automated EST analysis pipeline (ESTFrontier) and database for red seaweed <i>Eucheuma denticulatum</i> . <i>Bioinformatics</i> , 2011, 7, 157-162.	0.2	1
3940	Mining functional microsatellites in legume unigenes. <i>Bioinformatics</i> , 2011, 7, 264-270.	0.2	9
3941	Microsatellites in palm (<i>Arecaceae</i>) sequences. <i>Bioinformatics</i> , 2011, 7, 347-351.	0.2	10
3942	Analysis of expressed sequence tags (ESTs) from cocoa (<i>Theobroma cacao</i> L) upon infection with <i>Phytophthora megakarya</i> . <i>Bioinformatics</i> , 2012, 8, 65-69.	0.2	8
3943	A classification scoring schema to validate protein interactors. <i>Bioinformatics</i> , 2012, 8, 92-97.	0.2	13
3944	Towards an efficient computational mining approach to identify EST-SSR markers. <i>Bioinformatics</i> , 2012, 8, 201-202.	0.2	6
3945	ESMP: A high-throughput computational pipeline for mining SSR markers from ESTs. <i>Bioinformatics</i> , 2012, 8, 206-208.	0.2	7
3946	Mining for SSRs and FDMs from expressed sequence tags of <i>Camellia sinensis</i> . <i>Bioinformatics</i> , 2012, 8, 260-266.	0.2	19
3947	Suppression subtractive hybridization (SSH) combined with bioinformatics method: an integrated functional annotation approach for analysis of differentially expressed immune-genes in insects. <i>Bioinformatics</i> , 2013, 9, 216-221.	0.2	10
3948	Mining, characterization and validation of EST derived microsatellites from the transcriptome database of <i>Allium sativum</i> L. <i>Bioinformatics</i> , 2015, 11, 145-150.	0.2	10
3949	Computer aided gene mining for gingerol biosynthesis. <i>Bioinformatics</i> , 2015, 11, 316-321.	0.2	3
3950	In silico analysis of onion chitinases using transcriptome data. <i>Bioinformatics</i> , 2018, 14, 440-445.	0.2	3
3951	Computational analysis of transcriptome of Indian major carp, <i>Labeo rohita</i> (Hamilton-Buchanan, 1822) for functional annotation. <i>Bioinformatics</i> , 2012, 8, 1005-1011.	0.2	4
3952	Transcriptional signatures of somatic neoblasts and germline cells in <i>Macrostomum lignano</i> . <i>ELife</i> , 2016, 5, .	2.8	41
3953	<i>celsr1a</i> is essential for tissue homeostasis and onset of aging phenotypes in the zebrafish. <i>ELife</i> , 2020, 9, .	2.8	5

#	ARTICLE	IF	CITATIONS
3954	Structure of a mitochondrial ATP synthase with bound native cardiolipin. <i>ELife</i> , 2019, 8, .	2.8	69
3955	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	2.8	33
3956	GenomePeekâ€”an online tool for prokaryotic genome and metagenome analysis. <i>PeerJ</i> , 2015, 3, e1025.	0.9	12
3957	Comparative analysis of tissue-specific transcriptomes in the funnel-web spider <i>Macrothele calpeiana</i> (Araneae, Hexathelidae). <i>PeerJ</i> , 2015, 3, e1064.	0.9	14
3958	Targeted genomic enrichment and sequencing of CyHV-3 from carp tissues confirms low nucleotide diversity and mixed genotype infections. <i>PeerJ</i> , 2016, 4, e2516.	0.9	27
3959	Transcriptome analysis of <i>Polygonum minus</i> reveals candidate genes involved in important secondary metabolic pathways of phenylpropanoids and flavonoids. <i>PeerJ</i> , 2017, 5, e2938.	0.9	37
3960	290 metagenome-assembled genomes from the Mediterranean Sea: a resource for marine microbiology. <i>PeerJ</i> , 2017, 5, e3558.	0.9	71
3961	The complete mitochondrial genome of the grooved carpet shell, <i>Ruditapes decussatus</i> (Bivalvia), Tj ETQq1 10,784314, rgBT /Ove	0.9	16
3962	MetaCRIST: reference-guided extraction of CRISPR spacers from unassembled metagenomes. <i>PeerJ</i> , 2017, 5, e3788.	0.9	41
3963	The sugarcane mitochondrial genome: assembly, phylogenetics and transcriptomics. <i>PeerJ</i> , 2019, 7, e7558.	0.9	15
3964	A draft genome and transcriptome of common milkweed (<i>Asclepias syriaca</i>) as resources for evolutionary, ecological, and molecular studies in milkweeds and Apocynaceae. <i>PeerJ</i> , 2019, 7, e7649.	0.9	19
3965	Identification of an ancestral haplotype in the mitochondrial phylogeny of the ovine haplogroup B. <i>PeerJ</i> , 2019, 7, e7895.	0.9	14
3966	Classification and Phylogenetic Studies of Cephalopods from four countries of South-East Asia. <i>Korean Journal of Malacology</i> , 2016, 32, 55-62.	0.1	2
3967	Development, Characterization and Transferability of Peach Genic SSRs to some Rosaceae species. <i>Advances in Research</i> , 2015, 3, 165-180.	0.3	3
3968	Isolation and Identification of Cellulolytic and Xylanolytic Bacteria from Huancarhuaz Hot Spring, Peru. <i>Annual Research & Review in Biology</i> , 2014, 4, 2920-2930.	0.4	11
3969	Characterization of Expressed Genes Under Ozone Stress in Soybean. <i>Plant Breeding and Biotechnology</i> , 2013, 1, 270-276.	0.3	1
3970	Genetic Evidence of the Black Death in the Abbey of San Leonardo (Apulia Region, Italy): Tracing the Cause of Death in Two Individuals Buried with Coins. <i>Pathogens</i> , 2021, 10, 1354.	1.2	2
3971	SeekFusion - A Clinically Validated Fusion Transcript Detection Pipeline for PCR-Based Next-Generation Sequencing of RNA. <i>Frontiers in Genetics</i> , 2021, 12, 739054.	1.1	9

#	ARTICLE	IF	CITATIONS
3972	Metagenomic sequencing determines complete infectious bronchitis virus (avian Gammacoronavirus) vaccine strain genomes and associated viromes in chicken clinical samples. <i>Virus Genes</i> , 2021, 57, 529-540.	0.7	4
3973	Microbial Diversity Under the Influence of Natural Gas Storage in a Deep Aquifer. <i>Frontiers in Microbiology</i> , 2021, 12, 688929.	1.5	7
3974	Single-Nucleotide Polymorphisms in MICA and MICB Genes Could Play a Role in the Outcome in AML Patients after HSCT. <i>Journal of Clinical Medicine</i> , 2021, 10, 4636.	1.0	2
3975	bHLH Transcription Factors Undergo Alternative Splicing During Cold Acclimation in a Eucalyptus hybrid. <i>Plant Molecular Biology Reporter</i> , 0, , 1.	1.0	2
3977	Ubericin K, a New Pore-Forming Bacteriocin Targeting mannose-PTS. <i>Microbiology Spectrum</i> , 2021, 9, e0029921.	1.2	11
3981	GiSA: A Grid System for Genome Sequences Assembly. <i>Lecture Notes in Computer Science</i> , 2004, , 831-833.	1.0	0
3982	Large-Scale Biological Sequence Assembly and Alignment by Using Computing Grid. <i>Lecture Notes in Computer Science</i> , 2004, , 26-33.	1.0	0
3983	EST Projects for the Study of Genome Evolution in Legumes. , 2004, , .		0
3985	Methods of Computational Genomics. , 2004, , 279-342.		0
3986	Charting Contig-Component Relationships within the Triticeae. , 2005, , 109-120.		0
3987	Computer-Aided DNA Base Calling from Forward and Reverse Electropherograms. <i>Lecture Notes in Computer Science</i> , 2005, , 1-13.	1.0	1
3988	DNA Sequencing for Genome Analysis. , 2005, , .		0
3990	An Approach to Correcting DNA Sequencing Error. <i>Ruan Jian Xue Bao/Journal of Software</i> , 2006, 17, 193.	0.3	1
3991	Finding Data Broadness Via Generalized Nearest Neighbors. <i>Lecture Notes in Computer Science</i> , 2006, , 645-663.	1.0	2
3992	DNA Fragment Assembly: An Ant Colony System Approach. <i>Lecture Notes in Computer Science</i> , 2006, , 231-242.	1.0	1
3993	Analysis of hepatic gene expression in chickens with hormonallyâ€­induced lean and fat phenotypes. <i>FASEB Journal</i> , 2006, 20, A523.	0.2	0
3995	GoSh: a goat and sheep ESTs database. <i>Italian Journal of Animal Science</i> , 2007, 6, 60-62.	0.8	0
3996	Identification of the Putative Class 3 R Genes in <i>Coffea arabica</i> from CafEST Database. <i>Lecture Notes in Computer Science</i> , 2007, , 171-175.	1.0	0

#	ARTICLE	IF	CITATIONS
3997	Large-scale EST Sequencing. CGB Technical Report, 2007, 2007, .	1.5	0
3998	ASKGene, um sistema para processamento automatizado de DNA. Revista Electronica De Comunicacao, Informacao & Inovacao Em Saude: RECIIS, 2007, 1, .	0.2	0
3999	Gene/Protein Sequence Analysis. Springer Protocols, 2008, , 323-347.	0.1	0
4000	CHARACTERIZATION OF APHID-TRANSMITTED VIRUS ASSOCIATED WITH BLACK RASPBERRY DECLINE IN OREGON. Acta Horticulturae, 2008, , 327-332.	0.1	1
4001	Increasing ecological inference from high throughput sequencing of fungi in the environment through a tagging approach. Molecular Ecology Resources, 2008, .	2.2	0
4002	A family of GHF5 endo-1,4-beta-glucanases in the migratory plant-parasitic nematode Radopholus similis. Plant Pathology, 2008, .	1.2	0
4005	Fuzzy Genome Sequence Assembly for Single and Environmental Genomes. Studies in Fuzziness and Soft Computing, 2009, , 19-44.	0.6	0
4006	Functional Analysis of Expressed Sequence Tags from Hanwoo (Korean Cattle) cDNA Libraries. Journal of Animal Science and Technology, 2009, 51, 1-8.	0.8	4
4007	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0
4008	Chicken skeletal muscle-associated macroarray for gene discovery. Genetics and Molecular Research, 2010, 9, 188-207.	0.3	0
4009	PMSGGA: A FAST DNA FRAGMENT ASSEMBLER. , 2010, , .		0
4010	Construction of Web-Based Database for Anisakis Research. Journal of Life Science, 2010, 20, 411-415.	0.2	0
4011	Bioinformatics: Strategies, Trends, and Perspectives. , 0, , .		1
4012	Role of Bioinformatics as a Tool. , 2010, , 263-289.		2
4013	Granules. , 2010, , 201-225.		1
4014	ESTs and their Role in Functional Genomics. , 2010, , 104-119.		0
4015	Bioinformatics Resources of the Korean Bioinformation Center (KOBIC). Genomics and Informatics, 2010, 8, 165-169.	0.4	0
4016	Identification of Anthracnose Resistance Markers in Lentil through Comparative Screening with Marker Sequences from the Model Legume >Medicago truncatula. Atlas Journal of Biotechnology, 2011, 1, 9-20.	0.3	0

#	ARTICLE	IF	CITATIONS
4017	EST Analysis Pipeline: Use of Distributed Computing Resources. <i>Methods in Molecular Biology</i> , 2011, 722, 103-120.	0.4	0
4018	Functional analysis of expressed sequence tags from the liver and brain of Korean Jindo dogs. <i>BMB Reports</i> , 2011, 44, 238-243.	1.1	1
4019	Análisis de la estructura secundaria del LSU rRNA mitocondrial de caracoles terrestres peruanos (Orthalicidae: Gastropoda). <i>Revista Peruana De Biología</i> , 2011, 17, .	0.1	3
4021	Posición evolutiva de caracoles terrestres peruanos (Orthalicidae) entre los Stylommatophora (Mollusca: Gastropoda). <i>Revista Peruana De Biología</i> , 2011, 16, .	0.1	5
4022	Intraspecific divergence and DNA barcodes in <i>Systrophia helicycloides</i> (Gastropoda, Scolodontidae). <i>Revista Peruana De Biología</i> , 2011, 18, 201-208.	0.1	4
4024	Many-Core Processor Bioinformatics and Next-Generation Sequencing. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2012, , 172-188.	0.2	1
4025	Highly Efficient Parallel Approach to the Next-Generation DNA Sequencing. <i>Lecture Notes in Computer Science</i> , 2012, , 262-271.	1.0	0
4026	DGraph: Algorithms for Shotgun Reads Assembly Using De Bruijn Graph. <i>Lecture Notes in Computer Science</i> , 2012, , 14-21.	1.0	0
4028	Nature Inspired Algorithms To Solve DNA Fragment Assembly Problem: A Survey. <i>International Journal on Bioinformatics & Biosciences</i> , 2012, 2, 45-50.	0.2	1
4029	Development of an SNP Identification Pipeline for Highly Heterozygous Crops. , 2013, , 131-139.		0
4030	Characterization of de novo assemblies of quasispecies from next-generation sequencing via complex network modeling. <i>Scientific Research and Essays</i> , 2012, 7, .	0.1	0
4032	Transcriptome-based identification of enzymes involved in amino acid biosynthesis in the small brown planthopper, <i>Laodelphax striatellus</i> . <i>Open Access Insect Physiology</i> , 0, , 19.	0.8	0
4033	Degradación de tiocianato por hongos aislados de ambientes mineros y evaluación de su capacidad degradativa. <i>Revista Peruana De Biología</i> , 2012, 19, 081-088.	0.1	0
4034	RKN Lethal DB: A database for the identification of Root Knot Nematode (<i>Meloidogyne</i> spp.) candidate lethal genes. <i>Bioinformation</i> , 2012, 8, 950-952.	0.2	1
4036	Use of Bacterial Artificial Chromosomes in Metagenomics Studies, Overview. , 2013, , 1-12.		0
4037	Mapping and Analysis of Illumina Reads for Transcriptome of <i>Medicago truncatula</i> During the Early Organogenesis of the Nodule. <i>Bio-protocol</i> , 2013, 3, .	0.2	2
4038	Genetic diversity of soft corals of the family Alcyoniidae along Nang Rong Beach, Jorake Island and Juang Island, Amphur Sattahip, Chonburi Province, Thailand. <i>Galaxea</i> , 2013, 15, 182-188.	0.2	0
4039	De Novo Assembly Algorithms. <i>SpringerBriefs in Systems Biology</i> , 2013, , 55-83.	0.1	0

#	ARTICLE	IF	CITATIONS
4041	OrthoRBH: A streamlined pipeline for mining large gene family sequences in related species. <i>Bioinformatics</i> , 2013, 9, 267-269.	0.2	0
4042	SOFTvenom: an omics drug discovery approach from animal venoms. <i>EMBnet Journal</i> , 2013, 19, 91.	0.2	0
4043	Identification, sequence characterization and expression analysis of the arginine kinase gene in response to laminarin challenge from the Oriental land snail, <i>Nesiohelix samarangae</i> . <i>Korean Journal of Malacology</i> , 2013, 29, 171-179.	0.1	2
4044	The Sequence Reconstruction Problem. <i>Natural Computing Series</i> , 2014, , 23-43.	2.2	1
4045	Identification of Lettuce Germplasms and Commercial Cultivars Using SSR Markers Developed from EST. <i>Horticultural Science and Technology</i> , 2013, 31, 772-781.	0.9	5
4047	Transcriptome Analysis of Tessellated and Green Leaves in <i>Paphiopedilum</i> Orchids Using Illumina Paired-End Sequencing and Discovery Simple Sequence Repeat Markers. <i>Journal of Plant Biochemistry & Physiology</i> , 2014, 02, .	0.5	1
4048	Why Assembling Plant Genome Sequences Is So Challenging. , 2014, , 27-54.		0
4049	New Lymphocytic Choriomeningitis Virus-Like Arenavirus Infections. , 0, , 95-107.		0
4051	Performances of Bioinformatics Pipelines for the Identification of Pathogens in Clinical Samples with the De Novo Assembly Approaches: Focus on 2009 Pandemic Influenza A (H1N1). <i>Open Bioinformatics Journal</i> , 2014, 8, 1-5.	1.0	0
4052	Annotation Pipelines for Next-Generation Sequencing Projects. <i>Computational Biology</i> , 2015, , 325-367.	0.1	0
4053	Use of Bacterial Artificial Chromosomes in Metagenomics Studies, Overview. , 2015, , 671-680.		1
4054	High quality SNPs/Indels mining and characterization in ginger from ESTs data base. <i>Bioinformatics</i> , 2015, 11, 85-89.	0.2	2
4056	Genomic and Genotyping Characterization of Haplotype-Based Polymorphic Microsatellites in <i>Prunus</i> . <i>Journal of Genetics and Genome Research</i> , 2015, 2, .	0.3	1
4057	Mangomics: Information Systems Supporting Advanced Mango Breeding. , 2015, , 281-307.		0
4059	Health Services Data: Big Data Analytics for Deriving Predictive Healthcare Insights. , 2016, , 1-17.		2
4063	A Mitochondrial Cytochrome Oxidase I gene based identification of <i>Corbicula</i> ssp. commercially available in South Korea. <i>Korean Journal of Malacology</i> , 2016, 32, 127-131.	0.1	1
4064	Bioinformatics - Updated Features and Applications. , 2016, , .		4
4068	Workflow Integration and Orchestration, Opportunities and the Challenges. <i>Computer Communications and Networks</i> , 2017, , 137-156.	0.8	0

#	ARTICLE	IF	CITATIONS
4077	Isolation, identification and diversity of oleaginous yeasts from Kuching, Sarawak, Malaysia. <i>Biodiversitas</i> , 2018, 19, 1266-1272.	0.2	3
4083	Isolation, characterization and molecular identification of a novel aquareovirus that infects endangered fountain darter <i>Etheostoma fonticola</i> . <i>Diseases of Aquatic Organisms</i> , 2018, 130, 95-108.	0.5	0
4085	Mining of miRNAs using Next Generation Sequencing (NGS) data generated for Okra (<i>Abelmoschus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5	0.1	1
4087	Efficient Gene Assembly and Identification for Many Genome Samples. <i>Lecture Notes in Computer Science</i> , 2019, , 1-11.	1.0	0
4088	On the use of algebraic topology concepts to check the consistency of genome assembly. <i>Biophysics and Physicobiology</i> , 2019, 16, 444-451.	0.5	0
4089	DNA Fragment Assembly Using Quantum-Inspired Genetic Algorithm. <i>Advances in Computer and Electrical Engineering Book Series</i> , 2019, , 80-98.	0.2	1
4090	Development and validation of polymorphic EST-SSR markers for genetic diversity analysis in <i>Actinidia arguta</i> . <i>Fruits</i> , 2019, 74, 25-37.	0.3	2
4093	The first evidence of <i>Acidithiobacillus albertensis</i> in weathered ore samples from active gold mine HodruÅ¡ja-HÄ¡mre (Slovakia). <i>Nova Biotechnologica Et Chimica</i> , 2019, 18, 18-24.	0.1	1
4094	Analysis of Mitochondrial Genome from Labrador (<i>Canis lupus familiaris</i>) with Mammary Gland Tumour Reveals Novel Mutations and Polymorphisms. <i>Annals of Animal Science</i> , 2019, 19, 619-632.	0.6	6
4096	2HybridTools, a handy software to facilitate clone identification and mutation mapping from yeast two-hybrid screening. <i>PeerJ</i> , 2019, 7, e7245.	0.9	0
4099	Evaluating the role of wheat histone variant genes in development and response to abiotic stress in <i>Arabidopsis</i> . <i>Biologia Plantarum</i> , 0, , .	1.9	0
4102	Exploring Toxin Evolution: Venom Protein Transcript Sequencing and Transcriptome-Guided High-Throughput Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2068, 97-127.	0.4	3
4103	From EST to structure models for functional inference of APP, BACE1, PSEN1, PSEN2 genes. <i>Bioinformatics</i> , 2019, 15, 760-771.	0.2	0
4104	Constitutive expression of the wheat TaSOD5 gene enhances salinity tolerance of <i>Arabidopsis thaliana</i> . <i>Biologia Plantarum</i> , 0, 63, 750-756.	1.9	0
4106	OBSOLETE: NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2020, , .		0
4110	Active Fractions of Methanol Crude Obtained from Acacia Seyal Gum and their Antiproliferative Effects against Human Breast Cancer Cell Lines. <i>Global Journal of Science Frontier Research</i> , 2020, , 51-64.	0.1	2
4112	First report of begomoviruses infecting <i>Cucumis sativus</i> L. in North America and identification of a proposed new begomovirus species. <i>PeerJ</i> , 2020, 8, e9245.	0.9	4
4113	Genome Survey Sequencing of an Iconic "Trophy" Sportfish, the Roosterfish <i>Nematistius pectoralis</i> : Genome Size, Repetitive Elements, Nuclear RNA Gene Operon, and Microsatellite Discovery. <i>Genes</i> , 2021, 12, 1710.	1.0	6

#	ARTICLE	IF	CITATIONS
4114	Genomic evidence for adaptive differentiation among <i>Microhyla fissipes</i> populations: Implications for conservation. <i>Diversity and Distributions</i> , 2022, 28, 2665-2680.	1.9	5
4115	Discordance of genetic diversification between deep and shallow water species of <i>Kobeltocochlea Lindholm, 1909</i> (Caenogastropoda: Truncatelloidea: Benedictiidae) endemic to Lake Baikal with the description of a new species, review of the genus, and notes on its origin. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 0, .	0.6	4
4117	Bringing to light the molecular evolution of GUX genes in plants. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180208.	0.6	1
4120	Genome survey sequencing of the Caribbean spiny lobster <i>Panulirus argus</i> : Genome size, nuclear rRNA operon, repetitive elements, and microsatellite discovery. <i>PeerJ</i> , 2020, 8, e10554.	0.9	4
4122	New Insights into the Ecology and Physiology of Methanomassiliicoccales from Terrestrial and Aquatic Environments. <i>Microorganisms</i> , 2021, 9, 30.	1.6	23
4123	Genomic and transcriptomic identification of the cathepsin superfamily in the Mediterranean mussel <i>Mytilus galloprovincialis</i> . <i>Developmental and Comparative Immunology</i> , 2022, 127, 104286.	1.0	9
4125	Discovery and Analysis of RNA Viruses in Insects. <i>Springer Protocols</i> , 2020, , 191-200.	0.1	0
4127	Phylogenetic relationships of Iranian <i>Allium</i> species using the <i>matK</i> (cpDNA gene) region. <i>Journal of Plant Biotechnology</i> , 2020, 47, 15-25.	0.1	3
4131	Data Intensive Computing for Bioinformatics. , 0, , 287-321.		4
4132	Data Intensive Computing for Bioinformatics. <i>Advances in Systems Analysis, Software Engineering, and High Performance Computing Book Series</i> , 0, , 207-241.	0.5	1
4135	Sequencing the Human Genome: A Historical Perspective on Challenges for Systems Integration. , 2006, , 365-399.		0
4136	Sequencing Genes and Gene Islands by Gene Enrichment. , 2009, , 673-689.		1
4138	Characterization of nuclear mitochondrial insertions in the whole genomes of primates. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa089.	1.5	14
4142	Genetic analysis of chromosome 20-related posterior polymorphous corneal dystrophy: genetic heterogeneity and exclusion of three candidate genes. <i>Molecular Vision</i> , 2008, 14, 71-80.	1.1	31
4143	Expression profiles during dedifferentiation in newt lens regeneration revealed by expressed sequence tags. <i>Molecular Vision</i> , 2010, 16, 72-8.	1.1	29
4144	Serologic prevalence of MPV1 in mouse strains in a commercial laboratory mouse colony determined by using VP1 antigen. <i>Journal of the American Association for Laboratory Animal Science</i> , 2010, 49, 437-42.	0.6	10
4145	Isolation and cultivation of fungal strains from in vitro cell cultures of two marine sponges (Porifera: Halichondrida and Haplosclerida). <i>Brazilian Journal of Microbiology</i> , 2011, 42, 1560-8.	0.8	3
4147	Identification of plasmids from Brazilian <i>Chromobacterium violaceum</i> strains. <i>Canadian Journal of Microbiology</i> , 2022, 68, 45-54.	0.8	3

#	ARTICLE	IF	CITATIONS
4148	Virus-derived sequences from the transcriptomes of two snail vectors of schistosomiasis, <i>Biomphalaria pfeifferi</i> and <i>Bulinus globosus</i> from Kenya. PeerJ, 2021, 9, e12290.	0.9	3
4149	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. Nature Microbiology, 2021, 6, 1561-1574.	5.9	57
4150	Production and characterization of naturally occurring antibacterial magnetite nanoparticles from magnetotactic <i>Bacillus</i> sp. MTB17. Journal of Applied Microbiology, 2022, 132, 2683-2693.	1.4	1
4152	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. Genome Research, 2001, 11, 281-289.	2.4	19
4153	Comparative genomics and antibiotic resistance of <i>Yersinia enterocolitica</i> obtained from a pork production chain and human clinical cases in Brazil. Food Research International, 2022, 152, 110917.	2.9	4
4154	Phylogeny of <i>Anopheles darlingi</i> (Diptera:Culicidae) based on the antimicrobial peptide genes cecropin and defensin. Acta Tropica, 2022, 227, 106285.	0.9	1
4155	Performance evaluation of three mesophilic upflow anaerobic sludge blanket bioreactors treating olive mill wastewater: Flocculent and granular inocula tests, organic loading rate effect and anaerobic consortia structure. Fuel, 2022, 313, 122951.	3.4	10
4156	Response surface methodology mediated optimization of Lignin peroxidase from <i>Bacillus mycoides</i> isolated from Simlipal Biosphere Reserve, Odisha, India. Journal of Genetic Engineering and Biotechnology, 2022, 20, 2.	1.5	5
4157	Construction of integrative transcriptome to boost systematic exploration of Bougainvillea. Scientific Reports, 2022, 12, 923.	1.6	2
4158	Taming the massive genome of Scots pine with PiSy50k, a new genotyping array for conifer research. Plant Journal, 2022, 109, 1337-1350.	2.8	13
4159	<sc>slag</sc>: A program for seeded local assembly of genes in complex genomes. Molecular Ecology Resources, 2022, 22, 1999-2017.	2.2	4
4160	Sporophyte Stage Genes Exhibit Stronger Selection Than Gametophyte Stage Genes in Haplodiplontic Giant Kelp. Frontiers in Marine Science, 2022, 8, .	1.2	5
4161	Complete mitochondrial genomes and phylogenetic analysis of four Baikal endemic <i>Batrachocottus</i> species (Scorpaeniformes: Cottidae). Mitochondrial DNA Part B: Resources, 2022, 7, 123-124.	0.2	1
4162	Finding and Characterizing Repeats in Plant Genomes. Methods in Molecular Biology, 2022, 2443, 327-385.	0.4	2
4163	Genome survey sequencing of the phyto-parasitic nematode <i>Hoplolaimus galeatus</i> . PeerJ, 2022, 10, e12749.	0.9	2
4165	Characterisation of <i>Trichoderma</i> strains using FTIR-ATR spectroscopy and molecular analysis. European Journal of Plant Pathology, 2022, 162, 945-956.	0.8	3
4166	Exploring Virome Diversity in Public Data in South America as an Approach for Detecting Viral Sources From Potentially Emerging Viruses. Frontiers in Genetics, 2021, 12, 722857.	1.1	2
4167	Genome survey sequencing of the long-legged spiny lobster <i>Panulirus longipes</i> (A.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 nuclear repetitive elements classification, and SSR marker discovery. Journal of Crustacean Biology, 2022, 42, .	0.3	2

#	ARTICLE	IF	CITATIONS
4168	Host range and molecular variability of the sadwavirus dioscorea mosaic associated virus. Archives of Virology, 2022, 167, 917-922.	0.9	3
4169	A robust, cost-effective and widely applicable whole-genome sequencing protocol for capripoxviruses. Journal of Virological Methods, 2022, 301, 114464.	1.0	5
4170	Antarctic fungi applied to textile dye bioremediation. Anais Da Academia Brasileira De Ciencias, 2022, 94, e20210234.	0.3	4
4171	Novel patterns of expression and recruitment of new genes on the <i>t</i> -haplotype, a mouse selfish chromosome. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20211985.	1.2	3
4172	Lack of Fetal Protection against Bovine Viral Diarrhea Virus in a Vaccinated Heifer. Viruses, 2022, 14, 311.	1.5	7
4173	Side-by-Side Comparison of Post-Entry Quarantine and High Throughput Sequencing Methods for Virus and Viroid Diagnosis. Biology, 2022, 11, 263.	1.3	12
4176	A Fast-Growing Oleaginous Strain of Coelastrella Capable of Astaxanthin and Canthaxanthin Accumulation in Phototrophy and Heterotrophy. Life, 2022, 12, 334.	1.1	7
4177	Substantive Morphological Descriptions, Phylogenetic Analysis and Single Nucleotide Polymorphisms of Aspergillus Species From Foeniculum vulgare. Frontiers in Microbiology, 2022, 13, 832320.	1.5	2
4178	Sugarcane Transcriptomics in Response to Abiotic and Biotic Stresses: A Review. Sugar Tech, 2022, 24, 1295-1318.	0.9	5
4179	The Identification of Ethidium Bromide-Degrading Bacteria from Laboratory Gel Electrophoresis Waste. BioTech, 2022, 11, 4.	1.3	1
4180	Sequences Encoding a Novel Toursvirus Identified from Southern and Northern Corn Rootworms (Coleoptera: Chrysomelidae). Viruses, 2022, 14, 397.	1.5	1
4181	Characterization of Streptomyces nymphaeiformis sp. nov., and its taxonomic relatedness to other polyhydroxybutyrate-degrading streptomycetes. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
4182	Characterization of Halophilic Inulinase Producing Strains of Bacillus and Klebsiella Species Isolated From the Salt Mines of Pakistan. Geomicrobiology Journal, 0, , 1-6.	1.0	0
4183	Novel viral RNA genomes of the vine mealybug Planococcus ficus. Journal of General Virology, 2022, 103, .	1.3	3
4184	Dissecting the Species-Specific Virome in Culicoides of Thrace. Frontiers in Microbiology, 2022, 13, 802577.	1.5	3
4185	Discovery of a Novel Species of Trichomonasvirus in the Human Parasite Trichomonas vaginalis Using Transcriptome Mining. Viruses, 2022, 14, 548.	1.5	2
4186	The Singular Evolution of Olea Genome Structure. Frontiers in Plant Science, 2022, 13, 869048.	1.7	4
4187	High diversity of trematode metacercariae that parasitize freshwater gastropods in Bangkok, Thailand, and their infective situations, morphologies and phylogenetic relationships. Parasitology, 2022, , 1-21.	0.7	1

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4188	Development of SSR and SNP markers for identifying opium poppy. <i>International Journal of Legal Medicine</i> , 2022, 136, 1261-1271.	1.2	6
4189	Characterization of parainfluenza virus 5 from diarrheic piglet highlights its zoonotic potential. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	8
4190	Complete genome sequence of a novel fusarivirus from the phytopathogenic fungus <i>Corynespora cassiicola</i> . <i>Archives of Virology</i> , 2022, 167, 1375-1379.	0.9	2
4191	The life cycle of <i>Puccinia digitariae</i> on <i>Digitaria eriantha</i> and <i>Solanum</i> species in South Africa. <i>Mycologia</i> , 2022, , 1-18.	0.8	0
4193	Gut associated culturable bacterial community in intertidal polychaete worms (Annelida: Polychaeta), their characterization and implications in captive shrimp aquaculture. <i>Regional Studies in Marine Science</i> , 2022, 52, 102274.	0.4	4
4194	Using Simulated Annealing to solve the DNA Fragment Assembly Problem. , 2012, , 25-34.		0
4195	CottonGen: The Community Database for Cotton Genomics, Genetics, and Breeding Research. <i>Plants</i> , 2021, 10, 2805.	1.6	42
4197	Single-Larva RNA Sequencing Identifies Markers of Copper Toxicity and Exposure in Early <i>Mytilus californianus</i> Larvae. <i>Frontiers in Physiology</i> , 2021, 12, 647482.	1.3	1
4198	Limited Introgression between Rock-Wallabies with Extensive Chromosomal Rearrangements. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	17
4200	Recruitment of lysosomal cathepsins B, L and D as digestive enzymes in Coleoptera. <i>Insect Molecular Biology</i> , 2022, 31, 225-240.	1.0	4
4201	Functional screening of a human saliva metagenomic DNA reveal novel resistance genes against sodium hypochlorite and chlorhexidine. <i>BMC Oral Health</i> , 2021, 21, 632.	0.8	1
4202	Three phylogenetically distinct and culturable diazotrophs are perennial symbionts of leaf-cutting ants. <i>Ecology and Evolution</i> , 2021, 11, 17686-17699.	0.8	4
4203	Fungal dye-decolorizing peroxidase diversity: roles in either intra- or extracellular processes. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 2993-3007.	1.7	3
4205	CTREP-finder: A web service for quick identification and visualization of clean transgenic and genome-edited plants. , 2022, 1, 100003.		1
4206	Defining Virus-Carrier Networks that Shape the Composition of the Mosquito Core Virome of a Local Ecosystem. <i>Virus Evolution</i> , 2022, 8, veac036.	2.2	10
4313	Computational approaches toward single-nucleotide polymorphism discovery and its applications in plant breeding. , 2022, , 513-536.		0
4314	Mitogenome-wise codon usage pattern from comparative analysis of the first mitogenome of <i>Blepharipa</i> sp. (Muga uzifly) with other Oestroid flies. <i>Scientific Reports</i> , 2022, 12, 7028.	1.6	4
4315	In-Depth Satellitome Analyses of 37 <i>Drosophila</i> Species Illuminate Repetitive DNA Evolution in the <i>Drosophila</i> Genus. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	16

#	ARTICLE	IF	CITATIONS
4316	Characterization and expression of the Pirin gene family in <i>Triticum aestivum</i> . <i>Genome</i> , 2022, 65, 349-362.	0.9	6
4317	A mutation increases the specificity to plant compounds in an insect chemosensory protein. <i>Journal of Molecular Graphics and Modelling</i> , 2022, 114, 108191.	1.3	0
4318	Bracovirus Sneaks Into Apoptotic Bodies Transmitting Immunosuppressive Signaling Driven by Integration-Mediated eIF5A Hypusination. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	5
4320	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, .		4
4321	Genomic Survey and Resources for the Boring Giant Clam <i>Tridacna crocea</i> . <i>Genes</i> , 2022, 13, 903.	1.0	4
4322	RetroSnake: A Modular End-to-End Pipeline for Detection of Human Endogenous Retrovirus (HERV) Transposable Elements in Next Generation Sequencing (NGS) Data. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4323	Analysis of Complementary Sex-Determiner (csd) Allele Diversity in Different Honeybee Subspecies from Italy Based on NGS Data. <i>Genes</i> , 2022, 13, 991.	1.0	0
4324	Inter-Specific Genetic Exchange Despite Strong Divergence in Deep-Sea Hydrothermal Vent Gastropods of the Genus <i>Alviniconcha</i> . <i>Genes</i> , 2022, 13, 985.	1.0	5
4326	Plant growth-promoting characteristics of halotolerant endophytic bacteria isolated from <i>Sporobolus specatus</i> (Vahr) Kunth and <i>Cyperus laevigatus</i> L. of Ethiopian rift valley lakes. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	8
4327	Transcriptome of the synganglion in the tick <i>Ixodes ricinus</i> and evolution of the cys-loop ligand-gated ion channel family in ticks. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
4328	Transcriptomic Characterization of <i>Miscanthus sacchariflorus</i> – <i>M. lutarioriparius</i> and Its Implications for Energy Crop Development in the Semiarid Mine Area. <i>Plants</i> , 2022, 11, 1568.	1.6	4
4329	4-methyl-12-dodecahydro-1H-pyrrolo[3,4-b]quinoline-6-one produced by Endophytic Fungi <i>Aspergillus niger</i> E12 obtained from <i>Dodonaea viscosa</i> Plant Leaves as a Novel Antibacterial Compound. <i>Applied Biochemistry and Biotechnology</i> , 2022, 194, 5132-5150.	1.4	1
4330	Detection of non-reference porcine endogenous retrovirus loci in the Vietnamese native pig genome. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
4331	Genome sequence and experimental infection of calves with bovine gammaherpesvirus 4 (BoHV-4). <i>Archives of Virology</i> , 0, , .	0.9	0
4332	Reference-aided full-length transcript assembly, cDNA cloning, and molecular characterization of coronatine-insensitive 1b (COI1b) gene in coconut (<i>Cocos nucifera</i> L.). <i>Molecular Biology Reports</i> , 2022, 49, 8401-8411.	1.0	0
4333	Pseudomonas fluorescens group bacteria as responsible for chromatic alteration on rabbit carcasses. Possible hygienic implications. <i>Italian Journal of Food Safety</i> , 2022, 11, .	0.5	0
4334	Evaluation of the Bioefficacy and Insecticide Compatibility of Entomopathogens for Management of Whitefly (Hemiptera: Aleyrodidae) on Upland Cotton Under Laboratory and Polyhouse Conditions. <i>Neotropical Entomology</i> , 2022, 51, 600-612.	0.5	3
4335	Transcriptome sequencing and signal transduction for the enhanced tanshinone production in <i>Salvia miltiorrhiza</i> hairy roots induced by <i>Trichoderma atroviride</i> D16 polysaccharide fraction. <i>Bioscience, Biotechnology and Biochemistry</i> , 0, , .	0.6	2

#	ARTICLE	IF	CITATIONS
4336	Fungal Flora in Adult Females of the Rearing Population of Ambrosia Beetle <i>Euwallacea interjectus</i> (Blandford) (Coleoptera: Curculionidae: Scolytinae): Does It Differ from the Wild Population?. <i>Diversity</i> , 2022, 14, 535.	0.7	3
4337	Chromosome-scale assembly and annotation of the perennial ryegrass genome. <i>BMC Genomics</i> , 2022, 23, .	1.2	17
4338	Association of voltage-gated sodium channel mutations with field-evolved pyrethroid resistant phenotypes in soybean aphid and genetic markers for their detection. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
4339	Characterization of the complete chloroplast genome sequences of six <i>Dalbergia</i> species and its comparative analysis in the subfamily of Papilionoideae (Fabaceae). <i>PeerJ</i> , 0, 10, e13570.	0.9	4
4340	Implementation of GA-VirReport, a Web-Based Bioinformatics Toolkit for Post-Entry Quarantine Screening of Virus and Viroids in Plants. <i>Viruses</i> , 2022, 14, 1480.	1.5	3
4341	Rapid, in-field deployable, avian influenza virus haemagglutinin characterisation tool using MinION technology. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
4342	Emerging Computational Approaches for Antimicrobial Peptide Discovery. <i>Antibiotics</i> , 2022, 11, 936.	1.5	12
4343	Co-invading ectomycorrhizal fungal succession in pine-invaded mountain grasslands. <i>Fungal Ecology</i> , 2022, 60, 101176.	0.7	3
4344	Genetic diversity and antimicrobial susceptibility of <i>Staphylococcus aureus</i> isolated from bovine mastitis in Minas Gerais, Brazil. <i>Ciencia Rural</i> , 2023, 53, .	0.3	2
4345	Identification and characterization of a new geminivirus from soybean plants and determination of V2 as a pathogenicity factor and silencing suppressor. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	10
4346	Transcriptome analysis of emamectin benzoate caused midgut damage by inducing oxidative stress, energy metabolism disorder and apoptosis in gypsy moth (<i>Lymantria dispar</i>). <i>Pest Management Science</i> , 2022, 78, 4628-4637.	1.7	5
4347	Molecular identification and phylogenetic analysis of <i>Pseudomonas</i> sp. and <i>Aeromonas</i> sp. isolated from mine drainage water in Slovinky and MarkuÅ¡ovce (Slovakia). , 0, , .		0
4348	A Pipeline NanoTRF as a New Tool for De Novo Satellite DNA Identification in the Raw Nanopore Sequencing Reads of Plant Genomes. <i>Plants</i> , 2022, 11, 2103.	1.6	3
4350	Expanding the environmental virome: Infection profile in a native rainforest tree species. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
4351	Organic Farm Bedded Pack System Microbiomes: A Case Study with Comparisons to Similar and Different Bedded Packs. <i>Dairy</i> , 2022, 3, 587-607.	0.7	1
4352	Investigation of Peptide Toxin Diversity in Ribbon Worms (Nemertea) Using a Transcriptomic Approach. <i>Toxins</i> , 2022, 14, 542.	1.5	2
4353	Pathway elucidation of bioactive rhamnosylated ginsenosides in <i>Panax ginseng</i> and their de novo high-level production by engineered <i>Saccharomyces cerevisiae</i> . <i>Communications Biology</i> , 2022, 5, .	2.0	6
4354	Combined physiological responses and differential expression of drought-responsive genes preliminarily explain the drought resistance mechanism of <i>Lotus corniculatus</i> . <i>Functional Plant Biology</i> , 2022, , .	1.1	0

#	ARTICLE	IF	CITATIONS
4355	Genome analysis of <i>Phrixothrix hirtus</i> (Phengodidae) railroad worm shows the expansion of odorant-binding gene families and positive selection on morphogenesis and sex determination genes. <i>Gene</i> , 2023, 850, 146917.	1.0	1
4357	EukProt: A database of genome-scale predicted proteins across the diversity of eukaryotes. , 0, 2, .		57
4359	Exploring Conflicts in Whole Genome Phylogenetics: A Case Study Within Manakins (Aves: Pipridae). <i>Systematic Biology</i> , 2023, 72, 161-178.	2.7	2
4360	RetroSnake: A modular pipeline to detect human endogenous retroviruses in genome sequencing data. <i>IScience</i> , 2022, 25, 105289.	1.9	1
4361	Nuclear-embedded mitochondrial DNA sequences in 66,083 human genomes. <i>Nature</i> , 2022, 611, 105-114.	13.7	69
4362	hAssembler: A hybrid de novo genome assembly approach for large genomes. , 2020, 90, 2000-2005.		0
4365	The Complete Mitochondrial Genome of Eurasian Minnow (<i>Phoxinus cf. Phoxinus</i>) from the Heilongjiang River, and Its Phylogenetic Implications. <i>Animals</i> , 2022, 12, 2960.	1.0	1
4366	First Record of <i>Colletotrichum anthrisci</i> Causing Anthracnose on Avocado Fruits in Chile. <i>Pathogens</i> , 2022, 11, 1204.	1.2	3
4367	The <i>Amidella</i> Clade in Europe (Basidiomycota: Amanitaceae): Clarification of the Contentious <i>Amanita valens</i> (E.-J. Gilbert) Bertault and the Importance of Taxon-Specific PCR Primers for Identification. <i>Cryptogamie, Mycologie</i> , 2022, 43, .	0.2	1
4368	<i>Ā</i> <i>Cecinothofagus</i> Nieves-Aldrey & Lijlblad (Hymenoptera, Cynipidae) is likely an endoparasitoid of the gall-maker genus <i>Aditrochus</i> RÅ¼bsaamen (Hymenoptera, Pteromalidae). <i>Journal of Hymenoptera Research</i> , 0, 93, 33-42.	0.8	2
4369	Conventional and Omics Approaches for Understanding the Abiotic Stress Response in Cereal Cropsâ€”An Updated Overview. <i>Plants</i> , 2022, 11, 2852.	1.6	7
4370	Endophytic Fungi <i>Fusarium Equiseti</i> EF2 Isolated from <i>Leucas Aspera</i> : A Novel Biocontrol Agent Against <i>Culex</i> Sp. <i>International Journal of Life Science and Pharma Research</i> , 0, , L107-L117.	0.1	0
4372	<i>Bacillus velezensis</i> MT9 and <i>Pseudomonas chlororaphis</i> MT5 as biocontrol agents against citrus sooty mold and associated insect pests. <i>Biological Control</i> , 2022, 176, 105091.	1.4	3
4373	Computational Genomic Signatures. <i>Synthesis Lectures on Biomedical Engineering</i> , 2011, , .	0.1	0
4374	Lactoferrin gene polymorphisms associated with clinical mastitis in Honduran Holstein inheritance cows. <i>Molecular Biology Reports</i> , 0, , .	1.0	0
4375	First Study Case of Microbial Biocontrol Agents Isolated from Aquaponics Through the Mining of High-Throughput Sequencing Data to Control <i>Pythium aphanidermatum</i> on Lettuce. <i>Microbial Ecology</i> , 2023, 86, 1107-1119.	1.4	2
4376	The highest-elevation frog provides insights into mechanisms and evolution of defenses against high UV radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
4380	Detection by Block- and Band-Permuted Data. <i>IEEE Transactions on Signal Processing</i> , 2022, 70, 5778-5790.	3.2	0

#	ARTICLE	IF	CITATIONS
4381	Interactions among deep-sea mussels and their epibiotic and endosymbiotic chemoautotrophic bacteria: Insights from multi-omics analysis. <i>Zoological Research</i> , 2023, 44, 106-125.	0.9	4
4382	De-novo transcriptome assembly for discovery of putative microsatellite markers and transcription factors in black pepper (<i>Piper nigrum</i>). , 2019, 89, .		0
4383	Dominant Elongase Activity of Elov15a but Higher Expression of Elov15b in Common Carp (<i>Cyprinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	3
4384	Comparative genomics reveals insight into the evolutionary origin of massively scrambled genomes. <i>ELife</i> , 0, 11, .	2.8	5
4385	Polymorphisms in alternative oxidase genes from ecotypes of <i>Arabidopsis</i> and rice revealed an environmentâ€nduced linkage to altitude and rainfall. <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	2
4386	Chloroplast genome assemblies and comparative analyses of commercially important <i>Vaccinium</i> Âberry crops. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
4387	Widespread, human-associated redondoviruses infect the commensal protozoan <i>Entamoeba gingivalis</i> . <i>Cell Host and Microbe</i> , 2023, 31, 58-68.e5.	5.1	7
4389	Novel Virus Identification through Metagenomics: A Systematic Review. <i>Life</i> , 2022, 12, 2048.	1.1	7
4390	Functional Characterization of the Ryanodine Receptor Gene in <i>Diaphorina citri</i> . <i>Life</i> , 2022, 12, 2005.	1.1	1
4391	Transcriptome analyses of different edible tissues of <i>Clanis bilineata tsingtauca</i> (Lepidoptera:) Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 5	2.1	6
4392	Genome assembly of the acoe flatworm <i>Symsagittifera roscoffensis</i>, a model for research on body plan evolution and photosymbiosis. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	4
4393	Clade 2.3.4.4b H5N8 Subtype Avian Influenza Viruses Were Identified from the Common Crane Wintering in Yunnan Province, China. <i>Viruses</i> , 2023, 15, 38.	1.5	2
4394	Uncovering novel MHC alleles from RNA-Seq data: expanding the spectrum of MHC class I alleles in sheep. <i>BMC Genomic Data</i> , 2023, 24, .	0.7	1
4395	Development of novel microsatellite markers for population differentiation and detection of natural selection in wild populations of butter catfish, <i>Ompok bimaculatus</i> (Bloch, 1794). <i>Molecular Biology Reports</i> , 2023, 50, 2435-2444.	1.0	1
4396	Mycoparasites, Gut Dwellers, and Saprotrophs: Phylogenomic Reconstructions and Comparative Analyses of Kickxellomycotina Fungi. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	6
4397	Convergent genomics of longevity in rockfishes highlights the genetics of human life span variation. <i>Science Advances</i> , 2023, 9, .	4.7	5
4398	No evidence for sex chromosomes in natural populations of the cichlid fish <i>Astatotilapia burtoni</i>. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	5
4399	Unique Populations of Sulfur-Oxidizing Bacteria in Natural Cold Sulfur Springs in Slovakia. <i>Geomicrobiology Journal</i> , 2023, 40, 315-324.	1.0	5

#	ARTICLE	IF	CITATIONS
4400	Current Progress of Bioinformatics for Human Health. <i>Translational Bioinformatics</i> , 2023, , 145-162.	0.0	0
4401	Molecular characterization of potent antibacterial compound 4-(3-methylazetidin-1-yl)pentan-2-ol from <i>Calophyllum inophyllum</i> seed oil. <i>Biocatalysis and Agricultural Biotechnology</i> , 2023, 47, 102617.	1.5	1
4402	Influence of Substrate on the Fermentation Characteristics and Culture-Dependent Microbial Composition of Water Kefir. <i>Fermentation</i> , 2023, 9, 28.	1.4	10
4403	Genome Survey Sequencing of the Mole Cricket <i>Gryllotalpa orientalis</i> . <i>Genes</i> , 2023, 14, 255.	1.0	0
4404	High-throughput sequencing application in the detection and discovery of viruses associated with the regulated citrus leprosis disease complex. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
4405	PlantTribes2: Tools for comparative gene family analysis in plant genomics. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
4406	In Silico Mining and Characterization of High-Quality SNP/Indels in Some Agro-Economically Important Species Belonging to the Family Euphorbiaceae. <i>Genes</i> , 2023, 14, 332.	1.0	0
4407	The InBIO Barcoding Initiative Database: contribution to the knowledge on DNA barcodes of cuckoo wasps, with the description of new species from the Iberian Peninsula (Hymenoptera, Chrysididae). <i>Biodiversity Data Journal</i> , 0, 11, .	0.4	2
4408	Cryptic Chemical Variation in a Marine Red Alga as Revealed by Nontargeted Metabolomics. <i>ACS Omega</i> , 0, , .	1.6	0
4409	Rickettsia and relapsing fever <i>Borrelia</i> in <i>Alectorobius kelleyi</i> (Ixodida: Argasidae) from peri domestic bats in the northeastern United States. <i>Ticks and Tick-borne Diseases</i> , 2023, 14, 102157.	1.1	0
4413	Whole-genome sequence of synthetically derived <i>Brassica napus</i> inbred cultivar Da-Ae. G3: <i>Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	0
4414	Characterization of the microbiota dynamics associated with <i>Moniliophthora roreri</i> , causal agent of cocoa frosty pod rot disease, reveals new viral species. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
4415	Uncovering a Complex Virome Associated with the Cacao Pathogens <i>Ceratocystis cacaofunesta</i> and <i>Ceratocystis fimbriata</i> . <i>Pathogens</i> , 2023, 12, 287.	1.2	3
4416	<i>Rickettsia parkeri</i> hijacks tick hemocytes to manipulate cellular and humoral transcriptional responses. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	10
4417	Walnut witches' broom disease threatens butternut restoration efforts in Indiana. <i>Plant Disease</i> , 0, , .	0.7	0
4418	Evolutionary History of the <i>Poecilia picta</i> Sex Chromosomes. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	4
4420	Phenotypic and genotypic characterization of antibiotic resistance of <i>Salmonella Heidelberg</i> in the south of Brazil. <i>International Journal of Food Microbiology</i> , 2023, 391-393, 110151.	2.1	2
4421	Two major chromosome evolution events with unrivaled conserved gene content in pomegranate. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0

#	ARTICLE	IF	CITATIONS
4422	Antiviral immune response reveals host-specific virus infections in natural ant populations. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
4424	<i>Sida chlorotic leaf virus</i> : a new recombinant begomovirus found in non-cultivated plants and <i>Cucumis sativus</i> L. PeerJ, 0, 11, e15047.	0.9	0
4426	Evolution of tetraspanin antigens in the zoonotic Asian blood fluke <i>Schistosoma japonicum</i> . <i>Parasites and Vectors</i> , 2023, 16, .	1.0	0
4427	Antibiotic Resistance and Genetic Variability of <i>Acinetobacter</i> spp. from Wastewater Treatment Plant in KokÅ¡ov-BakÅ¡ja (Košice, Slovakia). <i>Microorganisms</i> , 2023, 11, 840.	1.6	2
4428	Purified cellulase-mediated simultaneous sugar utilization by <i>Bacillus albus</i> isolated from Similipal, Odisha, India. <i>Journal of Basic Microbiology</i> , 2023, 63, 759-780.	1.8	3
4429	Complete variable domain sequences of monoclonal antibody light chains identified from untargeted RNA sequencing data. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
4430	The whole genome of <i>Colletes collaris</i> (Hymenoptera: Colletidae): an important step in comparative genomics of cellophane bees. <i>Genome Biology and Evolution</i> , 0, , .	1.1	1
4431	Morphologic and molecular characterization of <i>Apertospathula pilata</i> n. sp., a novel freshwater spathidiid (Ciliophora, Litostomatea) from Idaho, USA. <i>European Journal of Protistology</i> , 2023, 89, 125990.	0.5	1
4444	Complete genome sequence of a novel bacteriophage vB_Pci_PCMW57 infecting phytobacteria <i>Pseudomonas cichorii</i> . <i>Molecular Biology Reports</i> , 0, , .	1.0	1
4505	Natural co-infection of pigs with African swine fever virus and porcine reproductive and respiratory syndrome virus in India. <i>Brazilian Journal of Microbiology</i> , 2024, 55, 1017-1022.	0.8	0
4506	Determination of the Mycovirome of a Necrotrophic Fungus. <i>Methods in Molecular Biology</i> , 2024, , 83-101.	0.4	0
4516	Overview of the Bioinformatics Databases and Tools for Genome Research and Crop Improvement. <i>Springer Protocols</i> , 2024, , 229-246.	0.1	0