ProtTest: selection of best-fit models of protein evolutio

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Citation Report

#	Article	IF	Citations
1	Lineage-specific variations of congruent evolution among DNA sequences from three genomes, and relaxed selective constraints on rbcL in Cryptomonas (Cryptophyceae). BMC Evolutionary Biology, 2005, 5, 56.	3.2	13
2	In silico characterization of the family of PARP-like poly(ADP-ribosyl)transferases (pARTs). BMC Genomics, 2005, 6, 139.	1.2	224
3	Molecular Evolution of the Plant Virus Family Bromoviridae Based on RNA3-Encoded Proteins. Journal of Molecular Evolution, 2005, 61, 697-705.	0.8	21
4	Serine proteinases of the human body louse (Pediculus humanus): sequence characterization and expression patterns. Parasitology Research, 2005, 97, 486-500.	0.6	14
5	ModelTest Server: a web-based tool for the statistical selection of models of nucleotide substitution online. Nucleic Acids Research, 2006, 34, W700-W703.	6.5	296
6	Genes coding for intermediate filament proteins closely related to the hagfish â€œthread keratins (TK)â€•Î± and Î³ also exist in lamprey, teleosts and amphibians. Experimental Cell Research, 2006, 312, 1447-1462.	1.2	31
7	A molecular phylogeny of the genus Echinococcus inferred from complete mitochondrial genomes. Parasitology, 2006, 134, 713-722.	0.7	389
8	Molecular Characterization of Crustacean Visual Pigments and the Evolution of Pancrustacean Opsins. Molecular Biology and Evolution, 2006, 24, 253-268.	3.5	79
9	A phylogenomic analysis of the Ascomycota. Fungal Genetics and Biology, 2006, 43, 715-725.	0.9	128
10	SmPKC1, a new protein kinase C identified in the platyhelminth parasite Schistosoma mansoni. Biochemical and Biophysical Research Communications, 2006, 345, 1138-1148.	1.0	18
11	On the phylogenetic position of a rare Iberian endemic mammal, the Pyrenean desman (Galemys) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.0	47
12	Full-length sequence and expression analysis of Toll-like receptor 9 in the gilthead seabream (Sparus) Tj ETQq1 1 0.784314 rgBT /Over	1.0	51
13	Evolutionarily Distinct Residues in the Uncoupling Protein UCP1 Are Essential for Its Characteristic Basal Proton Conductance. Journal of Molecular Biology, 2006, 359, 1010-1022.	2.0	21
14	Using Evolutionary Information and Ancestral Sequences to Understand the Sequenceâ€“Function Relationship in GLP-1 Agonists. Journal of Molecular Biology, 2006, 363, 977-988.	2.0	23
15	Sequence characterization and expression patterns of defensin and lysozyme encoding genes from the gut of the reduviid bug Triatoma brasiliensis. Insect Biochemistry and Molecular Biology, 2006, 36, 547-560.	1.2	92
16	A Gbx homeobox gene in amphioxus: Insights into ancestry of the ANTP class and evolution of the midbrain/hindbrain boundary. Developmental Biology, 2006, 295, 40-51.	0.9	98
17	The genomic repertoire for cell cycle control and DNA metabolism in S. purpuratus. Developmental Biology, 2006, 300, 238-251.	0.9	48
18	Biochemical and biological activities of the venom of the Chinese pitviper Zhaoermia mangshanensis, with the complete amino acid sequence and phylogenetic analysis of a novel Arg49 phospholipase A2 myotoxin. Toxicon, 2006, 47, 797-811.	0.8	34

#	Article	IF	Citations
19	Differential regulation of the zebrafish orthopedia 1 gene during fate determination of diencephalic neurons. BMC Developmental Biology, 2006, 6, 50.	2.1	63
20	Three rounds (1R/2R/3R) of genome duplications and the evolution of the glycolytic pathway in vertebrates. BMC Biology, 2006, 4, 16.	1.7	105
21	Morphological and gene expression similarities suggest that the ascidian neural gland may be osmoregulatory and homologous to vertebrate peri-ventricular organs. European Journal of Neuroscience, 2006, 24, 2299-2308.	1.2	36
22	The hemoglobin genes of Drosophila. FEBS Journal, 2006, 273, 468-480.	2.2	54
23	Combined Heat Shock Protein 90 and Ribosomal RNA Sequence Phylogeny Supports Multiple Replacements of Dinoflagellate Plastids. Journal of Eukaryotic Microbiology, 2006, 53, 217-224.	0.8	61
24	Genetic structure of the star sea squirt,Botryllus schlosseri, introduced in southern European harbours. Molecular Ecology, 2006, 15, 3957-3967.	2.0	55
25	An integrated view of protein evolution. Nature Reviews Genetics, 2006, 7, 337-348.	7.7	460
26	A PCR survey for posterior Hox genes in amphibians. Molecular Phylogenetics and Evolution, 2006, 38, 449-458.	1.2	15
27	Complete DNA sequence of the mitochondrial genome of the sea-slug, Aplysia californica: Conservation of the gene order in Euthyneura. Molecular Phylogenetics and Evolution, 2006, 38, 459-469.	1.2	64
28	Isolation and phylogeny of novel cytochrome P450 genes from tunicates (Ciona spp.): A CYP3 line in early deuterostomes?. Molecular Phylogenetics and Evolution, 2006, 40, 760-771.	1.2	19
29	Manganese superoxide dismutase based phylogeny of pathogenic fungi. Molecular Phylogenetics and Evolution, 2006, 41, 28-39.	1.2	28
30	Evolution of teleostean hatching enzyme genes and their paralogous genes. Development Genes and Evolution, 2006, 216, 769-784.	0.4	46
31	Evidence for a Diverse Cys-Loop Ligand-Gated Ion Channel Superfamily in Early Bilateria. Journal of Molecular Evolution, 2006, 62, 523-535.	0.8	79
32	The Complete Mitochondrial Genome of the Entomopathogenic Nematode Steinernema carpocapsae: Insights into Nematode Mitochondrial DNA Evolution and Phylogeny. Journal of Molecular Evolution, 2006, 62, 211-225.	0.8	24
33	Actinobacteria Cyclophilins: Phylogenetic Relationships and Description of New Class- and Order-Specific Paralogues. Journal of Molecular Evolution, 2006, 63, 719-732.	0.8	9
34	Novel Relationships Among Ten Fish Model Species Revealed Based on a Phylogenomic Analysis Using ESTs. Journal of Molecular Evolution, 2006, 62, 772-784.	0.8	150
35	Multiple Gene Duplication and Rapid Evolution in the groEL Gene: Functional Implications. Journal of Molecular Evolution, 2006, 63, 781-787.	0.8	60
36	Characterization and phylogenetic analysis of a cnidarian LMP X-like cDNA. Immunogenetics, 2006, 58, 454-464.	1.2	0

#	Article	IF	Citations
37	Polymorphism, natural selection, and structural modeling of class Ia MHC in the African clawed frog (Xenopus laevis). Immunogenetics, 2006, 58, 433-442.	1.2	14
38	Phylogenetics by likelihood: Evolutionary modeling as a tool for understanding the genome. Journal of Biomedical Informatics, 2006, 39, 51-61.	2.5	27
39	Evolution of â€˜front-endâ€™ desaturases in Echium (Boraginaceae). Biochemical Systematics and Ecology, 2006, 34, 327-337.	0.6	2
40	Schistosoma mansoni CBP/p300 has a conserved domain structure and interacts functionally with the nuclear receptor SmFtz-F1. Molecular and Biochemical Parasitology, 2006, 146, 180-191.	0.5	32
41	Assessment of methods for amino acid matrix selection and their use on empirical data shows that ad hoc assumptions for choice of matrix are not justified. BMC Evolutionary Biology, 2006, 6, 29.	3.2	977
42	Differential gene transfers and gene duplications in primary and secondary endosymbioses. BMC Evolutionary Biology, 2006, 6, 38.	3.2	6
43	Many genes in fish have species-specific asymmetric rates of molecular evolution. BMC Genomics, 2006, 7, 20.	1.2	100
44	High degree of conservancy among secreted salivary gland proteins from two geographically distant Phlebotomus duboscqi sandflies populations (Mali and Kenya). BMC Genomics, 2006, 7, 226.	1.2	93
45	The complete mitochondrial genome of a basal teleost, the Asian arowana (Scleropages formosus,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	73
46	Huntingtin gene evolution in Chordata and its peculiar features in the ascidian Ciona genus. BMC Genomics, 2006, 7, 288.	1.2	24
47	Comparative salivary gland transcriptomics of sandfly vectors of visceral leishmaniasis. BMC Genomics, 2006, 7, 52.	1.2	148
48	Asymmetric localization of Numb:EGFP in dividing neuroepithelial cells during neurulation inDanio rerio. Developmental Dynamics, 2006, 235, 934-948.	0.8	36
49	Ancient complexity of the non-Hox ANTP gene complement in the anthozoanNematostella vectensis. Implications for the evolution of the ANTP superclass. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2006, 306B, 589-596.	0.6	26
50	Heterotachy Processes in Rhodophyte-Derived Secondhand Plastid Genes: Implications for Addressing the Origin and Evolution of Dinoflagellate Plastids. Molecular Biology and Evolution, 2006, 23, 1504-1515.	3.5	50
51	Origin and Evolution of the Chloroplast trnK (matK) Intron: A Model for Evolution of Group II Intron RNA Structures. Molecular Biology and Evolution, 2006, 23, 380-391.	3.5	92
52	MtArt: A New Model of Amino Acid Replacement for Arthropoda. Molecular Biology and Evolution, 2006, 24, 1-5.	3.5	159
53	An unusual choanoflagellate protein released by Hedgehog autocatalytic processing. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 401-407.	1.2	56
54	Evolution of Glutamine Synthetase in Heterokonts: Evidence for Endosymbiotic Gene Transfer and the Early Evolution of Photosynthesis. Molecular Biology and Evolution, 2006, 23, 1048-1055.	3.5	36

#	Article	IF	Citations
55	Red blood with blue-blood ancestry: Intriguing structure of a snail hemoglobin. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12011-12016.	3.3	50
56	Genome of Crocodilepox Virus. Journal of Virology, 2006, 80, 4978-4991.	1.5	60
57	Monophyly of Rhizaria and Multigene Phylogeny of Unicellular Bikonts. Molecular Biology and Evolution, 2006, 23, 1922-1930.	3.5	42
58	Telomere-associated endonuclease-deficient Penelope-like retroelements in diverse eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9352-9357.	3.3	127
59	Nnalâ€like proteins are active metallocarboxypeptidases of a new and diverse M14 subfamily. FASEB Journal, 2007, 21, 851-865.	0.2	95
60	Lateral gene transfer between obligate intracellular bacteria: Evidence from the Rickettsia massiliae genome. Genome Research, 2007, 17, 1657-1664.	2.4	123
61	Cytochrome P450 1 Genes in Early Deuterostomes (Tunicates and Sea Urchins) and Vertebrates (Chicken and Frog): Origin and Diversification of the CYP1 Gene Family. Molecular Biology and Evolution, 2007, 24, 2619-2631.	3.5	84
62	The Î±D-Globin Gene Originated via Duplication of an Embryonic Î±-Like Globin Gene in the Ancestor of Tetrapod Vertebrates. Molecular Biology and Evolution, 2007, 24, 1982-1990.	3.5	46
63	Evolution and Functional Characterization of the RH50 Gene from the Ammonia-Oxidizing Bacterium Nitrosomonas europaea. Journal of Bacteriology, 2007, 189, 9090-9100.	1.0	23
64	Testing the Neutral Fixation of Hetero-Oligomerism in the Archaeal Chaperonin CCT. Molecular Biology and Evolution, 2007, 24, 1384-1396.	3.5	13
65	Plasmids derived from Gifsy-1/Gifsy-2, lambdoid prophages contributing to the virulence of Salmonella enterica serovar Typhimurium: implications for the evolution of replication initiation proteins of lambdoid phages and enterobacteria. Microbiology (United Kingdom), 2007, 153, 1884-1896.	0.7	10
66	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. Nucleic Acids Research, 2007, 35, W38-W42.	6.5	47
67	Mitochondrial Genome and Nuclear Sequence Data Support Myzostomida As Part of the Annelid Radiation. Molecular Biology and Evolution, 2007, 24, 1690-1701.	3.5	98
68	Metagenomic Characterization of Chesapeake Bay Virioplankton. Applied and Environmental Microbiology, 2007, 73, 7629-7641.	1.4	199
69	A Complete Set of Flagellar Genes Acquired by Horizontal Transfer Coexists with the Endogenous Flagellar System in Rhodobacter sphaeroides. Journal of Bacteriology, 2007, 189, 3208-3216.	1.0	73
70	Phylogenomic Analysis Supports the Monophyly of Cryptophytes and Haptophytes and the Association of Rhizaria with Chromalveolates. Molecular Biology and Evolution, 2007, 24, 1702-1713.	3.5	218
71	Comparison of Cyanopeptolin Genes in Planktothrix , Microcystis , and Anabaena Strains: Evidence for Independent Evolution within Each Genus. Applied and Environmental Microbiology, 2007, 73, 7322-7330.	1.4	60
72	Convergent Domestication of pogo-like Transposases into Centromere-Binding Proteins in Fission Yeast and Mammals. Molecular Biology and Evolution, 2007, 25, 29-41.	3.5	112

#	Article	IF	Citations
73	Non-Mendelian Inheritance of Paralogs of 2 Cytoskeletal Genes in the Ciliate Chilodonella uncinata. Molecular Biology and Evolution, 2007, 24, 2495-2503.	3.5	16
74	Selective Pressures of HLA Genotypes and Antiviral Therapy on Human Immunodeficiency Virus Type 1 Sequence Mutation at a Population Level. Vaccine Journal, 2007, 14, 1266-1273.	3.2	14
75	The Hox gene complement of a pelagic chaetognath, Flaccisagitta enflata. Integrative and Comparative Biology, 2007, 47, 854-864.	0.9	15
76	Functional Divergence in the Arabidopsis Â-1,3-Glucanase Gene Family Inferred by Phylogenetic Reconstruction of Expression States. Molecular Biology and Evolution, 2007, 24, 1045-1055.	3.5	148
77	The Complete Mitochondrial Genome of the Onychophoran Epiperipatus biolleyi Reveals a Unique Transfer RNA Set and Provides Further Support for the Ecdysozoa Hypothesis. Molecular Biology and Evolution, 2007, 25, 42-51.	3.5	51
78	Functional Characterization and Evolutionary History of Two Aryl Hydrocarbon Receptor Isoforms (AhR1 and AhR2) from Avian Species. Toxicological Sciences, 2007, 99, 101-117.	1.4	78
79	Spiralian Phylogenomics Supports the Resurrection of Bryozoa Comprising Ectoprocta and Entoprocta. Molecular Biology and Evolution, 2007, 24, 2723-2729.	3.5	105
80	Phylogenomic Data Analyses Provide Evidence that Xenarthra and Afrotheria Are Sister Groups. Molecular Biology and Evolution, 2007, 24, 2059-2068.	3.5	115
81	Characterization and Evolution of the Cell Cycle-Associated Mob Domain-Containing Proteins in Eukaryotes. Evolutionary Bioinformatics, 2007, 3, 117693430700300.	0.6	14
82	The complete mitochondrial DNA sequence of the Mekong giant catfish (Pangasianodon gigas), and the phylogenetic relationships among Siluriformes. Gene, 2007, 387, 49-57.	1.0	67
83	Comparative and phylogenetic analysis of Î±-l-fucosidase genes. Gene, 2007, 392, 34-46.	1.0	42
84	Homologs of eukaryotic Ras superfamily proteins in prokaryotes and their novel phylogenetic correlation with their eukaryotic analogs. Gene, 2007, 396, 116-124.	1.0	55
85	Characterization of an indoleamine 2,3-dioxygenase-like protein found in humans and mice. Gene, 2007, 396, 203-213.	1.0	400
86	Hemoglobin structure/function and globin-gene evolution in the Arctic fish Liparis tunicatus. Gene, 2007, 406, 58-68.	1.0	12
87	Molecular evolutionary analyses of the Arabidopsis L7 ribosomal protein gene family. Gene, 2007, 403, 143-150.	1.0	3
88	Where do animal Î±â€amylases come from? An interkingdom trip. FEBS Letters, 2007, 581, 3927-3935.	1.3	30
89	Characterization of the cDNAs Encoding Three GnRH Forms in the Pejerrey Fish Odontesthes bonariensis (Atheriniformes) and the Evolution of GnRH Precursors. Journal of Molecular Evolution, 2007, 64, 614-627.	0.8	36
90	Distinctive expression and functional regulation of the maize (Zea mays L.) TOR kinase ortholog. Molecular BioSystems, 2007, 3, 794.	2.9	42

#	Article	IF	Citations
91	Function, Structure, and Evolution of the RubisCO-Like Proteins and Their RubisCO Homologs. Microbiology and Molecular Biology Reviews, 2007, 71, 576-599.	2.9	310
92	Tracing the Evolution of the Light-Harvesting Antennae in Chlorophyll a/b-Containing Organisms. Plant Physiology, 2007, 143, 1802-1816.	2.3	179
93	Divergent Evolution of Function in the ROK Sugar Kinase Superfamily:â€‰ Role of Enzyme Loops in Substrate Specificity. Biochemistry, 2007, 46, 13564-13572.	1.2	30
94	Complete mitochondrial genome of a Chinese scorpionMesobuthus martensii(Chelicerata,) Tj ETQq1 1 0.784314 rgBT /Overlo	0.7	21
95	Expressed Sequence Tags as a Tool for Phylogenetic Analysis of Placental Mammal Evolution. PLoS ONE, 2007, 2, e775.	1.1	7
96	A Type II Polyketide Synthase is Responsible for Anthraquinone Biosynthesis in Photorhabdus luminescens. ChemBioChem, 2007, 8, 1721-1728.	1.3	111
97	Development of oral and pharyngeal teeth in the medaka (Oryzias latipes): comparison of morphology and expression of eve1 gene. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 693-708.	0.6	43
98	Ancient linkage of a POU class 6 and an anterior hoxâ€like gene in cnidaria: implications for the evolution of homeobox genes. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 777-784.	0.6	6
99	Molecular phylogeny of Clupeiformes (Actinopterygii) inferred from nuclear and mitochondrial DNA sequences. Molecular Phylogenetics and Evolution, 2007, 44, 386-398.	1.2	89
100	Phylogeny of Calvin cycle enzymes supports Plantae monophyly. Molecular Phylogenetics and Evolution, 2007, 45, 384-391.	1.2	75
101	Mitogenomic analyses of caniform relationships. Molecular Phylogenetics and Evolution, 2007, 45, 863-874.	1.2	125
102	The complete mitochondrial genome of Scutigerella causeyae (Myriapoda: Symphyla) and the phylogenetic position of Symphyla. Molecular Phylogenetics and Evolution, 2007, 45, 251-260.	1.2	28
103	EST sequencing of Onychophora and phylogenomic analysis of Metazoa. Molecular Phylogenetics and Evolution, 2007, 45, 942-951.	1.2	92
104	vasa-related genes and their expression in stem cells of colonial parasitic rhizocephalan barnacle Polyascus polygenea (Arthropoda: Crustacea: Cirripedia: Rhizocephala). Cell Biology International, 2007, 31, 97-108.	1.4	27
105	Increasing genetic distance to HIV-1 subtype B and F1 consensus sequences in the Brazilian epidemic: A challenge for vaccine strategies based on central immunogens?. Infection, Genetics and Evolution, 2007, 7, 594-599.	1.0	5
106	New methods for inferring population dynamics from microbial sequences. Infection, Genetics and Evolution, 2007, 7, 24-43.	1.0	18
107	Structural and functional comparison of the non-structural protein 4B in flaviviridae. Journal of Molecular Graphics and Modelling, 2007, 26, 546-557.	1.3	29
108	Molecular characterization, gene expression and dependence on thyroid hormones of two type I keratin genes (sseKer1 and sseKer2) in the flatfish Senegalese sole (Solea senegalensis Kaup). BMC Developmental Biology, 2007, 7, 118.	2.1	21

#	Article	IF	Citations
109	Characterization, developmental expression and evolutionary features of the huntingtin gene in the amphioxus Branchiostoma floridae. BMC Developmental Biology, 2007, 7, 127.	2.1	11
110	The non-dosage compensated Lsp1Î± gene of Drosophila melanogaster escapes acetylation by MOF in larval fat body nuclei, but is flanked by two dosage compensated genes. BMC Molecular Biology, 2007, 8, 35.	3.0	7
111	The Gas family of proteins ofSaccharomyces cerevisiae: characterization and evolutionary analysis. Yeast, 2007, 24, 297-308.	0.8	99
112	Phylogenetic analysis of haloalkane dehalogenases. Proteins: Structure, Function and Bioinformatics, 2007, 67, 305-316.	1.5	82
113	A model of restriction endonuclease MvaI in complex with DNA: A template for interpretation of experimental data and a guide for specificity engineering. Proteins: Structure, Function and Bioinformatics, 2007, 68, 324-336.	1.5	13
114	Multilocus sequence analysis of biocontrol fluorescent Pseudomonas spp. producing the antifungal compound 2,4-diacetylphloroglucinol. Environmental Microbiology, 2007, 9, 1939-1955.	1.8	73
115	Characterization of two globin genes from the malaria mosquito Anopheles gambiae: Divergent origin of nematoceran haemoglobins. Insect Molecular Biology, 2007, 16, 133-142.	1.0	23
116	Major ampullate spidroins from Euprosthenops australis: multiplicity at protein, mRNA and gene levels. Insect Molecular Biology, 2007, 16, 551-561.	1.0	46
117	Expression of Pax gene family members in the anthozoan cnidarian, Nematostella vectensis. Evolution & Development, 2007, 9, 25-38.	1.1	81
118	RATES OF MOLECULAR EVOLUTION IN BACTERIA ARE RELATIVELY CONSTANT DESPITE SPORE DORMANCY. Evolution; International Journal of Organic Evolution, 2007, 61, 280-288.	1.1	22
119	Diversification of the insulin receptor family in the helminth parasite Schistosoma mansoni. FEBS Journal, 2007, 274, 659-676.	2.2	78
120	Phylogenomic analyses of KCNA gene clusters in vertebrates: why do gene clusters stay intact?. BMC Evolutionary Biology, 2007, 7, 139.	3.2	22
121	Apolipocrustacein, formerly vitellogenin, is the major egg yolk precursor protein in decapod crustaceans and is homologous to insect apolipophorin II/I and vertebrate apolipoprotein B. BMC Evolutionary Biology, 2007, 7, 3.	3.2	113
122	Tic62: a protein family from metabolism to protein translocation. BMC Evolutionary Biology, 2007, 7, 43.	3.2	45
123	A practical approach to phylogenomics: the phylogeny of ray-finned fish (Actinopterygii) as a case study. BMC Evolutionary Biology, 2007, 7, 44.	3.2	322
124	Evolution of pigment synthesis pathways by gene and genome duplication in fish. BMC Evolutionary Biology, 2007, 7, 74.	3.2	191
125	The ancestor of the Paulinella chromatophore obtained a carboxysomal operon by horizontal gene transfer from a Nitrococcus-like Î³-proteobacterium. BMC Evolutionary Biology, 2007, 7, 85.	3.2	90
126	CR1 clade of non-LTR retrotransposons from Maculinea butterflies (Lepidoptera: Lycaenidae): evidence for recent horizontal transmission. BMC Evolutionary Biology, 2007, 7, 93.	3.2	23

#	Article	IF	Citations
127	Methods for selecting fixed-effect models for heterogeneous codon evolution, with comments on their application to gene and genome data. BMC Evolutionary Biology, 2007, 7, S5.	3.2	15
128	The complete mitochondrial genome of the sea spider Achelia bituberculata (Pycnogonida,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.2	27
129	The complete mitochondrial genome of Pseudocellus pearsei (Chelicerata: Ricinulei) and a comparison of mitochondrial gene rearrangements in Arachnida. BMC Genomics, 2007, 8, 386.	1.2	39
130	RCAN3, a novel calcineurin inhibitor that down-regulates NFAT-dependent cytokine gene expression. Biochimica Et Biophysica Acta - Molecular Cell Research, 2007, 1773, 330-341.	1.9	41
131	Making the most of mitochondrial genomes â€“ Markers for phylogeny, molecular ecology and barcodes in Schistosoma (Platyhelminthes: Digenea). International Journal for Parasitology, 2007, 37, 1401-1418.	1.3	78
132	Furcation, field-splitting, and the evolutionary origins of novelty in arthropod photoreceptors. Arthropod Structure and Development, 2007, 36, 386-400.	0.8	30
133	A Multigene Analysis of Corallomyxa tenera sp. nov. Suggests its Membership in a Clade that Includes Gromia, Haplosporidia and Foraminifera. Protist, 2007, 158, 457-472.	0.6	28
134	The developmental expression of foxl2 in the dogfish Scyliorhinus canicula. Gene Expression Patterns, 2007, 7, 793-797.	0.3	23
135	Recent independent evolution of msp1 polymorphism in Plasmodium vivax and related simian malaria parasites. Molecular and Biochemical Parasitology, 2007, 156, 74-79.	0.5	45
136	High Transcript Level of Fatty Acid-Binding Protein 11 but Not of Very Low-Density Lipoprotein Receptor Is Correlated to Ovarian Follicle Atresia in a Teleost Fish (Solea senegalensis)1. Biology of Reproduction, 2007, 77, 504-516.	1.2	62
137	The first lines of divergence in the Bacteria domain seem to be the hyperthermophilic organisms: a check using an outgroup of sequences from mesophiles in phylogenetic analysis. Annals of Microbiology, 2007, 57, 645-649.	1.1	0
138	Toxoplasma gondii Expresses Two Mitogen-Activated Protein Kinase Genes That Represent Distinct Protozoan Subfamilies. Journal of Molecular Evolution, 2007, 64, 4-14.	0.8	36
139	The VARL Gene Family and the Evolutionary Origins of the Master Cell-Type Regulatory Gene, regA, in Volvox carteri. Journal of Molecular Evolution, 2007, 65, 1-11.	0.8	39
140	Molecular Evolution of Hemojuvelin and the Repulsive Guidance Molecule Family. Journal of Molecular Evolution, 2007, 65, 68-81.	0.8	23
141	Tryptophan Biosynthesis in Stramenopiles: Eukaryotic Winners in the Diatom Complex Chloroplast. Journal of Molecular Evolution, 2007, 65, 496-511.	0.8	23
142	Antarctic Fish Mitochondrial Genomes Lack ND6 Gene. Journal of Molecular Evolution, 2007, 65, 519-528.	0.8	38
143	Evolution of Receptors for Growth Hormone and Somatolactin in Fish and Land Vertebrates: Lessons from the Lungfish and Sturgeon Orthologues. Journal of Molecular Evolution, 2007, 65, 359-372.	0.8	80
144	A Three-Gene Dinoflagellate Phylogeny Suggests Monophyly of Prorocentrales and a Basal Position for Amphidinium and Heterocapsa. Journal of Molecular Evolution, 2007, 65, 463-474.	0.8	97

#	Article	IF	Citations
145	Demarcation of ilarviruses based on the phylogeny of RNA2-encoded RdRp and a generic ramped annealing RT-PCR. Archives of Virology, 2007, 152, 1687-1698.	0.9	20
146	FGF signaling in gastrulation and neural development in Nematostella vectensis, an anthozoan cnidarian. Development Genes and Evolution, 2007, 217, 137-148.	0.4	91
147	Identification and analysis of cabut orthologs in invertebrates and vertebrates. Development Genes and Evolution, 2007, 217, 289-298.	0.4	17
148	Characterization of twist and snail gene expression during mesoderm and nervous system development in the polychaete annelid Capitella sp. I. Development Genes and Evolution, 2007, 217, 435-447.	0.4	39
149	Dating the early evolution of plants: detection and molecular clock analyses of orthologs. Molecular Genetics and Genomics, 2007, 278, 393-402.	1.0	103
150	The mitochondrial DNA of Xenoturbella bocki: genomic architecture and phylogenetic analysis. Theory in Biosciences, 2007, 126, 35-42.	0.6	47
151	Structural and phylogenetic relationship of ORF 31 from the Anticarsia gemmatalis MNPV to poly (ADP-ribose) polymerases (PARP). Virus Genes, 2008, 37, 177-184.	0.7	2
152	Species differences and effects of soft coral extracts from SinnulariaÂmaximus on the expression of cytochrome P4501A and 2N in butterflyfishes (Chaetodon spp.). Fish Physiology and Biochemistry, 2008, 34, 483-492.	0.9	13
153	Phylogeny of Dinoflagellate Plastid Genes Recently Transferred to the Nucleus Supports a Common Ancestry with Red Algal Plastid Genes. Journal of Molecular Evolution, 2008, 66, 175-184.	0.8	12
154	Comparative Analysis of Mitochondrial Genomes in Bombina (Anura; Bombinatoridae). Journal of Molecular Evolution, 2008, 67, 246-256.	0.8	18
155	The Phylogenetic Informativeness of Nucleotide and Amino Acid Sequences for Reconstructing the Vertebrate Tree. Journal of Molecular Evolution, 2008, 67, 437-447.	0.8	61
156	The Myofibrillar Protein, Projectin, is Highly Conserved Across Insect Evolution Except for Its PEVK Domain. Journal of Molecular Evolution, 2008, 67, 653-669.	0.8	24
157	Genetic diversity of the movement and coat protein genes of South American isolates of Prunus necrotic ringspot virus. Archives of Virology, 2008, 153, 909-919.	0.9	26
158	Cloning and Use of a Coral 36B4 Gene to Study the Differential Expression of Coral Genes Between Light and Dark Conditions. Marine Biotechnology, 2008, 10, 653-663.	1.1	28
159	TGFÎ² signaling in Tribolium: vertebrate-like components in a beetle. Development Genes and Evolution, 2008, 218, 203-213.	0.4	63
160	Comprehensive survey and classification of homeobox genes in the genome of amphioxus, Branchiostoma floridae. Development Genes and Evolution, 2008, 218, 579-590.	0.4	69
161	Centromeric retrotransposon lineages predate the maize/rice divergence and differ in abundance and activity. Molecular Genetics and Genomics, 2008, 279, 133-147.	1.0	50
162	Molecular characterization and expression analysis of five different elongation factor 1 alpha genes in the flatfish Senegalese sole (Solea senegalensis Kaup): Differential gene expression and thyroid hormones dependence during metamorphosis. BMC Molecular Biology, 2008, 9, 19.	3.0	36

#	Article	IF	Citations
163	Double-stranded RNA-activated protein kinase PKR of fishes and amphibians: Varying the number of double-stranded RNA binding domains and lineage-specific duplications. BMC Biology, 2008, 6, 12.	1.7	73
164	Expression of FoxC, FoxF, FoxL1, and FoxQ1 genes in the dogfish Scyliorhinus canicula defines ancient and derived roles for fox genes in vertebrate development. Developmental Dynamics, 2008, 237, 1590-1603.	0.8	32
165	Phylogenetic and structural information on glyceraldehyde-3-phosphate dehydrogenase (G3PDH) in Plasmodium provides functional insights. Infection, Genetics and Evolution, 2008, 8, 205-212.	1.0	7
166	Multigene analysis of lophophorate and chaetognath phylogenetic relationships. Molecular Phylogenetics and Evolution, 2008, 46, 206-214.	1.2	84
167	Phylogenetic placement of diverse amoebae inferred from multigene analyses and assessment of clade stability within â€˜Amoebozoaâ€™ upon removal of varying rate classes of SSU-rDNA. Molecular Phylogenetics and Evolution, 2008, 47, 339-352.	1.2	82
168	Evolution of mitochondrial gene orders in echinoderms. Molecular Phylogenetics and Evolution, 2008, 47, 855-864.	1.2	73
169	The complete mitochondrial genome of the demosponge Negombata magnifica (Poecilosclerida). Molecular Phylogenetics and Evolution, 2008, 47, 1238-1243.	1.2	21
170	Structure and evolution of the mitochondrial genomes of Haematobia irritans and Stomoxys calcitrans: The Muscidae (Diptera: Calyptratae) perspective. Molecular Phylogenetics and Evolution, 2008, 48, 850-857.	1.2	52
171	Hemocyanin in molluskâ€”A molecular survey and new data on hemocyanin genes in Solenogastres and Caudofoveataâ€ . Molecular Phylogenetics and Evolution, 2008, 49, 382-385.	1.2	19
172	Evolution of the Multivesicular Body ESCRT Machinery; Retention Across the Eukaryotic Lineage. Traffic, 2008, 9, 1698-1716.	1.3	243
173	New insights into evolution of crustacean hyperglycaemic hormone in decapods â€“ first characterization in Anomura. FEBS Journal, 2008, 275, 1039-1052.	2.2	12
174	Phylogenetic and Primary Sequence Characterization of Cathepsin B Cysteine Proteases from the Oxymonad Flagellate Monocercomonoides. Journal of Eukaryotic Microbiology, 2008, 55, 9-17.	0.8	12
175	Triosephosphate Isomerase Genes in Two Trophic Modes of Euglenoids (Euglenophyceae) and Their Phylogenetic Analysis. Journal of Eukaryotic Microbiology, 2008, 55, 170-177.	0.8	12
176	Characterization of a type A response regulator in the common bean (Phaseolus vulgaris) in response to phosphate starvation. Physiologia Plantarum, 2008, 132, 272-282.	2.6	8
177	The structure of CCTâ€“Hsc70NBD suggests a mechanism for Hsp70 delivery of substrates to the chaperonin. Nature Structural and Molecular Biology, 2008, 15, 858-864.	3.6	85
178	Exploiting the mosaic structure of trans-acyltransferase polyketide synthases for natural product discovery and pathway dissection. Nature Biotechnology, 2008, 26, 225-233.	9.4	362
179	Developmental expression of foxA and gata genes during gut formation in the polychaete annelid, Capitella sp. I. Evolution & Development, 2008, 10, 89-105.	1.1	79
180	AINTEGUMENTA homolog expression in Gnetum (gymnosperms) and implications for the evolution of ovulate axes in seed plants. Evolution & Development, 2008, 10, 280-287.	1.1	24

#	Article	IF	Citations
181	Chordate phylogeny and evolution: a not so simple threeâ€taxon problem. Journal of Zoology, 2008, 276, 117-141.	0.8	69
182	Phylogenetic analysis of 1.5ÂMbp and platypus EST data refute the Marsupionta hypothesis and unequivocally support Monotremata as sister group to Marsupialia/Placentalia. Zoologica Scripta, 2008, 37, 115-127.	0.7	18
183	Adaptive eukaryoteâ€toâ€eukaryote lateral gene transfer: stressâ€related genes of algal origin in the closest unicellular relatives of animals. Journal of Evolutionary Biology, 2008, 21, 1852-1860.	0.8	43
184	Ancestral roles of eukaryotic frataxin: mitochondrial frataxin function and heterologous expression of hydrogenosomal Trichomonas homologues in trypanosomes. Molecular Microbiology, 2008, 69, 94-109.	1.2	35
185	Funybase: a Fungal phylogenomic database. BMC Bioinformatics, 2008, 9, 456.	1.2	60
186	Diversification and adaptive sequence evolution of Caenorhabditis lysozymes (Nematoda: Rhabditidae). BMC Evolutionary Biology, 2008, 8, 114.	3.2	67
187	Evidence of a chimeric genome in the cyanobacterial ancestor of plastids. BMC Evolutionary Biology, 2008, 8, 117.	3.2	42
188	Broadly sampled multigene trees of eukaryotes. BMC Evolutionary Biology, 2008, 8, 14.	3.2	130
189	Unraveling the evolutionary history of the phosphoryl-transfer chain of the phosphoenolpyruvate:phosphotransferase system through phylogenetic analyses and genome context. BMC Evolutionary Biology, 2008, 8, 147.	3.2	23
190	Bioinformatic analysis of the neprilysin (M13) family of peptidases reveals complex evolutionary and functional relationships. BMC Evolutionary Biology, 2008, 8, 16.	3.2	71
191	Chlamydial genes shed light on the evolution of photoautotrophic eukaryotes. BMC Evolutionary Biology, 2008, 8, 203.	3.2	85
192	Molecular phylogeny of diplomonads and enteromonads based on SSU rRNA, alpha-tubulin and HSP90 genes: Implications for the evolutionary history of the double karyomastigont of diplomonads. BMC Evolutionary Biology, 2008, 8, 205.	3.2	41
193	Phylogenetic analyses suggest multiple changes of substrate specificity within the Glycosyl hydrolase 20 family. BMC Evolutionary Biology, 2008, 8, 214.	3.2	51
194	The evolutionary origin of the Runx/CBF-beta transcription factors - studies of the most basal metazoans. BMC Evolutionary Biology, 2008, 8, 228.	3.2	44
195	Evidence for positive selection acting on microcystin synthetase adenylation domains in three cyanobacterial genera. BMC Evolutionary Biology, 2008, 8, 256.	3.2	46
196	Structural and functional divergence of two fish aquaporin-1 water channels following teleost-specific gene duplication. BMC Evolutionary Biology, 2008, 8, 259.	3.2	57
197	Evolution of a family of metazoan active-site-serine enzymes from penicillin-binding proteins: a novel facet of the bacterial legacy. BMC Evolutionary Biology, 2008, 8, 26.	3.2	35
198	The Caenorhabditis globin gene family reveals extensive nematode-specific radiation and diversification. BMC Evolutionary Biology, 2008, 8, 279.	3.2	32

#	Article	IF	Citations
199	Evolutionary history of histone demethylase families: distinct evolutionary patterns suggest functional divergence. BMC Evolutionary Biology, 2008, 8, 294.	3.2	82
200	Factors affecting the concordance between orthologous gene trees and species tree in bacteria. BMC Evolutionary Biology, 2008, 8, 300.	3.2	20
201	Module evolution and substrate specificity of fungal nonribosomal peptide synthetases involved in siderophore biosynthesis. BMC Evolutionary Biology, 2008, 8, 328.	3.2	87
202	EST based phylogenomics of Syndermata questions monophyly of Eurotatoria. BMC Evolutionary Biology, 2008, 8, 345.	3.2	44
203	Evolution of gastropod mitochondrial genome arrangements. BMC Evolutionary Biology, 2008, 8, 61.	3.2	157
204	Molecular evolution and functional divergence of the bestrophin protein family. BMC Evolutionary Biology, 2008, 8, 72.	3.2	30
205	The complete mitochondrial genome sequence of the hydrothermal vent galatheid crab Shinkaia crosnieri (Crustacea: Decapoda: Anomura): A novel arrangement and incomplete tRNA suite. BMC Genomics, 2008, 9, 257.	1.2	65
206	Exploring the mialome of ticks: An annotated catalogue of midgut transcripts from the hard tick, Dermacentor variabilis (Acari: Ixodidae). BMC Genomics, 2008, 9, 552.	1.2	109
207	Recombination and selectional forces in cyanopeptolin NRPS operons from highly similar, but geographically remote Planktothrix strains. BMC Microbiology, 2008, 8, 141.	1.3	27
208	Expression of zebrafish aldh1a3 (raldh3) and absence of aldh1a1 in teleosts. Gene Expression Patterns, 2008, 8, 141-147.	0.3	54
209	Genetic characterization and phylogenetic position of Echinococcus felidis (Cestoda: Taeniidae) from the African lion. International Journal for Parasitology, 2008, 38, 861-868.	1.3	242
210	Planomonadida ord. nov. (Apusozoa): Ultrastructural Affinity with Micronuclearia podoventralis and Deep Divergences within Planomonas gen. nov.. Protist, 2008, 159, 535-562.	0.6	31
211	The sporadic occurrence of a group I intron-like element in the mtDNA rnl gene of Ophiostoma novo-ulmi subsp. americana. Mycological Research, 2008, 112, 564-582.	2.5	12
212	Evolutionary analysis of the transferrin gene in Antarctic Notothenioidei: A history of adaptive evolution and functional divergence. Marine Genomics, 2008, 1, 95-101.	0.4	7
213	Concerted gene recruitment in early plant evolution. Genome Biology, 2008, 9, R109.	13.9	46
214	Phylogenetic Position of Nemertea Derived from Phylogenomic Data. Molecular Biology and Evolution, 2008, 25, 728-736.	3.5	83
216	Methods for Analyzing Viral Evolution. , 2008, , 165-204.		5
217	Plant Virus Evolution. , 2008, , .		23

#	Article	IF	Citations
218	The PMS2 Subunit of Human MutLÎ± Contains a Metal Ion Binding Domain of the Iron-Dependent Repressor Protein Family. Journal of Molecular Biology, 2008, 382, 610-627.	2.0	55
219	Immunoglobulin light chain isotypes in the teleost Trematomus bernacchii. Molecular Immunology, 2008, 45, 3096-3106.	1.0	20
220	Dynamic evolutionary pattern of Î±2-macroglobulin in a model organism, the zebrafish (Danio rerio). Molecular Immunology, 2008, 45, 3312-3318.	1.0	8
221	Evolutionary relationships of virus species belonging to a distinct lineage within the Ampelovirus genus. Virus Research, 2008, 135, 125-135.	1.1	40
222	The Hedgehog gene family of the cnidarian, Nematostella vectensis, and implications for understanding metazoan Hedgehog pathway evolution. Developmental Biology, 2008, 313, 501-518.	0.9	127
223	Sequencing and Phylogenomic Analysis of Whole Mitochondrial Genomes of Animals. Methods in Molecular Biology, 2008, 422, 185-200.	0.4	4
224	Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Research, 2008, 36, W465-W469.	6.5	4,135
225	The evolution of transposon repeat-induced point mutation in the genome of Colletotrichum cereale: Reconciling sex, recombination and homoplasy in an â€˜â€˜asexualâ€•pathogen. Fungal Genetics and Biology, 2008, 45, 190-206.	0.9	44
226	Molecular characterization, phylogeny, and expression of c-type and g-type lysozymes in brill (Scophthalmus rhombus). Fish and Shellfish Immunology, 2008, 25, 57-65.	1.6	109
227	Detecting molecular adaptation at individual codons in the pattern recognition protein, lipopolysaccharide- and Î²-1,3-glucan-binding protein of decapods. Fish and Shellfish Immunology, 2008, 24, 638-648.	1.6	9
228	Complete mitochondrial genomes of three neobatrachian anurans: A case study of divergence time estimation using different data and calibration settings. Gene, 2008, 407, 116-129.	1.0	68
229	Complete nucleotide sequence and organization of the mitogenome of the silk moth Caligula boisduvalii (Lepidoptera: Saturniidae) and comparison with other lepidopteran insects. Gene, 2008, 413, 49-57.	1.0	88
230	Molecular evolution and characterization of hepcidin gene products in vertebrates. Gene, 2008, 415, 40-48.	1.0	102
231	Phylogenetic information from three mitochondrial genomes of Terebelliformia (Annelida) worms and duplication of the methionine tRNA. Gene, 2008, 416, 11-21.	1.0	42
232	Molecular characterization, gene expression and transcriptional regulation of cytosolic HSP90 genes in the flatfish Senegalese sole (Solea senegalensis Kaup). Gene, 2008, 416, 77-84.	1.0	94
233	The complete mitochondrial genome of Fusarium oxysporum: Insights into fungal mitochondrial evolution. Gene, 2008, 419, 7-15.	1.0	72
234	Molecular cloning and sequencing of metallothionein in squamates: New insights into the evolution of the metallothionein genes in vertebrates. Gene, 2008, 423, 48-56.	1.0	19
235	Evolution and functional divergence of monocarboxylate transporter genes in vertebrates. Gene, 2008, 423, 14-22.	1.0	11

#	Article	IF	Citations
236	The mitochondrial view of Blastocladiella emersonii. Gene, 2008, 424, 33-39.	1.0	14
237	The complete mitochondrial genome of Parafronurus youi (Insecta: Ephemeroptera) and phylogenetic position of the Ephemeroptera. Gene, 2008, 424, 18-24.	1.0	85
238	The phylogeny of the aromatic amino acid hydroxylases revisited by characterizing phenylalanine hydroxylase from Dictyostelium discoideum. Gene, 2008, 427, 86-92.	1.0	27
239	Molecular characterization and gene expression of six trypsinogens in the flatfish Senegalese sole (Solea senegalensis Kaup) during larval development and in tissues. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2008, 149, 334-344.	0.7	35
240	The archaebacterial origin of eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20356-20361.	3.3	306
241	Comparative and Evolutionary Genomics of Globin Genes in Fish. Methods in Enzymology, 2008, 436, 511-538.	0.4	6
242	Phylogeny of endocytic components yields insight into the process of nonendosymbiotic organelle evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 588-593.	3.3	120
243	Genesis and Expansion of Metazoan Transcription Factor Gene Classes. Molecular Biology and Evolution, 2008, 25, 980-996.	3.5	262
244	Evolution of Soldier-Specific Venomous Protease in Social Aphids. Molecular Biology and Evolution, 2008, 25, 2627-2641.	3.5	14
245	Natural Host Relationships and Genetic Diversity of Rodent-Associated Hantaviruses in Southeastern Brazil. Intervirology, 2008, 51, 299-310.	1.2	20
246	Intraphylum Diversity and Complex Evolution of Cyanobacterial Aminoacyl-tRNA Synthetases. Molecular Biology and Evolution, 2008, 25, 2369-2389.	3.5	23
247	Evolution of the Insulin Receptor Family and Receptor Isoform Expression in Vertebrates. Molecular Biology and Evolution, 2008, 25, 1043-1053.	3.5	90
248	Evolutionary analysis and molecular dissection of caveola biogenesis. Journal of Cell Science, 2008, 121, 2075-2086.	1.2	110
249	Mitochondrial cob and cox1 Genes and Editing of the Corresponding mRNAs in Dinophysis acuminata from Narragansett Bay, with Special Reference to the Phylogenetic Position of the Genus Dinophysis. Applied and Environmental Microbiology, 2008, 74, 1546-1554.	1.4	40
250	Carbonic Anhydrase in the Scleractinian Coral Stylophora pistillata. Journal of Biological Chemistry, 2008, 283, 25475-25484.	1.6	221
251	Molecular analysis of the diversity of the sulfideâ€Š:â€Šquinone reductase (sqr) gene in sediment environments. Microbiology (United Kingdom), 2008, 154, 3112-3121.	0.7	42
252	The promiscuous evolutionary history of the family Bromoviridae. Journal of General Virology, 2008, 89, 1739-1747.	1.3	48
253	Gene Expansion and Retention Leads to a Diverse Tyrosine Kinase Superfamily in Amphioxus. Molecular Biology and Evolution, 2008, 25, 1841-1854.	3.5	79

#	Article	IF	Citations
254	Inferring Evolution of Fish Proteins: The Globin Case Study. Methods in Enzymology, 2008, 436, 539-570.	0.4	36
255	Reductive Evolution of the Mitochondrial Processing Peptidases of the Unicellular Parasites Trichomonas vaginalis and Giardia intestinalis. PLoS Pathogens, 2008, 4, e1000243.	2.1	56
256	Conserved Features and Evolutionary Shifts of the EDA Signaling Pathway Involved in Vertebrate Skin Appendage Development. Molecular Biology and Evolution, 2008, 25, 912-928.	3.5	42
257	Synonymous Substitutions Substantially Improve Evolutionary Inference from Highly Diverged Proteins. Systematic Biology, 2008, 57, 367-377.	2.7	44
258	Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies. Systematic Biology, 2008, 57, 613-627.	2.7	162
259	Evolutionary Diversification in Polyamine Biosynthesis. Molecular Biology and Evolution, 2008, 25, 2119-2128.	3.5	150
260	Frequent and Widespread Parallel Evolution of Protein Sequences. Molecular Biology and Evolution, 2008, 25, 1943-1953.	3.5	98
261	Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. PLoS Computational Biology, 2008, 4, e1000214.	1.5	30
262	Anti-Fungal Innate Immunity in C. elegans Is Enhanced by Evolutionary Diversification of Antimicrobial Peptides. PLoS Pathogens, 2008, 4, e1000105.	2.1	212
263	Were class C iron-containing superoxide dismutases of trypanosomatid parasites initially imported into a complex plastid? A hypothesis based on analyses of their N-terminal targeting signals. Parasitology, 2008, 135, 1101-1110.	0.7	6
264	Origins and Evolution of the Formin Multigene Family That Is Involved in the Formation of Actin Filaments. Molecular Biology and Evolution, 2008, 25, 2717-2733.	3.5	65
265	Group II introns in Eubacteria and Archaea: ORF-less introns and new varieties. Rna, 2008, 14, 1704-1713.	1.6	81
266	EXOG, a novel paralog of Endonuclease G in higher eukaryotes. Nucleic Acids Research, 2008, 36, 1369-1379.	6.5	68
267	Phylogenetic and evolutionary relationships of RubisCO and the RubisCO-like proteins and the functional lessons provided by diverse molecular forms. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 2629-2640.	1.8	134
268	Novel reptilian uncoupling proteins: molecular evolution and gene expression during cold acclimation. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 979-985.	1.2	19
269	Evolution of Genes and Repeats in the Nimrod Superfamily. Molecular Biology and Evolution, 2008, 25, 2337-2347.	3.5	64
270	Analysis of Two Genomes from the Mitochondrion-Like Organelle of the Intestinal Parasite Blastocystis: Complete Sequences, Gene Content, and Genome Organization. Molecular Biology and Evolution, 2008, 25, 2475-2482.	3.5	59
271	Phylogeography of the ancient Parabathynellidae (Crustacea:Bathynellacea) from the Yilgarn region of Western Australia. Invertebrate Systematics, 2008, 22, 205.	0.5	70

#	Article	IF	Citations
272	Dissection of Functional Residues in Receptor Activity-Modifying Proteins through Phylogenetic and Statistical Analyses. Evolutionary Bioinformatics, 2008, 4, EBO.S705.	0.6	7
273	CYP3 phylogenomics: evidence for positive selection of CYP3A4 and CYP3A7. Pharmacogenetics and Genomics, 2008, 18, 53-66.	0.7	39
274	Emergence of Xin Demarcates a Key Innovation in Heart Evolution. PLoS ONE, 2008, 3, e2857.	1.1	23
275	Complete Genome Viral Phylogenies Suggests the Concerted Evolution of Regulatory Cores and Accessory Satellites. PLoS ONE, 2008, 3, e3500.	1.1	15
276	Genomic Organization and Expression Demonstrate Spatial and Temporal Hox Gene Colinearity in the Lophotrochozoan Capitella sp. I. PLoS ONE, 2008, 3, e4004.	1.1	104
277	Phylogenetic Analyses: A Toolbox Expanding towards Bayesian Methods. International Journal of Plant Genomics, 2008, 2008, 1-16.	2.2	7
278	Evolutionary Origins and Functions of the Carotenoid Biosynthetic Pathway in Marine Diatoms. PLoS ONE, 2008, 3, e2896.	1.1	134
279	Characterization of the complete mitochondrial genome of the giant silkworm moth, Eriogyna pyretorum (Lepidoptera: Saturniidae). International Journal of Biological Sciences, 2009, 5, 351-365.	2.6	111
280	The Impact of Outgroup Choice and Missing Data on Major Seed Plant Phylogenetics Using Genome-Wide EST Data. PLoS ONE, 2009, 4, e5764.	1.1	54
281	Analysis of Blood Stem Cell Activity and Cystatin Gene Expression in a Mouse Model Presenting a Chromosomal Deletion Encompassing Csta and Stfa2l1. PLoS ONE, 2009, 4, e7500.	1.1	15
282	Complete mitogenome sequence of the jewel beetle,Chrysochroa fulgidissima(Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	50
283	[FeFe] Hydrogenase Genetic Diversity Provides Insight into Molecular Adaptation in a Saline Microbial Mat Community. Applied and Environmental Microbiology, 2009, 75, 4620-4623.	1.4	48
284	Pyriform Spidroin 1, a Novel Member of the Silk Gene Family That Anchors Dragline Silk Fibers in Attachment Discs of the Black Widow Spider, Latrodectus hesperus. Journal of Biological Chemistry, 2009, 284, 29097-29108.	1.6	89
285	Pigmentation Pathway Evolution after Whole-Genome Duplication in Fish. Genome Biology and Evolution, 2009, 1, 479-493.	1.1	104
286	Regulation of stem cell maintenance by the Polycomb protein FIE has been conserved during land plant evolution. Development (Cambridge), 2009, 136, 2433-2444.	1.2	133
287	Discrete Shoot and Root Stem Cell-Promoting WUS/WOX5 Functions Are an Evolutionary Innovation of Angiosperms. Molecular Biology and Evolution, 2009, 26, 1745-1755.	3.5	115
288	Nodavirus Infection of Sea Bass (Dicentrarchus labrax) Induces Up-Regulation of Galectin-1 Expression with Potential Anti-Inflammatory Activity. Journal of Immunology, 2009, 183, 6600-6611.	0.4	62
289	Molecular Evolution of VEF -Domain-Containing PcG Genes in Plants. Molecular Plant, 2009, 2, 738-754.	3.9	41

#	Article	IF	Citations
290	Molecular diversity of visual pigments in Stomatopoda (Crustacea). Visual Neuroscience, 2009, 26, 255-265.	0.5	55
291	A novel phylogeny for the genus Echinococcus, based on nuclear data, challenges relationships based on mitochondrial evidence. Parasitology, 2009, 136, 317-328.	0.7	146
292	No Rosetta Stone for a Senseâ€“Antisense Origin of Aminoacyl tRNA Synthetase Classes. Molecular Biology and Evolution, 2009, 26, 445-450.	3.5	14
293	Molecular Characterization of Visual Pigments in Branchiopoda and the Evolution of Opsins in Arthropoda. Molecular Biology and Evolution, 2009, 26, 299-311.	3.5	39
294	Phylogenetic Relationships and Molecular Adaptation Dynamics of Human Rhinoviruses. Molecular Biology and Evolution, 2009, 26, 969-981.	3.5	30
295	Outbreaks of Disease Possibly Due to a Natural Avian Herpesvirus Infection in a Colony of Young Magnificent Frigatebirds (Fregata magnificens)in French Guiana. Journal of Wildlife Diseases, 2009, 45, 802-807.	0.3	25
296	Molecular mimicry: an important virulence strategy employed byLegionella pneumophilato subvert host functions. Future Microbiology, 2009, 4, 691-701.	1.0	49
297	The Endothelin System: Evolution of Vertebrate-Specific Ligand-Receptor Interactions by Three Rounds of Genome Duplication. Molecular Biology and Evolution, 2009, 26, 783-799.	3.5	81
298	A Broadscale Phylogenetic Analysis of Group II Intron RNAs and Intron-Encoded Reverse Transcriptases. Molecular Biology and Evolution, 2009, 26, 2795-2808.	3.5	33
299	Parallel Evolution between Aromatase and Androgen Receptor in the Animal Kingdom. Molecular Biology and Evolution, 2009, 26, 123-129.	3.5	14
300	Phylogenomics of Unusual Histone H2A Variants in Bdelloid Rotifers. PLoS Genetics, 2009, 5, e1000401.	1.5	26
301	Hemocyanin Suggests a Close Relationship of Remipedia and Hexapoda. Molecular Biology and Evolution, 2009, 26, 2711-2718.	3.5	60
302	A key role for the peroxisomalABCD2transporter in fatty acid homeostasis. American Journal of Physiology - Endocrinology and Metabolism, 2009, 296, E211-E221.	1.8	91
303	A New Malaria Agent in African Hominids. PLoS Pathogens, 2009, 5, e1000446.	2.1	127
304	A Phylogenomic Approach to Resolve the Basal Pterygote Divergence. Molecular Biology and Evolution, 2009, 26, 2719-2730.	3.5	66
305	Longicorn beetle that vectors pinewood nematode carries manyWolbachiagenes on an autosome. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 3791-3798.	1.2	55
306	Distribution of Endogenous Retroviruses in Crocodilians. Journal of Virology, 2009, 83, 10305-10308.	1.5	12
307	High-Level Molecular Diversity of Copper-Zinc Superoxide Dismutase Genes among and within Species of Arbuscular Mycorrhizal Fungi. Applied and Environmental Microbiology, 2009, 75, 1970-1978.	1.4	25

#	Article	IF	Citations
308	Statistical Comparison of Nucleotide, Amino Acid, and Codon Substitution Models for Evolutionary Analysis of Protein-Coding Sequences. Systematic Biology, 2009, 58, 199-210.	2.7	39
309	On the evolution of the Hysteriaceae and Mytilinidiaceae (Pleosporomycetidae, Dothideomycetes,) Tj ETQq1 1 0.784314 rgBT /Overlo	2.5	68
310	Seven Gene Phylogeny of Heterokonts. Protist, 2009, 160, 191-204.	0.6	118
311	Multigene Evidence for the Placement of a Heterotrophic Amoeboid Lineage Leukarachnion sp. among Photosynthetic Stramenopiles. Protist, 2009, 160, 376-385.	0.6	36
312	Two flavodoxin genes in Trichodesmium (Oscillatoriales, Cyanophyceae): Remarkable sequence divergence and possible functional diversification. Journal of Experimental Marine Biology and Ecology, 2009, 371, 93-101.	0.7	5
313	Phylogeny and evolution of Rab7 and Rab9 proteins. BMC Evolutionary Biology, 2009, 9, 101.	3.2	28
314	The evolution of nuclear auxin signalling. BMC Evolutionary Biology, 2009, 9, 126.	3.2	115
315	Temporal pattern of loss/persistence of duplicate genes involved in signal transduction and metabolic pathways after teleost-specific genome duplication. BMC Evolutionary Biology, 2009, 9, 127.	3.2	57
316	The evolution of YidC/Oxa/Alb3 family in the three domains of life: a phylogenomic analysis. BMC Evolutionary Biology, 2009, 9, 137.	3.2	39
317	Friend or foe? Evolutionary history of glycoside hydrolase family 32 genes encoding for sucrolytic activity in fungi and its implications for plant-fungal symbioses. BMC Evolutionary Biology, 2009, 9, 148.	3.2	77
318	On the phylogenetic position of Myzostomida: Can 77 genes get it wrong?. BMC Evolutionary Biology, 2009, 9, 150.	3.2	52
319	Domain duplication, divergence, and loss events in vertebrate Msx paralogs reveal phylogenomically informed disease markers. BMC Evolutionary Biology, 2009, 9, 18.	3.2	30
320	Neogastropod phylogenetic relationships based on entire mitochondrial genomes. BMC Evolutionary Biology, 2009, 9, 210.	3.2	116
321	Nuclear receptor complement of the cnidarian Nematostella vectensis: phylogenetic relationships and developmental expression patterns. BMC Evolutionary Biology, 2009, 9, 230.	3.2	52
322	An EST screen from the annelid Pomatoceros lamarckii reveals patterns of gene loss and gain in animals. BMC Evolutionary Biology, 2009, 9, 240.	3.2	40
323	The hydrogenosomes of Psalteriomonas lanterna. BMC Evolutionary Biology, 2009, 9, 287.	3.2	29
324	Molecular evolution of sex-biased genes in the Drosophila ananassae subgroup. BMC Evolutionary Biology, 2009, 9, 291.	3.2	21
325	Relaxin gene family in teleosts: phylogeny, syntenic mapping, selective constraint, and expression analysis. BMC Evolutionary Biology, 2009, 9, 293.	3.2	44

#	Article	IF	Citations
326	Gain and loss of elongation factor genes in green algae. BMC Evolutionary Biology, 2009, 9, 39.	3.2	29
327	Rodent phylogeny revised: analysis of six nuclear genes from all major rodent clades. BMC Evolutionary Biology, 2009, 9, 71.	3.2	242
328	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. BMC Evolutionary Biology, 2009, 9, 90.	3.2	92
329	Evolution from a respiratory ancestor to fill syntrophic and fermentative niches: comparative fenomics of six Geobacteraceae species. BMC Genomics, 2009, 10, 103.	1.2	45
330	The complete mitochondrial genome of the house dust mite Dermatophagoides pteronyssinus (Trouessart): a novel gene arrangement among arthropods. BMC Genomics, 2009, 10, 107.	1.2	69
331	A close phylogenetic relationship between Sipuncula and Annelida evidenced from the complete mitochondrial genome sequence of Phascolosoma esculenta. BMC Genomics, 2009, 10, 136.	1.2	60
332	Recent dermatophyte divergence revealed by comparative and phylogenetic analysis of mitochondrial genomes. BMC Genomics, 2009, 10, 238.	1.2	46
333	Analysis of salivary transcripts and antigens of the sand fly Phlebotomus arabicus. BMC Genomics, 2009, 10, 282.	1.2	79
334	Divergence in function and expression of the NOD26-like intrinsic proteins in plants. BMC Genomics, 2009, 10, 313.	1.2	76
335	A genome-wide analysis of nonribosomal peptide synthetase gene clusters and their peptides in a Planktothrix rubescens strain. BMC Genomics, 2009, 10, 396.	1.2	89
336	Comparative analysis of plant genomes allows the definition of the "Phytolongins": a novel non-SNARE longin domain protein family. BMC Genomics, 2009, 10, 510.	1.2	23
337	Eurotatorian paraphyly: Revisiting phylogenetic relationships based on the complete mitochondrial genome sequence of Rotaria rotatoria (Bdelloidea: Rotifera: Syndermata). BMC Genomics, 2009, 10, 533.	1.2	50
338	Evolutionary diversification of an ancient gene family (rhs) through C-terminal displacement. BMC Genomics, 2009, 10, 584.	1.2	99
339	The cellulose synthase superfamily in fully sequenced plants and algae. BMC Plant Biology, 2009, 9, 99.	1.6	143
340	Molecular characterization, gene expression and transcriptional regulation of thyroid hormone receptors in Senegalese sole. General and Comparative Endocrinology, 2009, 160, 139-147.	0.8	58
341	Differential expression of zebrafish gpia and gpib during development. Gene Expression Patterns, 2009, 9, 238-245.	0.3	6
342	An expression screen for RhoGEF genes involved in C. elegans gonadogenesis. Gene Expression Patterns, 2009, 9, 397-403.	0.3	15
343	Evolution of the apicoplast and its hosts: From heterotrophy to autotrophy and back again. International Journal for Parasitology, 2009, 39, 1-12.	1.3	79

#	Article	IF	Citations
344	Distribution and phylogeny of the blue light receptors aureochromes in eukaryotes. Planta, 2009, 230, 543-552.	1.6	74
345	Members of the Dof transcription factor family in Triticum aestivum are associated with light-mediated gene regulation. Functional and Integrative Genomics, 2009, 9, 485-498.	1.4	99
346	Complete Mitochondrial Genome Sequence of the Yellow-Spotted Long-Horned Beetle Psacothea hilaris (Coleoptera: Cerambycidae) and Phylogenetic Analysis among Coleopteran Insects. Molecules and Cells, 2009, 27, 429-442.	1.0	58
347	Complete Nucleotide Sequence and Organization of the Mitogenome of the Red-Spotted Apollo Butterfly, Parnassius bremeri (Lepidoptera: Papilionidae) and Comparison with Other Lepidopteran Insects. Molecules and Cells, 2009, 28, 347-364.	1.0	111
348	Expression of genes involved in symbiotic carbon and nitrogen transport in Pinus taeda mycorrhizal roots exposed to CO2 enrichment and nitrogen fertilization. Mycorrhiza, 2009, 19, 469-479.	1.3	14
349	Complete genome analysis and immunodetection of a member of a novel virus species belonging to the genus Ampelovirus. Archives of Virology, 2009, 154, 209-218.	0.9	28
350	Sequence and gene organization of 24 circles from the Cotesia plutellae bracovirus genome. Archives of Virology, 2009, 154, 1313-1327.	0.9	21
351	Molecular insights into the phylogeny of canine parvovirus 2 (CPV-2) with emphasis on Korean isolates: a Bayesian approach. Archives of Virology, 2009, 154, 1353-1360.	0.9	40
352	The complete mitogenome sequence of the Japanese oak silkmoth, Antheraea yamamai (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	81
353	Characterisation of a novel ilarvirus causing grapevine angular mosaic disease. European Journal of Plant Pathology, 2009, 125, 203-211.	0.8	7
354	Evolutionary history of Na,K-ATPases and their osmoregulatory role. Genetica, 2009, 136, 479-490.	0.5	70
355	Molecular phylogeny, long-term evolution, and functional divergence of flavin-containing monooxygenases. Genetica, 2009, 137, 173-187.	0.5	22
356	Widespread Gene Conversion of Alpha-2-Fucosyltransferase Genes in Mammals. Journal of Molecular Evolution, 2009, 69, 22-31.	0.8	24
357	Aplysia cys-loop Glutamate-Gated Chloride Channels Reveal Convergent Evolution of Ligand Specificity. Journal of Molecular Evolution, 2009, 69, 125-141.	0.8	44
358	The NfeD Protein Family and Its Conserved Gene Neighbours Throughout Prokaryotes: Functional Implications for Stomatin-Like Proteins. Journal of Molecular Evolution, 2009, 69, 657-667.	0.8	11
359	Identification and characterisation of a novel immune-type receptor (NITR) gene cluster in the European sea bass, Dicentrarchus labrax, reveals recurrent gene expansion and diversification by positive selection. Immunogenetics, 2009, 61, 773-788.	1.2	18
360	Loss of the insulator protein CTCF during nematode evolution. BMC Molecular Biology, 2009, 10, 84.	3.0	78
361	The relative ages of ectomycorrhizal mushrooms and their plant hosts estimated using Bayesian relaxed molecular clock analyses. BMC Biology, 2009, 7, 13.	1.7	152

#	Article	IF	Citations
362	The cell morphogenesis gene SPIRRIG in Arabidopsis encodes a WD/BEACH domain protein. Plant Journal, 2009, 59, 612-621.	2.8	36
363	Identification of pyrethroid resistance associated mutations in the para sodium channel of the twoâ€spotted spider mite Tetranychus urticae (Acari: Tetranychidae). Insect Molecular Biology, 2009, 18, 583-593.	1.0	99
364	Functional metagenomics reveals diverse Î²-lactamases in a remote Alaskan soil. ISME Journal, 2009, 3, 243-251.	4.4	462
365	The Distribution of Elongation Factorâ€1 Alpha (EFâ€1Î±), Elongation Factorâ€Like (EFL), and a Nonâ€Canonical Genetic Code in the Ulvophyceae: Discrete Genetic Characters Support a Consistent Phylogenetic Framework. Journal of Eukaryotic Microbiology, 2009, 56, 367-372.	0.8	21
366	The Single ENTHâ€Domain Protein of Trypanosomes; Endocytic Functions and Evolutionary Relationship with Epsin. Traffic, 2009, 10, 894-911.	1.3	38
367	Analysis of the Arabidopsis Floral Proteome: Detection of over 2â€ƒ000 Proteins and Evidence for Posttranslational Modifications. Journal of Integrative Plant Biology, 2009, 51, 207-223.	4.1	13
368	Haloarchaeal assimilatory nitrate-reducing communities from a saline alkaline soil. FEMS Microbiology Letters, 2009, 298, 56-66.	0.7	11
369	Phylogenetic analyses suggest thatPsammomitra(Ciliophora, Urostylida) should represent an urostylid family, based on small subunit rRNA and alpha-tubulin gene sequence information. Zoological Journal of the Linnean Society, 2009, 157, 227-236.	1.0	31
370	Functional replacement of a primary metabolic pathway via multiple independent eukaryoteâ€toâ€eukaryote gene transfers and selective retention. Journal of Evolutionary Biology, 2009, 22, 1882-1894.	0.8	15
371	Monophyly of terrestrial adephagan beetles as indicated by three nuclear genes (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	61
372	Molecular markers comparing the extremely simple body plan of dicyemids to that of lophotrochozoans: insight from the expression patterns of Hox, Otx, and brachyury. Evolution & Development, 2009, 11, 582-589.	1.1	9
373	The mitochondrial genome sequence of the arbuscular mycorrhizal fungus Glomus intraradices isolate 494 and implications for the phylogenetic placement of Glomus. New Phytologist, 2009, 183, 200-211.	3.5	85
374	The evolution of the adenylate-forming protein family in beetles: Multiple luciferase gene paralogues in fireflies and glow-worms. Molecular Phylogenetics and Evolution, 2009, 50, 93-101.	1.2	29
375	Arachnid relationships based on mitochondrial genomes: Asymmetric nucleotide and amino acid bias affects phylogenetic analyses. Molecular Phylogenetics and Evolution, 2009, 50, 117-128.	1.2	77
376	Comprehensive phylogenetic analysis of evolutionarily conserved rRNA adenine dimethyltransferase suggests diverse bacterial contributions to the nucleus-encoded plastid proteome. Molecular Phylogenetics and Evolution, 2009, 50, 282-289.	1.2	15
377	Phylogenetic analyses of complete mitochondrial genome of Urechis unicinctus (Echiura) support that echiurans are derived annelids. Molecular Phylogenetics and Evolution, 2009, 52, 558-562.	1.2	27
378	Interrelationships of chromalveolates within a broadly sampled tree of photosynthetic protists. Molecular Phylogenetics and Evolution, 2009, 53, 202-211.	1.2	35
379	Examining the utility of categorical models and alleviating artifacts in phylogenetic reconstruction of the Squamata (Reptilia). Molecular Phylogenetics and Evolution, 2009, 52, 784-796.	1.2	5

#	Article	IF	Citations
380	Support for the monophyletic origin of Gnathifera from phylogenomics. Molecular Phylogenetics and Evolution, 2009, 53, 1037-1041.	1.2	44
381	Estimating Maximum Likelihood Phylogenies with PhyML. Methods in Molecular Biology, 2009, 537, 113-137.	0.4	771
382	The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. Systematic Biology, 2009, 58, 224-239.	2.7	581
383	Phylogenetic methods in natural product research. Natural Product Reports, 2009, 26, 1585.	5.2	25
384	Ecology, Genetic Diversity, and Phylogeographic Structure of Andes Virus in Humans and Rodents in Chile. Journal of Virology, 2009, 83, 2446-2459.	1.5	60
385	The Cryphonectria parasitica mitochondrial rns gene: Plasmid-like elements, introns and homing endonucleases. Fungal Genetics and Biology, 2009, 46, 837-848.	0.9	41
386	The complete mitogenome of the hydrothermal vent crab Xenograpsus testudinatus (Decapoda,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 Genomics and Proteomics, 2009, 4, 290-299.	0.4	33
387	Molecular cloning, mRNA expression, and characterization of HSP90 gene from Chinese mitten crab Eriocheir japonica sinensis. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2009, 153, 229-235.	0.7	25
388	Genomic characterization and gene expression analysis of four hepcidin genes in the redbanded seabream (Pagrus auriga). Fish and Shellfish Immunology, 2009, 26, 483-491.	1.6	57
389	Tracing back EFL gene evolution in the cryptomonadsâ€“haptophytes assemblage: Separate origins of EFL genes in haptophytes, photosynthetic cryptomonads, and goniomonads. Gene, 2009, 441, 126-131.	1.0	20
390	Effect of taxon sampling on recovering the phylogeny of squamate reptiles based on complete mitochondrial genome and nuclear gene sequence data. Gene, 2009, 441, 12-21.	1.0	66
391	Electric charge divergence in proteins: insights into the evolution of their three-dimensional properties. Gene, 2009, 441, 3-11.	1.0	5
392	Identification and characterization of globin genes from two lepidopteran insects, Bombyx mori and Samia cynthia ricini. Gene, 2009, 431, 33-38.	1.0	9
393	The complete mitochondrial genome of the ridgetail white prawn Exopalaemon carinicauda Holthuis, 1950 (Crustacean: Decapoda: Palaemonidae) revealed a novel rearrangement of tRNA genes. Gene, 2009, 437, 1-8.	1.0	42
394	The complete mitochondrial genome of Cephalothrix simula (Iwata) (Nemertea: Palaeonemertea). Gene, 2009, 442, 8-17.	1.0	15
395	Evolutionary and functional diversity of green fluorescent proteins in cephalochordates. Gene, 2009, 446, 41-49.	1.0	11
396	Complete nucleotide sequence and gene organization of the mitochondrial genome of Paa spinosa (Anura: Ranoidae). Gene, 2009, 447, 86-96.	1.0	56
397	Multiple chicken repeat 1 lineages in the genomes of oestroid flies. Gene, 2009, 448, 40-45.	1.0	3

#	Article	IF	Citations
398	Regulatory back-up circuit of medaka Wt1 co-orthologs ensures PGC maintenance. Developmental Biology, 2009, 325, 179-188.	0.9	34
399	A novel role for dpp in the shaping of bivalve shells revealed in a conserved molluscan developmental program. Developmental Biology, 2009, 329, 152-166.	0.9	76
400	More constraint on ParaHox than Hox gene families in early metazoan evolution. Developmental Biology, 2009, 328, 173-187.	0.9	35
401	Vasa and the germ line lineage in a colonial urochordate. Developmental Biology, 2009, 331, 113-128.	0.9	68
402	Molecular and functional characterization of a cDNA encoding 4-hydroxy-3-methylbut-2-enyl diphosphate reductase from Dunaliella salina. Journal of Plant Physiology, 2009, 166, 968-977.	1.6	20
403	Steroid metabolism in cnidarians: Insights from Nematostella vectensis. Molecular and Cellular Endocrinology, 2009, 301, 27-36.	1.6	34
404	Systematic Analysis of the Twin Cx9C Protein Family. Journal of Molecular Biology, 2009, 393, 356-368.	2.0	153
405	Discovery of marine Bacillus species by 16S rRNA and rpoB comparisons and their usefulness for species identification. Journal of Microbiological Methods, 2009, 77, 48-57.	0.7	104
406	Genes of cathepsin L-like proteases in Trypanosoma rangeli isolates: Markers for diagnosis, genotyping and phylogenetic relationships. Acta Tropica, 2009, 112, 249-259.	0.9	32
407	Surveillance of Mosquito-Borne Viruses in Alberta Using Reverse Transcription Polymerase Chain Reaction With Generic Primers. Journal of Medical Entomology, 2009, 46, 640-648.	0.9	31
408	Repeated secondary loss of adaptin complex genes in the Apicomplexa. Parasitology International, 2009, 58, 86-94.	0.6	42
409	15-P003 An EST screen from the annelid Pomatoceros lamarckii reveals patterns of gene loss and gain in animals. Mechanisms of Development, 2009, 126, S247-S248.	1.7	1
410	Resident Microbiota of the Gypsy Moth Midgut Harbors Antibiotic Resistance Determinants. DNA and Cell Biology, 2009, 28, 109-117.	0.9	79
411	A highly divergent South African geminivirus species illuminates the ancient evolutionary history of this family. Virology Journal, 2009, 6, 36.	1.4	70
412	A novel putative virus of Gremmeniella abietina type B (Ascomycota: Helotiaceae) has a composite genome with endornavirus affinities. Journal of General Virology, 2009, 90, 2299-2305.	1.3	45
413	A Single-Copy IS5-Like Transposon in the Genome of a Bdelloid Rotifer. Molecular Biology and Evolution, 2009, 26, 1921-1929.	3.5	18
414	Revaluation of deuterostome phylogeny and evolutionary relationships among chordate subphyla using mitogenome data. Journal of Genetics and Genomics, 2009, 36, 151-160.	1.7	9
415	Evolution of vacuolar targeting in algae. Botanica Marina, 2009, 52, 117-128.	0.6	4

#	Article	IF	Citations
416	Phylogenetic analysis of new Prasinoviruses (Phycodnaviridae) that infect the green unicellular algae Ostreococcus, Bathycoccus and Micromonas. Environmental Microbiology Reports, 2009, 1, 114-123.	1.0	35
417	Phylogeny of the "Forgotten" Cellular Slime Mold, Fonticula alba, Reveals a Key Evolutionary Branch within Opisthokonta. Molecular Biology and Evolution, 2009, 26, 2699-2709.	3.5	138
418	Contribution of recombination and selection to molecular evolution of Citrus tristeza virus. Journal of General Virology, 2009, 90, 1527-1538.	1.3	74
419	Spectral sensitivity, visual pigments and screening pigments in two life history stages of the ontogenetic migrator Gnathophausia ingens. Journal of the Marine Biological Association of the United Kingdom, 2009, 89, 119-129.	0.4	22
420	A novel motif at the C-terminus of palmitoyltransferases is essential for Swf1 and Pfa3 function in vivo. Biochemical Journal, 2009, 419, 301-308.	1.7	39
421	The Effect of Chaperonin Buffering on Protein Evolution. Genome Biology and Evolution, 2010, 2, 609-619.	1.1	73
422	Genome-Wide Influence of Indel Substitutions on Evolution of Bacteria of the PVC Superphylum, Revealed Using a Novel Computational Method. Genome Biology and Evolution, 2010, 2, 870-886.	1.1	23
423	Polymorphism of the cox1 gene in cercariae isolates of bird schistosomes (Trematoda:Schistosomatidae) from ponds of Moscow and Moscow region. Russian Journal of Genetics, 2010, 46, 873-880.	0.2	8
424	Molecular systematics: A synthesis of the common methods and the state of knowledge. Cellular and Molecular Biology Letters, 2010, 15, 311-41.	2.7	51
425	Evolutionary History of Plant Multisubunit RNA Polymerases IV and V: Subunit Origins via Genome-Wide and Segmental Gene Duplications, Retrotransposition, and Lineage-Specific Subfunctionalization. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 285-297.	2.0	53
426	Evolutionary Dynamics of the wnt Gene Family: A Lophotrochozoan Perspective. Molecular Biology and Evolution, 2010, 27, 1645-1658.	3.5	115
427	ALTER: program-oriented conversion of DNA and protein alignments. Nucleic Acids Research, 2010, 38, W14-W18.	6.5	367
428	Molecular evidence for species separation in the water mite Hygrobates nigromaculatus Lebert, 1879 (Acari, Hydrachnidia): evolutionary consequences of the loss of larval parasitism. Aquatic Sciences, 2010, 72, 347-360.	0.6	68
429	Evolutionary Bases of Carbohydrate Recognition and Substrate Discrimination in the ROK Protein Family. Journal of Molecular Evolution, 2010, 70, 545-556.	0.8	40
430	Evidence for the Heparin-Binding Ability of the Ascidian Xlink Domain and Insight into the Evolution of the Xlink Domain in Chordates. Journal of Molecular Evolution, 2010, 71, 51-59.	0.8	6
431	Understanding the Effect of Secondary Structures and Aggregation on Human Protein Folding Class Evolution. Journal of Molecular Evolution, 2010, 71, 60-69.	0.8	8
432	Evolutionary History and Functional Diversification of Phosphomannomutase Genes. Journal of Molecular Evolution, 2010, 71, 119-127.	0.8	11
433	Actin Gene Family Dynamics in Cryptomonads and Red Algae. Journal of Molecular Evolution, 2010, 71, 169-179.	0.8	4

#	Article	IF	Citations
434	Evolution of the Cinnamyl/Sinapyl Alcohol Dehydrogenase (CAD/SAD) Gene Family: The Emergence of Real Lignin is Associated with the Origin of Bona Fide CAD. Journal of Molecular Evolution, 2010, 71, 202-218.	0.8	61
435	A Tandem Duplication of Manganese Superoxide Dismutase in Nosema bombycis and Its Evolutionary Origins. Journal of Molecular Evolution, 2010, 71, 401-414.	0.8	11
436	Patterns of molecular evolution and predicted function in thaumatin-like proteins of Populus trichocarpa. Planta, 2010, 232, 949-962.	1.6	38
437	Decreased ROS level and activation of antioxidant gene expression in Agrobacterium rhizogenes pRiA4-transformed calli of Rubia cordifolia. Planta, 2010, 232, 1023-1032.	1.6	33
438	Expansion, diversification, and expression of T-box family genes in Porifera. Development Genes and Evolution, 2010, 220, 251-262.	0.4	18
439	Expression of Distal-less, dachshund, and optomotor blind in Neanthes arenaceodentata (Annelida,) Tj ETQq1 1 0.784314 rgBT /Overl Development Genes and Evolution, 2010, 220, 275-295.	0.4	19
440	Auxin-related gene families in abiotic stress response in Sorghum bicolor. Functional and Integrative Genomics, 2010, 10, 533-546.	1.4	240
441	The amino terminus of the salmonid alphavirus capsid protein determines subcellular localization and inhibits cellular proliferation. Archives of Virology, 2010, 155, 1281-1293.	0.9	12
442	A novel species of mastrevirus (family Geminiviridae) isolated from Digitaria didactyla grass from Australia. Archives of Virology, 2010, 155, 1529-1534.	0.9	10
443	Physicochemical evolution and positive selection of the gymnosperm matK proteins. Journal of Genetics, 2010, 89, 81-89.	0.4	7
444	The mitochondrial genome of Euphausia superba (Prydz Bay) (Crustacea: Malacostraca: Euphausiacea) reveals a novel gene arrangement and potential molecular markers. Molecular Biology Reports, 2010, 37, 771-784.	1.0	35
445	A comparative analysis of the complete mitochondrial genome of the Eurasian otter Lutra lutra (Carnivora; Mustelidae). Molecular Biology Reports, 2010, 37, 1943-1955.	1.0	38
446	Complete mitochondrial genome of the Asian paddle crab Charybdis japonica (Crustacea: Decapoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf decapods. Molecular Biology Reports, 2010, 37, 2559-2569.	1.0	51
447	A clade in the QUASIMODO2 family evolved with vascular plants and supports a role for cell wall composition in adaptation to environmental changes. Plant Molecular Biology, 2010, 73, 605-615.	2.0	9
448	Control of somatic embryogenesis and embryo development by AP2 transcription factors. Plant Molecular Biology, 2010, 74, 313-326.	2.0	140
449	Comparative sequence analysis of CP12, a small protein involved in the formation of a Calvin cycle complex in photosynthetic organisms. Photosynthesis Research, 2010, 103, 183-194.	1.6	57
450	The evolutionary diversification of LSF and Grainyhead transcription factors preceded the radiation of basal animal lineages. BMC Evolutionary Biology, 2010, 10, 101.	3.2	37
451	Evolution of nectarivory in phyllostomid bats (Phyllostomidae Gray, 1825, Chiroptera: Mammalia). BMC Evolutionary Biology, 2010, 10, 165.	3.2	117

#	Article	IF	Citations
452	The origin and evolution of ARGFX homeobox loci in mammalian radiation. BMC Evolutionary Biology, 2010, 10, 182.	3.2	10
453	A phylogenetic mosaic plastid proteome and unusual plastid-targeting signals in the green-colored dinoflagellate Lepidodinium chlorophorum. BMC Evolutionary Biology, 2010, 10, 191.	3.2	62
454	Filoviruses are ancient and integrated into mammalian genomes. BMC Evolutionary Biology, 2010, 10, 193.	3.2	158
455	A new lysozyme from the eastern oyster, Crassostrea virginica, and a possible evolutionary pathway for i-type lysozymes in bivalves from host defense to digestion. BMC Evolutionary Biology, 2010, 10, 213.	3.2	48
456	Taxonomic distribution and origins of the extended LHC (light-harvesting complex) antenna protein superfamily. BMC Evolutionary Biology, 2010, 10, 233.	3.2	124
457	Untangling spider silk evolution with spidroin terminal domains. BMC Evolutionary Biology, 2010, 10, 243.	3.2	135
458	Phylogenomics reveals subfamilies of fungal nonribosomal peptide synthetases and their evolutionary relationships. BMC Evolutionary Biology, 2010, 10, 26.	3.2	184
459	The WTX/AMER1 gene family: evolution, signature and function. BMC Evolutionary Biology, 2010, 10, 280.	3.2	19
460	Molecular evolution and the role of oxidative stress in the expansion and functional diversification of cytosolic glutathione transferases. BMC Evolutionary Biology, 2010, 10, 281.	3.2	71
461	Unusual duplication of the insulin-like receptor in the crustacean Daphnia pulex. BMC Evolutionary Biology, 2010, 10, 305.	3.2	34
462	Evolutionary history of the poly(ADP-ribose) polymerase gene family in eukaryotes. BMC Evolutionary Biology, 2010, 10, 308.	3.2	108
463	Mutational dynamics of murine angiogenin duplicates. BMC Evolutionary Biology, 2010, 10, 310.	3.2	6
464	Evolutionary divergence of chloroplast FAD synthetase proteins. BMC Evolutionary Biology, 2010, 10, 311.	3.2	19
465	Evolution and functional divergence of the anoctamin family of membrane proteins. BMC Evolutionary Biology, 2010, 10, 319.	3.2	49
466	The synapsin gene family in basal chordates: evolutionary perspectives in metazoans. BMC Evolutionary Biology, 2010, 10, 32.	3.2	25
467	Chlorophyll-binding proteins revisited - a multigenic family of light-harvesting and stress proteins from a brown algal perspective. BMC Evolutionary Biology, 2010, 10, 365.	3.2	93
468	The globin gene family of the cephalochordate amphioxus: implications for chordate globin evolution. BMC Evolutionary Biology, 2010, 10, 370.	3.2	36
469	Evolution of spliceosomal introns following endosymbiotic gene transfer. BMC Evolutionary Biology, 2010, 10, 57.	3.2	23

#	Article	IF	Citations
470	Molecular evolution of the crustacean hyperglycemic hormone family in ecdysozoans. BMC Evolutionary Biology, 2010, 10, 62.	3.2	70
471	New insights into the evolution of subtilisin-like serine protease genes in Pezizomycotina. BMC Evolutionary Biology, 2010, 10, 68.	3.2	64
472	Comprehensive analysis of MHC class I genes from the U-, S-, and Z-lineages in Atlantic salmon. BMC Genomics, 2010, 11, 154.	1.2	50
473	Transcriptome analysis reveals nuclear-encoded proteins for the maintenance of temporary plastids in the dinoflagellate Dinophysis acuminata. BMC Genomics, 2010, 11, 366.	1.2	94
474	Evolution of electron transfer out of the cell: comparative genomics of six Geobacter genomes. BMC Genomics, 2010, 11, 40.	1.2	170
475	The genome of Geobacter bemidjiensis, exemplar for the subsurface clade of Geobacter species that predominate in Fe(III)-reducing subsurface environments.. BMC Genomics, 2010, 11, 490.	1.2	52
476	Conservation, duplication, and loss of the Tor signaling pathway in the fungal kingdom. BMC Genomics, 2010, 11, 510.	1.2	59
477	The venom composition of the parasitic wasp Chelonus inanitus resolved by combined expressed sequence tags analysis and proteomic approach. BMC Genomics, 2010, 11, 693.	1.2	102
478	Molecular and phylogenetic characterization of the sieve element occlusion gene family in Fabaceae and non-Fabaceaeplants. BMC Plant Biology, 2010, 10, 219.	1.6	61
479	The Puf family of RNA-binding proteins in plants: phylogeny, structural modeling, activity and subcellular localization. BMC Plant Biology, 2010, 10, 44.	1.6	73
480	Dynamic escape of pre-existing raltegravir-resistant HIV-1 from raltegravir selection pressure. Antiviral Research, 2010, 88, 281-286.	1.9	28
481	Ammonia uptake in Manduca sexta midgut is mediated by an amiloride sensitive cation/proton exchanger: Transport studies and mRNA expression analysis of NHE7, 9, NHE8, and V-ATPase (subunit D). Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2010, 157, 364-376.	0.8	21
482	Comparative genomic and phylogenetic analysis of vitellogenin and other large lipid transfer proteins in metazoans. FEBS Letters, 2010, 584, 1273-1278.	1.3	74
483	Substrate specificity and evolutionary implications of a NifDK enzyme carrying NifBâ€¢co at its active site. FEBS Letters, 2010, 584, 1487-1492.	1.3	34
484	Ecdysone receptor homologs from mollusks, leeches and a polychaete worm. FEBS Letters, 2010, 584, 4458-4462.	1.3	19
485	Phylogenetic analysis and evolution of aromatic amino acid hydroxylase. FEBS Letters, 2010, 584, 4775-4782.	1.3	29
486	Genetic analysis of Akabane virus isolates from cattle in Korea. Veterinary Microbiology, 2010, 140, 49-55.	0.8	13
487	The genome of the nematode Pristionchus pacificus encodes putative homologs of RXR/Usp and EcR. General and Comparative Endocrinology, 2010, 167, 11-17.	0.8	18

#	Article	IF	Citations
488	Molecular characterization and gene expression of thyrotropin receptor (TSHR) and a truncated TSHR-like in Senegalese sole. General and Comparative Endocrinology, 2010, 168, 431-439.	0.8	14
489	Molecular evolution and phylogeny of the angiosperm ycf2 gene. Journal of Systematics and Evolution, 2010, 48, 240-248.	1.6	44
491	Probing Enzyme Promiscuity of SGNH Hydrolases. ChemBioChem, 2010, 11, 2158-2167.	1.3	71
492	The nuclear genes Mtfr1 and Dufd1 regulate mitochondrial dynamic and cellular respiration. Journal of Cellular Physiology, 2010, 225, 767-776.	2.0	42
493	Extensive survey on the prevalence and genetic diversity of SIVs in primate bushmeat provides insights into risks for potential new cross-species transmissions. Infection, Genetics and Evolution, 2010, 10, 386-396.	1.0	100
494	An introduction to a novel population genetic approach for HIV characterization. Infection, Genetics and Evolution, 2010, 10, 1155-1164.	1.0	3
495	New defensins from hard and soft ticks: Similarities, differences, and phylogenetic analyses. Veterinary Parasitology, 2010, 167, 298-303.	0.7	31
496	Polyphyly of the Zaprionus genus group (Diptera: Drosophilidae). Molecular Phylogenetics and Evolution, 2010, 55, 335-339.	1.2	25
497	Evolutionary placement of Xanthomonadales based on conserved protein signature sequences. Molecular Phylogenetics and Evolution, 2010, 54, 524-534.	1.2	30
498	Evolution of Picornaviridae: An examination of phylogenetic relationships and cophylogeny. Molecular Phylogenetics and Evolution, 2010, 54, 995-1005.	1.2	23
499	Combination of molecular data support the existence of three main lineages in the phylogeny of aphids (Hemiptera: Aphididae) and the basal position of the subfamily Lachninae. Molecular Phylogenetics and Evolution, 2010, 55, 305-317.	1.2	82
500	Molecular phylogeny of acariform mites (Acari, Arachnida): Strong conflict between phylogenetic signal and long-branch attraction artifacts. Molecular Phylogenetics and Evolution, 2010, 56, 222-241.	1.2	272
501	Mitochondrial genome evolution in Ophiuroidea, Echinoidea, and Holothuroidea: Insights in phylogenetic relationships of Echinodermata. Molecular Phylogenetics and Evolution, 2010, 56, 201-211.	1.2	66
502	Nucleotide substitution rates for the full set of mitochondrial protein-coding genes in Coleoptera. Molecular Phylogenetics and Evolution, 2010, 56, 796-807.	1.2	141
503	Differential expansion of the merozoite surface protein (msp)-7 gene family in Plasmodium species under a birth-and-death model of evolution. Molecular Phylogenetics and Evolution, 2010, 55, 399-408.	1.2	17
504	Conservation and variation in mitochondrial genomes of gastropods Oncomelania hupensis and Tricula hortensis, intermediate host snails of Schistosoma in China. Molecular Phylogenetics and Evolution, 2010, 57, 215-226.	1.2	21
505	Rare genomic changes and mitochondrial sequences provide independent support for congruent relationships among the sea spiders (Arthropoda, Pycnogonida). Molecular Phylogenetics and Evolution, 2010, 57, 59-70.	1.2	31
506	Conservation of MAP kinase activity and MSP genes in parthenogenetic nematodes. BMC Developmental Biology, 2010, 10, 51.	2.1	10

#	Article	IF	Citations
507	The structure and evolution of the murine inhibitor of carbonic anhydrase: A member of the transferrin superfamily. Protein Science, 2010, 19, 1616-1626.	3.1	16
508	Structure and expression of conserved Wnt pathway components in the demosponge Amphimedon queenslandica. Evolution & Development, 2010, 12, 494-518.	1.1	112
509	Origin of animal epithelia: insights from the sponge genome. Evolution & Development, 2010, 12, 601-617.	1.1	94
510	CHARACTERIZATION AND EXPRESSION ANALYSIS OF THE Lhcf GENE FAMILY IN EMILIANIA HUXLEYI (HAPTOPHYTA) REVEALS DIFFERENTIAL RESPONSES TO LIGHT AND CO21. Journal of Phycology, 2010, 46, 123-134.	1.0	21
511	Phylogenetic diversity of T4-like bacteriophages in Lake Baikal, East Siberia. FEMS Microbiology Letters, 2010, 309, no-no.	0.7	33
512	Functions and cellular localization of cysteine desulfurase and selenocysteine lyase in Trypanosomaâ€ƒbrucei. FEBS Journal, 2010, 277, 383-393.	2.2	21
513	Expression profile of PIN, AUX/LAX and PGP auxin transporter gene families in Sorghumâ€ƒbicolor under phytohormone and abiotic stress. FEBS Journal, 2010, 277, 2954-2969.	2.2	139
514	New members of the brachyurins family in lobster include a trypsinâ€like enzyme with amino acid substitutions in the substrateâ€binding pocket. FEBS Journal, 2010, 277, 3489-3501.	2.2	14
515	Arabidopsis Qa-SNARE SYP2 proteins localized to different subcellular regions function redundantly in vacuolar protein sorting and plant development. Plant Journal, 2010, 64, 924-935.	2.8	46
516	Sugar transporters of the major facilitator superfamily in aphids; from gene prediction to functional characterization. Insect Molecular Biology, 2010, 19, 97-112.	1.0	50
517	cDNA cloning, homology modelling and evolutionary insights into novel endogenous cellulases of the borer beetleOncideres albomarginata chamela(Cerambycidae). Insect Molecular Biology, 2010, 19, 323-336.	1.0	38
518	Proposed new nomenclature for Bos taurus cytochromes P450 involved in xenobiotic drug metabolism. Journal of Veterinary Pharmacology and Therapeutics, 2010, 33, 528-536.	0.6	15
519	Ecological and evolutionary factors underlying global and local assembly of denitrifier communities. ISME Journal, 2010, 4, 633-641.	4.4	217
520	[FeFe]-hydrogenase in Yellowstone National Park: evidence for dispersal limitation and phylogenetic niche conservatism. ISME Journal, 2010, 4, 1485-1495.	4.4	63
521	Stepwise [FeFe]-hydrogenase H-cluster assembly revealed in the structure of HydAÎ”EFG. Nature, 2010, 465, 248-251.	13.7	295
522	A formal test of the theory of universal common ancestry. Nature, 2010, 465, 219-222.	13.7	187
523	Ribosomal protein genes of holometabolan insects reject the Halteria, instead revealing a close affinity of Strepsiptera with Coleoptera. Molecular Phylogenetics and Evolution, 2010, 55, 846-859.	1.2	33
524	Identification and characterization of new LuxR/Luxlâ€type quorum sensing systems from metagenomic libraries. Environmental Microbiology, 2010, 12, 105-117.	1.8	51

#	Article	IF	Citations
525	Identification of genes regulated by the MvaTâ€like paralogues TurA and TurB of Pseudomonas putida KT2440. Environmental Microbiology, 2010, 12, 254-263.	1.8	28
526	A thermophilic bacterial origin and subsequent constraints by redox, light and salinity on the evolution of the microbial mercuric reductase. Environmental Microbiology, 2010, 12, 2904-2917.	1.8	116
527	The complete mitogenome of the hydrothermal vent crab Gandalfus yunohana (Crustacea: Decapoda:) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.7	28
528	Phylogenetic position of Sipuncula derived from multi-gene and phylogenomic data and its implication for the evolution of segmentation. Journal of Zoological Systematics and Evolutionary Research, 2010, 48, 197.	0.6	38
529	Characterization and expression of AmphiBMP3â€Š/3b gene in amphioxus Branchiostoma japonicum. Development Growth and Differentiation, 2010, 52, 157-167.	0.6	3
531	Circadian Clock Proteins in Prokaryotes: Hidden Rhythms?. Frontiers in Microbiology, 2010, 1, 130.	1.5	36
532	Phylogenetic Analysis of Cellulolytic Enzyme Genes from Representative Lineages of Termites and a Related Cockroach. PLoS ONE, 2010, 5, e8636.	1.1	60
533	Platelet-Derived Growth Factor Receptor Î² Is Critical for Zebrafish Intersegmental Vessel Formation. PLoS ONE, 2010, 5, e11324.	1.1	46
534	A Score of the Ability of a Three-Dimensional Protein Model to Retrieve Its Own Sequence as a Quantitative Measure of Its Quality and Appropriateness. PLoS ONE, 2010, 5, e12483.	1.1	12
535	Light Entrained Rhythmic Gene Expression in the Sea Anemone Nematostella vectensis: The Evolution of the Animal Circadian Clock. PLoS ONE, 2010, 5, e12805.	1.1	80
536	Evolution and Diversity of a Fungal Self/Nonself Recognition Locus. PLoS ONE, 2010, 5, e14055.	1.1	52
537	DIVEIN: a web server to analyze phylogenies, sequence divergence, diversity, and informative sites. BioTechniques, 2010, 48, 405-408.	0.8	184
538	Complete nucleotide sequence and organization of the mitogenome of endangered Eumenis autonoe (Lepidoptera: Nymphalidae). African Journal of Biotechnology, 2010, 9, 735-754.	0.3	98
539	The application of cophylogenic tools to gene sets. Taxon, 2010, 59, 1843-1852.	0.4	1
540	Complex Regulation of Two Target Genes Encoding SPX-MFS Proteins by Rice miR827 in Response to Phosphate Starvation. Plant and Cell Physiology, 2010, 51, 2119-2131.	1.5	188
541	GIN Transposons: Genetic Elements Linking Retrotransposons and Genes. Molecular Biology and Evolution, 2010, 27, 1903-1911.	3.5	13
542	Tight Junctionâ€“associated MARVEL Proteins MarvelD3, Tricellulin, and Occludin Have Distinct but Overlapping Functions. Molecular Biology of the Cell, 2010, 21, 1200-1213.	0.9	264
543	Requirement of theLactobacillus caseiMaeKR Two-Component System for<scp>l</scp>-Malic Acid Utilization via a Malic Enzyme Pathway. Applied and Environmental Microbiology, 2010, 76, 84-95.	1.4	59

#	Article	IF	Citations
544	Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. Bioinformatics, 2010, 26, 2455-2457.	1.8	1,158
545	Characterization of the Possible Roles for B Class MADS Box Genes in Regulation of Perianth Formation in Orchid. Plant Physiology, 2010, 152, 837-853.	2.3	99
546	Transcriptional Diversification and Functional Conservation between DELLA Proteins in Arabidopsis. Molecular Biology and Evolution, 2010, 27, 1247-1256.	3.5	123
547	An atypical member of the light-harvesting complex stress-related protein family modulates diatom responses to light. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18214-18219.	3.3	258
548	The evolution of phototransduction from an ancestral cyclic nucleotide gated pathway. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 1963-1969.	1.2	75
549	Symbiosis-dependent gene expression in coralâ€“dinoflagellate association: cloning and characterization of a P-type H⁺-ATPase gene. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 87-95.	1.2	42
550	The BatR/BatS Two-Component Regulatory System Controls the Adaptive Response ofBartonella henselaeduring Human Endothelial Cell Infection. Journal of Bacteriology, 2010, 192, 3352-3367.	1.0	57
551	Marine Prasinovirus Genomes Show Low Evolutionary Divergence and Acquisition of Protein Metabolism Genes by Horizontal Gene Transfer. Journal of Virology, 2010, 84, 12555-12563.	1.5	87
552	Isolation of Prasinoviruses of the Green Unicellular Algae Ostreococcus spp. on a Worldwide Geographical Scale. Applied and Environmental Microbiology, 2010, 76, 96-101.	1.4	25
553	Internal and External Paralogy in the Evolution of Tropomyosin Genes in Metazoans. Molecular Biology and Evolution, 2010, 27, 1504-1517.	3.5	23
554	Arf3 Is Activated Uniquely at the trans-Golgi Network by Brefeldin A-inhibited Guanine Nucleotide Exchange Factors. Molecular Biology of the Cell, 2010, 21, 1836-1849.	0.9	49
555	Using Data-Display Networks for Exploratory Data Analysis in Phylogenetic Studies. Molecular Biology and Evolution, 2010, 27, 1044-1057.	3.5	44
556	Evolution of Hox Gene Clusters in Gnathostomes: Insights from a Survey of a Shark (Scyliorhinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	3.5	50
557	Different Phylogenomic Approaches to Resolve the Evolutionary Relationships among Model Fish Species. Molecular Biology and Evolution, 2010, 27, 2757-2774.	3.5	18
558	Opsin co-expression in Limulus photoreceptors: differential regulation by light and a circadian clock. Journal of Experimental Biology, 2010, 213, 2589-2601.	0.8	42
559	Insights into the organization of dorsal spinal cord pathways from an evolutionarily conserved raldh2 intronic enhancer. Development (Cambridge), 2010, 137, 507-518.	1.2	34
560	The Nuclear Component of a Cytonuclear Hybrid Incompatibility in Mimulus Maps to a Cluster of Pentatricopeptide Repeat Genes. Genetics, 2010, 184, 455-465.	1.2	85
561	Broadly Sampled Multigene Analyses Yield a Well-Resolved Eukaryotic Tree of Life. Systematic Biology, 2010, 59, 518-533.	2.7	212

#	Article	IF	Citations
562	Evolutionary Lineages and Functional Diversification of Plant Hexokinases. Molecular Plant, 2010, 3, 334-346.	3.9	70
563	An Evolutionary Analysis of Lateral Gene Transfer in Thymidylate Synthase Enzymes. Systematic Biology, 2010, 59, 212-225.	2.7	36
564	Bacterial Genes in the Aphid Genome: Absence of Functional Gene Transfer from Buchnera to Its Host. PLoS Genetics, 2010, 6, e1000827.	1.5	164
565	Birth-and-Death Long-Term Evolution Promotes Histone H2B Variant Diversification in the Male Germinal Cell Line. Molecular Biology and Evolution, 2010, 27, 1802-1812.	3.5	21
566	Endogenous Viral Elements in Animal Genomes. PLoS Genetics, 2010, 6, e1001191.	1.5	565
567	Allele-Specific Virulence Attenuation of the Pseudomonas syringae HopZ1a Type III Effector via the Arabidopsis ZAR1 Resistance Protein. PLoS Genetics, 2010, 6, e1000894.	1.5	151
568	A Metazoan/Plant-like Capping Enzyme and Cap Modified Nucleotides in the Unicellular Eukaryote Trichomonas vaginalis. PLoS Pathogens, 2010, 6, e1000999.	2.1	9
569	A Newly Classified Vertebrate Calpain Protease, Directly Ancestral to CAPN1 and 2, Episodically Evolved a Restricted Physiological Function in Placental Mammals. Molecular Biology and Evolution, 2010, 27, 1886-1902.	3.5	40
570	A Deviation from the Bipolar-Tetrapolar Mating Paradigm in an Early Diverged Basidiomycete. PLoS Genetics, 2010, 6, e1001052.	1.5	55
571	Ancient Protostome Origin of Chemosensory Ionotropic Glutamate Receptors and the Evolution of Insect Taste and Olfaction. PLoS Genetics, 2010, 6, e1001064.	1.5	680
572	Chitin Synthases from Saprolegnia Are Involved in Tip Growth and Represent a Potential Target for Anti-Oomycete Drugs. PLoS Pathogens, 2010, 6, e1001070.	2.1	61
573	Adaptive Divergence of Ancient Gene Duplicates in the Avian MHC Class II Â. Molecular Biology and Evolution, 2010, 27, 2360-2374.	3.5	66
574	The Evolution of Amastin Surface Glycoproteins in Trypanosomatid Parasites. Molecular Biology and Evolution, 2010, 27, 33-45.	3.5	80
575	Molecular Basis of the Waxy Endosperm Starch Phenotype in Broomcorn Millet (Panicum miliaceum) Tj ETQq1 1 0.784314 rgBT /Over	3.5	44
576	The Mixed Lineage Nature of Nitrogen Transport and Assimilation in Marine Eukaryotic Phytoplankton: A Case Study of Micromonas. Molecular Biology and Evolution, 2010, 27, 2268-2283.	3.5	66
577	Molecular identification of the causative agent of human strongyloidiasis acquired in Tanzania: Dispersal and diversity of Strongyloides spp. and their hosts. Parasitology International, 2010, 59, 407-413.	0.6	79
578	The diversity and evolution of circadian clock proteins in fungi. Mycologia, 2010, 102, 269-278.	0.8	63
579	Expression and phylogenetic analysis of the zic gene family in the evolution and development of metazoans. EvoDevo, 2010, 1, 12.	1.3	46

#	Article	IF	Citations
580	Conserved developmental expression of Fezf in chordates and Drosophila and the origin of the Zona Limitans Intrathalamica (ZLI) brain organizer. EvoDevo, 2010, 1, 7.	1.3	55
581	Floral symmetry genes and the origin and maintenance of zygomorphy in a plant-pollinator mutualism. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6388-6393.	3.3	134
582	Myosin Cross-reactive Antigen of Streptococcus pyogenes M49 Encodes a Fatty Acid Double Bond Hydratase That Plays a Role in Oleic Acid Detoxification and Bacterial Virulence. Journal of Biological Chemistry, 2010, 285, 10353-10361.	1.6	112
583	Piriform Spider Silk Sequences Reveal Unique Repetitive Elements. Biomacromolecules, 2010, 11, 3000-3006.	2.6	51
584	Origin and Diversification of Basic-Helix-Loop-Helix Proteins in Plants. Molecular Biology and Evolution, 2010, 27, 862-874.	3.5	503
585	Evolution and Cytological Diversification of the Green Seaweeds (Ulvophyceae). Molecular Biology and Evolution, 2010, 27, 2052-2061.	3.5	138
586	Lack of hemocyanin in Oriental Plecoptera and multifunctionality of the protein in Larvae. Oriental Insects, 2010, 44, 429-446.	0.1	1
587	Molecular cloning and characterization of a heat shock protein 70 gene in swimming crab (Portunus) Tj ETQq1 1 0.784314 rgBT /Ove	1.6	74
588	Molecular cloning and characterization of a serine proteinase homolog prophenoloxidase-activating factor in the swimming crab Portunus trituberculatus. Fish and Shellfish Immunology, 2010, 29, 679-686.	1.6	24
589	Clan CD of cysteine peptidases as an example of evolutionary divergences in related protein families across plant clades. Gene, 2010, 449, 59-69.	1.0	15
590	Mitochondrial rRNA secondary structures and genome arrangements distinguish chelicerates: Comparisons with a harvestman (Arachnida: Opiliones: Phalangium opilio). Gene, 2010, 449, 9-21.	1.0	28
591	Characterisation of capn1, capn2-like, capn3 and capn11 genes in Atlantic halibut (Hippoglossus) Tj ETQq1 1 0.784314 rgBT /Overlo nutritional states. Gene, 2010, 453, 45-58.	1.0	23
592	The impact of fossil calibrations, codon positions and relaxed clocks on the divergence time estimates of the native Australian rodents (Conilurini). Gene, 2010, 455, 22-31.	1.0	12
593	The complete mitochondrial genome and phylogenomics of a damselfly, Euphaea formosa support a basal Odonata within the Pterygota. Gene, 2010, 468, 20-29.	1.0	43
594	DNA barcoding for conservation and management of Amazonian commercial fish. Biological Conservation, 2010, 143, 1438-1443.	1.9	112
595	O-GlcNAc protein modification in plants: Evolution and function. Biochimica Et Biophysica Acta - General Subjects, 2010, 1800, 49-56.	1.1	131
596	The complete mitochondrial genome of the mantid shrimp Oratosquilla oratoria (Crustacea:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 112 T Stomatopoda. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2010, 5, 190-198.	0.4	12
597	Complete mtDNA of Meretrix lusoria (Bivalvia: Veneridae) reveals the presence of an atp8 gene, length variation and heteroplasmy in the control region. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2010, 5, 256-264.	0.4	18

#	Article	IF	Citations
598	Respiratory proteins in Sipunculus nudus â€" Implications for phylogeny and evolution of the hemerythrin family. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2010, 155, 171-177.	0.7	6
599	Molecular characterization and gene expression of thyrotropin-releasing hormone in Senegalese sole (Solea senegalensis). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2010, 157, 167-174.	0.7	16
600	The Genome of Naegleria gruberi Illuminates Early Eukaryotic Versatility. Cell, 2010, 140, 631-642.	13.5	399
601	Contrasting mitochondrial DNA diversity estimates in Austrian Scutovertex minutus and S. sculptus (Acari, Oribatida, Brachypylina, Scutoverticidae). Pedobiologia, 2010, 53, 203-211.	0.5	18
602	Evolution and functional divergence of enzymes involved in sesquiterpenoid hormone biosynthesis in crustaceans and insects. Peptides, 2010, 31, 451-455.	1.2	55
603	Expression analyses indicate the involvement of sunflower WRKY transcription factors in stress responses, and phylogenetic reconstructions reveal the existence of a novel clade in the Asteraceae. Plant Science, 2010, 178, 398-410.	1.7	32
604	Origin of Pax and Six gene families in sponges: Single PaxB and Six1/2 orthologs in Chalinula loosanoffi. Developmental Biology, 2010, 343, 106-123.	0.9	33
605	The Chlorella variabilis NC64A Genome Reveals Adaptation to Photosymbiosis, Coevolution with Viruses, and Cryptic Sex Â. Plant Cell, 2010, 22, 2943-2955.	3.1	441
606	Mitochondrial genome analysis of the predatory mitePhytoseiulus persimilisand a revisit of theMetaseiulus occidentalismitochondrial genome. Genome, 2010, 53, 285-301.	0.9	35
607	The role of multixenobiotic transporters in predatory marine molluscs as counter-defense mechanisms against dietary allelochemicals. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2010, 152, 288-300.	1.3	14
608	Genomic Fossils Calibrate the Long-Term Evolution of Hepadnaviruses. PLoS Biology, 2010, 8, e1000495.	2.6	126
609	Parallela Flint: its phylogenetic position in the Chlorophyceae and the polyphyly of Radiofilum Schmidle. Phycologia, 2010, 49, 373-383.	0.6	13
610	Identification of a methylase required for 2-methylhopanoid production and implications for the interpretation of sedimentary hopanes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8537-8542.	3.3	191
611	Natural and Engineered Photoactivated Nucleotidyl Cyclases for Optogenetic Applications. Journal of Biological Chemistry, 2010, 285, 41501-41508.	1.6	194
612	Bacterial and Eukaryotic Phosphoketolases: Phylogeny, Distribution and Evolution. Journal of Molecular Microbiology and Biotechnology, 2010, 18, 37-51.	1.0	31
613	The complete mitochondrial genome of the relict frogLeiopelma archeyi: Insights into the root of the frog Tree of Life. Mitochondrial DNA, 2010, 21, 173-182.	0.6	32
614	Environmental Regulation of Lateral Root Emergence inMedicago truncatulaRequires the HD-Zip I Transcription Factor HB1. Plant Cell, 2010, 22, 2171-2183.	3.1	156
615	The cereal rust miteAbacarus hystrix(Acari: Eriophyoidea) is a complex of species: evidence from mitochondrial and nuclear DNA sequences. Bulletin of Entomological Research, 2010, 100, 263-272.	0.5	114

#	Article	IF	Citations
616	Salmonid genomes have a remarkably expandedakirinfamily, coexpressed with genes from conserved pathways governing skeletal muscle growth and catabolism. Physiological Genomics, 2010, 42, 134-148.	1.0	48
617	Mitochondrial genomics in Orthoptera using MOSAS. Mitochondrial DNA, 2010, 21, 87-104.	0.6	65
618	Genome-Wide Classification and Evolutionary Analysis of the bHLH Family of Transcription Factors in Arabidopsis, Poplar, Rice, Moss, and Algae Â. Plant Physiology, 2010, 153, 1398-1412.	2.3	493
619	The Putative AKH Receptor of the Tobacco Hornworm,Manduca sexta, and Its Expression. Journal of Insect Science, 2011, 11, 1-20.	0.6	40
620	Molecular Identification of Novel Alpha- and Gammaherpesviruses from Cetaceans Stranded on Japanese Coasts. Zoological Science, 2011, 28, 126.	0.3	15
621	Diversity and Plasticity of the Intracellular Plant Pathogen and Insect Symbiont â€œCandidatus Liberibacter asiaticusâ€•as Revealed by Hypervariable Prophage Genes with Intragenic Tandem Repeats. Applied and Environmental Microbiology, 2011, 77, 6663-6673.	1.4	58
622	Reductive Evolution of Bacterial Genome in Insect Gut Environment. Genome Biology and Evolution, 2011, 3, 702-714.	1.1	147
623	Extraordinary Conservation, Gene Loss, and Positive Selection in the Evolution of an Ancient Neurotoxin. Molecular Biology and Evolution, 2011, 28, 1173-1182.	3.5	103
624	Biased gene transfer in microbial evolution. Nature Reviews Microbiology, 2011, 9, 543-555.	13.6	165
625	Molecular phylogenetics of the Gloeophyllales and relative ages of clades of Agaricomycotina producing a brown rot. Mycologia, 2011, 103, 510-524.	0.8	69
626	Sequence divergence at mitochondrial genes in animals: Applicability of DNA data in genetics of speciation and molecular phylogenetics. Marine Genomics, 2011, 4, 71-81.	0.4	26
627	Mitogenome of the small abalone Haliotis diversicolor Reeve and phylogenetic analysis within Gastropoda. Marine Genomics, 2011, 4, 253-262.	0.4	19
628	Complete mtDNA of the Meretrix lamarckii (Bivalvia: Veneridae) and molecular identification of suspected M. lamarckii based on the whole mitochondrial genome. Marine Genomics, 2011, 4, 263-271.	0.4	19
629	The role of stat1b in zebrafish hematopoiesis. Mechanisms of Development, 2011, 128, 442-456.	1.7	31
630	Phylogenetic Analysis of Protein Sequence Data Using the Randomized Axelerated Maximum Likelihood (<scp>RAXML</scp>) Program. Current Protocols in Molecular Biology, 2011, 96, Unit19.11.	2.9	43
631	Lafora disease E3-ubiquitin ligase malin is related to TRIM32 at both the phylogenetic and functional level. BMC Evolutionary Biology, 2011, 11, 225.	3.2	23
632	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic Xanthomonas spp. Journal of Bacteriology, 2011, 193, 5450-5464.	1.0	189
633	Strategies to Determine Diversity, Growth, and Activity of Ammonia-Oxidizing Archaea in Soil. Methods in Enzymology, 2011, 496, 3-34.	0.4	18

#	Article	IF	Citations
634	The complete mitochondrial genome sequence of Whitmania pigra (Annelida, Hirudinea): The first representative from the class Hirudinea. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 133-138.	0.4	12
635	Duplication of calsequestrin genes in teleosts: Molecular characterization in the Senegalese sole (Solea senegalensis). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2011, 158, 304-314.	0.7	15
636	Molecular characterization of a novel type II keratin gene (sseKer3) in the Senegalese sole (Solea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Physiology - B Biochemistry and Molecular Biology, 2011, 160, 15-23.	0.7	8
637	Neuropeptide Y/peptide YY receptor Y2 duplicate in zebrafish with unique introns displays distinct peptide binding properties. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2011, 160, 166-173.	0.7	21
638	A Mechanism for the Evolution of Phosphorylation Sites. Cell, 2011, 147, 934-946.	13.5	215
639	Individual sequence variability and functional activities of fibrinogen-related proteins (FREPs) in the Mediterranean mussel (Mytilus galloprovincialis) suggest ancient and complex immune recognition models in invertebrates. Developmental and Comparative Immunology, 2011, 35, 334-344.	1.0	94
640	TIR domain-containing adaptor SARM is a late addition to the ongoing microbeâ€“host dialog. Developmental and Comparative Immunology, 2011, 35, 461-468.	1.0	66
641	Three isoforms of anti-lipopolysaccharide factor identified from eyestalk cDNA library of swimming crab Portunus trituberculatus. Fish and Shellfish Immunology, 2011, 30, 583-591.	1.6	48
642	Multiple isoforms of immune-related genes from hemocytes and eyestalk cDNA libraries of swimming crab Portunus trituberculatus. Fish and Shellfish Immunology, 2011, 31, 29-42.	1.6	35
643	Characterization of the gilthead seabream (Sparus aurata L.) transferrin gene: Genomic structure, constitutive expression and SNP variation. Fish and Shellfish Immunology, 2011, 31, 548-56.	1.6	14
644	Genomic characterization, phylogeny and gene regulation of g-type lysozyme in sole (Solea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 T	1.6	37
645	The highly variable mitochondrial small-subunit ribosomal RNA gene of Ophiostoma minus. Fungal Biology, 2011, 115, 1122-1137.	1.1	8
646	Species of Heterobasidion host a diverse pool of partitiviruses with global distribution and interspecies transmission. Fungal Biology, 2011, 115, 1234-1243.	1.1	66
647	Analysis of lamprey clustered Fox genes: Insight into Fox gene evolution and expression in vertebrates. Gene, 2011, 489, 30-40.	1.0	18
648	Characterisation of the heat shock factor of the human thermodimorphic pathogen Paracoccidioides lutzii. Fungal Genetics and Biology, 2011, 48, 947-955.	0.9	4
649	Molecular evolution and selection pressure in alpha-class carbonic anhydrase family members. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1854-1861.	1.1	6
650	Evolutionary origins of the estrogen signaling system: Insights from amphioxus. Journal of Steroid Biochemistry and Molecular Biology, 2011, 127, 176-188.	1.2	56
651	Detection of members of the Tombusviridae in the Tallgrass Prairie Preserve, Osage County, Oklahoma, USA. Virus Research, 2011, 160, 256-263.	1.1	27

#	Article	IF	Citations
652	Evolutionary implications of morphogenesis and molecular patterning of the blind gut in the planarian Schmidtea polychroa. Developmental Biology, 2011, 352, 164-176.	0.9	52
653	Origin and evolutionary analysis of the plant-specific TIFY transcription factor family. Genomics, 2011, 98, 128-136.	1.3	167
654	Evaluating phylogenetic informativeness and data-type usage for new protein-coding genes across Vertebrata. Molecular Phylogenetics and Evolution, 2011, 61, 300-307.	1.2	32
655	A multi-locus analysis of phylogenetic relationships within cheilostome bryozoans supports multiple origins of ascophoran frontal shields. Molecular Phylogenetics and Evolution, 2011, 61, 351-362.	1.2	27
656	Mitogenome rearrangement in the cold-water scleractinian coral Lophelia pertusa (Cnidaria,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 T 61, 495-503.	1.2	39
657	Genomic organization of the glutathione S-transferase family in insects. Molecular Phylogenetics and Evolution, 2011, 61, 924-932.	1.2	88
658	Phylogenomic Evidence for the Presence of a Flagellum and cbb3 Oxidase in the Free-Living Mitochondrial Ancestor. Molecular Biology and Evolution, 2011, 28, 3285-3296.	3.5	124
659	The Organellar Genome and Metabolic Potential of the Hydrogen-Producing Mitochondrion of Nyctotherus ovalis. Molecular Biology and Evolution, 2011, 28, 2379-2391.	3.5	82
660	A multilocus sequence analysis approach to the phylogeny and taxonomy of the Halobacteriales. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 2984-2995.	0.8	54
661	Locusâ€specific protocol for nine different innate immune genes (antimicrobial peptides: Î²â€defensins) across passerine bird species reveals withinâ€species coding variation and a case of transâ€species polymorphisms. Molecular Ecology Resources, 2011, 11, 686-692.	2.2	38
662	Kakusan4 and Aminosan: two programs for comparing nonpartitioned, proportional and separate models for combined molecular phylogenetic analyses of multilocus sequence data. Molecular Ecology Resources, 2011, 11, 914-921.	2.2	608
663	Two new subfamilies of DNA mismatch repair proteins (MutS) specifically abundant in the marine environment. ISME Journal, 2011, 5, 1143-1151.	4.4	69
664	Complete mitochondrial DNA sequence and phylogenetic analysis of Zhikong scallop Chlamys farreri (Bivalvia: Pectinidae). Molecular Biology Reports, 2011, 38, 3067-3074.	1.0	32
665	Molecular evolution of RRM-containing proteins and glycine-rich RNA-binding proteins in plants. Nature Precedings, 2011, , .	0.1	0
666	Fusion of the subunits Î± and Î² of succinyl-CoA synthetase as a phylogenetic marker for Pezizomycotina fungi. Genetics and Molecular Biology, 2011, 34, 669-675.	0.6	1
667	Analysis of Duplicate Gene Families in Microbial Genomes and Application to the Study of Gene Duplication in M. tuberculosis. , 2011, , .		0
668	An Alternative Path for the Evolution of Biological Nitrogen Fixation. Frontiers in Microbiology, 2011, 2, 205.	1.5	105
669	Genomic and Experimental Evidence Suggests that Verrucomicrobium spinosum Interacts with Eukaryotes. Frontiers in Microbiology, 2011, 2, 211.	1.5	19

#	Article	IF	Citations
670	Contrasting 5' and 3' Evolutionary Histories and Frequent Evolutionary Convergence in Meis/hth Gene Structures. Genome Biology and Evolution, 2011, 3, 551-564.	1.1	16
671	Ancient Antimicrobial Peptides Kill Antibiotic-Resistant Pathogens: Australian Mammals Provide New Options. PLoS ONE, 2011, 6, e24030.	1.1	72
672	The First Molecular Phylogeny of Strepsiptera (Insecta) Reveals an Early Burst of Molecular Evolution Correlated with the Transition to Endoparasitism. PLoS ONE, 2011, 6, e21206.	1.1	39
673	Odorant Binding Proteins of the Red Imported Fire Ant, Solenopsis invicta: An Example of the Problems Facing the Analysis of Widely Divergent Proteins. PLoS ONE, 2011, 6, e16289.	1.1	42
674	Parallel Expansions of Sox Transcription Factor Group B Predating the Diversifications of the Arthropods and Jawed Vertebrates. PLoS ONE, 2011, 6, e16570.	1.1	25
675	Evolution of the Karyopherin-Î² Family of Nucleocytoplasmic Transport Factors; Ancient Origins and Continued Specialization. PLoS ONE, 2011, 6, e19308.	1.1	64
676	Spliced Leader RNAs, Mitochondrial Gene Frameshifts and Multi-Protein Phylogeny Expand Support for the Genus Perkinsus as a Unique Group of Alveolates. PLoS ONE, 2011, 6, e19933.	1.1	39
677	Discovery of Nuclear-Encoded Genes for the Neurotoxin Saxitoxin in Dinoflagellates. PLoS ONE, 2011, 6, e20096.	1.1	172
678	Identification of Fast-Evolving Genes in the Scleractinian Coral Acropora Using Comparative EST Analysis. PLoS ONE, 2011, 6, e20140.	1.1	20
679	Widespread Occurrence of Secondary Lipid Biosynthesis Potential in Microbial Lineages. PLoS ONE, 2011, 6, e20146.	1.1	74
680	Expression and Trans-Specific Polymorphism of Self-Incompatibility RNases in Coffea (Rubiaceae). PLoS ONE, 2011, 6, e21019.	1.1	57
681	Informational Gene Phylogenies Do Not Support a Fourth Domain of Life for Nucleocytoplasmic Large DNA Viruses. PLoS ONE, 2011, 6, e21080.	1.1	73
682	Role of Plant-Specific N-Terminal Domain of Maize CK2Î²1 Subunit in CK2Î² Functions and Holoenzyme Regulation. PLoS ONE, 2011, 6, e21909.	1.1	9
683	Multiple Independent Fusions of Glucose-6-Phosphate Dehydrogenase with Enzymes in the Pentose Phosphate Pathway. PLoS ONE, 2011, 6, e22269.	1.1	26
684	Beyond Biodiversity: Fish Metagenomes. PLoS ONE, 2011, 6, e22592.	1.1	18
685	Diversity in the Architecture of ATLs, a Family of Plant Ubiquitin-Ligases, Leads to Recognition and Targeting of Substrates in Different Cellular Environments. PLoS ONE, 2011, 6, e23934.	1.1	55
686	One Carbon Metabolism in SAR11 Pelagic Marine Bacteria. PLoS ONE, 2011, 6, e23973.	1.1	173
687	Evolutionary History of the Vertebrate Mitogen Activated Protein Kinases Family. PLoS ONE, 2011, 6, e26999.	1.1	53

#	Article	IF	Citations
688	The Mitochondrial Genome of Baylisascaris procyonis. PLoS ONE, 2011, 6, e27066.	1.1	45
689	Non-Negative Matrix Factorization for Learning Alignment-Specific Models of Protein Evolution. PLoS ONE, 2011, 6, e28898.	1.1	11
690	LTR Retrotransposons in Fungi. PLoS ONE, 2011, 6, e29425.	1.1	94
691	Stanniocalcin Has Deep Evolutionary Roots in Eukaryotes. Genome Biology and Evolution, 2011, 3, 284-294.	1.1	11
692	Genome sequences reveal divergence times of malaria parasite lineages. Parasitology, 2011, 138, 1737-1749.	0.7	50
693	Evolutionary History of the Non-Specific Lipid Transfer Proteins. Molecular Plant, 2011, 4, 947-964.	3.9	145
694	Diversity and distribution of microbial longâ€chain fatty acid biosynthetic genes in the marine environment. Environmental Microbiology, 2011, 13, 684-695.	1.8	37
695	Gene acquisition, duplication and metabolic specification: the evolution of fungal methylisocitrate lyases. Environmental Microbiology, 2011, 13, 1534-1548.	1.8	16
696	Alkane-degrading properties of Dietzia sp. H0B, a key player in the Prestige oil spill biodegradation (NW) Tj ETQq0 0 0 rgBT /Overlock 10	1.4	40
697	Root hairâ€specific expansins modulate root hair elongation in rice. Plant Journal, 2011, 66, 725-734.	2.8	143
698	Alternative targeting of Arabidopsis plastidic glucoseâ€6â€phosphate dehydrogenase G6PD1 involves cysteineâ€dependent interaction with G6PD4 in the cytosol. Plant Journal, 2011, 66, 745-758.	2.8	84
699	Cattle and chemokines: evidence for speciesâ€specific evolution of the bovine chemokine system. Animal Genetics, 2011, 42, 341-353.	0.6	24
700	CH4 production and oxidation processes in a boreal fen ecosystem after long-term water table drawdown. Global Change Biology, 2011, 17, 1311-1320.	4.2	98
701	Conserved function of the KrÃ¼ppel gap gene in the blowfly Lucilia sericata, despite anterior shift of expression. Insect Molecular Biology, 2011, 20, 257-265.	1.0	7
702	An actinâ€based cytoskeleton in archaea. Molecular Microbiology, 2011, 80, 1052-1061.	1.2	142
703	A late methanogen origin for molybdenumâ€dependent nitrogenase. Geobiology, 2011, 9, 221-232.	1.1	141
704	Evolution of the Alx homeobox gene family: parallel retention and independent loss of the vertebrate Alx3 gene. Evolution & Development, 2011, 13, 343-351.	1.1	37
705	Tail regression induced by elevated retinoic acid signaling in amphioxus larvae occurs by tissue remodeling, not cell death. Evolution & Development, 2011, 13, 427-435.	1.1	11

#	Article	IF	Citations
706	Coâ€orthology of<scp>P</scp>ax4and<scp>P</scp>ax6to the flyeyelessgene: molecular phylogenetic, comparative genomic, and embryological analyses. Evolution & Development, 2011, 13, 448-459.	1.1	16
707	Alkaline Phosphatase Gene Sequence And Transcriptional Regulation By Phosphate Limitation In Amphidinium Carterae (Dinophyceae)¹. Journal of Phycology, 2011, 47, 1110-1120.	1.0	56
708	The rice acylâ€CoAâ€binding protein gene family: phylogeny, expression and functional analysis. New Phytologist, 2011, 189, 1170-1184.	3.5	78
709	Phenotypic and genotypic heterogeneity among closely related soil-borne N2- and N2O-producing Bacillus isolates harboring the nosZ gene. FEMS Microbiology Ecology, 2011, 76, 541-552.	1.3	53
710	Phylogenetic relationships between Sophophora and Lordiphosa, with proposition of a hypothesis on the vicariant divergences of tropical lineages between the Old and New Worlds in the family Drosophilidae. Molecular Phylogenetics and Evolution, 2011, 60, 98-107.	1.2	42
711	What can the mitochondrial genome reveal about higher-level phylogeny of the molluscan class Cephalopoda?. Zoological Journal of the Linnean Society, 2011, 161, 573-586.	1.0	45
712	Diversity and distribution of single-stranded DNA phages in the North Atlantic Ocean. ISME Journal, 2011, 5, 822-830.	4.4	99
713	Phylogenomic analyses unravel annelid evolution. Nature, 2011, 471, 95-98.	13.7	357
714	Ancestral expression patterns and evolutionary diversification of YABBY genes in angiosperms. Plant Journal, 2011, 67, 26-36.	2.8	123
715	Characterization of the â€˜pristinamycin superclusterâ€™ of Streptomyces pristinaespiralis. Microbial Biotechnology, 2011, 4, 192-206.	2.0	119
716	An entropy-based approach for the identification of phylogenetically informative genomic regions of Papillomavirus. Infection, Genetics and Evolution, 2011, 11, 2026-2033.	1.0	21
717	Legionella bozemanae synthesizes phosphatidylcholine from exogenous choline. Microbiological Research, 2011, 166, 87-98.	2.5	9
718	Broad taxonomic sampling of mitochondrial cytochrome c oxidase subunit I does not solve the relationships between Rotifera and Acanthocephala. Zoologischer Anzeiger, 2011, 250, 80-85.	0.4	24
719	Heat shock protein expression during stress and diapause in the marine copepod Calanus finmarchicus. Journal of Insect Physiology, 2011, 57, 665-675.	0.9	83
720	Introns, Alternative Splicing, Spliced Leader trans-Splicing and Differential Expression of pcna and cyclin in Perkinsus marinus. Protist, 2011, 162, 154-167.	0.6	21
721	Subulatomonas tetraspora nov. gen. nov. sp. is a Member of a Previously Unrecognized Major Clade of Eukaryotes. Protist, 2011, 162, 762-773.	0.6	27
722	Divergence of duplicate POMC genes in gilthead sea bream Sparus auratus. General and Comparative Endocrinology, 2011, 173, 396-404.	0.8	27
723	Identification and gene expression analysis of three GnRH genes in female Atlantic cod during puberty provides insight into GnRH variant gene loss in fish. General and Comparative Endocrinology, 2011, 172, 458-467.	0.8	36

#	Article	IF	Citations
724	First evidence for a direct inhibitory effect of kisspeptins on LH expression in the eel, Anguilla anguilla. General and Comparative Endocrinology, 2011, 173, 216-225.	0.8	58
725	Four gonadotropin releasing hormone receptor genes in Atlantic cod are differentially expressed in the brain and pituitary during puberty. General and Comparative Endocrinology, 2011, 173, 333-345.	0.8	27
726	Biophysical and structural considerations for protein sequence evolution. BMC Evolutionary Biology, 2011, 11, 361.	3.2	50
727	Polymorphism, selection and tandem duplication of transferrin genes in Atlantic cod (Gadus morhua) - Conserved synteny between fish monolobal and tetrapod bilobal transferrin loci. BMC Genetics, 2011, 12, 51.	2.7	11
728	Uncharacterized conserved motifs outside the HD-Zip domain in HD-Zip subfamily I transcription factors; a potential source of functional diversity. BMC Plant Biology, 2011, 11, 42.	1.6	70
729	Drosophila metalloproteases in development and differentiation: The role of ADAM proteins and their relatives. European Journal of Cell Biology, 2011, 90, 770-778.	1.6	22
730	The HMGB protein gene family in zebrafish: Evolution and embryonic expression patterns. Gene Expression Patterns, 2011, 11, 3-11.	0.3	33
731	Evolution of the epithelial sodium channel and the sodium pump as limiting factors of aldosterone action on sodium transport. Physiological Genomics, 2011, 43, 844-854.	1.0	39
732	The role of vertical and horizontal transfer in the evolution of Paris-like elements in drosophilid species. Genetica, 2011, 139, 1487-1497.	0.5	3
733	Domain combination of the vertebrate-like TLR gene family: implications for their origin and evolution. Journal of Genetics, 2011, 90, 401-408.	0.4	24
734	On universal common ancestry, sequence similarity, and phylogenetic structure: the sins of P-values and the virtues of Bayesian evidence. Biology Direct, 2011, 6, 60.	1.9	17
735	Archaeorhizomycetes: Unearthing an Ancient Class of Ubiquitous Soil Fungi. Science, 2011, 333, 876-879.	6.0	249
736	Structural anatomy of telomere OB proteins. Critical Reviews in Biochemistry and Molecular Biology, 2011, 46, 409-435.	2.3	29
737	The evolutionary history of mariner-like elements in Neotropical drosophilids. Genetica, 2011, 139, 327-338.	0.5	8
738	Molecular evolution of the membrane associated progesterone receptor in the Brachionus plicatilis (Rotifera, Monogononta) species complex. Hydrobiologia, 2011, 662, 99-106.	1.0	9
739	The CO2-concentrating mechanism of Synechococcus WH5701 is composed of native and horizontally-acquired components. Photosynthesis Research, 2011, 109, 59-72.	1.6	38
740	Complete mitochondrial genome of the Chinese spiny lobster Panulirus stimpsoni (Crustacea:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 2011, 38, 403-410.	1.0	37
741	The complete mitochondrial genome of the hard clam Meretrix meretrix. Molecular Biology Reports, 2011, 38, 3401-3409.	1.0	28

#	Article	IF	Citations
742	Evolutionary significance of an algal gene encoding an [FeFe]-hydrogenase with F-domain homology and hydrogenase activity in Chlorella variabilis NC64A. Planta, 2011, 234, 829-843.	1.6	50
743	Eimeria maxima phosphatidylinositol 4-phosphate 5-kinase: locus sequencing, characterization, and cross-phylum comparison. Parasitology Research, 2011, 108, 611-620.	0.6	1
744	Bromus catharticus striate mosaic virus: a new mastrevirus infecting Bromus catharticus from Australia. Archives of Virology, 2011, 156, 335-341.	0.9	9
745	The genome sequence of pepper vein yellows virus (family Luteoviridae, genus Polerovirus). Archives of Virology, 2011, 156, 921-923.	0.9	28
746	Occurrence of a Silicatein Gene in Glass Sponges (Hexactinellida: Porifera). Marine Biotechnology, 2011, 13, 810-819.	1.1	23
747	A New Coral Carbonic Anhydrase in Stylophora pistillata. Marine Biotechnology, 2011, 13, 992-1002.	1.1	83
748	Comparative characterization, expression pattern and function analysis of the 12-oxo-phytodienoic acid reductase gene family in rice. Plant Cell Reports, 2011, 30, 981-995.	2.8	37
749	Ontogeny of globin expression in zebrafish (Danio rerio). Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology, 2011, 181, 1011-1021.	0.7	34
750	Characterization of a regulatory unit that controls melanization and affects longevity of mosquitoes. Cellular and Molecular Life Sciences, 2011, 68, 1929-1939.	2.4	110
751	Phylogenetic and Functional Analysis of the Vertebrate Cytochrome P450 2 Family. Journal of Molecular Evolution, 2011, 72, 56-71.	0.8	43
752	Prestin Shows Divergent Evolution Between Constant Frequency Echolocating Bats. Journal of Molecular Evolution, 2011, 73, 109-115.	0.8	13
753	Genome-Wide Comparative Analysis of pogo-Like Transposable Elements in Different Fusarium Species. Journal of Molecular Evolution, 2011, 73, 230-243.	0.8	20
754	Two Polymorphic Residues Account for the Differences in DNA Binding and Transcriptional Activation by NF-Î°B Proteins Encoded by Naturally Occurring Alleles in Nematostella vectensis. Journal of Molecular Evolution, 2011, 73, 325-336.	0.8	10
755	Molecular Characterization of Two Endothelin Pathways in East African Cichlid Fishes. Journal of Molecular Evolution, 2011, 73, 355-368.	0.8	16
756	Environmental Conditions Constrain the Distribution and Diversity of Archaeal merA in Yellowstone National Park, Wyoming, U.S.A.. Microbial Ecology, 2011, 62, 739-752.	1.4	33
757	Isolation and characterisation of KP34â€"a novel Ï†KMV-like bacteriophage for Klebsiella pneumoniae. Applied Microbiology and Biotechnology, 2011, 90, 1333-1345.	1.7	62
758	S-RNase-like Sequences in Styles of Coffea (Rubiaceae). Evidence for S-RNase Based Gametophytic Self-Incompatibility?. Tropical Plant Biology, 2011, 4, 237-249.	1.0	22
759	Prediction of sites under adaptive evolution in flavin-containing monooxygenases: Selection pattern revisited. Science Bulletin, 2011, 56, 1246-1255.	1.7	7

#	Article	IF	Citations
760	Transcriptional analysis of cell growth and morphogenesis in the unicellular green alga Micrasterias(Streptophyta), with emphasis on the role of expansin. BMC Plant Biology, 2011, 11, 128.	1.6	34
761	A highly conserved NB-LRR encoding gene cluster effective against Setosphaeria turcica in sorghum. BMC Plant Biology, 2011, 11, 151.	1.6	35
762	The taming of an impossible child: a standardized all-in approach to the phylogeny of Hymenoptera using public database sequences. BMC Biology, 2011, 9, 55.	1.7	54
763	Multiple origins of endosymbiosis within the Enterobacteriaceae (Î³-Proteobacteria): convergence of complex phylogenetic approaches. BMC Biology, 2011, 9, 87.	1.7	90
764	Biased gene transfer and its implications for the concept of lineage. Biology Direct, 2011, 6, 47.	1.9	36
765	Phylogenetic analysis reveals wide distribution of globin X. Biology Direct, 2011, 6, 54.	1.9	23
766	Rab23 is a flagellar protein in Trypanosoma brucei. BMC Research Notes, 2011, 4, 190.	0.6	14
767	Somatic and germline expression of piwi during development and regeneration in the marine polychaete annelid Capitella teleta. EvoDevo, 2011, 2, 10.	1.3	87
768	Gene expression in bryozoan larvae suggest a fundamental importance of pre-patterned blastemic cells in the bryozoan life-cycle. EvoDevo, 2011, 2, 13.	1.3	27
769	Developmental evolution of flowering plant pollen tube cell walls: callose synthase (CalS) gene expression patterns. EvoDevo, 2011, 2, 14.	1.3	38
770	Ciliary photoreceptors in the cerebral eyes of a protostome larva. EvoDevo, 2011, 2, 6.	1.3	67
771	SuiteMSA: visual tools for multiple sequence alignment comparison and molecular sequence simulation. BMC Bioinformatics, 2011, 12, 184.	1.2	16
772	Phylogenomic reconstruction of lactic acid bacteria: an update. BMC Evolutionary Biology, 2011, 11, 1.	3.2	312
773	Evolution of light-harvesting complex proteins from Chl c-containing algae. BMC Evolutionary Biology, 2011, 11, 101.	3.2	44
774	Reversal to air-driven sound production revealed by a molecular phylogeny of tongueless frogs, family Pipidae. BMC Evolutionary Biology, 2011, 11, 114.	3.2	47
775	The evolutionary history of the stearoyl-CoA desaturase gene family in vertebrates. BMC Evolutionary Biology, 2011, 11, 132.	3.2	90
776	A survey of green plant tRNA 3'-end processing enzyme tRNase Zs, homologs of the candidate prostate cancer susceptibility protein ELAC2. BMC Evolutionary Biology, 2011, 11, 219.	3.2	13
777	Molecular evolution of a chordate specific family of G protein-coupled receptors. BMC Evolutionary Biology, 2011, 11, 234.	3.2	16

#	Article	IF	Citations
778	Evidence for maintenance of sex determinants but not of sexual stages in red yeasts, a group of early diverged basidiomycetes. BMC Evolutionary Biology, 2011, 11, 249.	3.2	30
779	A holistic phylogeny of the coronin gene family reveals an ancient origin of the tandem-coronin, defines a new subfamily, and predicts protein function. BMC Evolutionary Biology, 2011, 11, 268.	3.2	53
780	Study of Sylvilagusrabbit TRIM5Î± species-specific domain: how ancient endoviruses could have shaped the antiviral repertoire in Lagomorpha. BMC Evolutionary Biology, 2011, 11, 294.	3.2	18
781	A multigene phylogeny of Olpidium and its implications for early fungal evolution. BMC Evolutionary Biology, 2011, 11, 331.	3.2	73
782	Evolutionary and functional insights into Leishmania META1: evidence for lateral gene transfer and a role for META1 in secretion. BMC Evolutionary Biology, 2011, 11, 334.	3.2	9
783	Evolutionary maintenance of filovirus-like genes in bat genomes. BMC Evolutionary Biology, 2011, 11, 336.	3.2	50
784	Evolutionary history of the OmpR/IIIA family of signal transduction two component systems in Lactobacillaceae and Leuconostocaceae. BMC Evolutionary Biology, 2011, 11, 34.	3.2	11
785	Pathogen-origin horizontally transferred genes contribute to the evolution of Lepidopteran insects. BMC Evolutionary Biology, 2011, 11, 356.	3.2	39
786	Phylogenetics and evolution of Su(var)3-9 SET genes in land plants: rapid diversification in structure and function. BMC Evolutionary Biology, 2011, 11, 63.	3.2	15
787	Mitochondrial genes support a common origin of rodent malaria parasites and Plasmodium falciparum's relatives infecting great apes. BMC Evolutionary Biology, 2011, 11, 70.	3.2	16
788	Evolution of Parallel Spindles Like genes in plants and highlight of unique domain architecture#. BMC Evolutionary Biology, 2011, 11, 78.	3.2	25
789	The midgut transcriptome of Phlebotomus (Larroussius) perniciosus, a vector of Leishmania infantum: comparison of sugar fed and blood fed sand flies. BMC Genomics, 2011, 12, 223.	1.2	30
790	BMP signaling components in embryonic transcriptomes of the hover fly Episyrphus balteatus (Syrphidae). BMC Genomics, 2011, 12, 278.	1.2	22
791	Unresolved orthology and peculiar coding sequence properties of lamprey genes: the KCNA gene family as test case. BMC Genomics, 2011, 12, 325.	1.2	70
792	The bacteriophage WORiC is the active phage element in wRi of Drosophila simulans and represents a conserved class of WO phages. BMC Microbiology, 2011, 11, 251.	1.3	11
793	Molecular architecture of muscles in an acoel and its evolutionary implications. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2011, 316B, 427-439.	0.6	13
794	Expression of a Musashiâ€like gene in sexual and asexual development of the colonial chordate Botryllus schlosseri and phylogenetic analysis of the protein group. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2011, 316B, 562-573.	0.6	10
796	Molecular analysis of neurogenic placode development in a basal rayâ€finned fish. Genesis, 2011, 49, 278-294.	0.8	24

#	Article	IF	Citations
797	Exploring the molecular phylogeny of phasmids with whole mitochondrial genome sequences. Molecular Phylogenetics and Evolution, 2011, 58, 43-52.	1.2	72
798	Reducing Model Complexity of the General Markov Model of Evolution. Molecular Biology and Evolution, 2011, 28, 3045-3059.	3.5	27
799	Interspersed DNA Repeats bcr1-bcr18 of Bacillus cereus Group Bacteria Form Three Distinct Groups with Different Evolutionary and Functional Patterns. Molecular Biology and Evolution, 2011, 28, 963-983.	3.5	13
800	New Data on the Presence of Hemocyanin in Plecoptera: Recomposing a Puzzle. Journal of Insect Science, 2011, 11, 1-20.	0.6	9
801	Multivesicular bodies in the enigmatic amoeboflagellateBreviata anathemaand the evolution of ESCRT 0. Journal of Cell Science, 2011, 124, 613-621.	1.2	35
802	Sea urchin tube feet are photosensory organs that express a rhabdomeric-like opsin and PAX6. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 3371-3379.	1.2	64
803	Conserved Meiotic Machinery in Glomus spp., a Putatively Ancient Asexual Fungal Lineage. Genome Biology and Evolution, 2011, 3, 950-958.	1.1	129
804	Eukaryotic Pyruvate Formate Lyase and Its Activating Enzyme Were Acquired Laterally from a Firmicute. Molecular Biology and Evolution, 2011, 28, 2087-2099.	3.5	66
805	Global Phylogeography of Chitinase Genes in Aquatic Metagenomes. Applied and Environmental Microbiology, 2011, 77, 1101-1106.	1.4	21
806	Paleozoic origin of insect large dsDNA viruses. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15931-15935.	3.3	136
807	The eisosome core is composed of BAR domain proteins. Molecular Biology of the Cell, 2011, 22, 2360-2372.	0.9	91
808	Expansion of Hexose Transporter Genes Was Associated with the Evolution of Aerobic Fermentation in Yeasts. Molecular Biology and Evolution, 2011, 28, 131-142.	3.5	82
809	Identification of a Perchlorate Reduction Genomic Island with Novel Regulatory and Metabolic Genes. Applied and Environmental Microbiology, 2011, 77, 7401-7404.	1.4	57
810	ProtTest 3: fast selection of best-fit models of protein evolution. Bioinformatics, 2011, 27, 1164-1165.	1.8	2,432
811	African Great Apes Are Naturally Infected with Polyomaviruses Closely Related to Merkel Cell Polyomavirus. Journal of Virology, 2011, 85, 916-924.	1.5	46
812	Evolution of the Insulin-Like Growth Factor Binding Protein (IGFBP) Family. Endocrinology, 2011, 152, 2278-2289.	1.4	123
813	Staphylococcus lugdunensis IsdG Liberates Iron from Host Heme. Journal of Bacteriology, 2011, 193, 4749-4757.	1.0	43
814	Rediscovery and genomic characterization of bovine astroviruses. Journal of General Virology, 2011, 92, 1888-1898.	1.3	77

#	Article	IF	Citations
815	The reconstructed ancestral subunit a functions as both V-ATPase isoforms Vph1p and Stv1p inSaccharomyces cerevisiae. Molecular Biology of the Cell, 2011, 22, 3176-3191.	0.9	25
816	Phylogenetic Study of Plant Q-type C2H2 Zinc Finger Proteins and Expression Analysis of Poplar Genes in Response to Osmotic, Cold and Mechanical Stresses. DNA Research, 2011, 18, 77-92.	1.5	53
817	Evolution of sodium channels predates the origin of nervous systems in animals. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9154-9159.	3.3	130
818	Parallel Evolution and Horizontal Gene Transfer of the pst Operon in Firmicutes from Oligotrophic Environments. International Journal of Evolutionary Biology, 2011, 2011, 1-10.	1.0	45
819	Phylogenetic Relationships of 3/3 and 2/2 Hemoglobins in Archaeplastida Genomes to Bacterial and Other Eukaryote Hemoglobins. Molecular Plant, 2011, 4, 42-58.	3.9	34
820	cAMP-dependent protein kinase fromPlasmodium falciparum: an update. Parasitology, 2011, 138, 1-25.	0.7	74
821	Functional Diversification of the Twin-Arginine Translocation Pathway Mediates the Emergence of Novel Ecological Adaptations. Molecular Biology and Evolution, 2011, 28, 3183-3193.	3.5	4
822	Stepwise assembly of the Nova -regulated alternative splicing network in the vertebrate brain. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5319-5324.	3.3	38
823	Genome Expansion and Differential Expression of Amino Acid Transporters at the Aphid/Buchnera Symbiotic Interface. Molecular Biology and Evolution, 2011, 28, 3113-3126.	3.5	66
824	Molecular Evolution of the Metazoan PHDâ€“HIF Oxygen-Sensing System. Molecular Biology and Evolution, 2011, 28, 1913-1926.	3.5	132
825	Quantifying the Phylodynamic Forces Driving Papillomavirus Evolution. Molecular Biology and Evolution, 2011, 28, 2101-2113.	3.5	114
826	Endosymbiotic Gene Transfer and Transcriptional Regulation of Transferred Genes in Paulinella chromatophora. Molecular Biology and Evolution, 2011, 28, 407-422.	3.5	110
827	New Insights on the Evolutionary History of Aphids and Their Primary Endosymbiont Buchnera aphidicola. International Journal of Evolutionary Biology, 2011, 2011, 1-9.	1.0	10
828	Substrate specificity of haloalkane dehalogenases. Biochemical Journal, 2011, 435, 345-354.	1.7	92
829	Overcoming Redundancy: An RNAi Enhancer Screen for Morphogenesis Genes inCaenorhabditis elegans. Genetics, 2011, 188, 549-564.	1.2	30
830	Evolution of the Insect Yellow Gene Family. Molecular Biology and Evolution, 2011, 28, 257-272.	3.5	114
831	Phylogenomic evidence for a common ancestor of mitochondria and the SAR11 clade. Scientific Reports, 2011, 1, 13.	1.6	133
832	High Prevalence of Simian Immunodeficiency Virus Infection in a Community of Savanna Chimpanzees. Journal of Virology, 2011, 85, 9918-9928.	1.5	94

#	Article	IF	Citations
833	A Membrane-bound Hemoglobin from Gills of the Green Shore Crab Carcinus maenas. Journal of Biological Chemistry, 2011, 286, 3185-3193.	1.6	25
834	Evolutionary reconstruction of the retromer complex and its function in Trypanosoma brucei. Journal of Cell Science, 2011, 124, 1496-1509.	1.2	102
835	Identification of an animal sucrose transporter. Journal of Cell Science, 2011, 124, 1984-1991.	1.2	57
836	Phylogenetic and Functional Characterization of the hAT Transposon Superfamily. Genetics, 2011, 188, 45-57.	1.2	69
837	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. Nucleic Acids Research, 2011, 39, W470-W474.	6.5	182
838	Evolutionary History of Arabidopsis thaliana Aminoacyl-tRNA Synthetase Dual-Targeted Proteins. Molecular Biology and Evolution, 2011, 28, 79-85.	3.5	21
839	The Plant Cell Wallâ€“Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. Science, 2011, 333, 762-765.	6.0	512
840	Evolution of the Nitric Oxide Synthase Family in Metazoans. Molecular Biology and Evolution, 2011, 28, 163-179.	3.5	123
841	Widespread Endogenization of Genome Sequences of Non-Retroviral RNA Viruses into Plant Genomes. PLoS Pathogens, 2011, 7, e1002146.	2.1	173
842	Comparative and Functional Genomics of Rhodococcus opacus PD630 for Biofuels Development. PLoS Genetics, 2011, 7, e1002219.	1.5	109
843	Independent Subtilases Expansions in Fungi Associated with Animals. Molecular Biology and Evolution, 2011, 28, 3395-3404.	3.5	51
844	Phylogenomic Analysis of the Uracil-DNA Glycosylase Superfamily. Molecular Biology and Evolution, 2011, 28, 1307-1317.	3.5	26
845	Differential Evolution of Voltage-Gated Sodium Channels in Tetrapods and Teleost Fishes. Molecular Biology and Evolution, 2011, 28, 859-871.	3.5	72
846	Global genetic diversity and geographical and host-species distribution of beak and feather disease virus isolates. Journal of General Virology, 2011, 92, 752-767.	1.3	71
847	Evolution of Structurally Disordered Proteins Promotes Neostructuralization. Molecular Biology and Evolution, 2011, 28, 59-62.	3.5	18
848	The Fifth Adaptor Protein Complex. PLoS Biology, 2011, 9, e1001170.	2.6	241
849	Adaptations to Endosymbiosis in a Cnidarian-Dinoflagellate Association: Differential Gene Expression and Specific Gene Duplications. PLoS Genetics, 2011, 7, e1002187.	1.5	91
850	Genome Reduction and Co-evolution between the Primary and Secondary Bacterial Symbionts of Psyllids. Molecular Biology and Evolution, 2012, 29, 3781-3792.	3.5	175

#	Article	IF	Citations
851	A Phylogenetic Analysis of the Brassicales Clade Based on an Alignment-Free Sequence Comparison Method. Frontiers in Plant Science, 2012, 3, 192.	1.7	41
852	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. Viruses, 2012, 4, 3209-3226.	1.5	156
853	Resurrecting prehistoric parvalbumins to explore the evolution of thermal compensation in extant Antarctic fish parvalbumins. Journal of Experimental Biology, 2012, 215, 3281-92.	0.8	7
854	Androglobin: A Chimeric Globin in Metazoans That Is Preferentially Expressed in Mammalian Testes. Molecular Biology and Evolution, 2012, 29, 1105-1114.	3.5	98
855	The Voltage-Gated Potassium Channel Subfamily KQT Member 4 (KCNQ4) Displays Parallel Evolution in Echolocating Bats. Molecular Biology and Evolution, 2012, 29, 1441-1450.	3.5	52
856	Repeated Evolution of Identical Domain Architecture in Metazoan Netrin Domain-Containing Proteins. Genome Biology and Evolution, 2012, 4, 883-899.	1.1	23
857	Characterization of Bean Necrotic Mosaic Virus: A Member of a Novel Evolutionary Lineage within the Genus Tospovirus. PLoS ONE, 2012, 7, e38634.	1.1	48
858	Phylogenetic Analysis and Classification of the Fungal bHLH Domain. Molecular Biology and Evolution, 2012, 29, 1301-1318.	3.5	29
859	Comparative Analysis of RNA Families Reveals Distinct Repertoires for Each Domain of Life. PLoS Computational Biology, 2012, 8, e1002752.	1.5	50
860	Salivary Gland Transcriptomes and Proteomes of Phlebotomus tobbi and Phlebotomus sergenti, Vectors of Leishmaniasis. PLoS Neglected Tropical Diseases, 2012, 6, e1660.	1.3	66
861	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. PLoS Pathogens, 2012, 8, e1003037.	2.1	595
862	Human Tetherin Exerts Strong Selection Pressure on the HIV-1 Group N Vpu Protein. PLoS Pathogens, 2012, 8, e1003093.	2.1	55
863	Phylogenetic Analysis of K+ Transporters in Bryophytes, Lycophytes, and Flowering Plants Indicates a Specialization of Vascular Plants. Frontiers in Plant Science, 2012, 3, 167.	1.7	91
864	Origin and Evolution of Laminin Gene Family Diversity. Molecular Biology and Evolution, 2012, 29, 1823-1836.	3.5	45
865	Computer-Based Annotation of Putative AraC/XylS-Family Transcription Factors of Known Structure but Unknown Function. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-14.	3.0	14
866	An expanding role for purine uptake permease-like transporters in plant secondary metabolism. Frontiers in Plant Science, 2012, 3, 78.	1.7	49
867	Molecular Evolution of Slow and Quick Anion Channels (SLACs and QUACs/ALMTs). Frontiers in Plant Science, 2012, 3, 263.	1.7	104
868	Reconstruction of Ancestral Metabolic Enzymes Reveals Molecular Mechanisms Underlying Evolutionary Innovation through Gene Duplication. PLoS Biology, 2012, 10, e1001446.	2.6	170

#	Article	IF	Citations
869	Genome Shrinkage and Loss of Nutrient-Providing Potential in the Obligate Symbiont of the Primitive Termite Mastotermes darwiniensis. Applied and Environmental Microbiology, 2012, 78, 204-210.	1.4	72
870	Taxon Influence Index: Assessing Taxon-Induced Incongruities in Phylogenetic Inference. Systematic Biology, 2012, 61, 337-345.	2.7	10
871	Analysis of Genome Content Evolution in PVC Bacterial Super-Phylum: Assessment of Candidate Genes Associated with Cellular Organization and Lifestyle. Genome Biology and Evolution, 2012, 4, 1375-1390.	1.1	51
872	Insights into the phylogeny of systematically controversial haptorian ciliates (Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 2012, 279, 2625-2635.	1.2	56
873	Endogenous Hepadnaviruses in the Genome of the Budgerigar (Melopsittacus undulatus) and the Evolution of Avian Hepadnaviruses. Journal of Virology, 2012, 86, 7688-7691.	1.5	25
874	Comparative Genome Analysis of Trichophyton rubrum and Related Dermatophytes Reveals Candidate Genes Involved in Infection. MBio, 2012, 3, e00259-12.	1.8	211
875	Evolutionary History and Functional Characterization of the Amphibian Xenosensor CAR. Molecular Endocrinology, 2012, 26, 14-26.	3.7	26
876	Tissue-Specific Alternative Splicing of Tak1 Is Conserved in Deuterostomes. Molecular Biology and Evolution, 2012, 29, 261-269.	3.5	21
877	Probabilistic Orthology Analysis of the ATP-Binding Cassette Transporters: Implications for the Development of Multiple Drug Resistance Phenotype. Drug Metabolism and Disposition, 2012, 40, 1397-1402.	1.7	4
878	Identification of Novel Positive-Strand RNA Viruses by Metagenomic Analysis of Archaea-Dominated Yellowstone Hot Springs. Journal of Virology, 2012, 86, 5562-5573.	1.5	107
879	Arabidopsis ECERIFERUM2 Is a Component of the Fatty Acid Elongation Machinery Required for Fatty Acid Extension to Exceptional Lengths Â Â. Plant Physiology, 2012, 160, 1164-1174.	2.3	133
880	Selfâ€regulated alternative splicing at the AHNAK locus. FASEB Journal, 2012, 26, 93-103.	0.2	24
881	Identification of MW Polyomavirus, a Novel Polyomavirus in Human Stool. Journal of Virology, 2012, 86, 10321-10326.	1.5	160
882	Vasopressin/Oxytocin-Related Signaling Regulates Gustatory Associative Learning in C. elegans. Science, 2012, 338, 543-545.	6.0	162
883	The Complete Mitochondrial Genome ofLeucoptera malifoliellaCosta (Lepidoptera: Lyonetiidae). DNA and Cell Biology, 2012, 31, 1508-1522.	0.9	28
884	Sculpting the endomembrane system in deep time: High resolution phylogenetics of Rab GTPases. Journal of Cell Science, 2012, 125, 2500-8.	1.2	139
885	Evolution of the FGF Gene Family. International Journal of Evolutionary Biology, 2012, 2012, 1-12.	1.0	42
886	Positive Selection and the Evolution of izumo Genes in Mammals. International Journal of Evolutionary Biology, 2012, 2012, 1-7.	1.0	27

#	Article	IF	Citations
887	Recurrent Horizontal Transfer of Bacterial Toxin Genes to Eukaryotes. Molecular Biology and Evolution, 2012, 29, 2223-2230.	3.5	91
888	An ancient genomic regulatory block conserved across bilaterians and its dismantling in tetrapods by retrogene replacement. Genome Research, 2012, 22, 642-655.	2.4	35
889	Eastern Chimpanzees, but Not Bonobos, Represent a Simian Immunodeficiency Virus Reservoir. Journal of Virology, 2012, 86, 10776-10791.	1.5	73
890	Actin polymerization controls the activation of multidrug efflux at fertilization by translocation and fine-scale positioning of ABCB1 on microvilli. Molecular Biology of the Cell, 2012, 23, 3663-3672.	0.9	14
891	Quantifying Homologous Replacement of Loci between Haloarchaeal Species. Genome Biology and Evolution, 2012, 4, 1223-1244.	1.1	55
892	Polyphenol oxidases in Physcomitrella: functional PPO1 knockout modulates cytokinin-dependent developmentin the moss Physcomitrella patens. Journal of Experimental Botany, 2012, 63, 5121-5135.	2.4	29
893	Emergent Complexity in Myosin V-Based Organelle Inheritance. Molecular Biology and Evolution, 2012, 29, 975-984.	3.5	11
894	On the Origin and Evolution of Thermophily: Reconstruction of Functional Precambrian Enzymes from Ancestors of Bacillus. Molecular Biology and Evolution, 2012, 29, 825-835.	3.5	83
895	Discovery of Retroviral Homologs in Bats: Implications for the Origin of Mammalian Gammaretroviruses. Journal of Virology, 2012, 86, 4288-4293.	1.5	52
896	C7orf30 specifically associates with the large subunit of the mitochondrial ribosome and is involved in translation. Nucleic Acids Research, 2012, 40, 4040-4051.	6.5	46
897	Integrating multi-origin expression data improves the resolution of deep phylogeny of ray-finned fish (Actinopterygii). Scientific Reports, 2012, 2, 665.	1.6	13
898	Mitochondrial Protein Acetylation and Sirtuin-Mediated Deacetylation. Oxidative Stress and Disease, 2012, , 245-267.	0.3	0
899	Comparative genomics of the Hedgehog loci in chordates and the origins of Shh regulatory novelties. Scientific Reports, 2012, 2, 433.	1.6	29
900	Phylogeny, integration and expression of sigma virus-like genes in Drosophila. Molecular Phylogenetics and Evolution, 2012, 65, 251-258.	1.2	32
901	The Light-Response BTB1 and BTB2 Proteins Assemble Nuclear Ubiquitin Ligases That Modify Phytochrome B and D Signaling in Arabidopsis Â Â. Plant Physiology, 2012, 160, 118-134.	2.3	49
902	The Repertoire of Chemical Defense Genes in the Coral Acropora digitifera Genome. Zoological Science, 2012, 29, 510.	0.3	17
903	Ilarviruses of Prunus spp.: A Continued Concern for Fruit Trees. Phytopathology, 2012, 102, 1108-1120.	1.1	104
904	Evolutionary relationships of flavobacterial and enterobacterial endosymbionts with their scale insect hosts (<scp>H</scp>emiptera: <scp>C</scp>occoidea). Journal of Evolutionary Biology, 2012, 25, 2357-2368.	0.8	64

#	Article	IF	Citations
905	Evolution of the Tbx6/16 Subfamily Genes in Vertebrates: Insights from Zebrafish. Molecular Biology and Evolution, 2012, 29, 3959-3983.	3.5	21
906	Expression of the pair-rule gene homologs runt, Pax3/7, even-skipped-1 and even-skipped-2 during larval and juvenile development of the polychaete annelid Capitella teleta does not support a role in segmentation. EvoDevo, 2012, 3, 8.	1.3	29
907	Proteomic characteristics of the liver and skeletal muscle in the Chinese tree shrew (Tupaia belangeri) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	4.8	11
908	Cysteine peptidases and their inhibitors in Tetranychus urticae: a comparative genomic approach. BMC Genomics, 2012, 13, 307.	1.2	38
909	The mitochondrial genome of stygobitic sponge Eunapius subterraneus: mtDNA is highly conserved in freshwater sponges. Hydrobiologia, 2012, 687, 49-59.	1.0	7
910	The genome of the polar eukaryotic microalga Coccomyxa subellipsoidea reveals traits of cold adaptation. Genome Biology, 2012, 13, R39.	13.9	289
911	Evolutionary Imprint of Catalytic Domains in Fungal PKSâ€“NRPS Hybrids. ChemBioChem, 2012, 13, 2363-2373.	1.3	34
912	Kinetic and phylogenetic analysis of plant polyamine uptake transporters. Planta, 2012, 236, 1261-1273.	1.6	41
913	Characterization of a plasma membrane Ca2+ ATPase expressed in olfactory receptor neurons of the moth Spodoptera littoralis. Cell and Tissue Research, 2012, 350, 239-250.	1.5	2
914	Convergent Evolution of Sodium Ion Selectivity in Metazoan Neuronal Signaling. Cell Reports, 2012, 2, 242-248.	2.9	67
915	Evolutionary analysis of Antarctic teleost Toll-like receptor 2. Fish and Shellfish Immunology, 2012, 33, 1076-1085.	1.6	11
916	Defensin like peptide from Panulirus argus relates structurally with beta defensin from vertebrates. Fish and Shellfish Immunology, 2012, 33, 872-879.	1.6	17
917	Expansion of transducin subunit gene families in early vertebrate tetraploidizations. Genomics, 2012, 100, 203-211.	1.3	28
918	Phylogenetics and evolution of Trx SET genes in fully sequenced land plants. Genome, 2012, 55, 269-280.	0.9	4
919	Mutation of Arabidopsis SPLICEOSOMAL TIMEKEEPER LOCUS1 Causes Circadian Clock Defects. Plant Cell, 2012, 24, 4066-4082.	3.1	112
920	Detection of members of the Secoviridae in the Tallgrass Prairie Preserve, Osage County, Oklahoma, USA. Virus Research, 2012, 167, 34-42.	1.1	26
921	Phylogenetic and functional analyses of the cytochrome P450 family 4. Molecular Phylogenetics and Evolution, 2012, 62, 458-471.	1.2	38
922	Distinct Bradyrhizbium communities nodulate legumes native to temperate and tropical monsoon Australia. Molecular Phylogenetics and Evolution, 2012, 63, 265-277.	1.2	49

#	Article	IF	Citations
923	Phylogeny of Bembidion and related ground beetles (Coleoptera: Carabidae: Trechinae: Bembidiini:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	55
924	Evolutionary history of synthesis pathway genes for phloroglucinol and cyanide antimicrobials in plant-associated fluorescent pseudomonads. Molecular Phylogenetics and Evolution, 2012, 63, 877-890.	1.2	29
925	Phylogenetic analysis of ticks (Acari: Ixodida) using mitochondrial genomes and nuclear rRNA genes indicates that the genus Amblyomma is polyphyletic. Molecular Phylogenetics and Evolution, 2012, 64, 45-55.	1.2	91
926	Phycoerythrin evolution and diversification of spectral phenotype in marine Synechococcus and related picocyanobacteria. Molecular Phylogenetics and Evolution, 2012, 64, 381-392.	1.2	41
927	Mipartoxin-I, a novel three-finger toxin, is the major neurotoxic component in the venom of the redtail coral snake Micrurus mipartitus (Elapidae). Toxicon, 2012, 60, 851-863.	0.8	41
928	Essential role of Dkk3 for head formation by inhibiting Wnt/Î²â€catenin and Nodal/Vg1 signaling pathways in the basal chordate amphioxus. Evolution & Development, 2012, 14, 338-350.	1.1	35
929	Adaptive horizontal transfer of a bacterial gene to an invasive insect pest of coffee. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4197-4202.	3.3	199
930	Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. Science, 2012, 337, 1661-1665.	6.0	637
931	Endosymbiotic bacteria as a source of carotenoids in whiteflies. Biology Letters, 2012, 8, 986-989.	1.0	158
932	Experimental Design in Phylogenetics: Testing Predictions from Expected Information. Systematic Biology, 2012, 61, 661-674.	2.7	14
933	Evaluating the Phylogenetic Position of Chinese Tree Shrew (Tupaia belangeri chinensis) Based on Complete Mitochondrial Genome: Implication for Using Tree Shrew as an Alternative Experimental Animal to Primates in Biomedical Research. Journal of Genetics and Genomics, 2012, 39, 131-137.	1.7	70
934	A Phylogenetic Analysis of Normal Modes Evolution in Enzymes and Its Relationship to Enzyme Function. Journal of Molecular Biology, 2012, 422, 442-459.	2.0	22
935	Phylogenetic and coevolutionary analysis of the Î²-barrel protein family comprised of mitochondrial porin (VDAC) and Tom40. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1502-1519.	1.4	42
936	Acyrthosiphon pisum AQP2: A multifunctional insect aquaglyceroporin. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 627-635.	1.4	34
937	Metallothionein primary structure in amphibians: Insights from comparative evolutionary analysis in vertebrates. Comptes Rendus - Biologies, 2012, 335, 480-487.	0.1	14
938	Gene expression analysis of clams Ruditapes philippinarum and Ruditapes decussatus following bacterial infection yields molecular insights into pathogen resistance and immunity. Developmental and Comparative Immunology, 2012, 36, 140-149.	1.0	51
939	Big defensins and mytimacins, new AMP families of the Mediterranean mussel Mytilus galloprovincialis. Developmental and Comparative Immunology, 2012, 36, 390-399.	1.0	106
940	Complete mitochondrial genome of Coelomactra antiquata (Mollusca: Bivalvia): The first representative from the family Mactridae with novel gene order and unusual tandem repeats. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2012, 7, 175-179.	0.4	16

#	Article	IF	Citations
941	Molecular characterization and transcriptional regulation of the sodium-dependent vitamin C transporter genes (slc23a1 and slc23a2) in a teleost fish, the Senegalese sole (Solea senegalensis). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2012, 161, 208-218.	0.7	8
942	Transcriptional responses of heat shock protein 70 (Hsp70) to thermal, bisphenol A, and copper stresses in the dinoflagellate Prorocentrum minimum. Chemosphere, 2012, 89, 512-520.	4.2	31
943	The mitochondrial genome of Moniliophthora roreri, the frosty pod rot pathogen of cacao. Fungal Biology, 2012, 116, 551-562.	1.1	29
944	A molecular phylogeny of thermophilic fungi. Fungal Biology, 2012, 116, 489-502.	1.1	114
945	The global distribution and evolution of deoxyribonucleoside kinases in bacteria. Gene, 2012, 492, 117-120.	1.0	6
946	Comparative analyses of the complete mitochondrial genomes of Ascaris lumbricoides and Ascaris suum from humans and pigs. Gene, 2012, 492, 110-116.	1.0	124
947	A novel Acetyl-CoA synthetase short-chain subfamily member 1 (Acss1) gene indicates a dynamic history of paralogue retention and loss in vertebrates. Gene, 2012, 497, 249-255.	1.0	12
948	Structure-based phylogeny of polyene macrolide antibiotic glycosyltransferases. Gene, 2012, 499, 288-296.	1.0	4
949	Alkaline phosphatase gene sequence characteristics and transcriptional regulation by phosphate limitation in Karenia brevis (Dinophyceae). Harmful Algae, 2012, 17, 14-24.	2.2	78
950	The function and structural influence of selective relaxed constraint at functional intracellular loop3 of 5-HT1A serotonin-1 receptor family. Gene, 2012, 508, 211-220.	1.0	2
951	Functional characterization and evolution of PTH/PTHrP receptors: insights from the chicken. BMC Evolutionary Biology, 2012, 12, 110.	3.2	74
952	Insights into the evolution of sorbitol metabolism: phylogenetic analysis of SDR196C family. BMC Evolutionary Biology, 2012, 12, 147.	3.2	6
953	Multiple functionally divergent and conserved copies of alpha tubulin in bdelloid rotifers. BMC Evolutionary Biology, 2012, 12, 148.	3.2	13
954	Evolutionary study of duplications of the miRNA machinery in aphids associated with striking rate acceleration and changes in expression profiles. BMC Evolutionary Biology, 2012, 12, 216.	3.2	13
955	The evolution of Dscam genes across the arthropods. BMC Evolutionary Biology, 2012, 12, 53.	3.2	55
956	Phylogenomics of the benzoxazinoid biosynthetic pathway of Poaceae: gene duplications and origin of the Bx cluster. BMC Evolutionary Biology, 2012, 12, 64.	3.2	74
957	A genome-wide study of recombination rate variation in Bartonella henselae. BMC Evolutionary Biology, 2012, 12, 65.	3.2	18
958	An ancient history of gene duplications, fusions and losses in the evolution of APOBEC3 mutators in mammals. BMC Evolutionary Biology, 2012, 12, 71.	3.2	130

#	Article	IF	Citations
959	Ancient origin of the divergent forms of leucyl-tRNA synthetases in the Halobacteriales. BMC Evolutionary Biology, 2012, 12, 85.	3.2	15
960	Molecular evolution of the polyamine oxidase gene family in Metazoa. BMC Evolutionary Biology, 2012, 12, 90.	3.2	38
961	Evolutionary genomics of mycovirus-related dsRNA viruses reveals cross-family horizontal gene transfer and evolution of diverse viral lineages. BMC Evolutionary Biology, 2012, 12, 91.	3.2	104
962	Expansion of CORE-SINEs in the genome of the Tasmanian devil. BMC Genomics, 2012, 13, 172.	1.2	10
963	Evolution and phylogeny of the mud shrimps (Crustacea: Decapoda) revealed from complete mitochondrial genomes. BMC Genomics, 2012, 13, 631.	1.2	62
964	Genome-wide analysis of the grapevine stilbene synthase multigenic family: genomic organization and expression profiles upon biotic and abiotic stresses. BMC Plant Biology, 2012, 12, 130.	1.6	275
965	Molecular characterization of the hexose transporter gene in benznidazole resistant and susceptible populations of Trypanosoma cruzi. Parasites and Vectors, 2012, 5, 161.	1.0	11
966	Genome-wide analysis of the sox family in the calcareous sponge Sycon ciliatum: multiple genes with unique expression patterns. EvoDevo, 2012, 3, 14.	1.3	59
967	ELMO Domains, Evolutionary and Functional Characterization of a Novel GTPase-activating Protein (GAP) Domain for Arf Protein Family GTPases. Journal of Biological Chemistry, 2012, 287, 39538-39553.	1.6	54
968	Sea Anemone (Cnidaria, Anthozoa, Actiniaria) Toxins: An Overview. Marine Drugs, 2012, 10, 1812-1851.	2.2	183
969	A Consistent Phylogenetic Backbone for the Fungi. Molecular Biology and Evolution, 2012, 29, 1319-1334.	3.5	129
970	A Novel Virus-Like Double-Stranded RNA in an Obligate Biotroph Arbuscular Mycorrhizal Fungus: A Hidden Player in Mycorrhizal Symbiosis. Molecular Plant-Microbe Interactions, 2012, 25, 1005-1012.	1.4	32
971	Phylogenetic Approaches to Natural Product Structure Prediction. Methods in Enzymology, 2012, 517, 161-182.	0.4	35
972	Divergence and Phylogeny of Firmicutes from the Cuatro CiÃ©negas Basin, Mexico: A Window to an Ancient Ocean. Astrobiology, 2012, 12, 674-684.	1.5	50
973	Distinct Expression Patterns of Glycoprotein Hormone Subunits in the Lophotrochozoan Aplysia: Implications for the Evolution of Neuroendocrine Systems in Animals. Endocrinology, 2012, 153, 5440-5451.	1.4	24
974	Regulation of cnidarianâ€“dinoflagellate mutualisms: Evidence that activation of a host TGFÎ² innate immune pathway promotes tolerance of the symbiont. Developmental and Comparative Immunology, 2012, 38, 525-537.	1.0	79
975	The evolution of catalytic residues and enzyme mechanism within the bacterial nucleoside phosphorylase superfamily 1. Gene, 2012, 510, 154-161.	1.0	4
976	The complete mitochondrial genome sequence of Oncicola luehei (Acanthocephala:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 67 T 2012, 61, 307-316.	0.6	30

#	Article	IF	Citations
977	Complete mitochondrial DNA sequence of Stenopus hispidus (Crustacea: Decapoda: Stenopodidea) and a novel tRNA gene cluster. Marine Genomics, 2012, 6, 7-15.	0.4	15
978	Characterization of the complete mitochondrial genomes of two whipworms Trichuris ovis and Trichuris discolor (Nematoda: Trichuridae). Infection, Genetics and Evolution, 2012, 12, 1635-1641.	1.0	54
979	Identification of diverse groups of endogenous gammaretroviruses in mega- and microbats. Journal of General Virology, 2012, 93, 2037-2045.	1.3	48
981	Molecular Phylogeny and Evolution of Parabasalia with Improved Taxon Sampling and New Protein Markers of Actin and Elongation Factor-1Î±. PLoS ONE, 2012, 7, e29938.	1.1	42
982	Whole-genome sequence of Schistosoma haematobium. Nature Genetics, 2012, 44, 221-225.	9.4	383
983	The evolution of the mitochondrial genetic code in arthropods revisited. Mitochondrial DNA, 2012, 23, 84-91.	0.6	27
984	A horizontally transferred cyanase gene in the spider mite Tetranychus urticae is involved in cyanate metabolism and is differentially expressed upon host plant change. Insect Biochemistry and Molecular Biology, 2012, 42, 881-889.	1.2	40
985	Insulin-Like Peptides. , 2012, , 63-92.		72
986	The complete mitochondrial genome of the black mud crab, Scylla serrata (Crustacea: Brachyura:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 39, 10921-10937.	1.0	14
987	The evolution of vertebrate somatostatin receptors and their gene regions involves extensive chromosomal rearrangements. BMC Evolutionary Biology, 2012, 12, 231.	3.2	46
988	The evolution of the class A scavenger receptors. BMC Evolutionary Biology, 2012, 12, 227.	3.2	52
989	Massive expansion of the calpain gene family in unicellular eukaryotes. BMC Evolutionary Biology, 2012, 12, 193.	3.2	34
990	MicroRNAs and essential components of the microRNA processing machinery are not encoded in the genome of the ctenophore Mnemiopsis leidyi. BMC Genomics, 2012, 13, 714.	1.2	43
991	Genomic organization, evolution, and expression of photoprotein and opsin genes in Mnemiopsis leidyi: a new view of ctenophore photocytes. BMC Biology, 2012, 10, 107.	1.7	107
992	Broad Phylogenomic Sampling and the Sister Lineage of Land Plants. PLoS ONE, 2012, 7, e29696.	1.1	234
993	Armadillo 1.1: An Original Workflow Platform for Designing and Conducting Phylogenetic Analysis and Simulations. PLoS ONE, 2012, 7, e29903.	1.1	38
994	A Phylogenetic Analysis of the Globins in Fungi. PLoS ONE, 2012, 7, e31856.	1.1	27
995	Primitive Duplicate Hox Clusters in the European Eel's Genome. PLoS ONE, 2012, 7, e32231.	1.1	128

#	Article	IF	Citations
996	The Complete Mitochondrial Genomes of Six Heterodont Bivalves (Tellinoidea and Solenoidea): Variable Gene Arrangements and Phylogenetic Implications. PLoS ONE, 2012, 7, e32353.	1.1	56
997	A Novel Serpin with Antithrombin-Like Activity in Branchiostoma japonicum: Implications for the Presence of a Primitive Coagulation System. PLoS ONE, 2012, 7, e32392.	1.1	8
998	The Evolution of Pepsinogen C Genes in Vertebrates: Duplication, Loss and Functional Diversification. PLoS ONE, 2012, 7, e32852.	1.1	19
999	Nitrile Hydratase Genes Are Present in Multiple Eukaryotic Supergroups. PLoS ONE, 2012, 7, e32867.	1.1	20
1000	The Diversification of the LIM Superclass at the Base of the Metazoa Increased Subcellular Complexity and Promoted Multicellular Specialization. PLoS ONE, 2012, 7, e33261.	1.1	50
1001	Toward a Global Phylogeny of the â€œLiving Fossil" Crustacean Order of the Notostraca. PLoS ONE, 2012, 7, e34998.	1.1	45
1002	Investigation of the Biosynthetic Potential of Endophytes in Traditional Chinese Anticancer Herbs. PLoS ONE, 2012, 7, e35953.	1.1	64
1003	Functional Study of Mammalian Neph Proteins in Drosophila melanogaster. PLoS ONE, 2012, 7, e40300.	1.1	30
1004	Comparative and Evolutionary Analysis of the HES/HEY Gene Family Reveal Exon/Intron Loss and Teleost Specific Duplication Events. PLoS ONE, 2012, 7, e40649.	1.1	26
1005	Cytochrome P450 2B Diversity and Dietary Novelty in the Herbivorous, Desert Woodrat (Neotoma) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	18
1006	Evolution of the Vertebrate Paralemmin Gene Family: Ancient Origin of Gene Duplicates Suggests Distinct Functions. PLoS ONE, 2012, 7, e41850.	1.1	18
1007	Global Transcriptome Analysis of the Scorpion Centruroides noxius: New Toxin Families and Evolutionary Insights from an Ancestral Scorpion Species. PLoS ONE, 2012, 7, e43331.	1.1	69
1008	GASP/WFIKKN Proteins: Evolutionary Aspects of Their Functions. PLoS ONE, 2012, 7, e43710.	1.1	8
1009	Identification and Sequence Analysis of Metazoan tRNA 3â€²-End Processing Enzymes tRNase Zs. PLoS ONE, 2012, 7, e44264.	1.1	9
1010	Multiple Kisspeptin Receptors in Early Osteichthyans Provide New Insights into the Evolution of This Receptor Family. PLoS ONE, 2012, 7, e48931.	1.1	57
1011	A Phylogenomic Approach to Vertebrate Phylogeny Supports a Turtle-Archosaur Affinity and a Possible Paraphyletic Lissamphibia. PLoS ONE, 2012, 7, e48990.	1.1	61
1012	An Integrated In Silico Approach to Design Specific Inhibitors Targeting Human Poly(A)-Specific Ribonuclease. PLoS ONE, 2012, 7, e51113.	1.1	15
1013	Unexplored Character Diversity in Onychophora (Velvet Worms): A Comparative Study of Three Peripatid Species. PLoS ONE, 2012, 7, e51220.	1.1	45

#	Article	IF	Citations
1014	Hippo Pathway Phylogenetics Predicts Monoubiquitylation of Salvador and Merlin/Nf2. PLoS ONE, 2012, 7, e51599.	1.1	2
1015	Scorpions from the primeval subgenus Archaeotityus produce putative homologs of Tityus serrulatus toxins active on voltage-gated sodium channels. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2012, 18, 432-440.	0.8	6
1016	Variable Regions of PI4P 5-Kinases Direct PtdIns(4,5)P2 Toward Alternative Regulatory Functions in Tobacco Pollen Tubes. Frontiers in Plant Science, 2011, 2, 114.	1.7	38
1017	The Mercury Resistance Operon: From an Origin in a Geothermal Environment to an Efficient Detoxification Machine. Frontiers in Microbiology, 2012, 3, 349.	1.5	209
1018	Xin proteins and intercalated disc maturation, signaling and diseases. Frontiers in Bioscience - Landmark, 2012, 17, 2566.	3.0	43
1019	Ribosomes from Trypanosomatids: Unique Structural and Functional Properties. , 2012, , .		0
1020	Evolution, expansion and expression of the Kunitz/BPTI gene family associated with long-term blood feeding in Ixodes Scapularis. BMC Evolutionary Biology, 2012, 12, 4.	3.2	62
1021	Lim homeobox genes in the Ctenophore Mnemiopsis leidyi: the evolution of neural cell type specification. EvoDevo, 2012, 3, 2.	1.3	36
1022	Structure based hypothesis of a mitochondrial ribosome rescue mechanism. Biology Direct, 2012, 7, 14.	1.9	31
1023	LRRC8 proteins share a common ancestor with pannexins, and may form hexameric channels involved in cellâ€cell communication. BioEssays, 2012, 34, 551-560.	1.2	140
1024	Interactions of SR45, an SRâ€like protein, with spliceosomal proteins and an intronic sequence: insights into regulated splicing. Plant Journal, 2012, 71, 936-947.	2.8	75
1025	The nonâ€hierarchical, nonâ€uniformly branching topology of a leuconoid sponge aquiferous system revealed by 3D reconstruction and morphometrics using corrosion casting and Xâ€ray microtomography. Acta Zoologica, 2012, 93, 160-170.	0.6	13
1026	Coral Comparative Genomics Reveal Expanded Hox Cluster in the Cnidarian-Bilaterian Ancestor. Integrative and Comparative Biology, 2012, 52, 835-841.	0.9	40
1027	Evolution of increased complexity in a molecular machine. Nature, 2012, 481, 360-364.	13.7	181
1028	J-Western Forms of Helicobacter pylori cagA Constitute a Distinct Phylogenetic Group with a Widespread Geographic Distribution. Journal of Bacteriology, 2012, 194, 1593-1604.	1.0	20
1029	Adenylate Cyclases of Trypanosoma brucei Inhibit the Innate Immune Response of the Host. Science, 2012, 337, 463-466.	6.0	130
1030	Molecular and Functional Evolution of Class I Chitinases for Plant Carnivory in the Caryophyllales. Molecular Biology and Evolution, 2012, 29, 2971-2985.	3.5	39
1031	Identification of Two Carbonic Anhydrases in the Mantle of the <scp>E</scp>uropean Abalone <scp>H</scp>aliotis tuberculata (<scp>G</scp>astropoda, Haliotidae): Phylogenetic Implications. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2012, 318, 353-367.	0.6	30

#	Article	IF	Citations
1032	The origins and evolution of ubiquitination sites. Molecular BioSystems, 2012, 8, 1865.	2.9	23
1033	A practical guide for the computational selection of residues to be experimentally characterized in protein families. Briefings in Bioinformatics, 2012, 13, 329-336.	3.2	10
1034	Activation of Hox genes during caudal regeneration of the polychaete annelid Platynereis dumerilii. Development Genes and Evolution, 2012, 222, 165-179.	0.4	53
1035	Peptidomics-Based Phylogeny and Biogeography of Mantophasmatodea (Hexapoda). Systematic Biology, 2012, 61, 609-629.	2.7	41
1036	Reference genome sequence of the model plant Setaria. Nature Biotechnology, 2012, 30, 555-561.	9.4	864
1037	Culturable Endophytes of Medicinal Plants and the Genetic Basis for Their Bioactivity. Microbial Ecology, 2012, 64, 431-449.	1.4	64
1038	Independent evolution of striated muscles in cnidarians and bilaterians. Nature, 2012, 487, 231-234.	13.7	221
1039	Epithelia, an Evolutionary Novelty of Metazoans. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2012, 318, 438-447.	0.6	75
1040	A comparative study of nemertean complete mitochondrial genomes, including two new ones for Nectonemertes cf. mirabilis and Zygeupolia rubens, may elucidate the fundamental pattern for the phylum Nemertea. BMC Genomics, 2012, 13, 139.	1.2	16
1041	Characterization of maspardin, responsible for human Mast syndrome, in an insect species and analysis of its evolution in metazoans. Die Naturwissenschaften, 2012, 99, 537-543.	0.6	1
1042	Two loci in sorghum with NB-LRR encoding genes confer resistance to Colletotrichum sublineolum. Theoretical and Applied Genetics, 2012, 124, 1005-1015.	1.8	34
1043	Molecular phylogeny of glass sponges (Porifera, Hexactinellida): increased taxon sampling and inclusion of the mitochondrial protein-coding gene, cytochrome oxidase subunit I. Hydrobiologia, 2012, 687, 11-20.	1.0	24
1044	A distinct tymovirus infecting Cassia hoffmannseggii in Brazil. Virus Genes, 2012, 45, 190-194.	0.7	11
1045	4-Hydroxyphenylglycine biosynthesis in Herpetosiphon aurantiacus: a case of gene duplication and catalytic divergence. Archives of Microbiology, 2012, 194, 557-566.	1.0	10
1046	Comparative Phylogenies of Ribosomal Proteins and the 16S rRNA Gene at Higher Ranks of the Class Actinobacteria. Current Microbiology, 2012, 65, 1-6.	1.0	8
1047	Complete mitochondrial genomes of two cockroaches, Blattella germanica and Periplaneta americana, and the phylogenetic position of termites. Current Genetics, 2012, 58, 65-77.	0.8	36
1048	Molecular cloning and characterization of seven class III peroxidases induced by overexpression of the agrobacterial rolB gene in Rubia cordifolia transgenic callus cultures. Plant Cell Reports, 2012, 31, 1009-1019.	2.8	20
1049	New Drosophila P-like elements and reclassification of Drosophila P-elements subfamilies. Molecular Genetics and Genomics, 2012, 287, 531-540.	1.0	5

#	Article	IF	Citations
1050	Vicilin Genes of Vigna luteola: Structure, Organization, Expression, and Variation. Biochemical Genetics, 2012, 50, 372-388.	0.8	0
1051	Conserved domains and evolution of secreted phospholipases A₂. FEBS Journal, 2012, 279, 636-649.	2.2	27
1052	Oesophagostomum dentatum and Oesophagostomum quadrispinulatum: Characterization of the complete mitochondrial genome sequences of the two pig nodule worms. Experimental Parasitology, 2012, 131, 1-7.	0.5	32
1053	Detecting adaptive evolution and functional divergence in aminocyclopropane-1-carboxylate synthase (ACS) gene family. Computational Biology and Chemistry, 2012, 38, 10-16.	1.1	11
1054	Genomic resources for the brown planthopper, Nilaparvata lugens: Transcriptome pyrosequencing and microarray design. Insect Science, 2012, 19, 1-12.	1.5	23
1055	PHYLOGENETIC ANALYSES UNRAVEL THE EVOLUTIONARY HISTORY OF NAC PROTEINS IN PLANTS. Evolution; International Journal of Organic Evolution, 2012, 66, 1833-1848.	1.1	87
1056	Horizontal gene transfer confers fermentative metabolism in the respiratory-deficient plant trypanosomatid Phytomonas serpens. Infection, Genetics and Evolution, 2012, 12, 539-548.	1.0	5
1057	A specific PCR assay for the identification and differentiation of Schistosoma japonicum geographical isolates in mainland China based on analysis of mitochondrial genome sequences. Infection, Genetics and Evolution, 2012, 12, 1027-1036.	1.0	17
1058	High-resolution picture of a venom gland transcriptome: Case study with the marine snail Conus consors. Toxicon, 2012, 59, 34-46.	0.8	76
1059	Convergent evolution led ribosome inactivating proteins to interact with ribosomal stalk. Toxicon, 2012, 59, 427-432.	0.8	19
1060	Analysis of Expressed Sequence Tags from the Marine Microalga Pseudochattonella farcimen (Dictyochophyceae). Protist, 2012, 163, 143-161.	0.6	14
1061	Phylogenetic study on Proales daphnicola Thompson, 1892 (Proalidae) and its relocation to Epiphanes (Rotifera: Epiphanidae). Zoologischer Anzeiger, 2012, 251, 180-196.	0.4	5
1062	EcPV2 DNA in equine genital squamous cell carcinomas and normal genital mucosa. Veterinary Microbiology, 2012, 158, 33-41.	0.8	44
1063	Population structure of a novel putative mycovirus infecting the conifer root-rot fungus Heterobasidion annosum sensu lato. Virology, 2012, 422, 366-376.	1.1	65
1064	Genetic characterization of TribeÄ•virus and Kemerovo virus, two tick-transmitted human-pathogenic Orbiviruses. Virology, 2012, 423, 68-76.	1.1	44
1065	A novel quadripartite dsRNA virus isolated from a phytopathogenic filamentous fungus, Rosellinia necatrix. Virology, 2012, 426, 42-50.	1.1	87
1066	The oxytocin/vasopressin receptor family has at least five members in the gnathostome lineage, inclucing two distinct V2 subtypes. General and Comparative Endocrinology, 2012, 175, 135-143.	0.8	88
1067	Differential regulation of the expression of cytochrome P450 aromatase, estrogen and androgen receptor subtypes in the brainâ€“pituitaryâ€“ovarian axis of the Japanese eel (Anguilla japonica) reveals steroid dependent and independent mechanisms. General and Comparative Endocrinology, 2012, 175, 163-172.	0.8	41

#	Article	IF	Citations
1068	The transcriptomic response to thermal stress is immediate, transient and potentiated by ultraviolet radiation in the sea anemone Anemonia viridis. Molecular Ecology, 2012, 21, 1158-1174.	2.0	66
1069	Genomic analysis of the potential for aromatic compounds biodegradation in Burkholderiales. Environmental Microbiology, 2012, 14, 1091-1117.	1.8	276
1070	Evolution of the biosynthesis of diâ€myoâ€inositol phosphate, a marker of adaptation to hot marine environments. Environmental Microbiology, 2012, 14, 691-701.	1.8	28
1071	The mitochondrial genomes of Cambaroides similis and Procambarus clarkii (Decapoda:) Tj ETQq1 1 0.784314 rgBT /Over	0.7	30
1072	The diversity and evolution of chelicerate hemocyanins. BMC Evolutionary Biology, 2012, 12, 19.	3.2	55
1073	Cellular, biochemical, and molecular characterization of nitric oxide synthase expressed in the nervous system of the prosobranch Stramonita haemastoma (Gastropoda, Neogastropoda). Journal of Comparative Neurology, 2012, 520, 364-383.	0.9	13
1074	The complete mitochondrial genome of the grand jackknife clam, Solen grandis (Bivalvia: Solenidae): a novel gene order and unusual non-coding region. Molecular Biology Reports, 2012, 39, 1287-1292.	1.0	23
1075	Determination of the complete mitochondrial DNA sequence of Octopus minor. Molecular Biology Reports, 2012, 39, 3461-3470.	1.0	30
1076	Morphological and molecular development of the eyes during embryogenesis of the freshwater planarian Schmidtea polychroa. Development Genes and Evolution, 2012, 222, 45-54.	0.4	25
1077	The modular respiratory complexes involved in hydrogen and sulfur metabolism by heterotrophic hyperthermophilic archaea and their evolutionary implications. FEMS Microbiology Reviews, 2013, 37, 182-203.	3.9	136
1078	Identification of diverse full-length endogenous betaretroviruses in megabats and microbats. Retrovirology, 2013, 10, 35.	0.9	45
1079	Virophages, polintons, and transpovirons: a complex evolutionary network of diverse selfish genetic elements with different reproduction strategies. Virology Journal, 2013, 10, 158.	1.4	99
1080	How protein targeting to primary plastids via the endomembrane system could have evolved? A new hypothesis based on phylogenetic studies. Biology Direct, 2013, 8, 18.	1.9	17
1081	Mitochondrial genomes of the genus Ephydatia Lamouroux, 1816: can palindromic elements be used in species-level studies?. Organisms Diversity and Evolution, 2013, 13, 127-134.	0.7	5
1082	Polyporales genomes reveal the genetic architecture underlying tetrapolar and bipolar mating systems. Mycologia, 2013, 105, 1374-1390.	0.8	42
1083	Expression of the Lhx genes apterous and lim1 in an errant polychaete: implications for bilaterian appendage evolution, neural development, and muscle diversification. EvoDevo, 2013, 4, 4.	1.3	11
1084	Evolution of plant Ash1 SET genes: structural divergence and functional differentiation. Genes and Genomics, 2013, 35, 463-473.	0.5	1
1085	Coexpression patterns indicate that GPI-anchored non-specific lipid transfer proteins are involved in accumulation of cuticular wax, suberin and sporopollenin. Plant Molecular Biology, 2013, 83, 625-649.	2.0	70

#	Article	IF	Citations
1086	Nitrogen-Fixing and Uricolytic Bacteria Associated with the Gut of Dendroctonus rhizophagus and Dendroctonus valens (Curculionidae: Scolytinae). Microbial Ecology, 2013, 66, 200-210.	1.4	121
1087	A new species of Eoperipatus (Onychophora) from Vietnam reveals novel morphological characters for the South-East Asian Peripatidae. Zoologischer Anzeiger, 2013, 252, 495-510.	0.4	23
1088	Bioinformatics Research and Applications. Lecture Notes in Computer Science, 2013, , .	1.0	0
1089	Molecular evolution of the moonlighting protein SMN in metazoans. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 220-230.	0.4	3
1090	Avihepadnavirus diversity in parrots is comparable to that found amongst all other avian species. Virology, 2013, 438, 98-105.	1.1	14
1091	Analyses of the radiation of birnaviruses from diverse host phyla and of their evolutionary affinities with other double-stranded RNA and positive strand RNA viruses using robust structure-based multiple sequence alignments and advanced phylogenetic methods. BMC Evolutionary Biology, 2013, 13, 154.	3.2	8
1092	Phylogeny, structural evolution and functional diversification of the plant PHOSPHATE1 gene family: a focus on Glycine max. BMC Evolutionary Biology, 2013, 13, 103.	3.2	25
1093	Evolution of S-domain receptor-like kinases in land plants and origination of S-locus receptor kinases in Brassicaceae. BMC Evolutionary Biology, 2013, 13, 69.	3.2	58
1094	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. BMC Evolutionary Biology, 2013, 13, 33.	3.2	123
1095	Comparative analysis of complete mitochondrial genome sequences confirms independent origins of plant-parasitic nematodes. BMC Evolutionary Biology, 2013, 13, 12.	3.2	57
1096	Evolutionary origins, molecular cloning and expression of carotenoid hydroxylases in eukaryotic photosynthetic algae. BMC Genomics, 2013, 14, 457.	1.2	31
1097	The complete mitochondrial genomes of three parasitic nematodes of birds: a unique gene order and insights into nematode phylogeny. BMC Genomics, 2013, 14, 414.	1.2	76
1098	A burst of ABC genes in the genome of the polyphagous spider mite Tetranychus urticae. BMC Genomics, 2013, 14, 317.	1.2	118
1099	Comparative analysis of fungal genomes reveals different plant cell wall degrading capacity in fungi. BMC Genomics, 2013, 14, 274.	1.2	473
1100	Analysis of the WUSCHEL-RELATED HOMEOBOX gene family in the conifer picea abiesreveals extensive conservation as well as dynamic patterns. BMC Plant Biology, 2013, 13, 89.	1.6	77
1101	Ancient origin of somatic and visceral neurons. BMC Biology, 2013, 11, 53.	1.7	38
1102	Morphology, Genome Plasticity, and Phylogeny in the Genus Ostreococcus Reveal a Cryptic Species, O. mediterraneus sp. nov. (Mamiellales, Mamiellophyceae). Protist, 2013, 164, 643-659.	0.6	48
1103	Genome and proteome analysis of phage <scp>E</scp>3 infecting the soilâ€borne actinomycete <scp>R</scp>hodococcus equi. Environmental Microbiology Reports, 2013, 5, 170-178.	1.0	21

#	Article	IF	Citations
1104	Duplicated STM-like KNOX I genes act in floral meristem activity in Eschscholzia californica (Papaveraceae). Development Genes and Evolution, 2013, 223, 289-301.	0.4	8
1105	Group 1 LEA proteins, an ancestral plant protein group, are also present in other eukaryotes, and in the archeae and bacteria domains. Molecular Genetics and Genomics, 2013, 288, 503-517.	1.0	47
1106	Classification and evolutionary analysis of the basic helix-loop-helix gene family in the green anole lizard, Anolis carolinensis. Molecular Genetics and Genomics, 2013, 288, 365-380.	1.0	12
1107	Serine/threonine kinases and E2-ubiquitin conjugating enzymes in Planctomycetes: unexpected findings. Antonie Van Leeuwenhoek, 2013, 104, 509-520.	0.7	12
1108	Novel cyclovirus discovered in the Florida woods cockroach Eurycotis floridana (Walker). Archives of Virology, 2013, 158, 1389-1392.	0.9	35
1109	A novel strategy for the determination of a rhabdovirus genome and its application to sequencing of Eggplant mottled dwarf virus. Virus Genes, 2013, 47, 105-113.	0.7	14
1110	Multilocus sequence analysis of Vibrio tapetis, the causative agent of Brown Ring Disease: Description of Vibrio tapetis subsp. britannicus subsp. nov. Systematic and Applied Microbiology, 2013, 36, 183-187.	1.2	29
1111	Inclusion of chloroplast genes that have undergone expansion misleads phylogenetic reconstruction in the Chlorophyta. American Journal of Botany, 2013, 100, 2194-2209.	0.8	11
1112	Pseudoplusia includens single nucleopolyhedrovirus: Genetic diversity, phylogeny and hypervariability of the pif-2 gene. Journal of Invertebrate Pathology, 2013, 114, 258-267.	1.5	19
1113	Isolation and expression of cytochrome P450 genes in the antennae and gut of pine beetle Dendroctonus rhizophagus (Curculionidae: Scolytinae) following exposure to host monoterpenes. Gene, 2013, 520, 47-63.	1.0	53
1114	Molecular characterization of three GnRH receptor paralogs in the European eel, Anguilla anguilla: Tissue-distribution and changes in transcript abundance during artificially induced sexual development. Molecular and Cellular Endocrinology, 2013, 369, 1-14.	1.6	35
1115	Identification and expression analysis of BMP signaling inhibitors genes of the DAN family in amphioxus. Gene Expression Patterns, 2013, 13, 377-383.	0.3	15
1116	Addressing Gene Tree Discordance and Non-Stationarity to Resolve a Multi-Locus Phylogeny of the Flatfishes (Teleostei: Pleuronectiformes). Systematic Biology, 2013, 62, 763-785.	2.7	116
1117	Protein evolution along phylogenetic histories under structurally constrained substitution models. Bioinformatics, 2013, 29, 3020-3028.	1.8	48
1118	Pheromone Evolution, Reproductive Genes, and Comparative Transcriptomics in Mediterranean Earthworms (Annelida, Oligochaeta, Hormogastridae). Molecular Biology and Evolution, 2013, 30, 1614-1629.	3.5	24
1119	Conservation of globin genes in the â€œliving fossilâ€•Latimeria chalumnae and reconstruction of the evolution of the vertebrate globin family. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1801-1812.	1.1	26
1120	Models and Algorithms for Genome Evolution. Computational Biology, 2013, , .	0.1	7
1121	Uncovering a Gene Duplication of the Photoreceptive Protein, Opsin, in Scallops (Bivalvia: Pectinidae). Integrative and Comparative Biology, 2013, 53, 68-77.	0.9	20

#	Article	IF	Citations
1122	Molecular characterization and phylogeny of whipworm nematodes inferred from DNA sequences of cox1 mtDNA and 18S rDNA. Parasitology Research, 2013, 112, 3933-3949.	0.6	51
1123	Description of new mitochondrial genomes (Spodoptera litura, Noctuoidea and Cnaphalocrocis) Tj ETQq1 1 0.784314 rgBT /Overlock 1 optimization schemes. Molecular Biology Reports, 2013, 40, 6333-6349.	1.0	37
1124	A Novel Clade of Unique Eukaryotic Ribonucleotide Reductase R2 Subunits is Exclusive to Apicomplexan Parasites. Journal of Molecular Evolution, 2013, 77, 92-106.	0.8	7
1125	Positive selection in the adhesion domain of Mus sperm Adam genes through gene duplications and function-driven gene complex formations. BMC Evolutionary Biology, 2013, 13, 217.	3.2	9
1126	Evolutionary diversification and characterization of the eubacterial gene family encoding DXR type II, an alternative isoprenoid biosynthetic enzyme. BMC Evolutionary Biology, 2013, 13, 180.	3.2	10
1127	Evidence for inter-specific recombination among the mitochondrial genomes of Fusarium species in the Gibberella fujikuroi complex. BMC Genomics, 2013, 14, 605.	1.2	52
1128	Evolution of clitellate phaosomes from rhabdomeric photoreceptor cells of polychaetes â€“ a study in the leech Helobdella robusta (Annelida, Sedentaria, Clitellata). Frontiers in Zoology, 2013, 10, 52.	0.9	16
1129	Elucidating the evolutionary history and expression patterns of nucleoside phosphorylase paralogs (vegetative storage proteins) in Populus and the plant kingdom. BMC Plant Biology, 2013, 13, 118.	1.6	17
1130	Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. Microbiome, 2013, 1, 22.	4.9	493
1131	Obligate mutualism within a host drives the extreme specialization of a fig wasp genome. Genome Biology, 2013, 14, R141.	13.9	85
1132	Transcriptomics-based screen for genes induced by flagellin and repressed by pathogen effectors identifies a cell wall-associated kinase involved in plant immunity. Genome Biology, 2013, 14, R139.	13.9	137
1133	Diversity and history of the long-chain acyl-CoA synthetase (Acsl) gene family in vertebrates. BMC Evolutionary Biology, 2013, 13, 271.	3.2	60
1134	Midgut transcriptome profiling of Anoplophora glabripennis, a lignocellulose degrading cerambycid beetle. BMC Genomics, 2013, 14, 850.	1.2	65
1135	Molecular Evolutionary Analysis of Vertebrate Transducins: A Role for Amino Acid Variation in Photoreceptor Deactivation. Journal of Molecular Evolution, 2013, 77, 231-245.	0.8	11
1136	An Ancestral Member of the Polysaccharide Lyase Family 2 Displays Endolytic Activity and Magnesium Dependence. Applied Biochemistry and Biotechnology, 2013, 171, 1911-1923.	1.4	6
1137	The vertebrate ancestral repertoire of visual opsins, transducin alpha subunits and oxytocin/vasopressin receptors was established by duplication of their shared genomic region in the two rounds of early vertebrate genome duplications. BMC Evolutionary Biology, 2013, 13, 238.	3.2	111
1138	Comparison of novel MLB-clade, VA-clade and classic human astroviruses highlights constrained evolution of the classic human astrovirus nonstructural genes. Virology, 2013, 436, 8-14.	1.1	72
1139	Phylogenetic analyses of endoparasitic Acanthocephala based on mitochondrial genomes suggest secondary loss of sensory organs. Molecular Phylogenetics and Evolution, 2013, 66, 182-189.	1.2	49

#	Article	IF	Citations
1140	De novo Ixodes ricinus salivary gland transcriptome analysis using two nextâ€generation sequencing methodologies. FASEB Journal, 2013, 27, 4745-4756.	0.2	88
1141	The unaccounted yet abundant nitrous oxide-reducing microbial community: a potential nitrous oxide sink. ISME Journal, 2013, 7, 417-426.	4.4	529
1142	Genomes of Stigonematalean Cyanobacteria (Subsection V) and the Evolution of Oxygenic Photosynthesis from Prokaryotes to Plastids. Genome Biology and Evolution, 2013, 5, 31-44.	1.1	234
1143	Functional Annotation and Comparative Analysis of a Zygopteran Transcriptome. G3: Genes, Genomes, Genetics, 2013, 3, 763-770.	0.8	5
1144	Multicellularity arose several times in the evolution of eukaryotes (Response to DOI) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td (10.1	1.2	57
1145	Molecular and immunohistochemical characterization of granulin gene encoded in Pieris rapae granulovirus genome. Journal of Invertebrate Pathology, 2013, 113, 7-17.	1.5	3
1146	Molecular and microscopic evidence of viruses in marine copepods. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1375-1380.	3.3	67
1147	Carbonic anhydrases in anthozoan coralsâ€"A review. Bioorganic and Medicinal Chemistry, 2013, 21, 1437-1450.	1.4	174
1148	GENETIC EXCHANGES OF INTEINS BETWEENPRASINOVIRUSES(PHYCODNAVIRIDAE). Evolution; International Journal of Organic Evolution, 2013, 67, 18-33.	1.1	14
1149	Transcriptome sequencing and annotation of the predatory mite Metaseiulus occidentalis (Acari:) Tj ETQq1 1 0.784314 rgBT /Overloc Applied Acarology, 2013, 59, 283-296.	0.7	32
1150	Phylogenetic Comparison of Opine Dehydrogenase Sequences from Marine Invertebrates. Biochemical Genetics, 2013, 51, 154-165.	0.8	5
1151	A family of diatom-like silicon transporters in the siliceous loricate choanoflagellates. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20122543.	1.2	39
1152	Deep metazoan phylogeny: When different genes tell different stories. Molecular Phylogenetics and Evolution, 2013, 67, 223-233.	1.2	242
1153	Loss, replacement and gain of proteins at the origin of the mitochondria. Biochimica Et Biophysica Acta - Bioenergetics, 2013, 1827, 224-231.	0.5	45
1154	A novel virus in the family Hypoviridae from the plant pathogenic fungus Fusarium graminearum. Virus Research, 2013, 174, 69-77.	1.1	78
1155	Carotenoids in unexpected places: Gall midges, lateral gene transfer, and carotenoid biosynthesis in animals. Molecular Phylogenetics and Evolution, 2013, 68, 221-228.	1.2	79
1156	Expression and phylogenetic analyses of the Gel/Gas proteins of Tuber melanosporum provide insights into the function and evolution of glucan remodeling enzymes in fungi. Fungal Genetics and Biology, 2013, 53, 10-21.	0.9	13
1157	The variability of the large genomic segment of ÅahyÅˆa orthobunyavirus and an all-atom exploration of its anti-viral drug resistance. Infection, Genetics and Evolution, 2013, 20, 304-311.	1.0	13

#	Article	IF	Citations
1158	Functional and evolutionary analysis of DXL1, a non-essential gene encoding a 1-deoxy-D-xylulose 5-phosphate synthase like protein in Arabidopsis thaliana. Gene, 2013, 524, 40-53.	1.0	32
1159	Evolutionary implications of intronâ€“exon distribution and the properties and sequences of the RPL10A gene in eukaryotes. Molecular Phylogenetics and Evolution, 2013, 66, 857-867.	1.2	31
1160	Middle ferritin genes from the icefish Chionodraco rastrospinosus: Comparative analysis and evolution of fish ferritins. Comptes Rendus - Biologies, 2013, 336, 134-141.	0.1	12
1161	Elucidating the origin of the ExbBD components of the TonB system through Bayesian inference and maximum-likelihood phylogenies. Molecular Phylogenetics and Evolution, 2013, 69, 674-686.	1.2	9
1162	Following Gene Duplication, Paralog Interference Constrains Transcriptional Circuit Evolution. Science, 2013, 342, 104-108.	6.0	103
1163	Zinc co-ordination by the DHHC cysteine-rich domain of the palmitoyltransferase Swf1. Biochemical Journal, 2013, 454, 427-435.	1.7	31
1164	Correlated Evolution of Gonadotropin-Releasing Hormone and Gonadotropin-Inhibitory Hormone and Their Receptors in Mammals. Neuroendocrinology, 2013, 97, 242-251.	1.2	6
1165	Spatiotemporal Seed Development Analysis Provides Insight into Primary Dormancy Induction and Evolution of theLepidium DELAY OF GERMINATION1Genes Â Â Â. Plant Physiology, 2013, 161, 1903-1917.	2.3	18
1166	Sequencing of the Î²-tubulin genes in the ascarid nematodes Parascaris equorum and Ascaridia galli. Molecular and Biochemical Parasitology, 2013, 190, 38-43.	0.5	17
1167	Characterization and embryonic expression of four amphioxus Frizzled genes with important functions during early embryogenesis. Gene Expression Patterns, 2013, 13, 445-453.	0.3	17
1168	A novel endogenous betaretrovirus group characterized from polar bears (Ursus maritimus) and giant pandas (Ailuropoda melanoleuca). Virology, 2013, 443, 1-10.	1.1	11
1169	Characterization of burdock mottle virus, a novel member of the genus Benyvirus, and the identification of benyvirus-related sequences in the plant and insect genomes. Virus Research, 2013, 177, 75-86.	1.1	31
1170	Cochliobolus heterostrophus Llm1 â€“ A Lae1-like methyltransferase regulates T-toxin production, virulence, and development. Fungal Genetics and Biology, 2013, 51, 21-33.	0.9	23
1171	Adaptin evolution in kinetoplastids and emergence of the variant surface glycoprotein coat in African trypanosomatids. Molecular Phylogenetics and Evolution, 2013, 67, 123-128.	1.2	44
1172	The evolutionary origins of chordate hematopoiesis and vertebrate endothelia. Developmental Biology, 2013, 375, 182-192.	0.9	52
1173	Phylogenetic analysis reveals the evolution and diversification of cyclins in eukaryotes. Molecular Phylogenetics and Evolution, 2013, 66, 1002-1010.	1.2	33
1174	Multiple ancient horizontal gene transfers and duplications in lepidopteran species. Insect Molecular Biology, 2013, 22, 72-87.	1.0	43
1175	Bioinformatics methods for the comparative analysis of metazoan mitochondrial genome sequences. Molecular Phylogenetics and Evolution, 2013, 69, 320-327.	1.2	31

#	Article	IF	Citations
1176	Diversity and expression of P450 genes from Dendroctonus valens LeConte (Curculionidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 T 417-432.	1.2	48
1177	Modular Evolution of Tn GBS s, a New Family of Integrative and Conjugative Elements Associating Insertion Sequence Transposition, Plasmid Replication, and Conjugation for Their Spreading. Journal of Bacteriology, 2013, 195, 1979-1990.	1.0	54
1178	Mitogenomic analysis of decapod crustacean phylogeny corroborates traditional views on their relationships. Molecular Phylogenetics and Evolution, 2013, 66, 776-789.	1.2	130
1179	The Mitochondrial Genome and a 60â€kb Nuclear DNA Segment from Naegleria fowleri, the Causative Agent of Primary Amoebic Meningoencephalitis. Journal of Eukaryotic Microbiology, 2013, 60, 179-191.	0.8	36
1180	Multigene Phylogenetic Reconstruction of the Tubulinea (Amoebozoa) Corroborates Four of the Six Major Lineages, while Additionally Revealing that Shell Composition Does not Predict Phylogeny in the Arcellinida. Protist, 2013, 164, 323-339.	0.6	45
1181	A dynamic history of gene duplications and losses characterizes the evolution of the SPARC family in eumetazoans. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20122963.	1.2	18
1182	Heat shock protein responses to salinity, food deprivation, and temperature in the invasive ground beetle Merizodus soledadinus at the Kerguelen Islands. Polar Biology, 2013, 36, 201-209.	0.5	6
1183	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. Science, 2013, 339, 1207-1210.	6.0	439
1184	Evolutionary History of Eukaryotic Î±-Glucosidases from the Î±-Amylase Family. Journal of Molecular Evolution, 2013, 76, 129-145.	0.8	33
1185	Arabidopsis homeodomain-leucine zipper IV proteins promote stomatal development and ectopically induce stomata beyond the epidermis. Development (Cambridge), 2013, 140, 1924-1935.	1.2	76
1186	You are where you live: parasitic nematode mitochondrial genome size is associated with the thermal environment generated by hosts. Journal of Evolutionary Biology, 2013, 26, 683-690.	0.8	18
1187	Potential contribution of P-glycoproteins to macrocyclic lactone resistance in the cattle parasitic nematode Cooperia oncophora. Molecular and Biochemical Parasitology, 2013, 188, 10-19.	0.5	33
1188	Assemblyâ€free metagenomic analysis reveals new metabolic capabilities in surface ocean bacterioplankton. Environmental Microbiology Reports, 2013, 5, 686-696.	1.0	8
1189	Inferring ancient divergences requires genes with strong phylogenetic signals. Nature, 2013, 497, 327-331.	13.7	541
1190	Arsenite oxidase gene diversity amongChloroflexiandProteobacteriafrom El Tatio Geyser Field, Chile. FEMS Microbiology Ecology, 2013, 83, 745-756.	1.3	53
1191	Comparative Genomics of a Plant-Pathogenic Fungus,Pyrenophora tritici-repentis, Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. G3: Genes, Genomes, Genetics, 2013, 3, 41-63.	0.8	167
1192	Characterization of the Mitochondrial Genome of the Diamondback MothPlutella xylostella(Lepidoptera: Plutellidae) and Phylogenetic Analysis of Advanced Moths and Butterflies. DNA and Cell Biology, 2013, 32, 173-187.	0.9	19
1193	Evolution of the vertebrate bone matrix: An expression analysis of the network forming collagen paralogues in amphibian osteoblasts. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2013, 320, 375-384.	0.6	12

#	Article	IF	Citations
1194	Influence of overlapping genes on the evolution of human hepatitis B virus. Virology, 2013, 441, 40-48.	1.1	30
1195	Localization and evolution of septins in algae. Plant Journal, 2013, 74, 605-614.	2.8	20
1196	Origin and Evolution of Yolk Proteins: Expansion and Functional Diversification of Large Lipid Transfer Protein Superfamily1. Biology of Reproduction, 2013, 88, 102.	1.2	35
1197	3-to-1: unraveling structural transitions in ureases. Die Naturwissenschaften, 2013, 100, 459-467.	0.6	32
1198	A 175 Million Year History of T Cell Regulatory Molecules Reveals Widespread Selection, with Adaptive Evolution of Disease Alleles. Immunity, 2013, 38, 1129-1141.	6.6	30
1199	Evidence for negative-strand RNA virus infection in fungi. Virology, 2013, 435, 201-209.	1.1	70
1200	Mutualism and asexual reproduction influence recognition genes in a fungal symbiont. Fungal Biology, 2013, 117, 439-450.	1.1	2
1201	The effects of model choice and mitigating bias on the ribosomal tree of life. Molecular Phylogenetics and Evolution, 2013, 69, 17-38.	1.2	53
1202	Evolutionary analyses of gap junction protein families. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 4-14.	1.4	109
1203	Functional divergence outlines the evolution of novel protein function in NifH/BchL protein family. Journal of Biosciences, 2013, 38, 733-740.	0.5	6
1204	Analyses of mitochondrial amino acid sequence datasets support the proposal that specimens of Hypodontus macropi from three species of macropodid hosts represent distinct species. BMC Evolutionary Biology, 2013, 13, 259.	3.2	17
1205	Advancing data reuse in phyloinformatics using an ontology-driven Semantic Web approach. BMC Medical Genomics, 2013, 6, S5.	0.7	5
1206	Analysis of Soluble Protein Contents from the Nematocysts of a Model Sea Anemone Sheds Light on Venom Evolution. Marine Biotechnology, 2013, 15, 329-339.	1.1	95
1207	Evolutionary Acquisition and Loss of Saxitoxin Biosynthesis in Dinoflagellates: the Second â€œCoreâ€• Gene, sxtG. Applied and Environmental Microbiology, 2013, 79, 2128-2136.	1.4	70
1208	Identification of Two Penelope-Like Elements with Different Structures and Chromosome Localization in Kuruma Shrimp Genome. Marine Biotechnology, 2013, 15, 115-123.	1.1	9
1209	Evolution of Substrate Specificity in a Recipientâ€™s Enzyme Following Horizontal Gene Transfer. Molecular Biology and Evolution, 2013, 30, 2024-2034.	3.5	32
1210	Adaptive evolution of tight junction protein claudin-14 in echolocating whales. Gene, 2013, 530, 208-214.	1.0	6
1211	The Ancient and Widespread Nature of the ERâ€“Mitochondria Encounter Structure. Molecular Biology and Evolution, 2013, 30, 2044-2049.	3.5	90

#	Article	IF	Citations
1212	A Novel Victorivirus from a Phytopathogenic Fungus, Rosellinia necatrix, Is Infectious as Particles and Targeted by RNA Silencing. Journal of Virology, 2013, 87, 6727-6738.	1.5	80
1213	Missing Data and Influential Sites: Choice of Sites for Phylogenetic Analysis Can Be As Important As Taxon Sampling and Model Choice. Genome Biology and Evolution, 2013, 5, 681-687.	1.1	23
1214	Identifying Cis-Regulatory Changes Involved in the Evolution of Aerobic Fermentation in Yeasts. Genome Biology and Evolution, 2013, 5, 1065-1078.	1.1	14
1215	Circadian Clocks in the Cnidaria: Environmental Entrainment, Molecular Regulation, and Organismal Outputs. Integrative and Comparative Biology, 2013, 53, 118-130.	0.9	50
1216	Phylogenetic, expression, and functional analyses of anoctamin homologs inCaenorhabditis elegans. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2013, 305, R1376-R1389.	0.9	19
1217	Evaluating Phylogenetic Informativeness as a Predictor of Phylogenetic Signal for Metazoan, Fungal, and Mammalian Phylogenomic Data Sets. BioMed Research International, 2013, 2013, 1-14.	0.9	17
1218	Biomphalysin, a New Î² Pore-forming Toxin Involved in Biomphalaria glabrata Immune Defense against Schistosoma mansoni. PLoS Pathogens, 2013, 9, e1003216.	2.1	93
1219	Comparative Genomics of Blattabacterium cuenoti: The Frozen Legacy of an Ancient Endosymbiont Genome. Genome Biology and Evolution, 2013, 5, 351-361.	1.1	64
1220	The Genome of Tolypocladium inflatum: Evolution, Organization, and Expression of the Cyclosporin Biosynthetic Gene Cluster. PLoS Genetics, 2013, 9, e1003496.	1.5	144
1221	Novel Polyomaviruses of Nonhuman Primates: Genetic and Serological Predictors for the Existence of Multiple Unknown Polyomaviruses within the Human Population. PLoS Pathogens, 2013, 9, e1003429.	2.1	35
1222	Divergent genetic mechanisms underlie reversals to radial floral symmetry from diverse zygomorphic flowered ancestors. Frontiers in Plant Science, 2013, 4, 302.	1.7	53
1223	Speciation inThaparocleidus(Monogenea: Dactylogyridae) Parasitizing Asian Pangasiid Catfishes. BioMed Research International, 2013, 2013, 1-14.	0.9	26
1224	A Gene Transfer Agent and a Dynamic Repertoire of Secretion Systems Hold the Keys to the Explosive Radiation of the Emerging Pathogen Bartonella. PLoS Genetics, 2013, 9, e1003393.	1.5	89
1225	The Extraordinary Evolutionary History of the Reticuloendotheliosis Viruses. PLoS Biology, 2013, 11, e1001642.	2.6	88
1226	The Evolution of the knirps Family of Transcription Factors in Arthropods. Molecular Biology and Evolution, 2013, 30, 1348-1357.	3.5	23
1227	The Continuing Debate on Deep Molluscan Phylogeny: Evidence for Serialia (Mollusca,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	60
1228	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across Cochliobolus Pathogens. PLoS Genetics, 2013, 9, e1003233.	1.5	232
1229	The identification and differential expression of Eucalyptus grandis pathogenesis-related genes in response to salicylic acid and methyl jasmonate. Frontiers in Plant Science, 2013, 4, 43.	1.7	31

#	Article	IF	Citations
1230	The Tissue-Specific RNA Binding Protein T-STAR Controls Regional Splicing Patterns of Neurexin Pre-mRNAs in the Brain. PLoS Genetics, 2013, 9, e1003474.	1.5	74
1231	Ancient Properties of Spider Silks Revealed by the Complete Gene Sequence of the Prey-Wrapping Silk Protein (AcSp1). Molecular Biology and Evolution, 2013, 30, 589-601.	3.5	76
1232	Sequential Duplications of an Ancient Member of the DnaJ-Family Expanded the Functional Chaperone Network in the Eukaryotic Cytosol. Molecular Biology and Evolution, 2013, 30, 985-998.	3.5	38
1233	Overview of organohalide-respiring bacteria and a proposal for a classification system for reductive dehalogenases. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120322.	1.8	266
1234	Patterns of Nucleotide Diversity of the ldpA Circadian Gene in Closely Related Species of Cyanobacteria from Extreme Cold Deserts. Applied and Environmental Microbiology, 2013, 79, 1516-1522.	1.4	6
1235	A novel gammaherpesvirus in a large flying fox (Pteropus vampyrus) with blepharitis. Journal of Veterinary Diagnostic Investigation, 2013, 25, 433-437.	0.5	10
1236	The Evolutionary Origins of Detoxifying Enzymes. Journal of Biological Chemistry, 2013, 288, 23914-23927.	1.6	112
1237	Evolution of Tre-2/Bub2/Cdc16 (TBC) Rab GTPase-activating proteins. Molecular Biology of the Cell, 2013, 24, 1574-1583.	0.9	57
1238	Genomic Makeup of the Marine Flavobacterium Nonlabens (Donghaeana) dokdonensis and Identification of a Novel Class of Rhodopsins. Genome Biology and Evolution, 2013, 5, 187-199.	1.1	84
1239	The Evolution of MicroRNA Pathway Protein Components in Cnidaria. Molecular Biology and Evolution, 2013, 30, 2541-2552.	3.5	57
1240	EF-hand proteins in onychophorans as compared to tardigrades and other ecdysozoans. Journal of Limnology, 2013, 72, .	0.3	0
1241	The Genetic Architecture of Degenerin/Epithelial Sodium Channels inDrosophila. G3: Genes, Genomes, Genetics, 2013, 3, 441-450.	0.8	85
1242	MORE THAN ONE WAY TO PRODUCE PROTEIN DIVERSITY: DUPLICATION AND LIMITED ALTERNATIVE SPLICING OF AN ADHESION MOLECULE GENE IN BASAL ARTHROPODS. Evolution; International Journal of Organic Evolution, 2013, 67, n/a-n/a.	1.1	25
1243	Structureâ€"function relationships of two paralogous single-stranded DNA-binding proteins from Streptomyces coelicolor: implication of SsbB in chromosome segregation during sporulation. Nucleic Acids Research, 2013, 41, 3659-3672.	6.5	17
1244	Heterogeneity in Neutralization Sensitivities of Viruses Comprising the Simian Immunodeficiency Virus SIVsmE660 Isolate and Vaccine Challenge Stock. Journal of Virology, 2013, 87, 5477-5492.	1.5	32
1245	A Genomic Survey of HECT Ubiquitin Ligases in Eukaryotes Reveals Independent Expansions of the HECT System in Several Lineages. Genome Biology and Evolution, 2013, 5, 833-847.	1.1	35
1246	The Complete Maternally and Paternally Inherited Mitochondrial Genomes of the Endangered Freshwater Mussel Solenaia carinatus (Bivalvia: Unionidae) and Implications for Unionidae Taxonomy. PLoS ONE, 2013, 8, e84352.	1.1	66
1247	Insight into the Family of Na+/Ca2+ Exchangers of Caenorhabditis elegans. Genetics, 2013, 195, 611-619.	1.2	16

#	Article	IF	Citations
1248	Extensive Trans-Specific Polymorphism at the Mating Type Locus of the Root Decay Fungus Heterobasidion. Molecular Biology and Evolution, 2013, 30, 2286-2301.	3.5	29
1249	A genome-wide analysis of annexins from parasitic organisms and their vectors. Scientific Reports, 2013, 3, 2893.	1.6	31
1250	The Expanding Roles of GÎ²Î³Subunits in G Proteinâ€“Coupled Receptor Signaling and Drug Action. Pharmacological Reviews, 2013, 65, 545-577.	7.1	202
1251	Evolution of the Class IV HD-Zip Gene Family in Streptophytes. Molecular Biology and Evolution, 2013, 30, 2347-2365.	3.5	31
1252	Convergent Evolution of Polysaccharide Debranching Defines a Common Mechanism for Starch Accumulation in Cyanobacteria and Plants. Plant Cell, 2013, 25, 3961-3975.	3.1	21
1253	Molecular phylogenetic analyses of albuminoids reveal the molecular evolution of allosteric properties. IUBMB Life, 2013, 65, 544-549.	1.5	6
1254	Structure and Evolution of Chlorate Reduction Composite Transposons. MBio, 2013, 4, .	1.8	64
1255	Ancient Complexity, Opisthokont Plasticity, and Discovery of the 11th Subfamily of Arf <scp>GAP</scp> Proteins. Traffic, 2013, 14, 636-649.	1.3	36
1256	The Rise of Statistical Phylogenetics. Australian and New Zealand Journal of Statistics, 2013, 55, 205-220.	0.4	5
1257	Phylogenetic and phenotypic characterisation of the 3-ketoacyl-CoA thiolase gene family from the opportunistic human pathogenic fungusCandida albicans. FEMS Yeast Research, 2013, 13, 553-564.	1.1	16
1258	Evolution of Bacterial-Like Phosphoprotein Phosphatases in Photosynthetic Eukaryotes Features Ancestral Mitochondrial or Archaeal Origin and Possible Lateral Gene Transfer Â Â Â. Plant Physiology, 2013, 163, 1829-1843.	2.3	34
1259	Saltatory Evolution of the Ectodermal Neural Cortex Gene Family at the Vertebrate Origin. Genome Biology and Evolution, 2013, 5, 1485-1502.	1.1	3
1260	Primary endosymbiosis events date to the later Proterozoic with cross-calibrated phylogenetic dating of duplicated ATPase proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12355-12360.	3.3	126
1261	Effects of Defective Interfering RNA on Symptom Induction by, and Replication of, a Novel Partitivirus from a Phytopathogenic Fungus, Rosellinia necatrix. Journal of Virology, 2013, 87, 2330-2341.	1.5	85
1262	Selective constraint and the evolution of the RNA Polymerase II C-Terminal Domain. Transcription, 2013, 4, 77-86.	1.7	10
1263	BOLA1 Is an Aerobic Protein That Prevents Mitochondrial Morphology Changes Induced by Glutathione Depletion. Antioxidants and Redox Signaling, 2013, 18, 129-138.	2.5	46
1264	A link between host plant adaptation and pesticide resistance in the polyphagous spider mite Tetranychus urticae. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E113-22.	3.3	347
1265	Linkage, Mobility, and Selfishness in the MazF Family of Bacterial Toxins: A Snapshot of Bacterial Evolution. Genome Biology and Evolution, 2013, 5, 2268-2284.	1.1	14

#	Article	IF	Citations
1266	Boronated tartrolon antibiotic produced by symbiotic cellulose-degrading bacteria in shipworm gills. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E295-304.	3.3	89
1267	Mannosylglucosylglycerate biosynthesis in the deep-branching phylum Planctomycetes: characterization of the uncommon enzymes from Rhodopirellula baltica. Scientific Reports, 2013, 3, 2378.	1.6	3
1268	PPR proteins of green algae. RNA Biology, 2013, 10, 1526-1542.	1.5	34
1269	The Origin of Parasitism Gene in Nematodes: Evolutionary Analysis through the Construction of Domain Trees. Evolutionary Bioinformatics, 2013, 9, EBO.S13032.	0.6	0
1270	Identification and characterization of two wheat Glycogen Synthase Kinase 3/ SHAGGY-like kinases. BMC Plant Biology, 2013, 13, 64.	1.6	14
1271	Examining new phylogenetic markers to uncover the evolutionary history of early-diverging fungi: comparing MCM7, TSR1 and rRNA genes for single- and multi-gene analyses of the <I>Kickxellomycotina</I>. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2013, 30, 106-125.	1.6	24
1272	Otx2 expression and implications for olfactory imprinting in the anemonefish, Amphiprion percula. Biology Open, 2013, 2, 907-915.	0.6	3
1273	Complete Mitochondrial Genome Sequence Data Provides Genetic Evidence That the Brown Dog Tick Rhipicephalus sanguineus (Acari: Ixodidae) Represents a Species Complex. International Journal of Biological Sciences, 2013, 9, 361-369.	2.6	90
1274	Candidate Chemosensory Genes in the Stemborer Sesamia nonagrioides. International Journal of Biological Sciences, 2013, 9, 481-495.	2.6	47
1275	Structural features of the two-component system LisR/LisK suggests multiple responses for the adaptation and survival of Listeria monocytogenes. Universitas Scientiarum, 2013, 18, 189.	0.2	2
1276	Cathelicidins Revisited. International Journal of Systems Biology and Biomedical Technologies, 2013, 2, 8-32.	0.2	1
1277	Diversification of SUMO-Activating Enzyme in Arabidopsis: Implications in SUMO Conjugation. Molecular Plant, 2013, 6, 1646-1660.	3.9	43
1278	Reconstruction of Family-Level Phylogenetic Relationships within Demospongiae (Porifera) Using Nuclear Encoded Housekeeping Genes. PLoS ONE, 2013, 8, e50437.	1.1	47
1279	De Novo Transcriptome Sequencing and Analysis for Venturia inaequalis, the Devastating Apple Scab Pathogen. PLoS ONE, 2013, 8, e53937.	1.1	32
1280	Comparative Genomic Analysis of East Asian and Non-Asian Helicobacter pylori Strains Identifies Rapidly Evolving Genes. PLoS ONE, 2013, 8, e55120.	1.1	27
1281	In Silico Analysis of Putative Paralytic Shellfish Poisoning Toxins Export Proteins in Cyanobacteria. PLoS ONE, 2013, 8, e55664.	1.1	10
1282	Phylogenetic Analysis of Glucosyltransferases and Implications for the Coevolution of Mutans Streptococci with Their Mammalian Hosts. PLoS ONE, 2013, 8, e56305.	1.1	30
1283	Evolution of the Ferric Reductase Domain (FRD) Superfamily: Modularity, Functional Diversification, and Signature Motifs. PLoS ONE, 2013, 8, e58126.	1.1	68

#	Article	IF	Citations
1284	The Complete Genome Sequence of the Plant Growth-Promoting Bacterium Pseudomonas sp. UW4. PLoS ONE, 2013, 8, e58640.	1.1	144
1285	Characterization of an Ancient Lepidopteran Lateral Gene Transfer. PLoS ONE, 2013, 8, e59262.	1.1	52
1286	Multiple Interkingdom Horizontal Gene Transfers in Pyrenophora and Closely Related Species and Their Contributions to Phytopathogenic Lifestyles. PLoS ONE, 2013, 8, e60029.	1.1	30
1287	A Comparison of the Olfactory Gene Repertoires of Adults and Larvae in the Noctuid Moth Spodoptera littoralis. PLoS ONE, 2013, 8, e60263.	1.1	109
1288	Tryptogalinin Is a Tick Kunitz Serine Protease Inhibitor with a Unique Intrinsic Disorder. PLoS ONE, 2013, 8, e62562.	1.1	32
1289	Selection and Phylogenetics of Salmonid MHC Class I: Wild Brown Trout (Salmo trutta) Differ from a Non-Native Introduced Strain. PLoS ONE, 2013, 8, e63035.	1.1	3
1290	Complete Mitochondrial DNA Sequences of the Threadfin Cichlid (Petrochromis trewavasae) and the Blunthead Cichlid (Tropheus moorii) and Patterns of Mitochondrial Genome Evolution in Cichlid Fishes. PLoS ONE, 2013, 8, e67048.	1.1	41
1291	Transcriptome Characterisation of the Ant Formica exsecta with New Insights into the Evolution of Desaturase Genes in Social Hymenoptera. PLoS ONE, 2013, 8, e68200.	1.1	14
1292	Revising the Taxonomic Distribution, Origin and Evolution of Ribosome Inactivating Protein Genes. PLoS ONE, 2013, 8, e72825.	1.1	37
1293	Unraveling the Evolution of the Atlantic Codâ€™s (Gadus morhua L.) Alternative Immune Strategy. PLoS ONE, 2013, 8, e74004.	1.1	64
1294	Molecular Phylogeny of a RING E3 Ubiquitin Ligase, Conserved in Eukaryotic Cells and Dominated by Homologous Components, the Muskelin/RanBPM/CTLH Complex. PLoS ONE, 2013, 8, e75217.	1.1	56
1295	The genome sequence of the colonial chordate, Botryllus schlosseri. ELife, 2013, 2, e00569.	2.8	209
1296	The Evolutionary Relationship between Microbial Rhodopsins and Metazoan Rhodopsins. Scientific World Journal, The, 2013, 2013, 1-10.	0.8	15
1297	Searching for convergent evolution in manganese superoxidase dismutase using hydrophobic cluster analysis. Genetics and Molecular Biology, 2014, 37, 460-470.	0.6	2
1298	Network Analysis Reveals Ecological Links between N-Fixing Bacteria and Wood-Decaying Fungi. PLoS ONE, 2014, 9, e88141.	1.1	129
1299	Transcriptome Data Reveal Syndermatan Relationships and Suggest the Evolution of Endoparasitism in Acanthocephala via an Epizoic Stage. PLoS ONE, 2014, 9, e88618.	1.1	40
1300	RNA Viral Metagenome of Whiteflies Leads to the Discovery and Characterization of a Whitefly-Transmitted Carlavirus in North America. PLoS ONE, 2014, 9, e86748.	1.1	46
1301	Isolation and Molecular Characterization of a Novel Picornavirus from Baitfish in the USA. PLoS ONE, 2014, 9, e87593.	1.1	34

#	Article	IF	Citations
1302	Independent Expansion of Zincin Metalloproteinases in Onygenales Fungi May Be Associated with Their Pathogenicity. PLoS ONE, 2014, 9, e90225.	1.1	35
1303	The Complete Mitochondrial Genome of Meloidogyne graminicola (Tylenchina): A Unique Gene Arrangement and Its Phylogenetic Implications. PLoS ONE, 2014, 9, e98558.	1.1	31
1304	Transcriptomic Analysis of Prunus domestica Undergoing Hypersensitive Response to Plum Pox Virus Infection. PLoS ONE, 2014, 9, e100477.	1.1	38
1305	Genome-Wide Prediction of the Polymorphic Ser Gene Family in Tetrahymena thermophila Based on Motif Analysis. PLoS ONE, 2014, 9, e105201.	1.1	0
1306	The Cytochrome P450 Superfamily Complement (CYPome) in the Annelid Capitella teleta. PLoS ONE, 2014, 9, e107728.	1.1	27
1307	Intragenic Recombination Has a Critical Role on the Evolution of Legionella pneumophila Virulence-Related Effector sidJ. PLoS ONE, 2014, 9, e109840.	1.1	16
1308	Molecular Evolution and Expansion Analysis of the NAC Transcription Factor in Zea mays. PLoS ONE, 2014, 9, e111837.	1.1	56
1309	Identification of Transcription Factor Genes and Their Correlation with the High Diversity of Stramenopiles. PLoS ONE, 2014, 9, e111841.	1.1	12
1310	Genetic Diversity of Candidatus Liberibacter asiaticus Based on Two Hypervariable Effector Genes in Thailand. PLoS ONE, 2014, 9, e112968.	1.1	21
1311	A Deg-protease family protein in marine Synechococcus is involved in outer membrane protein organization. Frontiers in Marine Science, 2014, 1, .	1.2	0
1312	Shotgun metagenomic data reveals significant abundance but low diversity of â€œCandidatus Scalinduaâ€• marine anammox bacteria in the Arabian Sea oxygen minimum zone. Frontiers in Microbiology, 2014, 5, 31.	1.5	41
1313	Fermentation couples Chloroflexi and sulfate-reducing bacteria to Cyanobacteria in hypersaline microbial mats. Frontiers in Microbiology, 2014, 5, 61.	1.5	61
1314	A novel single-stranded RNA virus isolated from a phytopathogenic filamentous fungus, Rosellinia necatrix, with similarity to hypo-like viruses. Frontiers in Microbiology, 2014, 5, 360.	1.5	75
1315	Complete Mitochondrial Genomes of Carcinoscorpius rotundicauda and Tachypleus tridentatus (Xiphosura, Arthropoda) and Implications for Chelicerate Phylogenetic Studies. International Journal of Biological Sciences, 2014, 10, 479-489.	2.6	19
1316	Type-IV Antifreeze Proteins are Essential for Epiboly and Convergence in Gastrulation of Zebrafish Embryos. International Journal of Biological Sciences, 2014, 10, 715-732.	2.6	25
1317	Computational analysis of 1,3-propanediol operon transcriptional regulators: Insights into Clostridium sp. glycerol metabolism regulation. Universitas Scientiarum, 2014, 20, 129.	0.2	2
1318	Evolution, divergence and loss of the Nodal signalling pathway: new data and a synthesis across the Bilateria. International Journal of Developmental Biology, 2014, 58, 521-532.	0.3	36
1319	Identification and characterization of a cathepsin-L-like peptidase in Eimeria tenella. Parasitology Research, 2014, 113, 4335-4348.	0.6	6

#	Article	IF	Citations
1320	Resolution of deep angiosperm phylogeny using conserved nuclear genes and estimates of early divergence times. Nature Communications, 2014, 5, 4956.	5.8	330
1321	Phylogenetic analysis of ligninolytic peroxidases: preliminary insights into the alternation of white-rot and brown-rot fungi in their lineage. Mycology, 2014, 5, 29-42.	2.0	6
1322	First evidence of the P-glycoprotein gene expression and multixenobiotic resistance modulation in earthworm. Arhiv Za Higijenu Rada I Toksikologiju, 2014, 65, 67-75.	0.4	13
1323	From all to (nearly) none. Cellular Logistics, 2014, 4, e28114.	0.9	22
1324	Simulation of Genome-Wide Evolution under Heterogeneous Substitution Models and Complex Multispecies Coalescent Histories. Molecular Biology and Evolution, 2014, 31, 1295-1301.	3.5	39
1325	Dynamic evolution of the alpha (Î±) and beta (Î²) keratins has accompanied integument diversification and the adaptation of birds into novel lifestyles. BMC Evolutionary Biology, 2014, 14, 249.	3.2	84
1326	Heterogeneous genetic diversity pattern in Plasmodium vivax genes encoding merozoite surface proteins (MSP) -7E, â^'7F and -7L. Malaria Journal, 2014, 13, 495.	0.8	24
1327	Positive selection at a seminal fluid gene within a QTL for conspecific sperm precedence. Genetica, 2014, 142, 537-543.	0.5	4
1328	Ball Python Nidovirus: a Candidate Etiologic Agent for Severe Respiratory Disease in Python regius. MBio, 2014, 5, e01484-14.	1.8	82
1329	Compositional Biases among Synonymous Substitutions Cause Conflict between Gene and Protein Trees for Plastid Origins. Molecular Biology and Evolution, 2014, 31, 1697-1709.	3.5	49
1330	Differential Expression of Conserved Germ Line Markers and Delayed Segregation of Male and Female Primordial Germ Cells in a Hermaphrodite, the Leech Helobdella. Molecular Biology and Evolution, 2014, 31, 341-354.	3.5	31
1331	Structural divergence of plant TCTPs. Frontiers in Plant Science, 2014, 5, 361.	1.7	14
1332	Characterization of a Proposed Dichorhavirus Associated with the Citrus Leprosis Disease and Analysis of the Host Response. Viruses, 2014, 6, 2602-2622.	1.5	34
1333	Vestigialization of an Allosteric Switch: Genetic and Structural Mechanisms for the Evolution of Constitutive Activity in a Steroid Hormone Receptor. PLoS Genetics, 2014, 10, e1004058.	1.5	39
1334	A Genome-Wide Identification of Basic Helix-Loop-Helix Motifs in Pediculus humanus corporis (Phthiraptera: Pediculidae). Journal of Insect Science, 2014, 14, 195.	0.6	6
1335	Genome sequence of mungbean and insights into evolution within Vigna species. Nature Communications, 2014, 5, 5443.	5.8	453
1336	A Fault Tolerant Workflow for Reproducible Research. , 2014, , .		1
1337	Thermodynamic System Drift in Protein Evolution. PLoS Biology, 2014, 12, e1001994.	2.6	78

#	Article	IF	Citations
1338	Evolution of the F0F1 ATP Synthase Complex in Light of the Patchy Distribution of Different Bioenergetic Pathways across Prokaryotes. PLoS Computational Biology, 2014, 10, e1003821.	1.5	38
1339	Rapid Evolution of PARP Genes Suggests a Broad Role for ADP-Ribosylation in Host-Virus Conflicts. PLoS Genetics, 2014, 10, e1004403.	1.5	163
1340	Comparative Analysis of Salivary Gland Transcriptomes of Phlebotomus orientalis Sand Flies from Endemic and Non-endemic Foci of Visceral Leishmaniasis. PLoS Neglected Tropical Diseases, 2014, 8, e2709.	1.3	53
1341	Leishmania infantum Ecto-Nucleoside Triphosphate Diphosphohydrolase-2 is an Apyrase Involved in Macrophage Infection and Expressed in Infected Dogs. PLoS Neglected Tropical Diseases, 2014, 8, e3309.	1.3	22
1342	A Novel Psittacine Adenovirus Identified During an Outbreak of Avian Chlamydiosis and Human Psittacosis: Zoonosis Associated with Virus-Bacterium Coinfection in Birds. PLoS Neglected Tropical Diseases, 2014, 8, e3318.	1.3	48
1343	Host-to-Pathogen Gene Transfer Facilitated Infection of Insects by a Pathogenic Fungus. PLoS Pathogens, 2014, 10, e1004009.	2.1	61
1344	Evolutionary analysis of the cystatin family in three Schistosoma species. Frontiers in Genetics, 2014, 5, 206.	1.1	13
1345	Identification of Giardia lamblia DHHC Proteins and the Role of Protein S-palmitoylation in the Encystation Process. PLoS Neglected Tropical Diseases, 2014, 8, e2997.	1.3	23
1346	Ancient Origins of Vertebrate-Specific Innate Antiviral Immunity. Molecular Biology and Evolution, 2014, 31, 140-153.	3.5	55
1347	The complete mitochondrial genome of Aphelenchoides besseyi (Nematoda: Aphelenchoididae), the first sequenced representative of the subfamily Aphelenchoidinae. Nematology, 2014, 16, 1167-1180.	0.2	5
1348	Quantitative Analysis of the Mitochondrial and Plastid Proteomes of the Moss Physcomitrella patens Reveals Protein Macrocompartmentation and Microcompartmentation. Plant Physiology, 2014, 164, 2081-2095.	2.3	61
1349	PhyloFlow: A fully customizable and automatic workflow for phylogenetic reconstruction. , 2014, , .		2
1350	Support for bioinformatics applications through volunteer and scalable computing frameworks. , 2014, , .		1
1351	The complete genome sequences of poxviruses isolated from a penguin and a pigeon in South Africa and comparison to other sequenced avipoxviruses. BMC Genomics, 2014, 15, 463.	1.2	37
1352	The mitochondrial and chloroplast genomes of the haptophyte Chrysochromulina tobin contain unique repeat structures and gene profiles. BMC Genomics, 2014, 15, 604.	1.2	30
1354	Promiscuous and Adaptable Enzymes Fill â€œHolesâ€•in the Tetrahydrofolate Pathway in Chlamydia Species. MBio, 2014, 5, e01378-14.	1.8	47
1355	Evolution of Bacterial Protein-Tyrosine Kinases and Their Relaxed Specificity Toward Substrates. Genome Biology and Evolution, 2014, 6, 800-817.	1.1	35
1356	TIR-domain-containing protein repertoire of nine anthozoan species reveals coralâ€“specific expansions and uncharacterized proteins. Developmental and Comparative Immunology, 2014, 46, 480-488.	1.0	80

#	Article	IF	Citations
1357	Secreted Proteomes of Different Developmental Stages of the Gastrointestinal Nematode Nippostrongylus brasiliensis. Molecular and Cellular Proteomics, 2014, 13, 2736-2751.	2.5	88
1358	Thylakoid FtsH Protease Contributes to Photosystem II and CytochromebÂ6 ÂfRemodeling inChlamydomonas reinhardtiiunder Stress Conditions. Plant Cell, 2014, 26, 373-390.	3.1	113
1359	Phylogenomics of â€œCandidatus Hepatoplasma crinochetorum,â€•a Lineage of Mollicutes Associated with Noninsect Arthropods. Genome Biology and Evolution, 2014, 6, 407-415.	1.1	35
1360	Genome sequence of the model sulfate reducer Desulfovibrio gigas: a comparative analysis within the Desulfovibrio genus. MicrobiologyOpen, 2014, 3, 513-530.	1.2	37
1361	Diversity and distribution of a key sulpholipid biosynthetic gene in marine microbial assemblages. Environmental Microbiology, 2014, 16, 774-787.	1.8	14
1362	Rhizobial plasmid pLPU83a is able to switch between different transfer machineries depending on its genomic background. FEMS Microbiology Ecology, 2014, 88, 565-578.	1.3	24
1363	Morphological diversity and genetic regulation of inflorescence abscission zones in grasses. American Journal of Botany, 2014, 101, 1759-1769.	0.8	45
1364	The <scp>L</scp>egionella pneumophila kai operon is implicated in stress response and confers fitness in competitive environments. Environmental Microbiology, 2014, 16, 359-381.	1.8	26
1365	New insights into the allergenicity of tropomyosin: a bioinformatics approach. Molecular Biology Reports, 2014, 41, 6509-6517.	1.0	15
1366	New insights into the evolution of vertebrate CRH (corticotropin-releasing hormone) and invertebrate DH44 (diuretic hormone 44) receptors in metazoans. General and Comparative Endocrinology, 2014, 209, 162-170.	0.8	36
1367	DNA topoisomerase VIII: a novel subfamily of type IIB topoisomerases encoded by free or integrated plasmids in Archaea and Bacteria. Nucleic Acids Research, 2014, 42, 8578-8591.	6.5	24
1368	Taste and odorant receptors of the coelacanthâ€”A gene repertoire in transition. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 403-414.	0.6	31
1369	The Holozoan Capsaspora owczarzaki Possesses a Diverse Complement of Active Transposable Element Families. Genome Biology and Evolution, 2014, 6, 949-963.	1.1	5
1370	Genome-Wide Analyses of a Plant-Specific LIM-Domain Gene Family Implicate Its Evolutionary Role in Plant Diversification. Genome Biology and Evolution, 2014, 6, 1000-1012.	1.1	24
1371	Cloning and structure of a histocompatibility class IIA gene (Lelo-DAA) in Chinese longsnout catfish (Leiocassis longirostris). Genes and Genomics, 2014, 36, 745-753.	0.5	10
1372	Evolutionary classification of ammonium, nitrate, and peptide transporters in land plants. BMC Evolutionary Biology, 2014, 14, 11.	3.2	127
1373	Looking for the bird Kiss: evolutionary scenario in sauropsids. BMC Evolutionary Biology, 2014, 14, 30.	3.2	31
1374	Comparison of environmental and isolate Sulfobacillus genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. BMC Genomics, 2014, 15, 1107.	1.2	65

#	Article	IF	Citations
1375	The translation initiation complex eIF3 in trypanosomatids and other pathogenic excavates â€“ identification of conserved and divergent features based on orthologue analysis. BMC Genomics, 2014, 15, 1175.	1.2	35
1376	Genome sequence of Erinnyis ello granulovirus (ErelGV), a natural cassava hornworm pesticide and the first sequenced sphingid-infecting betabaculovirus. BMC Genomics, 2014, 15, 856.	1.2	23
1377	Comparative genomics of the major fungal agents of human and animal Sporotrichosis: Sporothrix schenckii and Sporothrix brasiliensis. BMC Genomics, 2014, 15, 943.	1.2	121
1378	Phylogenomic analysis of glycogen branching and debranching enzymatic duo. BMC Evolutionary Biology, 2014, 14, 183.	3.2	27
1379	Diversity and evolution of myxozoan minicollagens and nematogalectins. BMC Evolutionary Biology, 2014, 14, 205.	3.2	43
1380	MitoCOGs: clusters of orthologous genes from mitochondria and implications for the evolution of eukaryotes. BMC Evolutionary Biology, 2014, 14, 237.	3.2	34
1381	Genome-wide annotation of the soybean WRKY family and functional characterization of genes involved in response to Phakopsora pachyrhiziinfection. BMC Plant Biology, 2014, 14, 236.	1.6	79
1382	Non-specific lipid transfer proteins in maize. BMC Plant Biology, 2014, 14, 281.	1.6	82
1383	Evolutionary Origin of Bone Morphogenetic Protein 15 and Growth and Differentiation Factor 9 and Differential Selective Pressure Between Mono- and Polyovulating Species1. Biology of Reproduction, 2014, 91, 83.	1.2	24
1384	Characterization of a UDP-N-acetylglucosamine biosynthetic pathway encoded by the giant DNA virus Mimivirus. Glycobiology, 2014, 24, 51-61.	1.3	24
1385	The Evolution of the Four Subunits of Voltage-Gated Calcium Channels: Ancient Roots, Increasing Complexity, and Multiple Losses. Genome Biology and Evolution, 2014, 6, 2210-2217.	1.1	50
1386	Ecology Drives the Distribution of Specialized Tyrosine Metabolism Modules in Fungi. Genome Biology and Evolution, 2014, 6, 121-132.	1.1	37
1387	At the Transition from Invertebrates to Vertebrates, a Novel GnRH-Like Peptide Emerges in Amphioxus. Molecular Biology and Evolution, 2014, 31, 765-778.	3.5	70
1388	Modularized Evolution in Archaeal Methanogens Phylogenetic Forest. Genome Biology and Evolution, 2014, 6, 3344-3359.	1.1	5
1389	The Globin Gene Repertoire of Lampreys: Convergent Evolution of Hemoglobin and Myoglobin in Jawed and Jawless Vertebrates. Molecular Biology and Evolution, 2014, 31, 2708-2721.	3.5	39
1390	Glycoprotein Hormones and Their Receptors Emerged at the Origin of Metazoans. Genome Biology and Evolution, 2014, 6, 1466-1479.	1.1	58
1391	Structural and functional analysis of amphioxus HIFÎ± reveals ancient features of the HIFÎ± family. FASEB Journal, 2014, 28, 1880-1890.	0.2	11
1392	Discovery of prosimian and afrotherian foamy viruses and potential cross species transmissions amidst stable and ancient mammalian co-evolution. Retrovirology, 2014, 11, 61.	0.9	45

#	Article	IF	Citations
1393	Molecular conservation of metazoan gut formation: evidence from expression of endomesoderm genes in Capitella teleta (Annelida). EvoDevo, 2014, 5, 39.	1.3	53
1394	Fungal negative-stranded RNA virus that is related to bornaviruses and nyaviruses. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12205-12210.	3.3	198
1395	Comparative Genomics of Taphrina Fungi Causing Varying Degrees of Tumorous Deformity in Plants. Genome Biology and Evolution, 2014, 6, 861-872.	1.1	33
1396	Synechococcus: 3 billion years of global dominance. Molecular Ecology, 2014, 23, 5538-5551.	2.0	88
1397	Current Immunological and Molecular Biological Perspectives on Seafood Allergy: A Comprehensive Review. Clinical Reviews in Allergy and Immunology, 2014, 46, 180-197.	2.9	89
1398	Longin and <scp>GAF</scp> Domains: Structural Evolution and Adaptation to the Subcellular Trafficking Machinery. Traffic, 2014, 15, 104-121.	1.3	40
1399	Ribosomal proteins: Toward a next generation standard for prokaryotic systematics?. Molecular Phylogenetics and Evolution, 2014, 75, 103-117.	1.2	30
1400	Connectivity of vertebrate genomes: Paired-related homeobox (Prrx) genes in spotted gar, basal teleosts, and tetrapods. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2014, 163, 24-36.	1.3	22
1401	Large-scale phylogenomic analysis reveals the phylogenetic position of the problematic taxon Protocruzia and unravels the deep phylogenetic affinities of the ciliate lineages. Molecular Phylogenetics and Evolution, 2014, 78, 36-42.	1.2	71
1402	Fitting CRISPR-associated Cas3 into the Helicase Family Tree. Current Opinion in Structural Biology, 2014, 24, 106-114.	2.6	59
1403	Generic detection of poleroviruses using an RT-PCR assay targeting the RdRp coding sequence. Journal of Virological Methods, 2014, 198, 1-11.	1.0	28
1404	The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants. Cell, 2014, 156, 691-704.	13.5	238
1405	Did the prion protein become vulnerable to misfolding after an evolutionary divide and conquer event?. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1074-1084.	2.0	2
1406	Complete genome sequence of Habenaria mosaic virus, a new potyvirus infecting a terrestrial orchid (Habenaria radiata) in Japan. Archives of Virology, 2014, 159, 163-166.	0.9	7
1407	Comparative genomics of enterohemorrhagic Escherichia coli O145:H28 demonstrates a common evolutionary lineage with Escherichia coli O157:H7. BMC Genomics, 2014, 15, 17.	1.2	84
1408	The Glycogen Synthase 2 Gene (Gys2) Displays Parallel Evolution Between Old World and New World Fruit Bats. Journal of Molecular Evolution, 2014, 78, 66-74.	0.8	5
1409	Structure, diversity and evolution of myriapod hemocyanins. FEBS Journal, 2014, 281, 1818-1833.	2.2	7
1410	FGF Signaling Emerged Concomitantly with the Origin of Eumetazoans. Molecular Biology and Evolution, 2014, 31, 310-318.	3.5	23

#	Article	IF	Citations
1411	The Phylogenetic Distribution and Evolution of Enzymes Within the Thymidine Kinase 2-like Gene Family in Metazoa. Journal of Molecular Evolution, 2014, 78, 202-216.	0.8	4
1412	The complete mitochondrial genome sequence of the world's largest fish, the whale shark (Rhincodon typus), and its comparison with those of related shark species. Gene, 2014, 539, 44-49.	1.0	34
1413	The evolutionary analysis reveals domain fusion of proteins with Frizzled-like CRD domain. Gene, 2014, 533, 229-239.	1.0	23
1414	Thirty-thousand-year-old distant relative of giant icosahedral DNA viruses with a pandoravirus morphology. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4274-4279.	3.3	468
1415	Conservation and divergence in the frog immunome: pyrosequencing and de novo assembly of immune tissue transcriptomes. Gene, 2014, 542, 98-108.	1.0	26
1416	Identification two novel nacrein-like proteins involved in the shell formation of the Pacific oyster Crassostrea gigas. Molecular Biology Reports, 2014, 41, 4273-4278.	1.0	32
1417	The evolution of paralogous enzymes MAT and MATX within the Euglenida and beyond. BMC Evolutionary Biology, 2014, 14, 25.	3.2	3
1418	On the Origin and Evolution of Plant Brassinosteroid Receptor Kinases. Journal of Molecular Evolution, 2014, 78, 118-129.	0.8	28
1419	Evolution, functional divergence and conserved exonâ€“intron structure of bHLH/PAS gene family. Molecular Genetics and Genomics, 2014, 289, 25-36.	1.0	20
1420	Production of a reference transcriptome and transcriptomic database (EdwardsiellaBase) for the lined sea anemone, Edwardsiella lineata, a parasitic cnidarian. BMC Genomics, 2014, 15, 71.	1.2	58
1421	Characterization of Rhizobium grahamii extrachromosomal replicons and their transfer among rhizobia. BMC Microbiology, 2014, 14, 6.	1.3	20
1422	Diversity and evolution of membrane intrinsic proteins. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 1468-1481.	1.1	199
1423	The evolution of the vertebrate cerebellum: absence of a proliferative external granule layer in a nonâ€teleost rayâ€finned fish. Evolution & Development, 2014, 16, 92-100.	1.1	36
1424	Identification of amino acids in mitochondrially encoded proteins that correlate with lifespan. Experimental Gerontology, 2014, 56, 53-58.	1.2	2
1425	Genomic Features of a Bumble Bee Symbiont Reflect Its Host Environment. Applied and Environmental Microbiology, 2014, 80, 3793-3803.	1.4	53
1426	Genome-wide Comparative Analysis of the GRAS Gene Family in Populus, Arabidopsis and Rice. Plant Molecular Biology Reporter, 2014, 32, 1129-1145.	1.0	107
1427	Bacterial origin of a diverse family of UDP-glycosyltransferase genes in the Tetranychus urticae genome. Insect Biochemistry and Molecular Biology, 2014, 50, 43-57.	1.2	59
1428	Mitochondrial genomes of Meloidogyne chitwoodi and M. incognita (Nematoda: Tylenchina): Comparative analysis, gene order and phylogenetic relationships with other nematodes. Molecular and Biochemical Parasitology, 2014, 194, 20-32.	0.5	26

#	Article	IF	Citations
1429	Taxonomic reorganization of family Partitiviridae and other recent progress in partitivirus research. Virus Research, 2014, 188, 128-141.	1.1	271
1430	Phylogeny of Rhigonematomorpha based on the complete mitochondrial genome of Rhigonema thysanophora (Nematoda: Chromadorea). Zoologica Scripta, 2014, 43, 289-303.	0.7	23
1431	Analysis of the complete plastid genome of the unicellular red alga Porphyridium purpureum. Journal of Plant Research, 2014, 127, 389-397.	1.2	45
1432	Illuminating the Base of the Annelid Tree Using Transcriptomics. Molecular Biology and Evolution, 2014, 31, 1391-1401.	3.5	268
1433	Mercuric reductase genes (merA) and mercury resistance plasmids in High Arctic snow, freshwater and sea-ice brine. FEMS Microbiology Ecology, 2014, 87, 52-63.	1.3	75
1434	A re-evaluation of the archaeal membrane lipid biosynthetic pathway. Nature Reviews Microbiology, 2014, 12, 438-448.	13.6	110
1435	A comparative analysis of trypanosomatid SNARE proteins. Parasitology International, 2014, 63, 341-348.	0.6	17
1436	Discovery and Evolution of Bunyavirids in Arctic Phantom Midges and Ancient Bunyavirid-Like Sequences in Insect Genomes. Journal of Virology, 2014, 88, 8783-8794.	1.5	80
1437	First molecular phylogeny of the subfamily Polycerinae (Mollusca, Nudibranchia, Polyceridae). Helgoland Marine Research, 2014, 68, 143-153.	1.3	16
1438	Recurrent gene loss correlates with the evolution of stomach phenotypes in gnathostome history. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20132669.	1.2	65
1439	De novo pyrimidine biosynthesis in the oomycete plant pathogen Phytophthora infestans. Gene, 2014, 537, 312-321.	1.0	24
1440	The ink sac clouds octopod evolutionary history. Hydrobiologia, 2014, 725, 215-235.	1.0	48
1441	Plant Expansins in Bacteria and Fungi: Evolution by Horizontal Gene Transfer and Independent Domain Fusion. Molecular Biology and Evolution, 2014, 31, 376-386.	3.5	95
1442	Multiple Sequence Alignment Methods. Methods in Molecular Biology, 2014, , .	0.4	14
1443	The complete mitochondrial genome of Toxascaris leonina: Comparison with other closely related species and phylogenetic implications. Infection, Genetics and Evolution, 2014, 21, 329-333.	1.0	27
1444	Habitat-specific type I polyketide synthases in soils and street sediments. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 75-85.	1.4	21
1445	Marine Tubeworm Metamorphosis Induced by Arrays of Bacterial Phage Tailâ€“Like Structures. Science, 2014, 343, 529-533.	6.0	223
1446	Spatiotemporal development of the embryonic nervous system of Saccoglossus kowalevskii. Developmental Biology, 2014, 386, 252-263.	0.9	32

#	Article	IF	Citations
1447	A dsRNA mycovirus, Magnaporthe oryzae chrysovirus 1-B, suppresses vegetative growth and development of the rice blast fungus. Virology, 2014, 448, 265-273.	1.1	65
1448	Metagenomic Evidence for Sulfide Oxidation in Extremely Acidic Cave Biofilms. Geomicrobiology Journal, 2014, 31, 194-204.	1.0	41
1449	De novo assembly of Eugenia uniflora L. transcriptome and identification of genes from the terpenoid biosynthesis pathway. Plant Science, 2014, 229, 238-246.	1.7	33
1450	Plant genomes enclose footprints of past infections by giant virus relatives. Nature Communications, 2014, 5, 4268.	5.8	92
1451	Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. ISME Journal, 2014, 8, 1440-1451.	4.4	119
1452	Dynamic expression of a Hydra FGF at boundaries and termini. Development Genes and Evolution, 2014, 224, 235-244.	0.4	19
1453	A novel papillomavirus in AdÃ©lie penguin (Pygoscelis adeliae) faeces sampled at the Cape Crozier colony, Antarctica. Journal of General Virology, 2014, 95, 1352-1365.	1.3	50
1454	Tanay virus, a new species of virus isolated from mosquitoes in the Philippines. Journal of General Virology, 2014, 95, 1390-1395.	1.3	53
1455	Zn-bis-glutathionate is the best co-substrate of the monomeric phytochelatin synthase from the photosynthetic heavy metal-hyperaccumulator Euglena gracilis. Metallomics, 2014, 6, 604.	1.0	13
1456	An eight-gene molecular phylogeny of the Kickxellomycotina, including the first phylogenetic placement of Asellariales. Mycologia, 2014, 106, 912-935.	0.8	29
1457	The Path to Triacylglyceride Obesity in the sta6 Strain of Chlamydomonas reinhardtii. Eukaryotic Cell, 2014, 13, 591-613.	3.4	143
1458	Phylogenetic analysis of barley WRKY proteins and characterization of HvWRKY1 and -2 as repressors of the pathogen-inducible gene HvGER4c. Molecular Genetics and Genomics, 2014, 289, 1331-1345.	1.0	38
1459	Detection and genetic characterisation of a novel mycovirus in Hymenoscyphus fraxineus, the causal agent of ash dieback. Infection, Genetics and Evolution, 2014, 28, 78-86.	1.0	43
1460	Gene Transfers Shaped the Evolution of De Novo NAD + Biosynthesis in Eukaryotes. Genome Biology and Evolution, 2014, 6, 2335-2349.	1.1	17
1461	Parvovirus-Derived Endogenous Viral Elements in Two South American Rodent Genomes. Journal of Virology, 2014, 88, 12158-12162.	1.5	23
1462	Lineageâ€specific evolution of cnidarian Wnt ligands. Evolution & Development, 2014, 16, 259-269.	1.1	14
1463	Using a five-gene phylogeny to test morphology-based hypotheses of Smittium and allies, endosymbiotic gut fungi (Harpellales) associated with arthropods. Molecular Phylogenetics and Evolution, 2014, 79, 23-41.	1.2	16
1464	Phylogenetic analysis and evolutionary studies of plant carotenoid cleavage dioxygenase gene. Gene, 2014, 548, 223-233.	1.0	41

#	Article	IF	Citations
1465	Dynamic recruitment of amino acid transporters to the insect/symbiont interface. Molecular Ecology, 2014, 23, 1608-1623.	2.0	57
1466	The diversity of rice phytocystatins. Molecular Genetics and Genomics, 2014, 289, 1321-1330.	1.0	12
1467	A transcriptome approach to ecdysozoan phylogeny. Molecular Phylogenetics and Evolution, 2014, 80, 79-87.	1.2	101
1468	Multiple occurrences of giant virus core genes acquired by eukaryotic genomes: The visible part of the iceberg?. Virology, 2014, 466-467, 53-59.	1.1	76
1469	Phylogenetic analysis of Merkel cell polyomavirus based on full-length LT and VP1 gene sequences derived from neoplastic tumours in Japanese patients. Journal of General Virology, 2014, 95, 135-141.	1.3	19
1470	Identification and phylogenetic analyses of VASt, an uncharacterized protein domain associated with lipid-binding domains in Eukaryotes. BMC Bioinformatics, 2014, 15, 222.	1.2	38
1471	Osiris: accessible and reproducible phylogenetic and phylogenomic analyses within the Galaxy workflow management system. BMC Bioinformatics, 2014, 15, 230.	1.2	36
1472	In silicosingle strand melting curve: a new approach to identify nucleic acid polymorphisms in Totiviridae. BMC Bioinformatics, 2014, 15, 243.	1.2	8
1473	The genome of the Tiger Milk mushroom, Lignosus rhinocerotis, provides insights into the genetic basis of its medicinal properties. BMC Genomics, 2014, 15, 635.	1.2	65
1474	Comparative genomics and transcriptomics in ants provide new insights into the evolution and function of odorant binding and chemosensory proteins. BMC Genomics, 2014, 15, 718.	1.2	82
1475	Molecular characterization and phylogenetics of Fennoscandian cowpox virus isolates based on the p4c and atip genes. Virology Journal, 2014, 11, 119.	1.4	11
1476	Evolutionary and sequence-based relationships in bacterial AdoMet-dependent non-coding RNA methyltransferases. BMC Research Notes, 2014, 7, 440.	0.6	13
1477	Complete mitochondrial genome sequences of two parasitic/commensal nemerteans, Gononemertes parasita and Nemertopsis tetraclitophila (Nemertea: Hoplonemertea). Parasites and Vectors, 2014, 7, 273.	1.0	6
1478	Characterization of the complete mitochondrial genomes of Nematodirus oiratianus and Nematodirus spathiger of small ruminants. Parasites and Vectors, 2014, 7, 319.	1.0	15
1479	The complete mitochondrial genome of the scab mite Psoroptes cuniculi (Arthropoda: Arachnida) provides insights into Acari phylogeny. Parasites and Vectors, 2014, 7, 340.	1.0	37
1480	Evolution of the Pax-Six-Eya-Dach network: the calcisponge case study. EvoDevo, 2014, 5, 23.	1.3	29
1481	An evolutionary preserved intergenic spacer in gadiform mitogenomes generates a long noncoding RNA. BMC Evolutionary Biology, 2014, 14, 182.	3.2	16
1482	Transcriptome Analysis of the Entomopathogenic Oomycete Lagenidium giganteum Reveals Putative Virulence Factors. Applied and Environmental Microbiology, 2014, 80, 6427-6436.	1.4	14

#	Article	IF	Citations
1483	The plastid ancestor originated among one of the major cyanobacterial lineages. Nature Communications, 2014, 5, 4937.	5.8	83
1484	Occurrence of Hemocyanin in Ostracod Crustaceans. Journal of Molecular Evolution, 2014, 79, 3-11.	0.8	11
1485	Pan-metazoan phylogeny of the DMRT gene family: a framework for functional studies. Development Genes and Evolution, 2014, 224, 175-181.	0.4	57
1486	Establishment of three new genera in the family Geminiviridae: Becurtovirus, Eragrovirus and Turncurtovirus. Archives of Virology, 2014, 159, 2193-2203.	0.9	218
1487	A high degree of African streak virus diversity within Nigerian maize fields includes a new mastrevirus from Axonopus compressus. Archives of Virology, 2014, 159, 2765-2770.	0.9	20
1488	Characterization of the AOX gene and cyanide-resistant respiration in Pyropia haitanensis (Rhodophyta). Journal of Applied Phycology, 2014, 26, 2425-2433.	1.5	4
1489	The fate of tandemly duplicated genes assessed by the expression analysis of a group of Arabidopsis thaliana RING-H2 ubiquitin ligase genes of the ATL family. Plant Molecular Biology, 2014, 84, 429-441.	2.0	1
1490	Expression of multiple Sox genes through embryonic development in the ctenophore Mnemiopsis leidyi is spatially restricted to zones of cell proliferation. EvoDevo, 2014, 5, 15.	1.3	46
1491	Characterization of two genes for the biosynthesis of abietane-type diterpenes in rosemary (Rosmarinus officinalis) glandular trichomes. Phytochemistry, 2014, 101, 52-64.	1.4	106
1492	The mitochondrial genome of Ifremeria nautilei and the phylogenetic position of the enigmatic deep-sea Abyssochrysoidea (Mollusca: Gastropoda). Gene, 2014, 547, 257-266.	1.0	23
1493	Cophylogenetic interactions between marine viruses and eukaryotic picophytoplankton. BMC Evolutionary Biology, 2014, 14, 59.	3.2	34
1494	Distribution and evolution of glycoside hydrolase family 45 cellulases in nematodes and fungi. BMC Evolutionary Biology, 2014, 14, 69.	3.2	37
1495	Identification of glutathione (GSH)-independent glyoxalase III from Schizosaccharomyces pombe. BMC Evolutionary Biology, 2014, 14, 86.	3.2	39
1496	Comparative genomics of type VI secretion systems in strains of Pantoea ananatisfrom different environments. BMC Genomics, 2014, 15, 163.	1.2	74
1497	The nuclear receptor gene family in the Pacific oyster, Crassostrea gigas, contains a novel subfamily group. BMC Genomics, 2014, 15, 369.	1.2	75
1498	Transcriptomic and metabolomic analysis of copper stress acclimation in Ectocarpus siliculosus highlights signaling and tolerance mechanisms in brown algae. BMC Plant Biology, 2014, 14, 116.	1.6	98
1499	Larval body patterning and apical organs are conserved in animal evolution. BMC Biology, 2014, 12, 7.	1.7	166
1500	Targeted Degradation of Abscisic Acid Receptors Is Mediated by the Ubiquitin Ligase Substrate Adaptor DDA1 in Arabidopsis. Plant Cell, 2014, 26, 712-728.	3.1	186

#	Article	IF	Citations
1501	Novel galanin receptors in teleost fish: Identification, expression and regulation by sex steroids. General and Comparative Endocrinology, 2014, 205, 109-120.	0.8	24
1502	Unveiling of the Diversity of Prasinoviruses (Phycodnaviridae) in Marine Samples by Using High-Throughput Sequencing Analyses of PCR-Amplified DNA Polymerase and Major Capsid Protein Genes. Applied and Environmental Microbiology, 2014, 80, 3150-3160.	1.4	30
1503	Molecular evolution of calcification genes in morphologically similar but phylogenetically unrelated scleractinian corals. Molecular Phylogenetics and Evolution, 2014, 77, 281-295.	1.2	11
1504	Calcitonin receptor family evolution and fishing for function using in silico promoter analysis. General and Comparative Endocrinology, 2014, 209, 61-73.	0.8	9
1505	Distribution and evolution of het gene homologs in the basidiomycota. Fungal Genetics and Biology, 2014, 64, 45-57.	0.9	27
1506	Evolutionary implications of dipluran hexamerins. Insect Biochemistry and Molecular Biology, 2014, 46, 17-24.	1.2	18
1507	Molecular cloning, organization, expression and 3D structural analysis of the MHC class Ia gene in the whitespotted bamboo shark (Chiloscyllium plagiosum). Veterinary Immunology and Immunopathology, 2014, 157, 111-118.	0.5	10
1508	Parallel Histories of Horizontal Gene Transfer Facilitated Extreme Reduction of Endosymbiont Genomes in Sap-Feeding Insects. Molecular Biology and Evolution, 2014, 31, 857-871.	3.5	180
1509	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6672-6677.	3.3	146
1510	Discovery of a SAR11 growth requirement for thiaminâ€™s pyrimidine precursor and its distribution in the Sargasso Sea. ISME Journal, 2014, 8, 1727-1738.	4.4	128
1511	Fish genomes provide novel insights into the evolution of vertebrate secretin receptors and their ligand. General and Comparative Endocrinology, 2014, 209, 82-92.	0.8	8
1512	Distribution of protein poly(ADP-ribosyl)ation systems across all domains of life. DNA Repair, 2014, 23, 4-16.	1.3	143
1513	VP6 genetic diversity, reassortment, intragenic recombination and classification of rotavirus B in American and Japanese pigs. Veterinary Microbiology, 2014, 172, 359-366.	0.8	26
1514	Molecular and functional characterization of Anopheles gambiae inward rectifier potassium (Kir1) channels: A novel role in egg production. Insect Biochemistry and Molecular Biology, 2014, 51, 10-19.	1.2	27
1515	Comparative genomic analysis provides insights into the evolution and niche adaptation of marine <scp>M</scp>agnetospira sp. <scp>QH</scp>â€2 strain. Environmental Microbiology, 2014, 16, 525-544.	1.8	66
1516	Novel hydrocarbon monooxygenase genes in the metatranscriptome of a natural deepâ€sea hydrocarbon plume. Environmental Microbiology, 2014, 16, 60-71.	1.8	59
1517	A predicted sex pheromone receptor of codling moth Cydia pomonella detects the plant volatile pear ester. Frontiers in Ecology and Evolution, 2014, 2, .	1.1	50
1518	Antibacterial gene transfer across the tree of life. ELife, 2014, 3, .	2.8	66

#	Article	IF	Citations
1519	A gene horizontally transferred from bacteria protects arthropods from host plant cyanide poisoning. ELife, 2014, 3, e02365.	2.8	135
1520	Virulence, Host-Selective Toxin Production, and Development of Three Cochliobolus Phytopathogens Lacking the Sfp-Type 4â€²-Phosphopantetheinyl Transferase Ppt1. Molecular Plant-Microbe Interactions, 2015, 28, 1130-1141.	1.4	9
1521	Regulation of transcription factors on sexual dimorphism of fig wasps. Scientific Reports, 2015, 5, 10696.	1.6	2
1522	Uncertainty Quantification of State Boundaries in Thin Beam Buckling Experiments. , 2015, , .		1
1524	Bats and Rodents Shape Mammalian Retroviral Phylogeny. Scientific Reports, 2015, 5, 16561.	1.6	31
1525	Horizontal functional gene transfer from bacteria to fishes. Scientific Reports, 2015, 5, 18676.	1.6	9
1526	Origin of marine planktonic cyanobacteria. Scientific Reports, 2015, 5, 17418.	1.6	143
1527	De Novo Assembly and Characterization of Four Anthozoan (Phylum Cnidaria) Transcriptomes. G3: Genes, Genomes, Genetics, 2015, 5, 2441-2452.	0.8	74
1528	Comprehensive genome-wide analysis reveals different classes of enigmatic old yellow enzyme in fungi. Scientific Reports, 2014, 4, 4013.	1.6	25
1529	Gnathostoma spinigerum Mitochondrial Genome Sequence: a Novel Gene Arrangement and its Phylogenetic Position within the Class Chromadorea. Scientific Reports, 2015, 5, 12691.	1.6	22
1530	Genome analysis of Daldinia eschscholtzii strains UM 1400 and UM 1020, wood-decaying fungi isolated from human hosts. BMC Genomics, 2015, 16, 966.	1.2	16
1531	Transition from two to one integument in Prunus species: expression pattern of <scp>INNER NO OUTER</scp> (<scp>INO</scp>), <scp>ABERRANT TESTA SHAPE</scp> (<scp>ATS</scp>) and <scp>ETTIN</scp> (<scp>ETT</scp>). New Phytologist, 2015, 208, 584-595.	3.5	26
1532	Saprophytic and pathogenic fungi in the Ceratocystidaceae differ in their ability to metabolize plant-derived sucrose. BMC Evolutionary Biology, 2015, 15, 273.	3.2	47
1533	Gonadal transcriptomics elucidate patterns of adaptive evolution within marine rockfishes (Sebastes). BMC Genomics, 2015, 16, 656.	1.2	8
1534	The Perchlorate Reduction Genomic Island: Mechanisms and Pathways of Evolution by Horizontal Gene Transfer. BMC Genomics, 2015, 16, 862.	1.2	39
1535	In silico hybridization enables transcriptomic illumination of the nature and evolution of Myxozoa. BMC Genomics, 2015, 16, 840.	1.2	22
1536	Prevalence of classic, MLB-clade and VA-clade Astroviruses in Kenya and The Gambia. Virology Journal, 2015, 12, 78.	1.4	73
1537	Molecular characterization of a cathepsin F-like protease in Trichinella spiralis. Parasites and Vectors, 2015, 8, 652.	1.0	19

#	Article	IF	Citations
1538	Depthâ€related distribution of a key gene of the tetraether lipid biosynthetic pathway in marine <scp>T</scp>haumarchaeota. Environmental Microbiology, 2015, 17, 3527-3539.	1.8	44
1539	Construction of a robust and sensitive arginine biosensor through ancestral protein reconstruction. Protein Science, 2015, 24, 1412-1422.	3.1	60
1540	Molecular evolution and speciesâ€specific expansion of the NAP members in plants. Journal of Integrative Plant Biology, 2015, 57, 673-687.	4.1	17
1541	Biochemical and biophysical characterisation of haloalkane dehalogenases <scp>DmrA</scp> and <scp>DmrB</scp> in <scp>M</scp>ycobacterium strain <scp>JS</scp>60 and their role in growth on haloalkanes. Molecular Microbiology, 2015, 97, 439-453.	1.2	19
1542	Evolutionary History of Cathepsin L (L-like) Family Genes in Vertebrates. International Journal of Biological Sciences, 2015, 11, 1016-1025.	2.6	27
1543	Genetic and Phylogenetic Characterization of Tataguine and Witwatersrand Viruses and Other Orthobunyaviruses of the Anopheles A, Capim, GuamÃ¡, Koongol, Mapputta, Tete, and Turlock Serogroups. Viruses, 2015, 7, 5987-6008.	1.5	36
1544	Molecular phylogeny and a taxonomic proposal for the genus Streptococcus. Genetics and Molecular Research, 2015, 14, 10905-10918.	0.3	33
1545	Genomic Mining Reveals Deep Evolutionary Relationships between Bornaviruses and Bats. Viruses, 2015, 7, 5792-5800.	1.5	10
1546	Biochemical and Structural Characterization of Enolase from Chloroflexus aurantiacus: Evidence for a Thermophilic Origin. Frontiers in Bioengineering and Biotechnology, 2015, 3, 74.	2.0	9
1547	A Guide to Phylogenetic Reconstruction Using Heterogeneous Modelsâ€"A Case Study from the Root of the Placental Mammal Tree. Computation, 2015, 3, 177-196.	1.0	17
1548	Evolution of two receptors detecting the same pheromone compound in crop pest moths of the genus Spodoptera. Frontiers in Ecology and Evolution, 2015, 3, .	1.1	35
1549	Trends in substitution models of molecular evolution. Frontiers in Genetics, 2015, 6, 319.	1.1	115
1550	The Evolution of the Scavenger Receptor Cysteine-Rich Domain of the Class A Scavenger Receptors. Frontiers in Immunology, 2015, 6, 342.	2.2	31
1551	Genomic comparison of closely related Giant Viruses supports an accordion-like model of evolution. Frontiers in Microbiology, 2015, 6, 593.	1.5	41
1552	Novel circular single-stranded DNA viruses identified in marine invertebrates reveal high sequence diversity and consistent predicted intrinsic disorder patterns within putative structural proteins. Frontiers in Microbiology, 2015, 6, 696.	1.5	69
1553	Comparative Genomic and Phylogenetic Analyses of Gammaproteobacterial glg Genes Traced the Origin of the Escherichia coli Glycogen glgBXCAP Operon to the Last Common Ancestor of the Sister Orders Enterobacteriales and Pasteurellales. PLoS ONE, 2015, 10, e0115516.	1.1	23
1554	Identification, Evolution and Expression of an Insulin-Like Peptide in the Cephalochordate Branchiostoma lanceolatum. PLoS ONE, 2015, 10, e0119461.	1.1	20
1555	Duplicated Leptin Receptors in Two Species of Eel Bring New Insights into the Evolution of the Leptin System in Vertebrates. PLoS ONE, 2015, 10, e0126008.	1.1	31

#	Article	IF	Citations
1556	Genome Sequence and Transcriptome Analyses of Chrysochromulina tobin: Metabolic Tools for Enhanced Algal Fitness in the Prominent Order Prymnesiales (Haptophyceae). PLoS Genetics, 2015, 11, e1005469.	1.5	58
1557	Phylogeny of Echinoderm Hemoglobins. PLoS ONE, 2015, 10, e0129668.	1.1	9
1558	Unravelling the Evolution of the Allatostatin-Type A, KISS and Galanin Peptide-Receptor Gene Families in Bilaterians: Insights from Anopheles Mosquitoes. PLoS ONE, 2015, 10, e0130347.	1.1	29
1559	"PP2C7s", Genes Most Highly Elaborated in Photosynthetic Organisms, Reveal the Bacterial Origin and Stepwise Evolution of PPM/PP2C Protein Phosphatases. PLoS ONE, 2015, 10, e0132863.	1.1	13
1560	Comprehensive Evolutionary and Expression Analysis of FCS-Like Zinc finger Gene Family Yields Insights into Their Origin, Expansion and Divergence. PLoS ONE, 2015, 10, e0134328.	1.1	22
1561	Transcriptome Analysis of the Emerald Ash Borer (EAB), Agrilus planipennis: De Novo Assembly, Functional Annotation and Comparative Analysis. PLoS ONE, 2015, 10, e0134824.	1.1	9
1562	Ancient Origin of the U2 Small Nuclear RNA Gene-Targeting Non-LTR Retrotransposons Utopia. PLoS ONE, 2015, 10, e0140084.	1.1	8
1563	Transcriptome Analysis Revealed Highly Expressed Genes Encoding Secondary Metabolite Pathways and Small Cysteine-Rich Proteins in the Sclerotium of Lignosus rhinocerotis. PLoS ONE, 2015, 10, e0143549.	1.1	17
1564	Two Cdc2 Kinase Genes with Distinct Functions in Vegetative and Infectious Hyphae in Fusarium graminearum. PLoS Pathogens, 2015, 11, e1004913.	2.1	42
1565	Structure, expression profile and phylogenetic inference of chalcone isomerase-like genes from the narrow-leafed lupin (Lupinus angustifolius L.) genome. Frontiers in Plant Science, 2015, 6, 268.	1.7	32
1566	Conservation of the abscission signaling peptide IDA during Angiosperm evolution: withstanding genome duplications and gain and loss of the receptors HAE/HSL2. Frontiers in Plant Science, 2015, 6, 931.	1.7	50
1568	Molecular cloning of RBCS genes in Selaginella and the evolution of the rbcS gene family. Archives of Biological Sciences, 2015, 67, 373-383.	0.2	1
1569	Species-Specific Transmission of Novel Picornaviruses in Lemurs. Journal of Virology, 2015, 89, 4002-4010.	1.5	9
1570	Molecular characterization of a bipartite double-stranded RNA virus and its satellite-like RNA co-infecting the phytopathogenic fungus Sclerotinia sclerotiorum. Frontiers in Microbiology, 2015, 6, 406.	1.5	70
1571	Identification of Xenologs and Their Characteristic Low Expression Levels in the Cyanobacterium Synechococcus elongatus. Journal of Molecular Evolution, 2015, 80, 292-304.	0.8	2
1572	Functional Pairing of Class B1 Ligand-GPCR in Cephalochordate Provides Evidence of the Origin of PTH and PACAP/Glucagon Receptor Family. Molecular Biology and Evolution, 2015, 32, 2048-2059.	3.5	21
1573	Bioinformatics and Biomedical Engineering. Lecture Notes in Computer Science, 2015, , .	1.0	3
1574	A Proposal for the Evolution of Cathepsin and Silicatein in Sponges. Journal of Molecular Evolution, 2015, 80, 278-291.	0.8	19

#	Article	IF	Citations
1575	Identification and expression of an atypical isoform of metallothionein in the African clawed frog Xenopus laevis. Comptes Rendus - Biologies, 2015, 338, 314-320.	0.1	3
1576	Coalescence vs. concatenation: Sophisticated analyses vs. first principles applied to rooting the angiosperms. Molecular Phylogenetics and Evolution, 2015, 91, 98-122.	1.2	77
1577	Transcriptomic characterization of the enzymatic antioxidants FeSOD, MnSOD, APX and KatG in the dinoflagellate genus Symbiodinium. BMC Evolutionary Biology, 2015, 15, 48.	3.2	50
1578	Mesodermal gene expression during the embryonic and larval development of the articulate brachiopod Terebratalia transversa. EvoDevo, 2015, 6, 10.	1.3	33
1579	Basal Gnathostomes Provide Unique Insights into the Evolution of Vitamin B12 Binders. Genome Biology and Evolution, 2015, 7, 457-464.	1.1	6
1580	Innexin7a forms junctions that stabilize the basal membrane during cellularization of the blastoderm in Tribolium castaneum. Development (Cambridge), 2015, 142, 2173-2183.	1.2	20
1581	Genes encoding defensins ofÂimportant Chagas disease vectors used for phylogenetic studies. Parasitology Research, 2015, 114, 4503-4511.	0.6	11
1582	Alternative splicing and co-option of transposable elements: the case of TMPO/LAP2Î± and ZNF451 in mammals. Bioinformatics, 2015, 31, 2257-2261.	1.8	33
1583	A New Class of SINEs with snRNA Gene-Derived Heads. Genome Biology and Evolution, 2015, 7, 1702-1712.	1.1	24
1584	The Full Globin Repertoire of Turtles Provides Insights into Vertebrate Globin Evolution and Functions. Genome Biology and Evolution, 2015, 7, 1896-1913.	1.1	17
1585	Assessing the prediction fidelity of ancestral reconstruction by a library approach. Protein Engineering, Design and Selection, 2015, 28, 507-518.	1.0	35
1586	The Intracellular Scots Pine Shoot Symbiont Methylobacterium extorquens DSM13060 Aggregates around the Host Nucleus and Encodes Eukaryote-Like Proteins. MBio, 2015, 6, .	1.8	44
1587	Tex19 and Sectm1 concordant molecular phylogenies support co-evolution of both eutherian-specific genes. BMC Evolutionary Biology, 2015, 15, 222.	3.2	2
1588	The transcriptome recipe for the venom cocktail of Tityus bahiensis scorpion. Toxicon, 2015, 95, 52-61.	0.8	61
1589	The mitochondrial genome of Dastarcus helophoroides (Coleoptera: Bothrideridae) and related phylogenetic analyses. Gene, 2015, 560, 15-24.	1.0	32
1590	Internal transcribed spacer (ITS) evolution in populations of the hyperparasitic European mistletoe pathogen fungus, Sphaeropsis visci (Botryosphaeriaceae): The utility of ITS2 secondary structures. Gene, 2015, 558, 54-64.	1.0	12
1591	<scp>L</scp>isteria monocytogenes exopolysaccharide: origin, structure, biosynthetic machinery and câ€diâ€<scp>GMP</scp>â€dependent regulation. Molecular Microbiology, 2015, 96, 728-743.	1.2	80
1592	Molecular characterization and transcriptional regulation of the reninâ€“angiotensin system genes in Senegalese sole (Solea senegalensis Kaup, 1858): Differential gene regulation by salinity. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2015, 184, 6-19.	0.8	10

#	Article	IF	Citations
1593	Genome characterization of a GII.6 norovirus strain identified in China. Infection, Genetics and Evolution, 2015, 31, 110-117.	1.0	20
1594	De Novo Characterisation of the Greenlip Abalone Transcriptome (Haliotis laevigata) with a Focus on the Heat Shock Protein 70 (HSP70) Family. Marine Biotechnology, 2015, 17, 23-32.	1.1	52
1595	Draft genome sequence of adzuki bean, Vigna angularis. Scientific Reports, 2015, 5, 8069.	1.6	144
1596	Mitochondrial genome plasticity among species of the nematode genus Meloidogyne (Nematoda:) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	18
1597	The MYB182 Protein Down-Regulates Proanthocyanidin and Anthocyanin Biosynthesis in Poplar by Repressing Both Structural and Regulatory Flavonoid Genes Â. Plant Physiology, 2015, 167, 693-710.	2.3	177
1598	Detection and Analysis of Non-retroviral RNA Virus-Like Elements in Plant, Fungal, and Insect Genomes. Methods in Molecular Biology, 2015, 1236, 73-88.	0.4	25
1599	Digestive peptidase evolution in holometabolous insects led to a divergent group of enzymes in Lepidoptera. Insect Biochemistry and Molecular Biology, 2015, 58, 1-11.	1.2	18
1600	Evolutionary relatedness does not predict competition and co-occurrence in natural or experimental communities of green algae. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20141745.	1.2	26
1601	A mitovirus related to plant mitochondrial gene confers hypovirulence on the phytopathogenic fungus Sclerotinia sclerotiorum. Virus Research, 2015, 197, 127-136.	1.1	83
1602	Functional characterization of hesp018, a baculovirus-encoded serpin gene. Journal of General Virology, 2015, 96, 1150-1160.	1.3	17
1603	Evolution of the Insect Desaturase Gene Family with an Emphasis on Social Hymenoptera. Molecular Biology and Evolution, 2015, 32, 456-471.	3.5	60
1604	The Same or Not the Same: Lineage-Specific Gene Expansions and Homology Relationships in Multigene Families in Nematodes. Journal of Molecular Evolution, 2015, 80, 18-36.	0.8	23
1605	HedgehogExpression During Development and Regeneration in the Hemichordate,Ptychodera flava. Zoological Science, 2015, 32, 33-37.	0.3	13
1606	Genome-wide identification and analysis of basic helix-loop-helix domains in dog, Canis lupus familiaris. Molecular Genetics and Genomics, 2015, 290, 633-648.	1.0	6
1607	High Gene Family Turnover Rates and Gene Space Adaptation in the Compact Genome of the Carnivorous Plant Utricularia gibba. Molecular Biology and Evolution, 2015, 32, 1284-1295.	3.5	53
1608	Ancient dynamin segments capture early stages of hostâ€“mitochondrial integration. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2800-2805.	3.3	41
1609	Domain repeats related to innate immunity in the South African abalone, Haliotis midae. Marine Genomics, 2015, 23, 41-43.	0.4	2
1610	Transcript levels of the soluble sperm factor protein phospholipase C zeta 1 (PLCÎ¶1) increase through induced spermatogenesis in European eel. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2015, 187, 168-176.	0.8	2

#	Article	IF	Citations
1611	Clustering of Two Genes Putatively Involved in Cyanate Detoxification Evolved Recently and Independently in Multiple Fungal Lineages. Genome Biology and Evolution, 2015, 7, 789-800.	1.1	32
1612	Evolution of alternative biosynthetic pathways for vitamin C following plastid acquisition in photosynthetic eukaryotes. ELife, 2015, 4, .	2.8	140
1613	Thermosensation and the TRPV channel in Rhodnius prolixus. Journal of Insect Physiology, 2015, 81, 145-156.	0.9	29
1614	Endogenization of mouse mammary tumor virus (MMTV)-like elements in genomes of pikas (Ochotona) Tj ETQq1 1 0.784314 rgBT /Ov	1.1	8
1615	Functional Operons in Secondary Metabolic Gene Clusters in Glarea lozoyensis (Fungi,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	1.8	15
1616	PACAP system evolution and its role in melanophore function in teleost fish skin. Molecular and Cellular Endocrinology, 2015, 411, 130-145.	1.6	13
1617	Antagonistic Roles for KNOX1 and KNOX2 Genes in Patterning the Land Plant Body Plan Following an Ancient Gene Duplication. PLoS Genetics, 2015, 11, e1004980.	1.5	137
1618	Early origin and adaptive evolution of the GW182 protein family, the key component of RNA silencing in animals. RNA Biology, 2015, 12, 761-770.	1.5	23
1619	The complete mitochondrial genome sequence of Southwellina hispida supports monophyly of Palaeacanthocephala (Acanthocephala: Polymorphida). Parasitology International, 2015, 64, 64-68.	0.6	17
1620	Alfalfa Leaf Curl Virus: an Aphid-Transmitted Geminivirus. Journal of Virology, 2015, 89, 9683-9688.	1.5	62
1621	Molecular Diversity and Gene Evolution of the Venom Arsenal of Terebridae Predatory Marine Snails. Genome Biology and Evolution, 2015, 7, 1761-1778.	1.1	36
1622	Overview of the Knottin scorpion toxin-like peptides in scorpion venoms: Insights on their classification and evolution. Toxicon, 2015, 107, 317-326.	0.8	41
1623	Coinfection with a novel fibropapilloma-associated herpesvirus and a novel Spirorchis sp. in an eastern box turtle (Terrapene carolina) in Florida. Journal of Veterinary Diagnostic Investigation, 2015, 27, 408-413.	0.5	31
1624	What RNA World? Why a Peptide/RNA Partnership Merits Renewed Experimental Attention. Life, 2015, 5, 294-320.	1.1	73
1625	Unusual biology across a group comprising more than 15% of domain Bacteria. Nature, 2015, 523, 208-211.	13.7	1,050
1626	Genetic Characterization of the Tick-Borne Orbiviruses. Viruses, 2015, 7, 2185-2209.	1.5	36
1627	Gene duplication, loss and selection in the evolution of saxitoxin biosynthesis in alveolates. Molecular Phylogenetics and Evolution, 2015, 92, 165-180.	1.2	48
1628	NLRC5 Exclusively Transactivates MHC Class I and Related Genes through a Distinctive SXY Module. PLoS Genetics, 2015, 11, e1005088.	1.5	81

#	Article	IF	Citations
1629	PROTEIN TARGETING TO STARCH Is Required for Localising GRANULE-BOUND STARCH SYNTHASE to Starch Granules and for Normal Amylose Synthesis in Arabidopsis. PLoS Biology, 2015, 13, e1002080.	2.6	139
1630	Genes encoding conserved hypothetical proteins localized in the conjugative transfer region of plasmid pRet42a from Rhizobium etli CFN42 participate in modulating transfer and affect conjugation from different donors. Frontiers in Microbiology, 2014, 5, 793.	1.5	19
1631	A specific indel marker for the Philippines Schistosoma japonicum revealed by analysis of mitochondrial genome sequences. Parasitology Research, 2015, 114, 2697-2704.	0.6	3
1632	Explosive Tandem and Segmental Duplications of Multigenic Families in Eucalyptus grandis. Genome Biology and Evolution, 2015, 7, 1068-1081.	1.1	42
1633	Novel CK2Î± and CK2Î² subunits in maize reveal functional diversification in subcellular localization and interaction capacity. Plant Science, 2015, 235, 58-69.	1.7	5
1634	The study of fkbp and ubiquitin reveals interesting aspects of Artemia stress history. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2015, 186, 8-19.	0.7	5
1635	RNase E in the Î³-Proteobacteria: conservation of intrinsically disordered noncatalytic region and molecular evolution of microdomains. Molecular Genetics and Genomics, 2015, 290, 847-862.	1.0	43
1636	Distinct expression patterns and functions of the pygopus genes in amphioxus and zebrafish early embryogenesis. Genes and Genomics, 2015, 37, 375-386.	0.5	1
1637	Extensive horizontal gene transfer, duplication, and loss of chlorophyll synthesis genes in the algae. BMC Evolutionary Biology, 2015, 15, 16.	3.2	52
1638	High pheromone diversity in the male cheek gland of the red-spotted newt Notophthalmus viridescens (Salamandridae). BMC Evolutionary Biology, 2015, 15, 54.	3.2	12
1639	The genome sequence of Pseudoplusia includens single nucleopolyhedrovirus and an analysis of p26 gene evolution in the baculoviruses. BMC Genomics, 2015, 16, 127.	1.2	22
1640	Molecular evolution and diversification of the Argonaute family of proteins in plants. BMC Plant Biology, 2015, 15, 23.	1.6	49
1641	Identification and characterization of diverse groups of endogenous retroviruses in felids. Retrovirology, 2015, 12, 26.	0.9	6
1642	The complete mitochondrial genome of the gullet worm Gongylonema pulchrum: gene content, arrangement, composition and phylogenetic implications. Parasites and Vectors, 2015, 8, 100.	1.0	20
1643	Molecular detection and phylogenetic analysis of bovine astrovirus in Brazil. Archives of Virology, 2015, 160, 1519-1525.	0.9	16
1644	Mitochondrial genomes advance phylogenetic hypotheses for Tylenchina (Nematoda: Chromadorea). Zoologica Scripta, 2015, 44, 446-462.	0.7	20
1645	Analysis of phylogenetic and functional diverge in plant nine-cis epoxycarotenoid dioxygenase gene family. Journal of Plant Research, 2015, 128, 519-534.	1.2	47
1646	An ancestral role in peroxisome assembly is retained by the divisional peroxin Pex11 in the yeast Yarrowia lipolytica. Journal of Cell Science, 2015, 128, 1327-1340.	1.2	16

#	Article	IF	Citations
1647	Transmission and Microevolution of USA300 MRSA in U.S. Households: Evidence from Whole-Genome Sequencing. MBio, 2015, 6, e00054.	1.8	97
1648	Massive expansion and functional divergence of innate immune genes in a protostome. Scientific Reports, 2015, 5, 8693.	1.6	226
1649	Transgenic switchgrass (Panicum virgatum L.) biomass is increased by overexpression of switchgrass sucrose synthase (PvSUS1). Biotechnology Journal, 2015, 10, 552-563.	1.8	45
1650	Identification and expression analysis of a Spsb gene in planarian Dugesia japonica. Gene, 2015, 564, 168-175.	1.0	6
1651	Mitogenomics reveals phylogeny and repeated motifs in control regions of the deep-sea family Siboglinidae (Annelida). Molecular Phylogenetics and Evolution, 2015, 85, 221-229.	1.2	62
1652	Metatranscriptomic Analysis of Diminutive Thiomargarita-Like Bacteria (â€œCandidatus Thiopilulaâ€•spp.) from Abyssal Cold Seeps of the Barbados Accretionary Prism. Applied and Environmental Microbiology, 2015, 81, 3142-3156.	1.4	20
1653	Evolution of Molybdenum Nitrogenase during the Transition from Anaerobic to Aerobic Metabolism. Journal of Bacteriology, 2015, 197, 1690-1699.	1.0	97
1654	Transcripts involved in hemostasis: Exploring salivary complexes from Haementeria vizottoi leeches through transcriptomics, phylogenetic studies and structural features. Toxicon, 2015, 106, 20-29.	0.8	12
1655	Comparative transcriptome resources of eleven Primulina species, a group of â€˜stone plantsâ€™ from a biodiversity hot spot. Molecular Ecology Resources, 2015, 15, 619-632.	2.2	45
1656	Time dependency of foamy virus evolutionary rate estimates. BMC Evolutionary Biology, 2015, 15, 119.	3.2	28
1657	Insights into the evolution of enzyme substrate promiscuity after the discovery of (Î²Î±)8 isomerase evolutionary intermediates from a diverse metagenome. BMC Evolutionary Biology, 2015, 15, 107.	3.2	16
1658	Characterization of a Novel Hepadnavirus in the White Sucker (Catostomus commersonii) from the Great Lakes Region of the United States. Journal of Virology, 2015, 89, 11801-11811.	1.5	39
1659	Provirophages in the Bigelowiella genome bear testimony to past encounters with giant viruses. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5318-26.	3.3	89
1660	KLF/SP Transcription Factor Family Evolution: Expansion, Diversification, and Innovation in Eukaryotes. Genome Biology and Evolution, 2015, 7, 2289-2309.	1.1	93
1661	Expansion and Functional Divergence of Jumonji C-Containing Histone Demethylases: Significance of Duplications in Ancestral Angiosperms and Vertebrates. Plant Physiology, 2015, 168, 1321-1337.	2.3	67
1662	Independent Co-Option of a Tailed Bacteriophage into a Killing Complex in Pseudomonas. MBio, 2015, 6, e00452.	1.8	66
1663	Neutralization Properties of Simian Immunodeficiency Viruses Infecting Chimpanzees and Gorillas. MBio, 2015, 6, .	1.8	25
1664	Evolution of Proteasome Regulators in Eukaryotes. Genome Biology and Evolution, 2015, 7, 1363-1379.	1.1	77

#	Article	IF	Citations
1665	The Evolutionary Fate of Alternatively Spliced Homologous Exons after Gene Duplication. Genome Biology and Evolution, 2015, 7, 1392-1403.	1.1	31
1666	Early life dynamics of the human gut virome and bacterial microbiome in infants. Nature Medicine, 2015, 21, 1228-1234.	15.2	523
1667	Identification, characterization and quantitative analysis of NAD-malate dehydrogenase from the marine rhodophyte Pyropia haitanensis. Botanica Marina, 2015, 58, 285-293.	0.6	3
1668	The complete mitochondrial genome of Strongylus equinus (Chromadorea: Strongylidae): Comparison with other closely related species and phylogenetic analyses. Experimental Parasitology, 2015, 159, 94-99.	0.5	16
1669	A deep phylogeny of viral and cellular right-hand polymerases. Infection, Genetics and Evolution, 2015, 36, 275-286.	1.0	10
1670	Plastid establishment did not require a chlamydial partner. Nature Communications, 2015, 6, 6421.	5.8	51
1671	Prevalence and complete genome characterization of turkey picobirnaviruses. Infection, Genetics and Evolution, 2015, 30, 134-139.	1.0	25
1672	Evolutionary origin of a streamlined marine bacterioplankton lineage. ISME Journal, 2015, 9, 1423-1433.	4.4	32
1673	A new and critically endangered species and genus of Onychophora (Peripatidae) from the Brazilian savannah â€“ a vulnerable biodiversity hotspot. Systematics and Biodiversity, 2015, 13, 211-233.	0.5	12
1674	Expression and evolution of hexamerins from the tobacco hornworm, Manduca sexta , and other Lepidoptera. Insect Biochemistry and Molecular Biology, 2015, 62, 226-234.	1.2	31
1675	Molecular and functional characterization of seven Na+/K+-ATPase Î² subunit paralogs in Senegalese sole (Solea senegalensis Kaup, 1858). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2015, 182, 14-26.	0.7	17
1676	Diagnosis and discovery of fungal viruses using deep sequencing of small RNAs. Journal of General Virology, 2015, 96, 714-725.	1.3	78
1677	The evolution of eukaryotic cells from the perspective of peroxisomes. BioEssays, 2015, 37, 195-203.	1.2	47
1678	Evidence of Novel Phylogenetic Lineages of Methanogenic Archaea from Hypersaline Microbial Mats. Microbial Ecology, 2015, 69, 106-117.	1.4	27
1679	Transferred interbacterial antagonism genes augment eukaryotic innate immune function. Nature, 2015, 518, 98-101.	13.7	82
1680	Identification of the MAT1 locus in Stagonosporopsis tanaceti, and exploring its potential for sexual reproduction in Australian pyrethrum fields. Fungal Biology, 2015, 119, 408-419.	1.1	18
1681	Embryonic development of the nervous system in the planarian Schmidtea polychroa. Developmental Biology, 2015, 397, 305-319.	0.9	24
1682	Highly Dynamic Genomic Loci Drive the Synthesis of Two Types of Capsular or Secreted Polysaccharides within the Mycoplasma mycoides Cluster. Applied and Environmental Microbiology, 2015, 81, 676-687.	1.4	29

#	Article	IF	Citations
1683	Heterobasidion wood decay fungi host diverse and globally distributed viruses related to Helicobasidium mompa partitivirus V70. Virus Research, 2015, 195, 119-123.	1.1	23
1684	Evolution of mitochondrial DNA and its relation to basal metabolic rate. Mitochondrial DNA, 2015, 26, 566-571.	0.6	6
1685	Nme family of proteinsâ€"clues from simple animals. Naunyn-Schmiedeberg's Archives of Pharmacology, 2015, 388, 133-142.	1.4	12
1686	Structural Molecular Components of Septate Junctions in Cnidarians Point to the Origin of Epithelial Junctions in Eukaryotes. Molecular Biology and Evolution, 2015, 32, 44-62.	3.5	69
1687	Molecular cloning and characterization of the CHS gene family in turmeric (Curcuma longa Linn.). Journal of Plant Biochemistry and Biotechnology, 2015, 24, 25-33.	0.9	9
1688	The Complete Mitochondrial Genome ofBrachmia macroscopa(Lepidoptera: Gelechiidae) and Its Related Phylogenetic Analysis. Journal of Insect Science, 2016, 16, 9.	0.6	8
1689	Betalains and expression of antioxidant enzymes during development andabiotic stress in Rivina humilis L. berries. Turkish Journal of Botany, 2016, 40, 28-36.	0.5	9
1690	Birth of Archaeal Cells: Molecular Phylogenetic Analyses of G1P Dehydrogenase, G3P Dehydrogenases, and Glycerol Kinase Suggest Derived Features of Archaeal Membranes Having G1P Polar Lipids. Archaea, 2016, 2016, 1-16.	2.3	13
1691	Molecular evolutionary analysis of the high-affinity K+ transporter gene family in angiosperms. Genetics and Molecular Research, 2016, 15, .	0.3	0
1692	Gene family expansions and contractions are associated with host range in plant pathogens of the genus Colletotrichum. BMC Genomics, 2016, 17, 555.	1.2	151
1693	An Insight into the Triabin Protein Family of American Hematophagous Reduviids: Functional, Structural and Phylogenetic Analysis. Toxins, 2016, 8, 44.	1.5	15
1694	Venom Gland Transcriptomic and Proteomic Analyses of the Enigmatic Scorpion Superstitionia donensis (Scorpiones: Superstitioniidae), with Insights on the Evolution of Its Venom Components. Toxins, 2016, 8, 367.	1.5	41
1695	Begomovirus-Associated Satellite DNA Diversity Captured Through Vector-Enabled Metagenomic (VEM) Surveys Using Whiteflies (Aleyrodidae). Viruses, 2016, 8, 36.	1.5	40
1696	The Microbial Opsin Homolog Sop1 is involved in Sclerotinia sclerotiorum Development and Environmental Stress Response. Frontiers in Microbiology, 2015, 6, 1504.	1.5	38
1697	Microevolution Analysis of Bacillus coahuilensis Unveils Differences in Phosphorus Acquisition Strategies and Their Regulation. Frontiers in Microbiology, 2016, 7, 58.	1.5	17
1698	The Role of Complement in Cnidarian-Dinoflagellate Symbiosis and Immune Challenge in the Sea Anemone Aiptasia pallida. Frontiers in Microbiology, 2016, 7, 519.	1.5	66
1699	Evolution of a Sigma Factor: An All-In-One of Gene Duplication, Horizontal Gene Transfer, Purifying Selection, and Promoter Differentiation. Frontiers in Microbiology, 2016, 7, 581.	1.5	13
1700	Single-Cell (Meta-)Genomics of a Dimorphic Candidatus Thiomargarita nelsonii Reveals Genomic Plasticity. Frontiers in Microbiology, 2016, 7, 603.	1.5	36

#	Article	IF	Citations
1701	Region 4 of Rhizobium etli Primary Sigma Factor (SigA) Confers Transcriptional Laxity in Escherichia coli. Frontiers in Microbiology, 2016, 7, 1078.	1.5	1
1702	Contribution of Multiple Inter-Kingdom Horizontal Gene Transfers to Evolution and Adaptation of Amphibian-Killing Chytrid, Batrachochytrium dendrobatidis. Frontiers in Microbiology, 2016, 7, 1360.	1.5	11
1703	Evolution and expression of the phosphodiesterase 6 genes unveils vertebrate novelty to control photosensitivity. BMC Evolutionary Biology, 2016, 16, 124.	3.2	46
1704	Arginine deiminase pathway enzymes: evolutionary history in metamonads and other eukaryotes. BMC Evolutionary Biology, 2016, 16, 197.	3.2	40
1705	PhyloBot: A Web Portal for Automated Phylogenetics, Ancestral Sequence Reconstruction, and Exploration of Mutational Trajectories. PLoS Computational Biology, 2016, 12, e1004976.	1.5	43
1706	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. PLoS Genetics, 2016, 12, e1005954.	1.5	105
1707	Comparative Genomics of the Sigatoka Disease Complex on Banana Suggests a Link between Parallel Evolutionary Changes in Pseudocercospora fijiensis and Pseudocercospora eumusae and Increased Virulence on the Banana Host. PLoS Genetics, 2016, 12, e1005904.	1.5	51
1708	Genome-Wide Comparative Analysis of Chemosensory Gene Families in Five Tsetse Fly Species. PLoS Neglected Tropical Diseases, 2016, 10, e0004421.	1.3	28
1709	Molecular Evolution and Characterization of Hemagglutinin (H) in Peste des Petits Ruminants Virus. PLoS ONE, 2016, 11, e0152587.	1.1	16
1710	Intron Derived Size Polymorphism in the Mitochondrial Genomes of Closely Related Chrysoporthe Species. PLoS ONE, 2016, 11, e0156104.	1.1	68
1711	Random Sampling of Squamate Reptiles in Spanish Natural Reserves Reveals the Presence of Novel Adenoviruses in Lacertids (Family Lacertidae) and Worm Lizards (Amphisbaenia). PLoS ONE, 2016, 11, e0159016.	1.1	11
1712	Carbonic Anhydrases in Cnidarians: Novel Perspectives from the Octocorallian Corallium rubrum. PLoS ONE, 2016, 11, e0160368.	1.1	27
1713	RAP2.4a Is Transported through the Phloem to Regulate Cold and Heat Tolerance in Papaya Tree (Carica) Tj ETQq0 0 0 rgBT /Overlock 10	1.1	27
1714	The Diversity of Yellow-Related Proteins in Sand Flies (Diptera: Psychodidae). PLoS ONE, 2016, 11, e0166191.	1.1	12
1715	TLR-2 Recognizes Propionibacterium acnes CAMP Factor 1 from Highly Inflammatory Strains. PLoS ONE, 2016, 11, e0167237.	1.1	51
1716	Small RNA-Based Antiviral Defense in the Phytopathogenic Fungus Colletotrichum higginsianum. PLoS Pathogens, 2016, 12, e1005640.	2.1	112
1717	Comparative genomic and transcriptomic analyses of the Fuzhuan brick tea-fermentation fungus Aspergillus cristatus. BMC Genomics, 2016, 17, 428.	1.2	55
1718	Evolution and Functional Insights of Different Ancestral Orthologous Clades of Chitin Synthase Genes in the Fungal Tree of Life. Frontiers in Plant Science, 2016, 7, 37.	1.7	15

#	Article	IF	Citations
1719	Evolution of Electrogenic Ammonium Transporters (AMTs). Frontiers in Plant Science, 2016, 7, 352.	1.7	57
1720	Assessment of Potential Risks of Dietary RNAi to a Soil Micro-arthropod, Sinella curviseta Brook (Collembola: Entomobryidae). Frontiers in Plant Science, 2016, 7, 1028.	1.7	37
1721	Genome-Wide Identification, Evolution, and Co-expression Network Analysis of Mitogen-Activated Protein Kinase Kinase Kinases in Brachypodium distachyon. Frontiers in Plant Science, 2016, 7, 1400.	1.7	25
1722	Phylogenetic characterisation of feline immunodeficiency virus in naturally infected cats in Croatia indicates additional heterogeneity of subtype B in Europe. Archives of Virology, 2016, 161, 2567-2573.	0.9	8
1723	Phylomitogenomic analyses strongly support the sister relationship of the <scp>C</scp>haetognatha and <scp>P</scp>rotostomia. Zoologica Scripta, 2016, 45, 187-199.	0.7	7
1724	Mitogenomic phylogeny of <scp>A</scp>canthocephala reveals novel <scp>C</scp>lass relationships. Zoologica Scripta, 2016, 45, 437-454.	0.7	29
1725	Complete sequence of a double-stranded RNA from the phytopathogenic fungus Erysiphe cichoracearum that might represent a novel endornavirus. Archives of Virology, 2016, 161, 2343-2346.	0.9	9
1726	Vermistella arctica n. sp. Nominates the Genus Vermistella as a Candidate for Taxon with Bipolar Distribution. Journal of Eukaryotic Microbiology, 2016, 63, 210-219.	0.8	4
1727	Structural distinctions of fast and slow bacterial luciferases revealed by phylogenetic analysis. Bioinformatics, 2016, 32, 3053-3057.	1.8	12
1728	De novo assembly and characterization of leaf and floral transcriptomes of the hybridizing bromeliad species (Pitcairnia spp.) adapted to Neotropical Inselbergs. Molecular Ecology Resources, 2016, 16, 1012-1022.	2.2	37
1729	Co-infection of a hypovirulent isolate of Sclerotinia sclerotiorum with a new botybirnavirus and a strain of a mitovirus. Virology Journal, 2016, 13, 92.	1.4	40
1730	Unique Loss of the PYHIN Gene Family in Bats Amongst Mammals: Implications for Inflammasome Sensing. Scientific Reports, 2016, 6, 21722.	1.6	113
1731	The All-Data-Based Evolutionary Hypothesis of Ciliated Protists with a Revised Classification of the Phylum Ciliophora (Eukaryota, Alveolata). Scientific Reports, 2016, 6, 24874.	1.6	271
1732	Evolutionary redesign of the Atlantic cod (Gadus morhua L.) Toll-like receptor repertoire by gene losses and expansions. Scientific Reports, 2016, 6, 25211.	1.6	89
1733	Insight into different environmental niches adaptation and allergenicity from the Cladosporium sphaerospermum genome, a common human allergy-eliciting Dothideomycetes. Scientific Reports, 2016, 6, 27008.	1.6	18
1734	The machinery underlying malaria parasite virulence is conserved between rodent and human malaria parasites. Nature Communications, 2016, 7, 11659.	5.8	61
1735	Identification of an orthologous clade of peroxidases that respond to feeding by greenbugs (Schizaphis graminum) in C4 grasses. Functional Plant Biology, 2016, 43, 1134.	1.1	12
1736	Late Mitochondrial Acquisition, Really?. Genome Biology and Evolution, 2016, 8, 2031-2035.	1.1	12

#	Article	IF	Citations
1737	Mitochondrial Phylogenomics yields Strongly Supported Hypotheses for Ascaridomorph Nematodes. Scientific Reports, 2016, 6, 39248.	1.6	26
1738	Expression and Localization of Carbonic Anhydrase Genes in the Serpulid Polychaete Hydroides elegans. Biological Bulletin, 2016, 231, 175-184.	0.7	5
1739	Genome Sequence of Hafnia alvei bta3_1, a Bacterium with Antimicrobial Properties Isolated from Honey Bee Gut. Genome Announcements, 2016, 4, .	0.8	17
1740	Efficient Detection of Repeating Sites to Accelerate Phylogenetic Likelihood Calculations. Systematic Biology, 2017, 66, syw075.	2.7	22
1741	Draft genome sequencing and secretome analysis of fungal phytopathogen Ascochyta rabiei provides insight into the necrotrophic effector repertoire. Scientific Reports, 2016, 6, 24638.	1.6	57
1742	Characterization of the complete mitochondrial genome of the cloacal tapeworm Cloacotaenia megalops (Cestoda: Hymenolepididae). Parasites and Vectors, 2016, 9, 490.	1.0	11
1743	Complex Ancestries of Isoprenoid Synthesis in Dinoflagellates. Journal of Eukaryotic Microbiology, 2016, 63, 123-137.	0.8	17
1744	Genetic Improvement of Industrially Important Fungal Strains. , 2016, , 61-72.		0
1745	Evolution of the SOUL Heme-Binding Protein Superfamily Across Eukarya. Journal of Molecular Evolution, 2016, 82, 279-290.	0.8	15
1746	Co-occurrence of analogous enzymes determines evolution of a novel (Î²Î±)8-isomerase sub-family after non-conserved mutations in flexible loop. Biochemical Journal, 2016, 473, 1141-1152.	1.7	6
1747	Ectomycorrhizal fungi decompose soil organic matter using oxidative mechanisms adapted from saprotrophic ancestors. New Phytologist, 2016, 209, 1705-1719.	3.5	264
1748	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. Virology, 2016, 493, 142-153.	1.1	40
1749	Two asian jumbo phages, Ï•RSL2 and Ï•RSF1, infect Ralstonia solanacearum and show common features of Ï•KZ-related phages. Virology, 2016, 494, 56-66.	1.1	56
1750	Multi-species protein similarity clustering reveals novel expanded immune gene families in the eastern oyster Crassostrea virginica. Fish and Shellfish Immunology, 2016, 53, 13-23.	1.6	45
1751	The complete mitochondrial genomes of four cockroaches (Insecta: Blattodea) and phylogenetic analyses within cockroaches. Gene, 2016, 586, 115-122.	1.0	50
1752	Sequencing and analysis of the complete organellar genomes of Parmales, a closely related group to Bacillariophyta (diatoms). Current Genetics, 2016, 62, 887-896.	0.8	31
1753	Molecular Evolution of Alternative Oxidase Proteins: A Phylogenetic and Structure Modeling Approach. Journal of Molecular Evolution, 2016, 82, 207-218.	0.8	27
1754	Evolution of IFN-Î» in tetrapod vertebrates and its functional characterization in green anole lizard (Anolis carolinensis). Developmental and Comparative Immunology, 2016, 61, 208-224.	1.0	32

#	Article	IF	Citations
1755	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. ISME Journal, 2016, 10, 2702-2714.	4.4	98
1756	The Entnerâ€“Doudoroff pathway is an overlooked glycolytic route in cyanobacteria and plants. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5441-5446.	3.3	160
1757	Molecular evolution analysis of WUSCHEL-related homeobox transcription factor family reveals functional divergence among clades in the homeobox region. Development Genes and Evolution, 2016, 226, 259-268.	0.4	10
1758	A Ralstonia solanacearum phage Ï•RP15 is closely related to Viunalikeviruses and encodes 19 tRNA-related sequences. Virology Reports, 2016, 6, 61-73.	0.4	6
1759	Characterization of Botrytis cinerea negative-stranded RNA virus 1, a new mycovirus related to plant viruses, and a reconstruction of host pattern evolution in negative-sense ssRNA viruses. Virology, 2016, 499, 212-218.	1.1	72
1760	An optimised phylogenetic method sheds more light on the main branching events of rhodopsin-like superfamily. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 20, 85-94.	0.4	17
1761	Astaxanthin biosynthetic pathway: Molecular phylogenies and evolutionary behaviour of Crt genes in eubacteria. Plant Gene, 2016, 8, 32-41.	1.4	4
1762	Identification of three somatostatin genes in lampreys. General and Comparative Endocrinology, 2016, 237, 89-97.	0.8	13
1763	Lytic bacteriophage PM16 specific for Proteus mirabilis: a novel member of the genus Phikmvvirus. Archives of Virology, 2016, 161, 2457-2472.	0.9	20
1764	Complete mitochondrial genome of Rhynchocinetes durbanensis (Rhynchocinetidae:) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	4
1765	Evolution of bacterial recombinase A (recA) in eukaryotes explained by addition of genomic data of key microbial lineages. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161453.	1.2	10
1766	Molecular Diversity of Terpene Synthases in the Liverwort Marchantia polymorpha. Plant Cell, 2016, 28, tpc.00062.2016.	3.1	48
1767	Cytochrome P450 complement (CYPome) of Candida oregonensis, a gut-associated yeast of bark beetle, Dendroctonus rhizophagus. Fungal Biology, 2016, 120, 1077-1089.	1.1	23
1768	Co-evolution of SNF spliceosomal proteins with their RNA targets in trans-splicing nematodes. Genetica, 2016, 144, 487-496.	0.5	1
1769	Spatiotemporal Expression Patterns and Antibody Reactivity of Taeniidae Endophilin B1. Journal of Clinical Microbiology, 2016, 54, 2553-2562.	1.8	9
1770	Diversity of cytosolic HSP70 Heat Shock Protein from decapods and their phylogenetic placement within Arthropoda. Gene, 2016, 591, 97-107.	1.0	15
1771	Complete mitochondrial genomes are not necessarily more informative than individual mitochondrial genes to recover a well-established annelid phylogeny. Gene Reports, 2016, 5, 10-17.	0.4	14
1772	Unusual Diversity of Myoglobin Genes in the Lungfish. Molecular Biology and Evolution, 2016, 33, 3033-3041.	3.5	22

#	Article	IF	Citations
1773	Molecular Evolution and Functional Characterization of a Bifunctional Decarboxylase Involved in Lycopodium Alkaloid Biosynthesis. Plant Physiology, 2016, 171, 2432-2444.	2.3	50
1774	Evolutionary conservation of candidate osmoregulation genes in plant phloem sapâ€feeding insects. Insect Molecular Biology, 2016, 25, 251-258.	1.0	20
1775	Molecular characterization of lipoamide dehydrogenase gene in Trypanosoma cruzi populations susceptible and resistant to benznidazole. Experimental Parasitology, 2016, 170, 1-9.	0.5	11
1776	Complete mitochondrial genomes of four entomopathogenic nematode species of the genus Steinernema. Parasites and Vectors, 2016, 9, 430.	1.0	8
1777	Ontogenetic onset of immune-relevant genes in the common sole (Solea solea). Fish and Shellfish Immunology, 2016, 57, 278-292.	1.6	24
1778	LRR-RLK family from two Citrus species: genome-wide identification and evolutionary aspects. BMC Genomics, 2016, 17, 623.	1.2	35
1779	FLDS: A Comprehensive dsRNA Sequencing Method for Intracellular RNA Virus Surveillance. Microbes and Environments, 2016, 31, 33-40.	0.7	84
1780	Disruption of Macrodomain Protein SCO6735 Increases Antibiotic Production in Streptomyces coelicolor. Journal of Biological Chemistry, 2016, 291, 23175-23187.	1.6	16
1781	Combined Transcriptomic and Proteomic Analysis of the Posterior Salivary Gland from the Southern Blue-Ringed Octopus and the Southern Sand Octopus. Journal of Proteome Research, 2016, 15, 3284-3297.	1.8	22
1782	Genome-wide analysis suggests divergent evolution of lipid phosphotases/phosphotransferase genes in plants. Genome, 2016, 59, 589-601.	0.9	4
1783	Concurrence of Iridovirus, Polyomavirus, and a Unique Member of a New Group of Fish Papillomaviruses in Lymphocystis Disease-Affected Gilthead Sea Bream. Journal of Virology, 2016, 90, 8768-8779.	1.5	79
1784	Molecular characterization and expression analyses of three RIG-I-like receptor signaling pathway genes (MDA5, LGP2 and MAVS) in Larimichthys crocea. Fish and Shellfish Immunology, 2016, 55, 535-549.	1.6	28
1785	Revisiting the phosphatidylethanolamineâ€binding protein (<scp>PEBP)</scp> gene family reveals cryptic FLOWERING LOCUS T gene homologs in gymnosperms and sheds new light on functional evolution. New Phytologist, 2016, 212, 730-744.	3.5	77
1787	The Identification of the Closest Living Relative(s) of Tetrapods: Phylogenomic Lessons for Resolving Short Ancient Internodes. Systematic Biology, 2016, 65, 1057-1075.	2.7	45
1788	Eukaryotic association module in phage WO genomes from Wolbachia. Nature Communications, 2016, 7, 13155.	5.8	133
1789	Evolutionary and Expression Analysis Provides Evidence for the Plant Glutamate-like Receptors Family is Involved in Woody Growth-related Function. Scientific Reports, 2016, 6, 32013.	1.6	16
1790	Biochemical characterization of predicted Precambrian RuBisCO. Nature Communications, 2016, 7, 10382.	5.8	112
1791	The complete mitogenome of a jumping spider Carrhotus xanthogramma (Araneae: Salticidae) and comparative analysis in four salticid mitogenomes. Genetica, 2016, 144, 699-709.	0.5	10

#	Article	IF	Citations
1792	The first complete mitochondrial genome for the subfamily Limacodidae and implications for the higher phylogeny of Lepidoptera. Scientific Reports, 2016, 6, 35878.	1.6	35
1793	The Salivary Protein Repertoire of the Polyphagous Spider Mite Tetranychus urticae: A Quest for Effectors. Molecular and Cellular Proteomics, 2016, 15, 3594-3613.	2.5	113
1794	Co-dependence between trypanosome nuclear lamina components in nuclear stability and control of gene expression. Nucleic Acids Research, 2016, 44, 10554-10570.	6.5	23
1795	Glycoside hydrolases family 20 (GH20) represent putative virulence factors that are shared by animal pathogenic oomycetes, but are absent in phytopathogens. BMC Microbiology, 2016, 16, 232.	1.3	12
1796	Discovery of parvovirus-related sequences in an unexpected broad range of animals. Scientific Reports, 2016, 6, 30880.	1.6	61
1797	Robustness of Reconstructed Ancestral Protein Functions to Statistical Uncertainty. Molecular Biology and Evolution, 2017, 34, msw223.	3.5	80
1798	Studying Evolutionary Dynamics of Gene Families Encoding SUMO-Activating Enzymes with SeaView and ProtTest. Methods in Molecular Biology, 2016, 1450, 273-284.	0.4	3
1799	Courtship Pheromone Use in a Model Urodele, the Mexican Axolotl (Ambystoma mexicanum). Scientific Reports, 2016, 6, 20184.	1.6	16
1800	Beyond sodefrin: evidence for a multi-component pheromone system in the model newt Cynops pyrrhogaster (Salamandridae). Scientific Reports, 2016, 6, 21880.	1.6	14
1801	Structural differences and differential expression among rhabdomeric opsins reveal functional change after gene duplication in the bay scallop, Argopecten irradians (Pectinidae). BMC Evolutionary Biology, 2016, 16, 250.	3.2	10
1802	Monoplacophoran mitochondrial genomes: convergent gene arrangements and little phylogenetic signal. BMC Evolutionary Biology, 2016, 16, 274.	3.2	10
1803	Evidence of functional divergence in MSP7 paralogous proteins: a molecular-evolutionary and phylogenetic analysis. BMC Evolutionary Biology, 2016, 16, 256.	3.2	17
1804	Retracing the path of planar cell polarity. BMC Evolutionary Biology, 2016, 16, 69.	3.2	24
1805	Functional test of PCDHB11, the most human-specific neuronal surface protein. BMC Evolutionary Biology, 2016, 16, 75.	3.2	1
1806	Comparative genome-wide analysis and evolutionary history of haemoglobin-processing and haem detoxification enzymes in malarial parasites. Malaria Journal, 2016, 15, 51.	0.8	11
1807	An evolutionary perspective of AMPKâ€“TOR signaling in the three domains of life. Journal of Experimental Botany, 2016, 67, 3897-3907.	2.4	72
1808	Functional conservation of the apoptotic machinery from coral to man: the diverse and complex Bcl-2 and caspase repertoires of Acropora millepora. BMC Genomics, 2016, 17, 62.	1.2	45
1809	Characteristics and expression patterns of histone-modifying enzyme systems in the migratory locust. Insect Biochemistry and Molecular Biology, 2016, 76, 18-28.	1.2	15

#	Article	IF	Citations
1810	Characterization of Function of the GlgA2 Glycogen/Starch Synthase in Cyanobacterium sp. Clg1 Highlights Convergent Evolution of Glycogen Metabolism into Starch Granule Aggregation. Plant Physiology, 2016, 171, 1879-1892.	2.3	15
1811	Modulation of NADPH-oxidase gene expression in rolB- transformed calli of Arabidopsis thaliana and Rubia cordifolia. Plant Physiology and Biochemistry, 2016, 105, 282-289.	2.8	10
1812	Corticotropin-releasing hormone family evolution: five ancestral genes remain in some lineages. Journal of Molecular Endocrinology, 2016, 57, 73-86.	1.1	52
1813	Comparative analysis of expression profiling of the trypsin and chymotrypsin genes from Lepidoptera species with different levels of sensitivity to soybean peptidase inhibitors. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2016, 196-197, 67-73.	0.7	18
1814	Reconstruction of ancestral chromosome architecture and gene repertoire reveals principles of genome evolution in a model yeast genus. Genome Research, 2016, 26, 918-932.	2.4	95
1815	Phylogenetic characterization of a novel herpesvirus found in the liver and lungs of a Chilean flamingo (Phoenicopterus chilensis). Journal of Veterinary Diagnostic Investigation, 2016, 28, 219-224.	0.5	3
1816	An effective approach for annotation of protein families with low sequence similarity and conserved motifs: identifying GDSL hydrolases across the plant kingdom. BMC Bioinformatics, 2016, 17, 91.	1.2	11
1817	The diversification of the basic leucine zipper family in eukaryotes correlates with the evolution of multicellularity. BMC Evolutionary Biology, 2016, 16, 28.	3.2	62
1818	A betabaculovirus encoding a gp64 homolog. BMC Genomics, 2016, 17, 94.	1.2	8
1819	Horizontal Gene Acquisitions, Mobile Element Proliferation, and Genome Decay in the Host-Restricted Plant PathogenErwinia Tracheiphila. Genome Biology and Evolution, 2016, 8, 649-664.	1.1	34
1820	Comparative Phylogenomics of Pathogenic and Nonpathogenic Species. G3: Genes, Genomes, Genetics, 2016, 6, 235-244.	0.8	38
1821	The transformer genes in the fig wasp <scp>C</scp>eratosolen solmsi provide new evidence for duplications independent of complementary sex determination. Insect Molecular Biology, 2016, 25, 191-201.	1.0	7
1822	Genome-Wide Survey of Gut Fungi (Harpellales) Reveals the First Horizontally Transferred Ubiquitin Gene from a Mosquito Host. Molecular Biology and Evolution, 2016, 33, 2544-2554.	3.5	28
1823	Patterns of expression of odorant receptor genes in a Chagas disease vector. Insect Biochemistry and Molecular Biology, 2016, 69, 71-81.	1.2	18
1824	Co-variation in methanotroph community composition and activity in three temperate grassland soils. Soil Biology and Biochemistry, 2016, 95, 78-86.	4.2	22
1825	A Novel Female-Specific and Sexual Reproduction-Associated Dmrt Gene Discovered in the Stony Coral, Euphyllia ancora1. Biology of Reproduction, 2016, 94, 40.	1.2	10
1826	The complete mitochondrial genome of Koerneria sudhausi (Diplogasteromorpha: Nematoda) supports monophyly of Diplogasteromorpha within Rhabditomorpha. Current Genetics, 2016, 62, 391-403.	0.8	8
1827	Identification and characterisation of hemocyanin of the fish louse Argulus (Crustacea: Branchiura). Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology, 2016, 186, 161-168.	0.7	10

#	Article	IF	Citations
1828	New poleroviruses associated with yellowing symptoms in different vegetable crops in Greece. Archives of Virology, 2016, 161, 431-436.	0.9	16
1829	Mycobacterial Pan-Genome Analysis Suggests Important Role of Plasmids in the Radiation of Type VII Secretion Systems. Genome Biology and Evolution, 2016, 8, 387-402.	1.1	81
1830	A multilocus assessment of nuclear and mitochondrial sequence data elucidates phylogenetic relationships among European spirlins (Alburnoides, Cyprinidae). Molecular Phylogenetics and Evolution, 2016, 94, 479-491.	1.2	34
1831	The complete mitochondrial genome of the dwarf tapeworm Hymenolepis nanaâ€"a neglected zoonotic helminth. Parasitology Research, 2016, 115, 1253-1262.	0.6	21
1832	New features of desiccation tolerance in the lichen photobiont Trebouxia gelatinosa are revealed by a transcriptomic approach. Plant Molecular Biology, 2016, 91, 319-339.	2.0	69
1833	The complete mitochondrial genome of Gasterophilus intestinalis, the first representative of the family Gasterophilidae. Parasitology Research, 2016, 115, 2573-2579.	0.6	10
1834	Phylogenetic characterization of Clonorchis sinensis proteins homologous to the sigma-class glutathione transferase and their differential expression profiles. Molecular and Biochemical Parasitology, 2016, 206, 46-55.	0.5	18
1835	Linear Plasmids and the Rate of Sequence Evolution in Plant Mitochondrial Genomes. Genome Biology and Evolution, 2016, 8, 364-374.	1.1	29
1836	Two Endopolygalacturonase Genes in Trichoderma virens: In Silico Characterization and Expression during Interaction with Plants. Journal of Phytopathology, 2016, 164, 18-28.	0.5	6
1837	Failed detection of Bovine viral diarrhea virus 2 subgenotype a (BVDV-2a) by direct fluorescent antibody test on tissue samples due to reduced reactivity of field isolates to raw anti-BVDV antibody. Journal of Veterinary Diagnostic Investigation, 2016, 28, 150-157.	0.5	7
1838	Ancestral Protein Reconstruction Yields Insights into Adaptive Evolution of Binding Specificity in Solute-Binding Proteins. Cell Chemical Biology, 2016, 23, 236-245.	2.5	84
1839	Cycloviruses, gemycircularviruses and other novel replication-associated protein encoding circular viruses in Pacific flying fox (Pteropus tonganus) faeces. Infection, Genetics and Evolution, 2016, 39, 279-292.	1.0	53
1840	Surgical management of an odontogenic tumor in a banded Gila monster (Heloderma suspectum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.0	8
1841	Structural and transcriptional characterization of a novel member of the soybean urease gene family. Plant Physiology and Biochemistry, 2016, 101, 96-104.	2.8	13
1842	The mitochondrial genome of Atrijuglans hetaohei Yang (Lepidoptera: Gelechioidea) and related phylogenetic analyses. Gene, 2016, 581, 66-74.	1.0	22
1843	An updated evolutionary study of Flaviviridae NS3 helicase and NS5 RNA-dependent RNA polymerase reveals novel invariable motifs as potential pharmacological targets. Molecular BioSystems, 2016, 12, 2080-2093.	2.9	34
1844	Rhizobial diversity, symbiotic effectiveness and structure of nodules of Vachellia macracantha. Soil Biology and Biochemistry, 2016, 96, 39-54.	4.2	22
1845	Selecting best-fit models for estimating the body mass from 3D data of the human calcaneus. Forensic Science International, 2016, 262, 37-45.	1.3	3

#	Article	IF	Citations
1846	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. Nature Communications, 2016, 7, 10476.	5.8	189
1847	The genomic basis of parasitism in the Strongyloides clade of nematodes. Nature Genetics, 2016, 48, 299-307.	9.4	226
1848	Allatostatin-type A, kisspeptin and galanin GPCRs and putative ligands as candidate regulatory factors of mantle function. Marine Genomics, 2016, 27, 25-35.	0.4	21
1849	Gene Family Expansions in Aphids Maintained by Endosymbiotic and Nonsymbiotic Traits. Genome Biology and Evolution, 2016, 8, 753-764.	1.1	27
1850	A single CRD C-type lectin from Eriocheir sinensis (EsLecB) with microbial-binding, antibacterial prophenoloxidase activation and hem-encapsulation activities. Fish and Shellfish Immunology, 2016, 50, 175-190.	1.6	32
1851	Evolutionary Genetics of Hypoxia Tolerance in Cetaceans during Diving. Genome Biology and Evolution, 2016, 8, 827-839.	1.1	64
1852	Three nuclear and two membrane estrogen receptors in basal teleosts, Anguilla sp.: Identification, evolutionary history and differential expression regulation. General and Comparative Endocrinology, 2016, 235, 177-191.	0.8	32
1853	The complete mitochondrial genome of Epicauta chinensis (Coleoptera: Meloidae) and phylogenetic analysis among Coleopteran insects. Gene, 2016, 578, 274-280.	1.0	35
1854	Molecular characterization of Botrytis ourmia-like virus, a mycovirus close to the plant pathogenic genus Ourmiavirus. Virology, 2016, 489, 158-164.	1.1	65
1855	Molecular evolution of the lysophosphatidic acid acyltransferase (LPAAT) gene family. Molecular Phylogenetics and Evolution, 2016, 96, 55-69.	1.2	51
1856	A novel Dreb2-type gene from Carica papaya confers tolerance under abiotic stress. Plant Cell, Tissue and Organ Culture, 2016, 125, 119-133.	1.2	24
1857	Molecular diversity of turncurtoviruses in Iran. Archives of Virology, 2016, 161, 551-561.	0.9	22
1858	Information Commons for Rice (IC4R). Nucleic Acids Research, 2016, 44, D1172-D1180.	6.5	41
1859	Characterization of the complete mitochondrial genome of the storage mite pest Tyrophagus longior (Gervais) (Acari: Acaridae) and comparative mitogenomic analysis of four acarid mites. Gene, 2016, 576, 807-819.	1.0	26
1860	Complete mitochondrial genome of Rhodeus ocellatus (Cypriniformes: Cyprinidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3489-3490.	0.7	2
1861	The complete mitochondrial genome of rabbit pinworm Passalurus ambiguus: genome characterization and phylogenetic analysis. Parasitology Research, 2016, 115, 423-429.	0.6	12
1862	Phylogenetic relationships of Hemiptera inferred from mitochondrial and nuclear genes. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4380-4389.	0.7	10
1863	Phylogeny of haemosporidian blood parasites revealed by a multi-gene approach. Molecular Phylogenetics and Evolution, 2016, 94, 221-231.	1.2	81

#	Article	IF	Citations
1864	Ancestral protein reconstruction: techniques and applications. Biological Chemistry, 2016, 397, 1-21.	1.2	121
1865	Complete mitochondrial genome of Parachromis managuensis (Perciformes: Cichlidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 2533-2534.	0.7	2
1866	MÃ¼ller glia reactivity follows retinal injury despite the absence of the glial fibrillary acidic protein gene in Xenopus. Developmental Biology, 2017, 426, 219-235.	0.9	26
1867	Phylogenomic analysis of lipid biosynthetic genes of Archaea shed light on the â€˜lipid divideâ€™. Environmental Microbiology, 2017, 19, 54-69.	1.8	77
1868	The Origin of Floral Organ Identity Quartets. Plant Cell, 2017, 29, 229-242.	3.1	44
1869	A new giant egg-laying onychophoran (Peripatopsidae) reveals evolutionary and biogeographical aspects of Australian velvet worms. Organisms Diversity and Evolution, 2017, 17, 375-391.	0.7	9
1870	Diversity and evolution of TIR-domain-containing proteins in bivalves and Metazoa: New insights from comparative genomics. Developmental and Comparative Immunology, 2017, 70, 145-164.	1.0	43
1871	Induction of resveratrol biosynthesis in Vitis amurensis cells by heterologous expression of the Arabidopsis constitutively active, Ca2+-independent form of the AtCPK1 gene. Process Biochemistry, 2017, 54, 144-155.	1.8	13
1872	Functional <scp>PTB</scp> phosphate transporters are present in streptophyte algae and early diverging land plants. New Phytologist, 2017, 214, 1158-1171.	3.5	25
1873	Relative benefits of aminoâ€acid, codon, degeneracy, DNA, and purineâ€pyrimidine character coding for phylogenetic analyses of exons. Journal of Systematics and Evolution, 2017, 55, 85-109.	1.6	24
1874	Capturing Compositional Variation in Denitrifying Communities: a Multiple-Primer Approach That Includes Epsilonproteobacteria. Applied and Environmental Microbiology, 2017, 83, .	1.4	9
1875	The Conservation of the Germline Multipotency Program, from Sponges to Vertebrates: A Stepping Stone to Understanding the Somatic and Germline Origins. Genome Biology and Evolution, 2017, 9, evw289.	1.1	39
1876	Characterization of Phytochrome Interacting Factors from the Moss Physcomitrella patens Illustrates Conservation of Phytochrome Signaling Modules in Land Plants. Plant Cell, 2017, 29, 310-330.	3.1	61
1877	Conserved Ankyrin Repeat Proteins and Their NIMA Kinase Partners Regulate Extracellular Matrix Remodeling and Intracellular Trafficking in Caenorhabditis elegans. Genetics, 2017, 205, 273-293.	1.2	25
1878	Functional Characterization of a 28-Kilobase Catabolic Island from Pseudomonas sp. Strain M1 Involved in Biotransformation of Î²-Myrcene and Related Plant-Derived Volatiles. Applied and Environmental Microbiology, 2017, 83, .	1.4	7
1879	Cloning and molecular characterization of the betaine aldehyde dehydrogenase involved in the biosynthesis of glycine betaine in white shrimp (Litopenaeus vannamei). Chemico-Biological Interactions, 2017, 276, 65-74.	1.7	7
1880	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. Environmental Microbiology, 2017, 19, 2320-2333.	1.8	57
1881	Duplication of Dio3 genes in teleost fish and their divergent expression in skin during flatfish metamorphosis. General and Comparative Endocrinology, 2017, 246, 279-293.	0.8	14

#	Article	IF	Citations
1882	Prophage WO genes recapitulate and enhance Wolbachia-induced cytoplasmic incompatibility. Nature, 2017, 543, 243-247.	13.7	366
1883	The ancient CYP716 family is a major contributor to the diversification of eudicot triterpenoid biosynthesis. Nature Communications, 2017, 8, 14153.	5.8	128
1884	Phylogenomic analysis of Copepoda (Arthropoda, Crustacea) reveals unexpected similarities with earlier proposed morphological phylogenies. BMC Evolutionary Biology, 2017, 17, 23.	3.2	38
1885	Phylogenomic resolution of the bacterial genus Pantoea and its relationship with Erwinia and Tatumella. Antonie Van Leeuwenhoek, 2017, 110, 1287-1309.	0.7	48
1886	Mitochondrial genome diversity in dagger and needle nematodes (Nematoda: Longidoridae). Scientific Reports, 2017, 7, 41813.	1.6	20
1887	Transcriptional comparison of the photogenic and non-photogenic tissues of Phrixothrix hirtus (Coleoptera: Phengodidae) and non-luminescent Chauliognathus flavipes (Coleoptera: Cantharidae) give insights on the origin of lanterns in railroad worms. Gene Reports, 2017, 7, 78-86.	0.4	16
1888	The glutathione transferase family of Chlamydomonas reinhardtii: Identification and characterization of novel sigma class-like enzymes. Algal Research, 2017, 24, 237-250.	2.4	16
1889	Phylogenetic positioning of the Antarctic alga Prasiola crispa (Trebouxiophyceae) using organellar genomes and their structural analysis. Journal of Phycology, 2017, 53, 908-915.	1.0	6
1890	Comparative Study of Chemosensory Organs of Shrimp From Hydrothermal Vent and Coastal Environments. Chemical Senses, 2017, 42, 319-331.	1.1	24
1891	The repertoire of bitter taste receptor genes in canids. Amino Acids, 2017, 49, 1159-1167.	1.2	13
1892	Molecular control of gut formation in the spider Parasteatoda tepidariorum. Genesis, 2017, 55, e23033.	0.8	15
1893	Ancestral Haloalkane Dehalogenases Show Robustness and Unique Substrate Specificity. ChemBioChem, 2017, 18, 1448-1456.	1.3	45
1894	Unique mitochondrial localization of arginase 1 and 2 in hepatocytes of air-breathing walking catfish, Clarias batrachus and their differential expression patterns under hyper-ammonia stress. Gene, 2017, 622, 13-22.	1.0	14
1895	Expression patterns of Passiflora edulis APETALA1/FRUITFULL homologues shed light onto tendril and corona identities. EvoDevo, 2017, 8, 3.	1.3	28
1896	ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods, 2017, 14, 587-589.	9.0	9,486
1897	Genome sequences of a capulavirus infecting Plantago lanceolata in the Ã…land archipelago of Finland. Archives of Virology, 2017, 162, 2041-2045.	0.9	39
1898	Differential Retention of Gene Functions in a Secondary Metabolite Cluster. Molecular Biology and Evolution, 2017, 34, 2002-2015.	3.5	41
1899	Evolution of specificity in cartilaginous fish glycoprotein hormones and receptors. General and Comparative Endocrinology, 2017, 246, 309-320.	0.8	13

#	Article	IF	Citations
1900	The complete mitochondrial genome of Clostera anachoreta (Lepidoptera: Notodontidae) and phylogenetic implications for Noctuoidea species. Genomics, 2017, 109, 221-226.	1.3	30
1901	Mitochondrial genome sequences effectively reveal deep branching events in aphids (Insecta:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.7	12
1902	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. Journal of Physiology, 2017, 595, 4611-4630.	1.3	11
1903	Identifying Optimal Models of Evolution. Methods in Molecular Biology, 2017, 1525, 379-420.	0.4	17
1904	Structural Characterization of a Eukaryotic Cyanase from Tetranychus urticae. Journal of Agricultural and Food Chemistry, 2017, 65, 5453-5462.	2.4	11
1905	Daily Activity of the Housefly,Musca domestica, Is Influenced by Temperature Independent of 3â€² UTRperiodGene Splicing. G3: Genes, Genomes, Genetics, 2017, 7, 2637-2649.	0.8	25
1906	Chronic stress impairs the local immune response during cutaneous repair in gilthead sea bream (Sparus aurata, L.). Molecular Immunology, 2017, 87, 267-283.	1.0	24
1907	A transfer RNA gene rearrangement in the lepidopteran mitochondrial genome. Biochemical and Biophysical Research Communications, 2017, 489, 149-154.	1.0	29
1908	Lineage-specific expansion and loss of tyrosinase genes across platyhelminths and their induction profiles in the carcinogenic oriental liver fluke, Clonorchis sinensis. Parasitology, 2017, 144, 1316-1327.	0.7	4
1909	SMS: Smart Model Selection in PhyML. Molecular Biology and Evolution, 2017, 34, 2422-2424.	3.5	1,572
1910	Evolutionary bottlenecks in brackish water habitats drive the colonization of fresh water by stingrays. Journal of Evolutionary Biology, 2017, 30, 1576-1591.	0.8	20
1911	Transcriptome sequencing and phylogenetic analysis of four species of luminescent beetles. Scientific Reports, 2017, 7, 1814.	1.6	30
1912	Gene rearrangement and sequence analysis of mitogenomes suggest polyphyly of Archaeobalanid and Balanid barnacles (Cirripedia: Balanomorpha). Zoologica Scripta, 2017, 46, 729-739.	0.7	15
1913	Molecular evolution of Coq1 gene family in eukaryotes. Journal of Systematics and Evolution, 2017, 55, 417-425.	1.6	1
1914	Complete mitochondrial genome sequence of Cucullaea labiata (Arcoida: Cucullaeidae) and phylogenetic implications. Genes and Genomics, 2017, 39, 867-875.	0.5	6
1915	Genomic and phylogenetic analysis of the complete mitochondrial DNA sequence of walnut leaf pest Paleosepharia posticata (Coleoptera: Chrysomeloidea). Journal of Asia-Pacific Entomology, 2017, 20, 840-853.	0.4	13
1916	Protein and pathway engineering for the biosynthesis of 5â€hydroxytryptophan in Escherichia coli. Engineering in Life Sciences, 2017, 17, 892-899.	2.0	13
1917	Subfunctionalization of COX4 paralogs in fish. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2017, 312, R671-R680.	0.9	5

#	Article	IF	Citations
1918	Biochemical characteristics and gene expression profiles of two paralogous luciferases from the Japanese firefly Pyrocoelia atripennis (Coleoptera, Lampyridae, Lampyrinae): insight into the evolution of firefly luciferase genes. Photochemical and Photobiological Sciences, 2017, 16, 1301-1310.	1.6	12
1919	Heterologous expression of cytotoxic sesquiterpenoids from the medicinal mushroom Lignosus rhinocerotis in yeast. Microbial Cell Factories, 2017, 16, 103.	1.9	40
1920	Phylogenetic and Evolutionary Analysis of Plant ARGONAUTES. Methods in Molecular Biology, 2017, 1640, 267-294.	0.4	9
1921	Genomic organization and spatio-temporal expression of the hemoglobin genes in European sea bass (Dicentrarchus labrax). Marine Biology, 2017, 164, 1.	0.7	26
1922	Scallop genome provides insights into evolution of bilaterian karyotype and development. Nature Ecology and Evolution, 2017, 1, 120.	3.4	353
1923	Nuclear and membrane progestin receptors in the European eel: Characterization and expression in vivo through spermatogenesis. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2017, 207, 79-92.	0.8	20
1924	Recurrent DCC gene losses during bird evolution. Scientific Reports, 2017, 7, 37569.	1.6	19
1925	Protein interaction evolution from promiscuity to specificity with reduced flexibility in an increasingly complex network. Scientific Reports, 2017, 7, 44948.	1.6	40
1926	Evolution of the endomembrane systems of trypanosomatids: conservation and specialisation. Journal of Cell Science, 2017, 130, 1421-1434.	1.2	23
1927	The complete mitochondrial genome of a threatened loach (Sinibotia reevesae) and its phylogeny. Genes and Genomics, 2017, 39, 767-778.	0.5	25
1928	Identification of a mammalian silicon transporter. American Journal of Physiology - Cell Physiology, 2017, 312, C550-C561.	2.1	45
1929	Structural reconstruction of protein ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3897-3902.	3.3	12
1930	Malaria parasites possess a telomere repeat-binding protein that shares ancestry with transcription factor IIIA. Nature Microbiology, 2017, 2, 17033.	5.9	17
1931	Identification and characterization of the Luc2â€type luciferase in the Japanese firefly, Luciola parvula, involved in a dim luminescence in immobile stages. Luminescence, 2017, 32, 924-931.	1.5	14
1932	Primary structures and partial toxicological characterization of two phospholipases A2 from Micrurus mipartitus and Micrurus dumerilii coral snake venoms. Biochimie, 2017, 137, 88-98.	1.3	18
1933	Reconstructing Ancient Proteins to Understand the Causes of Structure and Function. Annual Review of Biophysics, 2017, 46, 247-269.	4.5	129
1934	A novel cetacean adenovirus in stranded harbour porpoises from the North Sea: detection and molecular characterization. Archives of Virology, 2017, 162, 2035-2040.	0.9	14
1935	Duplication and concerted evolution of MiSp-encoding genes underlie the material properties of minor ampullate silks of cobweb weaving spiders. BMC Evolutionary Biology, 2017, 17, 78.	3.2	33

#	Article	IF	Citations
1936	Experimental recreation of the evolution of lignin-degrading enzymes from the Jurassic to date. Biotechnology for Biofuels, 2017, 10, 67.	6.2	41
1937	Novel RNA viruses producing simultaneous covert infections in Ceratitis capitata. Correlations between viral titers and host fitness, and implications for SIT programs. Journal of Invertebrate Pathology, 2017, 143, 50-60.	1.5	17
1938	Identification and genomic analysis of antifungal property of a tomato root endophyte Pseudomonas sp. p21. Antonie Van Leeuwenhoek, 2017, 110, 387-397.	0.7	16
1939	Analysis of the histone cluster in Senegalese sole (Solea senegalensis): evidence for a divergent evolution of two canonical histone clusters. Genome, 2017, 60, 441-453.	0.9	15
1940	Complete mitochondrial genomes of Gnathostoma nipponicum and Gnathostoma sp., and their comparison with other Gnathostoma species. Infection, Genetics and Evolution, 2017, 48, 109-115.	1.0	8
1941	Sexual selection for genetic compatibility: the role of the major histocompatibility complex on cryptic female choice in Chinook salmon (Oncorhynchus tshawytscha). Heredity, 2017, 118, 442-452.	1.2	29
1942	Legume isoflavone synthase genes have evolved by whole-genome and local duplications yielding transcriptionally active paralogs. Plant Science, 2017, 264, 149-167.	1.7	13
1943	Neofunctionalization of â€œJuvenile Hormone Esterase Duplicationâ€•in Drosophila as an odorant-degrading enzyme towards food odorants. Scientific Reports, 2017, 7, 12629.	1.6	24
1944	Back to the future: Rational maps for exploring acetylcholine receptor space and time. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1522-1528.	1.1	9
1945	Characterization, expression, and evolutionary analysis of new TLR3 and TLR5M genes cloned from the spiny eel Mastacembelus armatus. Developmental and Comparative Immunology, 2017, 77, 174-187.	1.0	15
1946	Deciphering the Origin and Evolution of Hepatitis B Viruses by Means of a Family of Non-enveloped Fish Viruses. Cell Host and Microbe, 2017, 22, 387-399.e6.	5.1	134
1947	Active subsite properties, subsite residues and targeting to lysosomes or midgut lumen of cathepsins L from the beetle Tenebrio molitor. Insect Biochemistry and Molecular Biology, 2017, 89, 17-30.	1.2	9
1948	Evolution of the 3-hydroxypropionate bicycle and recent transfer of anoxygenic photosynthesis into the Chloroflexi. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10749-10754.	3.3	108
1949	Giardiaâ€™s primitive GPL biosynthesis pathways with parasitic adaptation â€˜patchesâ€™: implications for Giardiaâ€™s evolutionary history and for finding targets against Giardiasis. Scientific Reports, 2017, 7, 9507.	1.6	15
1950	Chillingâ€responsive DEMETERâ€LIKE DNA demethylase mediates in poplar bud break. Plant, Cell and Environment, 2017, 40, 2236-2249.	2.8	69
1951	Characterization of the neuropeptidome of a Southern Ocean decapod, the Antarctic shrimp Chorismus antarcticus: Focusing on a new decapod ITP-like peptide belonging to the CHH peptide family. General and Comparative Endocrinology, 2017, 252, 60-78.	0.8	31
1952	The complete mitochondrial genome of Euproctis similis (Lepidoptera: Noctuoidea: Erebidae) and phylogenetic analysis. International Journal of Biological Macromolecules, 2017, 105, 219-227.	3.6	24
1953	Constraining the timing of the Great Oxidation Event within the Rubisco phylogenetic tree. Geobiology, 2017, 15, 628-640.	1.1	37

#	Article	IF	Citations
1954	Mitochondrial Genomes of Two Bombycoidea Insects and Implications for Their Phylogeny. Scientific Reports, 2017, 7, 6544.	1.6	22
1955	Neuronal patterning of the tubular collar cord is highly conserved among enteropneusts but dissimilar to the chordate neural tube. Scientific Reports, 2017, 7, 7003.	1.6	15
1956	Evolution, expression and association of the chemosensory protein genes with the outbreak phase of the two main pest locusts. Scientific Reports, 2017, 7, 6653.	1.6	23
1957	Mitochondrial Genome Assemblies of Elysia timida and Elysia cornigera and the Response of Mitochondrion-Associated Metabolism during Starvation. Genome Biology and Evolution, 2017, 9, 1873-1879.	1.1	9
1958	Molecular cloning and functional characterization of a monoterpene synthase isolated from the aromatic wild shrub Thymus albicans. Journal of Plant Physiology, 2017, 218, 35-44.	1.6	10
1959	Overexpression of DEMETER, a DNA demethylase, promotes early apical bud maturation in poplar. Plant, Cell and Environment, 2017, 40, 2806-2819.	2.8	32
1960	Early photosynthetic eukaryotes inhabited low-salinity habitats. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7737-E7745.	3.3	244
1961	Characterization of the piRNA pathway during development of the sea anemone Nematostella vectensis. RNA Biology, 2017, 14, 1727-1741.	1.5	49
1962	Insights Into the Etiology of Polerovirus-Induced Pepper Yellows Disease. Phytopathology, 2017, 107, 1567-1576.	1.1	18
1963	Conserved Gene Microsynteny Unveils Functional Interaction Between Protein Disulfide Isomerase and Rho Guanine-Dissociation Inhibitor Families. Scientific Reports, 2017, 7, 17262.	1.6	16
1964	Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals. Current Biology, 2017, 27, 3864-3870.e4.	1.8	244
1965	Early emergence of negative regulation of the tyrosine kinase Src by the C-terminal Src kinase. Journal of Biological Chemistry, 2017, 292, 18518-18529.	1.6	7
1966	Recognition cascade and metabolite transfer in a marine bacteriaâ€phytoplankton model system. Environmental Microbiology, 2017, 19, 3500-3513.	1.8	111
1967	Mitochondrial genome of Helice tientsinensis (Brachyura: Grapsoidea: Varunidae): Gene rearrangements and higher-level phylogeny of the Brachyura. Gene, 2017, 627, 307-314.	1.0	26
1968	Phylogenetic diversification and developmental implications of poly-(R)-3-hydroxyalkanoate gene cluster assembly in prokaryotes. FEMS Microbiology Letters, 2017, 364, .	0.7	10
1969	The malate sensing two-component system MaeKR is a non-canonical class of sensory complex for C4-dicarboxylates. Scientific Reports, 2017, 7, 2708.	1.6	5
1970	Transcriptomes from the photogenic and non-photogenetic tissues and life stages of the Aspisoma lineatum firefly (Coleoptera: Lampyridae): Implications for the evolutionary origins of bioluminescence and its associated light organs. Gene Reports, 2017, 8, 150-159.	0.4	14
1971	Phylogenomics of 2,4-Diacetylphloroglucinol-ProducingPseudomonasand Novel Antiglycation Endophytes fromPiper auritum. Journal of Natural Products, 2017, 80, 1955-1963.	1.5	35

#	Article	IF	Citations
1972	The first two complete mitochondrial genomes for the family Triglidae and implications for the higher phylogeny of Scorpaeniformes. Scientific Reports, 2017, 7, 1553.	1.6	9
1973	Ancestral Reconstruction Approach to Acetylcholine Receptor Structure and Function. Structure, 2017, 25, 1295-1302.e3.	1.6	9
1974	The complete mitochondrial genome of the copperhead (Agkistrodon contortrix) and phylogenetic analyses of Crotalinae (Serpentes; Colubroidea; Viperidae). Conservation Genetics Resources, 2017, 9, 607-611.	0.4	0
1975	Mechanochemical evolution of the giant muscle protein titin as inferred from resurrected proteins. Nature Structural and Molecular Biology, 2017, 24, 652-657.	3.6	30
1976	Diversity and evolution of mariner-like elements in aphid genomes. BMC Genomics, 2017, 18, 494.	1.2	23
1977	Evolution of the angiopoietin-like gene family in teleosts and their role in skin regeneration. BMC Evolutionary Biology, 2017, 17, 14.	3.2	24
1978	Retention of duplicated long-wavelength opsins in mosquito lineages by positive selection and differential expression. BMC Evolutionary Biology, 2017, 17, 84.	3.2	19
1979	Evolutionary history of versatile-lipases from Agaricales through reconstruction of ancestral structures. BMC Genomics, 2017, 18, 12.	1.2	9
1980	Valine/isoleucine variants drive selective pressure in the VP1 sequence of EV-A71 enteroviruses. BMC Infectious Diseases, 2017, 17, 333.	1.3	6
1982	Lipidomics. Methods in Molecular Biology, 2017, , .	0.4	10
1983	Computational Functional Analysis of Lipid Metabolic Enzymes. Methods in Molecular Biology, 2017, 1609, 195-216.	0.4	2
1984	Intronless and intron-containing type I IFN genes coexist in amphibian Xenopus tropicalis : Insights into the origin and evolution of type I IFNs in vertebrates. Developmental and Comparative Immunology, 2017, 67, 166-176.	1.0	50
1985	Expression of caspase 3 in ovarian follicle cells of the lizard Podarcis sicula. Cell and Tissue Research, 2017, 367, 397-404.	1.5	5
1986	Phylogenetic analysis of two Plectus mitochondrial genomes (Nematoda: Plectida) supports a sister group relationship between Plectida and Rhabditida within Chromadorea. Molecular Phylogenetics and Evolution, 2017, 107, 90-102.	1.2	39
1987	Characterization of Carboxylic Acid Reductases as Enzymes in the Toolbox for Synthetic Chemistry. ChemCatChem, 2017, 9, 1005-1017.	1.8	106
1988	A six-gene phylogeny provides new insights into choanoflagellate evolution. Molecular Phylogenetics and Evolution, 2017, 107, 166-178.	1.2	59
1989	Microbial and viral-like rhodopsins present in coastal marine sediments from four polar and subpolar regions. FEMS Microbiology Ecology, 2017, 93, fiw216.	1.3	9
1990	Phylogenomics of tubeworms (Siboglinidae, Annelida) and comparative performance of different reconstruction methods. Zoologica Scripta, 2017, 46, 200-213.	0.7	33

#	Article	IF	Citations
1991	Molecular characterization and evolution of carnivorous sundew (Drosera rotundifolia L.) class V Î²-1,3-glucanase. Planta, 2017, 245, 77-91.	1.6	6
1992	Monophyly of Anthozoa (Cnidaria): why do nuclear and mitochondrial phylogenies disagree?. Zoologica Scripta, 2017, 46, 363-371.	0.7	25
1993	Mitochondrial Genome of Prasinophyte Alga Pyramimonas parkeae. Journal of Eukaryotic Microbiology, 2017, 64, 360-369.	0.8	3
1994	Crown group Oxyphotobacteria postdate the rise of oxygen. Geobiology, 2017, 15, 19-29.	1.1	153
1995	Structural and evolutionary analyses reveal determinants of DNA binding specificities of nucleoid-associated proteins HU and IHF. Molecular Phylogenetics and Evolution, 2017, 107, 356-366.	1.2	35
1996	The transition from somatic to germline identity shows conserved and specialized features during angiosperm evolution. New Phytologist, 2017, 216, 495-509.	3.5	41
1997	Evolution and function of the Mycoplasma hyopneumoniae peroxiredoxin, a 2-Cys-like enzyme with a single Cys residue. Molecular Genetics and Genomics, 2017, 292, 297-305.	1.0	3
1998	RSL class I genes positively regulate root hair development in Oryza sativa. New Phytologist, 2017, 213, 314-323.	3.5	32
1999	Analysis of the Genes Involved in Thiocyanate Oxidation during Growth in Continuous Culture of the Haloalkaliphilic Sulfur-Oxidizing Bacterium Thioalkalivibrio thiocyanoxidans ARh 2 ^T Using Transcriptomics. MSystems, 2017, 2, .	1.7	9
2000	Rapid Evolution of Primate Type 2 Immune Response Factors Linked to Asthma Susceptibility. Genome Biology and Evolution, 2017, 9, 1757-1765.	1.1	7
2001	Genome-Wide Characterization and Expression Profiling of Sugar Transporter Family in the Whitefly, Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae). Frontiers in Physiology, 2017, 8, 322.	1.3	15
2002	Clathrin in Chara australis: Molecular Analysis and Involvement in Charasome Degradation and Constitutive Endocytosis. Frontiers in Plant Science, 2017, 8, 20.	1.7	18
2003	Evolutionary Analysis of the LAFL Genes Involved in the Land Plant Seed Maturation Program. Frontiers in Plant Science, 2017, 8, 439.	1.7	22
2004	Characterization of the Polycomb-Group Mark H3K27me3 in Unicellular Algae. Frontiers in Plant Science, 2017, 8, 607.	1.7	38
2005	Expression Analyses of Embryogenesis-Associated Genes during Somatic Embryogenesis of Adiantum capillus-veneris L. In vitro: New Insights into the Evolution of Reproductive Organs in Land Plants. Frontiers in Plant Science, 2017, 8, 658.	1.7	15
2006	Divergent Evolutionary Patterns of NAC Transcription Factors Are Associated with Diversification and Gene Duplications in Angiosperm. Frontiers in Plant Science, 2017, 8, 1156.	1.7	14
2007	Genome-Wide Comprehensive Analysis the Molecular Phylogenetic Evaluation and Tissue-Specific Expression of SABATH Gene Family in Salvia miltiorrhiza. Genes, 2017, 8, 365.	1.0	14
2008	Lamprey IGF-Binding Protein-3 Has IGF-Dependent and -Independent Actions. Frontiers in Endocrinology, 2017, 7, 174.	1.5	9

#	Article	IF	Citations
2009	Conservation of Three-Dimensional Helix-Loop-Helix Structure through the Vertebrate Lineage Reopens the Cold Case of Gonadotropin-Releasing Hormone-Associated Peptide. Frontiers in Endocrinology, 2017, 8, 207.	1.5	26
2010	Nucleated Teleost Erythrocytes Play an Nk-Lysin- and Autophagy-Dependent Role in Antiviral Immunity. Frontiers in Immunology, 2017, 8, 1458.	2.2	41
2011	Origin of the Animal Circadian Clock: Diurnal and Light-Entrained Gene Expression in the Sponge Amphimedon queenslandica. Frontiers in Marine Science, 2017, 4, .	1.2	15
2012	Novel Large Sulfur Bacteria in the Metagenomes of Groundwater-Fed Chemosynthetic Microbial Mats in the Lake Huron Basin. Frontiers in Microbiology, 2017, 8, 791.	1.5	29
2013	Pheno- and Genotyping of Hopanoid Production in Acidobacteria. Frontiers in Microbiology, 2017, 8, 968.	1.5	26
2014	Genome Data Provides High Support for Generic Boundaries in Burkholderia Sensu Lato. Frontiers in Microbiology, 2017, 8, 1154.	1.5	122
2015	Respiratory Pathways Reconstructed by Multi-Omics Analysis in Melioribacter roseus, Residing in a Deep Thermal Aquifer of the West-Siberian Megabasin. Frontiers in Microbiology, 2017, 8, 1228.	1.5	13
2016	Modulation of Zinc Homeostasis in Acanthamoeba castellanii as a Possible Antifungal Strategy against Cryptococcus gattii. Frontiers in Microbiology, 2017, 8, 1626.	1.5	9
2017	Rapid Gene Turnover as a Significant Source of Genetic Variation in a Recently Seeded Population of a Healthcare-Associated Pathogen. Frontiers in Microbiology, 2017, 8, 1817.	1.5	65
2018	MtDNA The small workhorse of evolutionary studies. Frontiers in Bioscience - Landmark, 2017, 22, 873-887.	3.0	55
2019	AS3MT-mediated tolerance to arsenic evolved by multiple independent horizontal gene transfers from bacteria to eukaryotes. PLoS ONE, 2017, 12, e0175422.	1.1	29
2020	Hypoxia Inducible Factor (HIF) transcription factor family expansion, diversification, divergence and selection in eukaryotes. PLoS ONE, 2017, 12, e0179545.	1.1	75
2021	The complete mitochondrial genome of Sesarmops sinensis reveals gene rearrangements and phylogenetic relationships in Brachyura. PLoS ONE, 2017, 12, e0179800.	1.1	34
2022	RNA-Seq de novo assembly and differential transcriptome analysis of the nematode Ascaridia galli in relation to in vivo exposure to flubendazole. PLoS ONE, 2017, 12, e0185182.	1.1	11
2023	Generality of toxins in defensive symbiosis: Ribosome-inactivating proteins and defense against parasitic wasps in Drosophila. PLoS Pathogens, 2017, 13, e1006431.	2.1	82
2024	Species-specific genes under selection characterize the co-evolution of slavemaker and host lifestyles. BMC Evolutionary Biology, 2017, 17, 237.	3.2	12
2025	Genome-wide comparative analysis of putative Pth11-related G protein-coupled receptors in fungi belonging to Pezizomycotina. BMC Microbiology, 2017, 17, 166.	1.3	11
2026	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and RÃ©union. Virology Journal, 2017, 14, 146.	1.4	20

#	Article	IF	Citations
2027	Sequencing of the complete mitochondrial genome of a fish-parasitic flatworm Paratetraonchoides inermis (Platyhelminthes: Monogenea): tRNA gene arrangement reshuffling and implications for phylogeny. Parasites and Vectors, 2017, 10, 462.	1.0	29
2028	The Evolutionary Landscape of Dbl-Like RhoGEF Families: Adapting Eukaryotic Cells to Environmental Signals. Genome Biology and Evolution, 2017, 9, 1471-1486.	1.1	47
2029	NaPi/S_X-RNase segregates as a functional S-RNase and is induced under phosphate deficiency in Nicotiana alata. Biologia Plantarum, 2018, 62, 261-268.	1.9	14
2030	Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions. Science, 2018, 359, 930-935.	6.0	51
2031	Structural and Mechanistic Analysis of the Choline Sulfatase from Sinorhizobium melliloti: A Class I Sulfatase Specific for an Alkyl Sulfate Ester. Journal of Molecular Biology, 2018, 430, 1004-1023.	2.0	18
2032	Modifications to a common phosphorylation network provide individualized control in caspases. Journal of Biological Chemistry, 2018, 293, 5447-5461.	1.6	29
2033	Evolution of cyclohexadienyl dehydratase from an ancestral solute-binding protein. Nature Chemical Biology, 2018, 14, 542-547.	3.9	79
2034	The Gastrodia elata genome provides insights into plant adaptation to heterotrophy. Nature Communications, 2018, 9, 1615.	5.8	170
2035	Identification and characterization of doublesex in Bemisia tabaci. Insect Molecular Biology, 2018, 27, 620-632.	1.0	29
2036	Dung application increases CH4 production potential and alters the composition and abundance of methanogen community in restored peatland soils from Europe. Biology and Fertility of Soils, 2018, 54, 533-547.	2.3	10
2037	Conservation analysis and decomposition of residue correlation networks in the phospholipase A2 superfamily (PLA2s): Insights into the structure-function relationships of snake venom toxins. Toxicon, 2018, 146, 50-60.	0.8	12
2038	De novo draft assembly of the Botrylloides leachii genome provides further insight into tunicate evolution. Scientific Reports, 2018, 8, 5518.	1.6	36
2039	A giant virus infecting green algae encodes key fermentation genes. Virology, 2018, 518, 423-433.	1.1	92
2040	High Levels of Intrinsic Tetracycline Resistance in Mycobacterium abscessus Are Conferred by a Tetracycline-Modifying Monooxygenase. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	53
2041	Phylogeny and evolution of the cholesterol transporter NPC1 in insects. Journal of Insect Physiology, 2018, 107, 157-166.	0.9	13
2042	A massive incorporation of microbial genes into the genome of Tetranychus urticae, a polyphagous arthropod herbivore. Insect Molecular Biology, 2018, 27, 333-351.	1.0	40
2043	Isolation and genomic characterization of Culex flaviviruses from mosquitoes in Myanmar. Virus Research, 2018, 247, 120-124.	1.1	8
2044	Evolutionary Genetics of Cytoplasmic Incompatibility Genes cifA and cifB in Prophage WO of Wolbachia. Genome Biology and Evolution, 2018, 10, 434-451.	1.1	143

#	Article	IF	Citations
2045	Amphioxus SYCP1: a case of retrogene replacement and co-option of regulatory elements adjacent to the ParaHox cluster. Development Genes and Evolution, 2018, 228, 13-30.	0.4	1
2046	Identification of Bacterial Species That Can Utilize Fructose-Asparagine. Applied and Environmental Microbiology, 2018, 84, .	1.4	15
2047	Genome-wide searches and molecular analyses highlight the unique evolutionary path of flavone synthase I (FNSI) in Apiaceae. Genome, 2018, 61, 103-109.	0.9	7
2048	A phylogenetic classification of gastropod aquaporins. Marine Genomics, 2018, 38, 59-65.	0.4	9
2049	Phenotypic plasticity of six unusual cercariae in nassariid gastropods and their relationships to the Acanthocolpidae and Brachycladiidae (Digenea). Parasitology International, 2018, 67, 225-232.	0.6	4
2050	Trypanosoma brucei EIF4E2 cap-binding protein binds a homolog of the histone-mRNA stem-loop-binding protein. Current Genetics, 2018, 64, 821-839.	0.8	21
2051	Duplicated membrane estrogen receptors in the European sea bass (Dicentrarchus labrax): Phylogeny, expression and regulation throughout the reproductive cycle. Journal of Steroid Biochemistry and Molecular Biology, 2018, 178, 234-242.	1.2	16
2052	Ancient duplications and functional divergence in the interferon regulatory factors of vertebrates provide insights into the evolution of vertebrate immune systems. Developmental and Comparative Immunology, 2018, 81, 324-333.	1.0	13
2053	Conserved roles of Osiris genes in insect development, polymorphism and protection. Journal of Evolutionary Biology, 2018, 31, 516-529.	0.8	43
2054	HLA Class I Downregulation by HIV-1 Variants from Subtype C Transmission Pairs. Journal of Virology, 2018, 92, .	1.5	8
2055	Higher tRNA gene duplication in mitogenomes of praying mantises (Dictyoptera, Mantodea) and the phylogeny within Mantodea. International Journal of Biological Macromolecules, 2018, 111, 787-795.	3.6	42
2056	Tracing the evolution of the heterotrimeric G protein Î± subunit in Metazoa. BMC Evolutionary Biology, 2018, 18, 51.	3.2	17
2057	Heterogeneous rates of genome rearrangement contributed to the disparity of species richness in Ascomycota. BMC Genomics, 2018, 19, 282.	1.2	17
2058	Molecular, phylogenetic and developmental analyses of Sall proteins in bilaterians. EvoDevo, 2018, 9, 9.	1.3	6
2059	Adaptive evolution of osmoregulatory-related genes provides insight into salinity adaptation in Chinese mitten crab, Eriocheir sinensis. Genetica, 2018, 146, 303-311.	0.5	14
2060	Interferons type II and their receptors R1 and R2 in fish species: Evolution, structure, and function. Fish and Shellfish Immunology, 2018, 79, 140-152.	1.6	19
2061	Structural Basis for Superoxide Activation of Flavobacterium johnsoniae Class I Ribonucleotide Reductase and for Radical Initiation by Its Dimanganese Cofactor. Biochemistry, 2018, 57, 2679-2693.	1.2	38
2062	Genome-wide dissection and expression profiling of unique glyoxalase III genes in soybean reveal the differential pattern of transcriptional regulation. Scientific Reports, 2018, 8, 4848.	1.6	12

#	Article	IF	Citations
2063	The complete genome sequence of the first hesperiid-infecting alphabaculovirus isolated from the leguminous pest Urbanus proteus (Lepidoptera: Hesperiidae). Virus Research, 2018, 249, 76-84.	1.1	12
2064	Transposase-DNA Complex Structures Reveal Mechanisms for Conjugative Transposition of Antibiotic Resistance. Cell, 2018, 173, 208-220.e20.	13.5	51
2065	Targeting symbiosis-related insect genes by RNAi in the pea aphid- Buchnera symbiosis. Insect Biochemistry and Molecular Biology, 2018, 95, 55-63.	1.2	71
2066	The mitochondrial genome ofAncylostoma tubaeformefrom cats in China. Journal of Helminthology, 2018, 92, 22-33.	0.4	12
2067	Characterization of the complete mitochondrial genome ofOrtleppascaris sinensis(Nematoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Helminthology, 2018, 92, 369-378.	0.4	7
2068	The first phleboâ€like virus infecting plants: a case study on the adaptation of negativeâ€stranded RNA viruses to new hosts. Molecular Plant Pathology, 2018, 19, 1075-1089.	2.0	72
2069	Evolution of the glucagon-like system across fish. General and Comparative Endocrinology, 2018, 264, 113-130.	0.8	9
2070	Elainella gen. nov.: a new tropical cyanobacterium characterized using a complex genomic approach. European Journal of Phycology, 2018, 53, 39-51.	0.9	27
2071	A Phytophthora palmivora Extracellular Cystatin-Like Protease Inhibitor Targets Papain to Contribute to Virulence on Papaya. Molecular Plant-Microbe Interactions, 2018, 31, 363-373.	1.4	88
2072	Molecular characterization and expression analyses of the Viperin gene in Larimichthys crocea (Family: Sciaenidae). Developmental and Comparative Immunology, 2018, 79, 59-66.	1.0	18
2073	The roles of mucusâ€forming mucins, peritrophins and peritrophins with mucin domains in the insect midgut. Insect Molecular Biology, 2018, 27, 46-60.	1.0	48
2074	Divergence time, historical biogeography and evolutionary rate estimation of the order Bangiales (Rhodophyta) inferred from multilocus data. Journal of Oceanology and Limnology, 2018, 36, 870-881.	0.6	13
2075	The first complete organellar genomes of an Antarctic red alga, Pyropia endiviifolia: insights into its genome architecture and phylogenetic position within genus Pyropia (Bangiales, Rhodophyta). Journal of Oceanology and Limnology, 2018, 36, 1315-1328.	0.6	12
2076	Metaproteomics of marine viral concentrates reveals key viral populations and abundant periplasmic proteins in the oligotrophic deep chlorophyll maximum of the South China Sea. Environmental Microbiology, 2018, 20, 477-491.	1.8	3
2077	Characterization of Pepper leafroll chlorosis virus, a New Polerovirus Causing Yellowing Disease of Bell Pepper in Saudi Arabia. Plant Disease, 2018, 102, 318-326.	0.7	14
2078	Determination of the diversity of astroviruses in feces from cats in Florida. Journal of Veterinary Diagnostic Investigation, 2018, 30, 275-279.	0.5	12
2079	Genome characterization of an Argentinean isolate of alfalfa leaf curl virus. Archives of Virology, 2018, 163, 799-803.	0.9	16
2080	Putative Independent Evolutionary Reversals from Genotypic to Temperature-Dependent Sex Determination are Associated with Accelerated Evolution of Sex-Determining Genes in Turtles. Journal of Molecular Evolution, 2018, 86, 11-26.	0.8	19

#	Article	IF	Citations
2081	Oligomannosidic glycans at Asn-110 are essential for secretion of human diamine oxidase. Journal of Biological Chemistry, 2018, 293, 1070-1087.	1.6	9
2082	Molecular cloning, tissue distribution, and effect of fasting and refeeding on the expression of neuropeptide Y in Channa argus. General and Comparative Endocrinology, 2018, 259, 147-153.	0.8	16
2083	Screening of polyhydroxyalkanoate-producing bacteria and PhaC-encoding genes in two hypersaline microbial mats from Guerrero Negro, Baja California Sur, Mexico. PeerJ, 2018, 6, e4780.	0.9	16
2084	Transcriptomic Characterization of the South American Freshwater Stingray Potamotrygon motoro Venom Apparatus. Toxins, 2018, 10, 544.	1.5	13
2085	Vertebrate SLRP family evolution and the subfunctionalization of osteoglycin gene duplicates in teleost fish. BMC Evolutionary Biology, 2018, 18, 191.	3.2	2
2086	Expression of a novel surfactant protein gene is associated with sites of extrapulmonary respiration in a lungless salamander. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181589.	1.2	4
2087	Basal position of two new complete mitochondrial genomes of parasitic Cymothoida (Crustacea:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Vectors, 2018, 11, 628.	1.0	18
2088	Evolutionary dynamics of origin and loss in the deep history of phospholipase D toxin genes. BMC Evolutionary Biology, 2018, 18, 194.	3.2	9
2089	Endogenous amdoparvovirus-related elements reveal insights into the biology and evolution of vertebrate parvoviruses. Virus Evolution, 2018, 4, vey026.	2.2	19
2090	Phylogenetic Analysis: Basic Concepts and Its Use as a Tool for Virology and Molecular Epidemiology. Acta Scientiae Veterinariae, 2018, 44, 20.	0.2	0
2091	Members of the Genus Methylobacter Are Inferred To Account for the Majority of Aerobic Methane Oxidation in Oxic Soils from a Freshwater Wetland. MBio, 2018, 9, .	1.8	64
2092	Caligus rogercresseyi acetylcholinesterase types and variants: a potential marker for organophosphate resistance. Parasites and Vectors, 2018, 11, 570.	1.0	9
2093	Virome analyses of Hevea brasiliensis using small RNA deep sequencing and PCR techniques reveal the presence of a potential new virus. Virology Journal, 2018, 15, 184.	1.4	10
2094	Mitochondrial genome of the garfish Hyporhamphus quoyi (Beloniformes: Hemiramphidae) and phylogenetic relationships within Beloniformes based on whole mitogenomes. PLoS ONE, 2018, 13, e0205025.	1.1	6
2095	Diversification of DNA binding specificities enabled SREBP transcription regulators to expand the repertoire of cellular functions that they govern in fungi. PLoS Genetics, 2018, 14, e1007884.	1.5	14
2096	Comparison of complex networks and tree-based methods of phylogenetic analysis and proposal of a bootstrap method. PeerJ, 2018, 6, e4349.	0.9	4
2097	The complete mitochondrial genome of the Caribbean spiny lobster Panulirus argus. Scientific Reports, 2018, 8, 17690.	1.6	31
2098	A Phylogenomic Framework and Divergence History of Cephalochordata Amphioxus. Frontiers in Physiology, 2018, 9, 1833.	1.3	11

#	Article	IF	Citations
2099	Structure-function analysis of Sedolisins: evolution of tripeptidyl peptidase and endopeptidase subfamilies in fungi. BMC Bioinformatics, 2018, 19, 464.	1.2	2
2100	Mitochondrial genomes of two diplectanids (Platyhelminthes: Monogenea) expose paraphyly of the order Dactylogyridea and extensive tRNA gene rearrangements. Parasites and Vectors, 2018, 11, 601.	1.0	37
2101	Molecular Characterization and Overexpression of SmJMT Increases the Production of Phenolic Acids in Salvia miltiorrhiza. International Journal of Molecular Sciences, 2018, 19, 3788.	1.8	21
2102	Generation and classification of transcriptomes in two Croomia species and molecular evolution of CYC/TB1 genes in Stemonaceae. Plant Diversity, 2018, 40, 253-264.	1.8	1
2103	The Westward Journey of Alfalfa Leaf Curl Virus. Viruses, 2018, 10, 542.	1.5	12
2104	Molecular dynamics and structure function analysis show that substrate binding and specificity are major forces in the functional diversification of Eqolisins. BMC Bioinformatics, 2018, 19, 338.	1.2	3
2105	Evidence of positive selection suggests possible role of aquaporins in the water-to-land transition of mudskippers. Organisms Diversity and Evolution, 2018, 18, 499-514.	0.7	8
2106	Evidence of two genetically different lymphotropic herpesviruses present among red deer, sambar, and milu herds in China. Journal of Veterinary Science, 2018, 19, 716.	0.5	3
2107	Unique Composition of Intronless and Intron-Containing Type I IFNs in the Tibetan Frog Nanorana parkeri Provides New Evidence To Support Independent Retroposition Hypothesis for Type I IFN Genes in Amphibians. Journal of Immunology, 2018, 201, 3329-3342.	0.4	37
2108	Impact of Dengue Virus Serotype 2 Strain Diversity on Serological Immune Responses to Dengue. ACS Infectious Diseases, 2018, 4, 1705-1717.	1.8	2
2109	Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. Plant Cell, 2018, 30, 2741-2760.	3.1	13
2110	Analysis of Scheduling Policies in Metaheuristics for Evolutionary Biology. , 2018, , .		0
2111	Evolutionary history of Mo25 gene in plants, a component of RAM/MOR signaling network. Mechanisms of Development, 2018, 153, 64-73.	1.7	4
2112	Two R2R3â€‹scp›MYB‹/scp› proteins are broad repressors of flavonoid and phenylpropanoid metabolism in poplar. Plant Journal, 2018, 96, 949-965.	2.8	137
2113	Three new Diplozoidae mitogenomes expose unusual compositional biases within the Monogenea class: implications for phylogenetic studies. BMC Evolutionary Biology, 2018, 18, 133.	3.2	28
2114	De novo assembly and annotation of Hyalomma dromedarii tick (Acari: Ixodidae) sialotranscriptome with regard to gender differences in gene expression. Parasites and Vectors, 2018, 11, 314.	1.0	21
2115	Molecular cloning, antiserum preparation and expression analysis during head regeneration of $$upalpha $$ Î± -crystallin type heat shock protein in Hydra vulgaris. Journal of Genetics, 2018, 97, 911-924.	0.4	0
2116	Complete Genome Sequence of a Novel RNA Virus Identified from a Deep-Sea Animal, <i>Osedax japonicus</i>. Microbes and Environments, 2018, 33, 446-449.	0.7	9

#	Article	IF	Citations
2117	Comparative genomic analysis of Acinetobacter spp. plasmids originating from clinical settings and environmental habitats. Scientific Reports, 2018, 8, 7783.	1.6	72
2118	Pan-genomic approach shows insight of genetic divergence and pathogenic-adaptation of Pasteurella multocida. Gene, 2018, 670, 193-206.	1.0	31
2119	Differential expression of multiple glutamine synthetase genes in air-breathing magur catfish, Clarias magur and their induction under hyper-ammonia stress. Gene, 2018, 671, 85-95.	1.0	16
2120	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6201-6206.	3.3	19
2121	Hotspots of Independent and Multiple Rounds of LTR-retrotransposon Bursts in Brassica Species. Horticultural Plant Journal, 2018, 4, 165-174.	2.3	13
2122	De Novo Sequencing of a Sparassis latifolia Genome and Its Associated Comparative Analyses. Canadian Journal of Infectious Diseases and Medical Microbiology, 2018, 2018, 1-12.	0.7	9
2123	Diversity, evolution, and function of myriapod hemocyanins. BMC Evolutionary Biology, 2018, 18, 107.	3.2	12
2124	New genomic data and analyses challenge the traditional vision of animal epithelium evolution. BMC Genomics, 2018, 19, 393.	1.2	50
2125	Single-strand DNA processing: phylogenomics and sequence diversity of a superfamily of potential prokaryotic HuH endonucleases. BMC Genomics, 2018, 19, 475.	1.2	5
2126	Individual components of paired typical NLR immune receptors are regulated by distinct E3 ligases. Nature Plants, 2018, 4, 699-710.	4.7	43
2127	The CaspBase: a curated database for evolutionary biochemical studies of caspase functional divergence and ancestral sequence inference. Protein Science, 2018, 27, 1857-1870.	3.1	21
2128	Multiple independent origins for a subtelomeric locus associated with growth rate in Fusarium circinatum. IMA Fungus, 2018, 9, 27-36.	1.7	14
2129	Evolution of DNMT2 in drosophilids: Evidence for positive and purifying selection and insights into new protein (pathways) interactions. Genetics and Molecular Biology, 2018, 41, 215-234.	0.6	14
2130	A novel non-segmented double-stranded RNA virus from an Arctic isolate of Pythium polare. Virology, 2018, 522, 234-243.	1.1	52
2131	Genome Reduction in Psychromonas Species within the Gut of an Amphipod from the Oceanâ€™s Deepest Point. MSystems, 2018, 3, .	1.7	21
2132	Whole Genome Analyses Suggests that Burkholderia sensu lato Contains Two Additional Novel Genera (Mycetohabitans gen. nov., and Trinickia gen. nov.): Implications for the Evolution of Diazotrophy and Nodulation in the Burkholderiaceae. Genes, 2018, 9, 389.	1.0	252
2133	Metabolic and Evolutionary Insights in the Transformation of Diphenylamine by a Pseudomonas putida Strain Unravelled by Genomic, Proteomic, and Transcription Analysis. Frontiers in Microbiology, 2018, 9, 676.	1.5	4
2134	Genome-Wide Characterization of Heat-Shock Protein 70s from Chenopodium quinoa and Expression Analyses of Cqhsp70s in Response to Drought Stress. Genes, 2018, 9, 35.	1.0	37

#	Article	IF	Citations
2135	The complete mitochondrial genome of Clostera anastomosis (Lepidoptera: Notodontidae) and implication for the phylogenetic relationships of Noctuoidea species. International Journal of Biological Macromolecules, 2018, 118, 1574-1583.	3.6	22
2136	A Novel Betabaculovirus Isolated from the Monocot Pest Mocis latipes (Lepidoptera: Noctuidae) and the Evolution of Multiple-Copy Genes. Viruses, 2018, 10, 134.	1.5	7
2137	Genome-wide analysis of the Glycerol-3-Phosphate Acyltransferase (GPAT) gene family reveals the evolution and diversification of plant GPATs. Genetics and Molecular Biology, 2018, 41, 355-370.	0.6	48
2138	Complete mitochondrial genome of the first deep-sea spongicolid shrimp Spongiocaris panglao (Decapoda: Stenopodidea): Novel gene arrangement and the phylogenetic position and origin of Stenopodidea. Gene, 2018, 676, 123-138.	1.0	14
2139	Genomic abundance and transcriptional activity of diverse gypsy and copia long terminal repeat retrotransposons in three wild sunflower species. BMC Plant Biology, 2018, 18, 6.	1.6	25
2140	Comparative genomic analysis reveals the evolution and environmental adaptation strategies of vibrios. BMC Genomics, 2018, 19, 135.	1.2	71
2141	Mt-rps3 is an ancient gene which provides insight into the evolution of fungal mitochondrial genomes. Molecular Phylogenetics and Evolution, 2018, 127, 74-86.	1.2	55
2142	Diversity and evolution of polyketide biosynthesis gene clusters in the Ceratocystidaceae. Fungal Biology, 2018, 122, 856-866.	1.1	19
2143	Nearly neutral evolution in IFNL3 gene retains the immune function to detect and clear the viral infection in HCV. Progress in Biophysics and Molecular Biology, 2018, 140, 107-116.	1.4	0
2144	Revision of Tasmanian viviparous velvet worms (Onychophora : Peripatopsidae) with descriptions of two new species. Invertebrate Systematics, 2018, 32, 909.	0.5	6
2145	Molecular Evolution and Functional Divergence of the IgLON Family. Evolutionary Bioinformatics, 2018, 14, 117693431877508.	0.6	29
2146	Characterization of MyD88 in Japanese eel, Anguilla japonica. Fish and Shellfish Immunology, 2018, 81, 374-382.	1.6	17
2147	Discovery of Culex pipiens associated tunisia virus: a new ssRNA(+) virus representing a new insect associated virus family. Virus Evolution, 2018, 4, vex040.	2.2	17
2148	Characterization of Gonadotropin-Releasing Hormone (GnRH) Genes From Cartilaginous Fish: Evolutionary Perspectives. Frontiers in Neuroscience, 2018, 12, 607.	1.4	21
2149	Identification and molecular characterization of a novel circular single-stranded DNA virus associated with yerba mate in Argentina. Archives of Virology, 2018, 163, 2811-2815.	0.9	3
2150	Uncoupling protein 1 in snakehead (Channa argus): Cloning, tissue distribution, and its expression in response to fasting and refeeding. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2018, 225, 1-6.	0.8	9
2151	Elemental sulfur reduction in the deepâ€sea vent thermophile, Thermovibrio ammonificans. Environmental Microbiology, 2018, 20, 2301-2316.	1.8	16
2152	Parkinson disease related ATP13A2 evolved early in animal evolution. PLoS ONE, 2018, 13, e0193228.	1.1	47

#	Article	IF	Citations
2153	Proteomic endorsed transcriptomic profiles of venom glands from Tityus obscurus and T. serrulatus scorpions. PLoS ONE, 2018, 13, e0193739.	1.1	55
2154	Harnessing the power of phylogenomics to disentangle the directionality and signatures of interkingdom host jumping in the parasitic fungal genus Tolypocladium. Mycologia, 2018, 110, 104-117.	0.8	12
2155	Evolutionary novelty in gravity sensing through horizontal gene transfer and high-order protein assembly. PLoS Biology, 2018, 16, e2004920.	2.6	14
2156	From Spatial Metagenomics to Molecular Characterization of Plant Viruses: A Geminivirus Case Study. Advances in Virus Research, 2018, 101, 55-83.	0.9	34
2157	Genome sequence of Jatropha curcas L., a nonâ€edible biodiesel plant, provides a resource to improve seedâ€related traits. Plant Biotechnology Journal, 2019, 17, 517-530.	4.1	56
2158	Resurrection of efficient Precambrian endoglucanases for lignocellulosic biomass hydrolysis. Communications Chemistry, 2019, 2, .	2.0	21
2159	Identification and expression analysis of NAC transcription factors potentially involved in leaf and petal senescence in Petunia hybrida. Plant Science, 2019, 287, 110195.	1.7	20
2160	Genome-Wide Comprehensive Analysis of the SABATH Gene Family inArabidopsisand Rice. Evolutionary Bioinformatics, 2019, 15, 117693431986086.	0.6	6
2161	The lichen symbiosis re-viewed through the genomes of Cladonia grayi and its algal partner Asterochloris glomerata. BMC Genomics, 2019, 20, 605.	1.2	98
2162	The First Co-Opted Endogenous Foamy Viruses and the Evolutionary History of Reptilian Foamy Viruses. Viruses, 2019, 11, 641.	1.5	13
2163	An Expanded Ribosomal Phylogeny of Cyanobacteria Supports a Deep Placement of Plastids. Frontiers in Microbiology, 2019, 10, 1612.	1.5	49
2164	The complete mitochondrial genome of Sinna extrema (Lepidoptera: Nolidae) and its implications for the phylogenetic relationships of Noctuoidea species. International Journal of Biological Macromolecules, 2019, 137, 317-326.	3.6	18
2165	The evolution of endogenous retroviral envelope genes in bats and their potential contribution to host biology. Virus Research, 2019, 270, 197645.	1.1	10
2166	Diversification of the gut fungi Smittium and allies (Harpellales) co-occurred with the origin of complete metamorphosis of their symbiotic insect hosts (lower Diptera). Molecular Phylogenetics and Evolution, 2019, 139, 106550.	1.2	8
2167	Variable genome evolution in fungi after transposon-mediated amplification of a housekeeping gene. Mobile DNA, 2019, 10, 37.	1.3	1
2168	A novel toti-like virus from a plant pathogenic oomycete Globisporangium splendens. Virology, 2019, 537, 165-171.	1.1	10
2169	Genome-wide identification of ABC transporters in monogeneans. Molecular and Biochemical Parasitology, 2019, 234, 111234.	0.5	9
2170	The Novel Serine/Threonine Protein Kinase LmjF.22.0810 from Leishmania major may be Involved in the Resistance to Drugs such as Paromomycin. Biomolecules, 2019, 9, 723.	1.8	8

#	Article	IF	Citations
2171	Evolutionary basis of high-frequency hearing in the cochleae of echolocators revealed by comparative genomics. Genome Biology and Evolution, 2020, 12, 3740-3753.	1.1	10
2172	The Complete Mitochondrial Genome of the Caecal Fluke of Poultry, Postharmostomum commutatum, as the First Representative from the Superfamily Brachylaimoidea. Frontiers in Genetics, 2019, 10, 1037.	1.1	13
2173	191 Early weaning in pigs induces long-term alterations in intestinal nutrient transporter function and expression partially via beta adrenergic enteric neural receptors. Journal of Animal Science, 2019, 97, 112-113.	0.2	0
2174	Hinge Region in DNA Packaging Terminase pUL15 of Herpes Simplex Virus: A Potential Allosteric Target for Antiviral Drugs. Biomolecules, 2019, 9, 603.	1.8	5
2175	The Role of Co-Deleted Genes in Neurofibromatosis Type 1 Microdeletions: An Evolutive Approach. Genes, 2019, 10, 839.	1.0	3
2176	Candidate genes in red pigment biosynthesis of a red-fleshed radish cultivar (Raphanus sativus L.) as revealed by transcriptome analysis. Biochemical Systematics and Ecology, 2019, 86, 103933.	0.6	3
2177	The Differential Expression of Mevalonate Pathway Genes in the Gut of the Bark Beetle Dendroctonus rhizophagus (Curculionidae: Scolytinae) Is Unrelated to the de Novo Synthesis of Terpenoid Pheromones. International Journal of Molecular Sciences, 2019, 20, 4011.	1.8	6
2178	Transcriptome analyses reveal alterations in muscle metabolism, immune responses and reproductive behavior of Japanese mantis shrimp (Oratosquilla oratoria) at different cold temperature. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 32, 100615.	0.4	9
2179	Independent evolution of complex development in animals and plants: deep homology and lateral gene transfer. Development Genes and Evolution, 2019, 229, 25-34.	0.4	9
2180	Insights Into the Evolution of Picocyanobacteria and Phycoerythrin Genes (mpeBA and cpeBA). Frontiers in Microbiology, 2019, 10, 45.	1.5	56
2181	MIPS: Functional dynamics in evolutionary pathways of plant kingdom. Genomics, 2019, 111, 1929-1945.	1.3	17
2182	Ancient complement and lineage-specific evolution of the Sec7 ARF GEF proteins in eukaryotes. Molecular Biology of the Cell, 2019, 30, 1846-1863.	0.9	21
2183	Evolution and functional differentiation of recently diverged phytochelatin synthase genes from Arundo donax L.. Journal of Experimental Botany, 2019, 70, 5391-5405.	2.4	15
2184	Metabolic versatility in a modern lineage of cyanobacteria from terrestrial hot springs. Free Radical Biology and Medicine, 2019, 140, 224-232.	1.3	20
2185	Metabolic Consequences of Cobalamin Scarcity in the Diatom Thalassiosira pseudonana as Revealed Through Metabolomics. Protist, 2019, 170, 328-348.	0.6	33
2186	Comparative Genomics of Thiohalobacter thiocyanaticus HRh1T and Guyparkeria sp. SCN-R1, Halophilic Chemolithoautotrophic Sulfur-Oxidizing Gammaproteobacteria Capable of Using Thiocyanate as Energy Source. Frontiers in Microbiology, 2019, 10, 898.	1.5	20
2187	Molecular cloning of two kcnk3 genes from the Northern snakehead (Channa argus) for quantification of their transcriptions in response to fasting and refeeding. General and Comparative Endocrinology, 2019, 281, 49-57.	0.8	9
2188	Evolution of folate biosynthesis and metabolism across algae and land plant lineages. Scientific Reports, 2019, 9, 5731.	1.6	35

#	Article	IF	Citations
2189	Protein Structure-Guided Hidden Markov Models (HMMs) as A Powerful Method in the Detection of Ancestral Endogenous Viral Elements. Viruses, 2019, 11, 320.	1.5	7
2190	Quantitative proteomics reveals the key molecular events occurring at different cell cycle phases of the in situ blooming dinoflagellate cells. Science of the Total Environment, 2019, 676, 62-71.	3.9	14
2191	Genome-wide analysis and evolution of plant thaumatin-like proteins: a focus on the origin and diversification of osmotins. Molecular Genetics and Genomics, 2019, 294, 1137-1157.	1.0	19
2192	Light-Emitting Dehalogenases: Reconstruction of Multifunctional Biocatalysts. ACS Catalysis, 2019, 9, 4810-4823.	5.5	33
2193	Genome-informed Bradyrhizobium taxonomy: where to from here?. Systematic and Applied Microbiology, 2019, 42, 427-439.	1.2	62
2194	A New Prevalent Densovirus Discovered in Acari. Insight from Metagenomics in Viral Communities Associated with Two-Spotted Mite (Tetranychus urticae) Populations. Viruses, 2019, 11, 233.	1.5	19
2195	OsAGO2 controls ROS production and the initiation of tapetal PCD by epigenetically regulating OsHXK1 expression in rice anthers. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7549-7558.	3.3	102
2196	Functional Characterization of OXYL, A SghC1qDC LacNAc-specific Lectin from The Crinoid Feather Star Anneissia Japonica. Marine Drugs, 2019, 17, 136.	2.2	11
2197	A reptilian endogenous foamy virus sheds light on the early evolution of retroviruses. Virus Evolution, 2019, 5, vez001.	2.2	19
2198	Diversity and Distribution of Sulfur Oxidation-Related Genes in Thioalkalivibrio, a Genus of Chemolithoautotrophic and Haloalkaliphilic Sulfur-Oxidizing Bacteria. Frontiers in Microbiology, 2019, 10, 160.	1.5	56
2199	Co-occurring genomic capacity for anaerobic methane and dissimilatory sulfur metabolisms discovered in the Korarchaeota. Nature Microbiology, 2019, 4, 614-622.	5.9	91
2200	Insight into the structure, function and conjugative transfer of pLPU83a, an accessory plasmid of Rhizobium favelukesii LPU83. Plasmid, 2019, 103, 9-16.	0.4	10
2201	Molecular evolution of Pr1 proteases depicts ongoing diversification in Metarhizium spp. Molecular Genetics and Genomics, 2019, 294, 901-917.	1.0	8
2202	A<scp>led</scp> D<scp>avies</scp>. The City of London and Social Democracy: The Political Economy of Finance in Britain, 1959â€“1979.. American Historical Review, 2019, 124, 335-336.	0.0	0
2203	In silico characterization of multiple genes encoding the GP63 virulence protein from Leishmania braziliensis: identification of sources of variation and putative roles in immune evasion. BMC Genomics, 2019, 20, 118.	1.2	15
2204	Sponges Lack ParaHox Genes. Genome Biology and Evolution, 2019, 11, 1250-1257.	1.1	11
2205	Developmental expression and evolution of hexamerin and haemocyanin from Folsomia candida (Collembola). Insect Molecular Biology, 2019, 28, 716-727.	1.0	5
2206	How to resurrect ancestral proteins as proxies for ancient biogeochemistry. Free Radical Biology and Medicine, 2019, 140, 260-269.	1.3	45

#	Article	IF	Citations
2207	Spatiotemporal distributions and environmental drivers of diversity and community structure of nosZ-type denitrifiers and anammox bacteria in sediments of the Bohai Sea and North Yellow Sea, China. Journal of Oceanology and Limnology, 2019, 37, 1211-1228.	0.6	6
2208	Neofunctionalisation of basic helixâ^'loopâ^'helix proteins occurred when embryophytes colonised the land. New Phytologist, 2019, 223, 993-1008.	3.5	18
2209	Delegating Sex: Differential Gene Expression in Stolonizing Syllids Uncovers the Hormonal Control of Reproduction. Genome Biology and Evolution, 2019, 11, 295-318.	1.1	13
2210	Evolution of squat lobsters (Crustacea, Galatheoidea): mitogenomic data suggest an early divergent Porcellanidae. Hydrobiologia, 2019, 833, 173-184.	1.0	5
2211	Roles of plasma membrane proton ATPases AHA2 and AHA7 in normal growth of roots and root hairs in <scp>Arabidopsis thaliana</scp>. Physiologia Plantarum, 2019, 166, 848-861.	2.6	36
2212	Phylogenetic relationships of five Oriental Apanteles species-groups (Hymenoptera: Braconidae:) Tj ETQq1 1 0.784314 rgBT /Overlock 1 22, 341-352.	0.4	3
2213	Wnt Gene Expression During Early Embryogenesis in the Nymphalid Butterfly Bicyclus anynana. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	18
2214	Diverse, Abundant, and Novel Viruses Infecting the Marine Roseobacter RCA Lineage. MSystems, 2019, 4, .	1.7	27
2215	In silico definition of new ligninolytic peroxidase sub-classes in fungi and putative relation to fungal life style. Scientific Reports, 2019, 9, 20373.	1.6	13
2216	Resolution of deep divergence of club fungi (phylum Basidiomycota). Synthetic and Systems Biotechnology, 2019, 4, 225-231.	1.8	6
2217	Natural Infection of Aedes aegypti by Chikungunya and Dengue type 2 Virus in a Transition Area of North-Northeast Brazil. Viruses, 2019, 11, 1126.	1.5	12
2218	Identification and evolution of avian endogenous foamy viruses. Virus Evolution, 2019, 5, vez049.	2.2	10
2219	The complete mitochondrial genome and description of a new cryptic species of Benedenia Diesing, 1858 (Monogenea: Capsalidae), a major pathogen infecting the yellowtail kingfish Seriola lalandi Valenciennes in the South-East Pacific. Parasites and Vectors, 2019, 12, 490.	1.0	22
2220	The genetic basis of adaptive evolution in parasitic environment from the Angiostrongylus cantonensis genome. PLoS Neglected Tropical Diseases, 2019, 13, e0007846.	1.3	9
2221	PacBio Long-Read Sequencing Reveals the Transcriptomic Complexity and Aux/IAA Gene Evolution in Gnetum (Gnetales). Forests, 2019, 10, 1043.	0.9	6
2222	Highly thermostable carboxylic acid reductases generated by ancestral sequence reconstruction. Communications Biology, 2019, 2, 429.	2.0	34
2223	Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. Nature Chemical Biology, 2019, 15, 1120-1128.	3.9	71
2224	Revision of the taxonomic status of <i>Synthesium elongatum</i> (Ozaki, 1935) (Brachycladiidae), an intestinal digenean of narrow-ridged finless porpoise (<i>Neophocaena) Tj ETQq1 1 0.784314 rgBT /Overlock	0.3	2

#	Article	IF	Citations
2225	Complete mitochodrial genome of the crab spider Ebrechtella tricuspidata (Araneae: Thomisidae): A novel tRNA rearrangement and phylogenetic implications for Araneae. Genomics, 2019, 111, 1266-1273.	1.3	6
2226	Comparative Analysis of the Complete Mitochondrial Genomes for Development Application. Frontiers in Genetics, 2019, 9, 651.	1.1	4
2227	Molecular characterization and expression analyses of two homologues of interferon-stimulated gene ISG15 in Larimichthys crocea (Family: Sciaenidae). Fish and Shellfish Immunology, 2019, 86, 846-857.	1.6	10
2228	ABCF ATPases Involved in Protein Synthesis, Ribosome Assembly and Antibiotic Resistance: Structural and Functional Diversification across the Tree of Life. Journal of Molecular Biology, 2019, 431, 3568-3590.	2.0	90
2229	Structural, thermodynamic and catalytic characterization of an ancestral triosephosphate isomerase reveal early evolutionary coupling between monomer association and function. FEBS Journal, 2019, 286, 882-900.	2.2	6
2230	Pelagiphages in the Podoviridae family integrate into host genomes. Environmental Microbiology, 2019, 21, 1989-2001.	1.8	50
2231	Comparison of the Malpighian tubules and fat body transcriptional profiles of Zophobas morio larvae (Coleoptera: Tenebrionidae). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 95-105.	0.4	6
2232	An analysis of characterized plant sesquiterpene synthases. Phytochemistry, 2019, 158, 157-165.	1.4	67
2233	Discovery of highly divergent lineages of plant-associated astro-like viruses sheds light on the emergence of potyviruses. Virus Research, 2019, 260, 38-48.	1.1	24
2234	The Evolutionary Traceability of a Protein. Genome Biology and Evolution, 2019, 11, 531-545.	1.1	23
2235	RNA-Seq analysis of the bioluminescent and non-bioluminescent species of Elateridae (Coleoptera): Comparison to others photogenic and non-photogenic tissues of Elateroidea species. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 154-165.	0.4	4
2236	Ancestral Sequence Reconstruction as a Tool for the Elucidation of a Stepwise Evolutionary Adaptation. Methods in Molecular Biology, 2019, 1851, 171-182.	0.4	4
2237	Evolution of the main skeleton-forming genes in sponges (phylum Porifera) with special focus on the marine Haplosclerida (class Demospongiae). Molecular Phylogenetics and Evolution, 2019, 131, 245-253.	1.2	13
2238	Balancing Specificity and Promiscuity in Enzyme Evolution: Multidimensional Activity Transitions in the Alkaline Phosphatase Superfamily. Journal of the American Chemical Society, 2019, 141, 370-387.	6.6	35
2239	The Influence of Protein Stability on Sequence Evolution: Applications to Phylogenetic Inference. Methods in Molecular Biology, 2019, 1851, 215-231.	0.4	9
2240	Computational Methods in Protein Evolution. Methods in Molecular Biology, 2019, , .	0.4	1
2241	Absence of Relationship between Mitochondrial DNA Evolutionary Rate and Longevity in Mammals except for CYTB. Journal of Mammalian Evolution, 2019, 26, 1-7.	1.0	1
2242	Model Choice, Missing Data, and Taxon Sampling Impact Phylogenomic Inference of Deep Basidiomycota Relationships. Systematic Biology, 2020, 69, 17-37.	2.7	34

#	Article	IF	Citations
2243	A chromosomeâ€level genome assembly of Pyropia haitanensis (Bangiales, Rhodophyta). Molecular Ecology Resources, 2020, 20, 216-227.	2.2	37
2244	Comparative genome/transcriptome analysis probes Boraginales' phylogenetic position, WGDs in Boraginales, and key enzyme genes in the alkannin/shikonin core pathway. Molecular Ecology Resources, 2020, 20, 228-241.	2.2	24
2245	Genomeâ€wide identification and analysis of genes encoding cuticular proteins in the endoparasitoid wasp Pteromalus puparum (Hymenoptera: Pteromalidae). Archives of Insect Biochemistry and Physiology, 2020, 103, e21628.	0.6	8
2246	Parallel Concerted Evolution of Ribosomal Protein Genes in Fungi and Its Adaptive Significance. Molecular Biology and Evolution, 2020, 37, 455-468.	3.5	14
2247	The Evolutionary History of Ephs and Ephrins: Toward Multicellular Organisms. Molecular Biology and Evolution, 2020, 37, 379-394.	3.5	13
2248	Evolution of P2A and P5A ATPases: ancient gene duplications and the red algal connection to green plants revisited. Physiologia Plantarum, 2020, 168, 630-647.	2.6	11
2249	Characterization of Nme5-Like Gene/Protein from the Red Alga Chondrus Crispus. Marine Drugs, 2020, 18, 13.	2.2	5
2250	Molecular characterization and ornithine-urea cycle genes expression in air-breathing magur catfish (Clarias magur) during exposure to high external ammonia. Genomics, 2020, 112, 2247-2260.	1.3	12
2251	Diversity and Expression Patterns of MADS-Box Genes in Gnetum luofuenseâ€"Implications for Functional Diversity and Evolution. Tropical Plant Biology, 2020, 13, 36-49.	1.0	8
2252	Characterization of two kcnk3 genes in Nile tilapia (Oreochromis niloticus): Molecular cloning, tissue distribution, and transcriptional changes in various salinity of seawater. Genomics, 2020, 112, 2213-2222.	1.3	8
2253	The family of amphioxus chitin synthases offers insight into the evolution of chitin formation in chordates. Molecular Phylogenetics and Evolution, 2020, 143, 106691.	1.2	3
2254	Variation of mitochondrial minichromosome composition in Hoplopleura lice (Phthiraptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	12
2255	Genome-wide identification and expression analysis of the carotenoid metabolic pathway genes in pepper (Capsicum annuum L.). Biotechnology and Biotechnological Equipment, 2020, 34, 1134-1149.	0.5	3
2256	Combined Comparative Genomics and Gene Expression Analyses Provide Insights into the Terpene Synthases Inventory in Trichoderma. Microorganisms, 2020, 8, 1603.	1.6	25
2257	Genome-Wide Analysis of Chemosensory Protein Genes (CSPs) Family in Fig Wasps (Hymenoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	4
2258	Evolutionary Dynamics of Transposable Elements Following a Shared Polyploidization Event in the Tribe Andropogoneae. G3: Genes, Genomes, Genetics, 2020, 10, 4387-4398.	0.8	9
2259	Single-Cell Transcriptomics of Abedinium Reveals a New Early-Branching Dinoflagellate Lineage. Genome Biology and Evolution, 2020, 12, 2417-2428.	1.1	11
2260	Genome-wide characterization of Toll-like receptors in black rockfish Sebastes schlegelii: Evolution and response mechanisms following Edwardsiella tarda infection. International Journal of Biological Macromolecules, 2020, 164, 949-962.	3.6	28

#	Article	IF	Citations
2261	The de novo genome assembly of Tapiscia sinensis and the transcriptomic and developmental bases of androdioecy. Horticulture Research, 2020, 7, 191.	2.9	3
2262	A conserved regulator controls asexual sporulation in the fungal pathogen Candida albicans. Nature Communications, 2020, 11, 6224.	5.8	10
2263	Molecular variation in a functionally divergent homolog of FCA regulates flowering time in Arabidopsis thaliana. Nature Communications, 2020, 11, 5830.	5.8	14
2264	Complete mitochondrial genome of Spilosoma lubricipedum (Noctuoidea: Erebidae) and implications for phylogeny of noctuid insects. Genomics, 2020, 112, 4577-4584.	1.3	5
2265	Assessing the utility of Hsp90 gene for inferring evolutionary relationships within the ciliate subclass Hypotricha (Protista, Ciliophora). BMC Evolutionary Biology, 2020, 20, 86.	3.2	1
2266	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. BMC Biology, 2020, 18, 90.	1.7	40
2267	Pathogenic Adaptations Revealed by Comparative Genome Analyses of Two Colletotrichum spp., the Causal Agent of Anthracnose in Rubber Tree. Frontiers in Microbiology, 2020, 11, 1484.	1.5	9
2268	Genomic Characterization and Expression of Juvenile Hormone Esterase-Like Carboxylesterase Genes in Pacific White Shrimp, Litopenaeus vannamei. International Journal of Molecular Sciences, 2020, 21, 5444.	1.8	6
2269	Contingency between Historical Substitutions in the Acetylcholine Receptor Pore. ACS Chemical Neuroscience, 2020, 11, 2861-2868.	1.7	5
2270	Ethylene-independent functions of the ethylene precursor ACC in Marchantia polymorpha. Nature Plants, 2020, 6, 1335-1344.	4.7	46
2271	Conserved sequence motifs in the abiotic stress response protein late embryogenesis abundant 3. PLoS ONE, 2020, 15, e0237177.	1.1	12
2272	Fragmented mitochondrial genomes evolved in opposite directions between closely related macaque louse Pedicinus obtusus and colobus louse Pedicinus badii. Genomics, 2020, 112, 4924-4933.	1.3	17
2273	Chikungunya virus Detection in Aedes aegypti and Culex quinquefasciatus during an Outbreak in the Amazon Region. Viruses, 2020, 12, 853.	1.5	8
2274	Infectivity and genes differentially expressed between young and aging theront cells of the marine fish parasite Cryptocaryon irritans. PLoS ONE, 2020, 15, e0238167.	1.1	7
2275	Natural variation of root lesion nematode antagonism in the biocontrol fungus Clonostachys rosea and identification of biocontrol factors through genomeâ€wide association mapping. Evolutionary Applications, 2020, 13, 2264-2283.	1.5	12
2276	Unravelling the developmental and functional significance of an ancient Argonaute duplication. Nature Communications, 2020, 11, 6187.	5.8	17
2277	A horizontally acquired expansin gene increases virulence of the emerging plant pathogen Erwinia tracheiphila. Scientific Reports, 2020, 10, 21743.	1.6	6
2278	Origins and Stepwise Expansion of R2R3-MYB Transcription Factors for the Terrestrial Adaptation of Plants. Frontiers in Plant Science, 2020, 11, 575360.	1.7	11

#	Article	IF	Citations
2279	Open gaps in the evolution of the eukaryotic nucleotide excision repair. DNA Repair, 2020, 95, 102955.	1.3	5
2280	Predicted AS3MT Proteins Methylate Arsenic and Support Two Major Phylogenetic AS3MT Groups. Chemical Research in Toxicology, 2020, 33, 3041-3047.	1.7	13
2281	Hemocyanin and hexamerinsÂexpression in response to hypoxia in stoneflies (Plecoptera, Insecta). Archives of Insect Biochemistry and Physiology, 2020, 105, e21743.	0.6	5
2282	Ancient origin and complex evolution of porcine endogenous retroviruses. Biosafety and Health, 2020, 2, 142-151.	1.2	7
2283	Assessment of Gene Flow to Wild Relatives and Nutritional Composition of Sugarcane in Brazil. Frontiers in Bioengineering and Biotechnology, 2020, 8, 598.	2.0	6
2284	New insights into the evolution and expression dynamics of invertase gene family in Solanum lycopersicum. Plant Growth Regulation, 2020, 92, 205-217.	1.8	5
2285	Microbial Metabolic Potential of Phenol Degradation in Wastewater Treatment Plant of Crude Oil Refinery: Analysis of Metagenomes and Characterization of Isolates. Microorganisms, 2020, 8, 652.	1.6	16
2286	Myriapod haemocyanin: the first three-dimensional reconstruction of Scolopendra subspinipes and preliminary structural analysis of S. viridicornis. Open Biology, 2020, 10, 190258.	1.5	1
2287	Selenoprotein T: An Essential Oxidoreductase Serving as a Guardian of Endoplasmic Reticulum Homeostasis. Antioxidants and Redox Signaling, 2020, 33, 1257-1275.	2.5	34
2288	More Than One-to-Four via 2R: Evidence of an Independent Amphioxus Expansion and Two-Gene Ancestral Vertebrate State for MyoD-Related Myogenic Regulatory Factors (MRFs). Molecular Biology and Evolution, 2020, 37, 2966-2982.	3.5	15
2289	Evolutionary Trends in the Mitochondrial Genome of Archaeplastida: How Does the GC Bias Affect the Transition from Water to Land?. Plants, 2020, 9, 358.	1.6	1
2290	Gene editing of three BnITPK genes in tetraploid oilseed rape leads to significant reduction of phytic acid in seeds. Plant Biotechnology Journal, 2020, 18, 2241-2250.	4.1	84
2291	A high-quality genome provides insights into the new taxonomic status and genomic characteristics of Cladopus chinensis (Podostemaceae). Horticulture Research, 2020, 7, 46.	2.9	11
2292	Exceptional diversity of opsin expression patterns in Neogonodactylus oerstedii (Stomatopoda) retinas. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8948-8957.	3.3	22
2293	New Insights into Evolution of Plant Heat Shock Factors (Hsfs) and Expression Analysis of Tea Genes in Response to Abiotic Stresses. Plants, 2020, 9, 311.	1.6	11
2294	The Coevolution of Fungal Mitochondrial Introns and Their Homing Endonucleases (GIY-YIG and) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	46
2295	A new phylogenetic protocol: dealing with model misspecification and confirmation bias in molecular phylogenetics. NAR Genomics and Bioinformatics, 2020, 2, lqaa041.	1.5	15
2296	The complete mitochondrial genome of the eusocial sponge-dwelling snapping shrimp Synalpheus microneptunus. Scientific Reports, 2020, 10, 7744.	1.6	12

#	Article	IF	Citations
2297	Cooperation between passive and active silicon transporters clarifies the ecophysiology and evolution of biosilicification in sponges. Science Advances, 2020, 6, eaba9322.	4.7	22
2298	Detecting Signatures of Positive Selection against a Backdrop of Compensatory Processes. Molecular Biology and Evolution, 2020, 37, 3353-3362.	3.5	2
2299	Genome-Based Metabolic Reconstruction Unravels the Key Role of B12 in Methionine Auxotrophy of an Ortho-Phenylphenol-Degrading Sphingomonas haloaromaticamans. Frontiers in Microbiology, 2019, 10, 3009.	1.5	8
2300	Holothurians have a reduced GPCR and odorant receptor-like repertoire compared to other echinoderms. Scientific Reports, 2020, 10, 3348.	1.6	16
2301	Shared Mutations in a Novel Glutaredoxin Repressor of Multicellular Trichome Fate Underlie Parallel Evolution of Antirrhinum Species. Current Biology, 2020, 30, 1357-1366.e4.	1.8	10
2302	Recombinant expression, characterization and phylogenetic studies of novels cystatins-like proteins of sweet orange (Citrus sinensis) and clementine (Citrus clementina). International Journal of Biological Macromolecules, 2020, 152, 546-553.	3.6	6
2303	Characterization of the mitogenome of Rhammatocerus brasiliensis and phylogenetic analysis of the family Acrididae (Orthoptera). Gene, 2020, 731, 144362.	1.0	2
2304	Proteome analysis of leaf, stem and callus in Viscum album and identification of lectins and viscotoxins with bioactive properties. Plant Cell, Tissue and Organ Culture, 2020, 141, 167-178.	1.2	7
2305	Identification and stable expression of vitellogenin receptor through vitellogenesis in the European eel. Animal, 2020, 14, 1213-1222.	1.3	12
2306	Molecular characterization of two leptin genes and their transcriptional changes in response to fasting and refeeding in Northern snakehead (Channa argus). Gene, 2020, 736, 144420.	1.0	16
2307	Maize E2F transcription factors. Expression, association to promoters of S-phase genes and interaction with the RBR1 protein in chromatin during seed germination. Plant Science, 2020, 296, 110491.	1.7	5
2308	Draft genomes of two Atlantic bay scallop subspecies Argopecten irradians irradians and A. i. concentricus. Scientific Data, 2020, 7, 99.	2.4	37
2309	Complete mitogenomic and phylogenetic characteristics of the speckled wood-pigeon (Columba) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	6
2310	Characterization of the Complete Mitochondrial Genome of Epicauta impressicornis (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock Science, 2020, 20, .	0.6	8
2311	Rubisco and carbonâ€concentrating mechanism coâ€evolution across chlorophyte and streptophyte green algae. New Phytologist, 2020, 227, 810-823.	3.5	28
2312	Genomic Organization and Comparative Phylogenic Analysis of NBS-LRR Resistance Gene Family inSolanum pimpinellifoliumandArabidopsis thaliana. Evolutionary Bioinformatics, 2020, 16, 117693432091105.	0.6	14
2313	Insight into the Functional Diversification of Lipases in the Endoparasitoid Pteromalus puparum (Hymenoptera: Pteromalidae) by Genome-scale Annotation and Expression Analysis. Insects, 2020, 11, 227.	1.0	7
2314	Characterization and expression analysis of Nod-like receptor 3 (NLRC3) against infection with Piscirickettsia salmonis in Atlantic salmon. Developmental and Comparative Immunology, 2021, 114, 103865.	1.0	13

#	Article	IF	Citations
2315	The complete mitochondrial genome of the red-jointed brackish-water fiddler crab Minuca minax (LeConte 1855) (Brachyura: Ocypodidae): New family gene order, and purifying selection and phylogenetic informativeness of protein coding genes. Genomics, 2021, 113, 565-572.	1.3	8
2316	Culturing novel and abundant pelagiphages in the ocean. Environmental Microbiology, 2021, 23, 1145-1161.	1.8	27
2317	Unexpected Discovery and Expression of Amphibian Class II Endogenous Retroviruses. Journal of Virology, 2021, 95, .	1.5	5
2318	Multiple Sequence Alignment for Large Heterogeneous Datasets Using SATÃ©, PASTA, and UPP. Methods in Molecular Biology, 2021, 2231, 99-119.	0.4	1
2319	Discovery of divided RdRp sequences and a hitherto unknown genomic complexity in fungal viruses. Virus Evolution, 2021, 7, veaa101.	2.2	33
2320	Characterization of five caspase genes and their transcriptional changes in response to exogenous iridescent virus challenge in the whiteleg shrimp (Litopenaeus vannamei). Aquaculture, 2021, 534, 736192.	1.7	8
2321	Cloning and characterisation of NMDA receptors in the Pacific oyster, Crassostrea gigas (Thunberg,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 144-159.	0.9	5
2322	Comparative multi-omics analyses reveal differential expression of key genes relevant for parasitism between non-encapsulated and encapsulated Trichinella. Communications Biology, 2021, 4, 134.	2.0	4
2323	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. Briefings in Bioinformatics, 2021, 22, 631-641.	3.2	38
2324	Mitogenome of Coprophanaeus ensifer and phylogenetic analysis of the Scarabaeidae family (Coleoptera). Genetics and Molecular Biology, 2021, 44, e20200417.	0.6	1
2325	Combined whole cell wall analysis and streamlined in silico carbohydrate-active enzyme discovery to improve biocatalytic conversion of agricultural crop residues. Biotechnology for Biofuels, 2021, 14, 16.	6.2	15
2326	Endogenization of a Prosimian Retrovirus during Lemur Evolution. Viruses, 2021, 13, 383.	1.5	2
2327	Paracellular and Transcellular Leukocytes Diapedesis Are Divergent but Interconnected Evolutionary Events. Genes, 2021, 12, 254.	1.0	20
2328	Exopolysaccharide Characterization of Rhizobium favelukesii LPU83 and Its Role in the Symbiosis With Alfalfa. Frontiers in Plant Science, 2021, 12, 642576.	1.7	7
2329	Association of T2/S-RNase With Self-Incompatibility of Japanese Citrus Accessions Examined by Transcriptomic, Phylogenetic, and Genetic Approaches. Frontiers in Plant Science, 2021, 12, 638321.	1.7	10
2330	A novel vieuvirus from multidrug-resistant Acinetobacter baumannii. Archives of Virology, 2021, 166, 1401-1408.	0.9	6
2331	Convergent Biochemical Pathways for Xanthine Alkaloid Production in Plants Evolved from Ancestral Enzymes with Different Catalytic Properties. Molecular Biology and Evolution, 2021, 38, 2704-2714.	3.5	6
2332	The myxozoan minicollagen gene repertoire was not simplified by the parasitic lifestyle: computational identification of a novel myxozoan minicollagen gene. BMC Genomics, 2021, 22, 198.	1.2	4

#	Article	IF	Citations
2333	Distinct plastid fructose bisphosphate aldolases function in photosynthetic and non-photosynthetic metabolism in Arabidopsis. Journal of Experimental Botany, 2021, 72, 3739-3755.	2.4	19
2334	The Crown Pearl: a draft genome assembly of the European freshwater pearl musselMargaritifera margaritifera(Linnaeus, 1758). DNA Research, 2021, 28, .	1.5	15
2335	Utilization of Cobalamin Is Ubiquitous in Early-Branching Fungal Phyla. Genome Biology and Evolution, 2021, 13, .	1.1	9
2336	Characterization of the Ergosterol Biosynthesis Pathway in Ceratocystidaceae. Journal of Fungi (Basel, Switzerland), 2021, 7, 237.	1.5	0
2337	MRAP2 Interaction with Melanocortin-4 Receptor in SnakeHead (Channa argus). Biomolecules, 2021, 11, 481.	1.8	23
2338	Ascorbate Peroxidase Neofunctionalization at the Origin of APX-R and APX-L: Evidence from Basal Archaeplastida. Antioxidants, 2021, 10, 597.	2.2	11
2339	A phylogenetic study of the members of the MAPK and MEK families across Viridiplantae. PLoS ONE, 2021, 16, e0250584.	1.1	4
2340	Genome-wide evolution of MAPKs family and their expression in response to bacterial infection in seahorse Hippocampus erectus. Journal of Oceanology and Limnology, 2021, 39, 2309-2321.	0.6	4
2341	A highly conserved mechanism for the detoxification and assimilation of the toxic phytoproduct L-azetidine-2-carboxylic acid in Aspergillus nidulans. Scientific Reports, 2021, 11, 7391.	1.6	3
2342	Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. Molecular Systems Biology, 2021, 17, e9880.	3.2	33
2343	Highly rearranged mitochondrial genome in Falcolipeurus lice (Phthiraptera: Philopteridae) from endangered eagles. Parasites and Vectors, 2021, 14, 269.	1.0	6
2344	Listeria cossartiae sp. nov., Listeria immobilis sp. nov., Listeria portnoyi sp. nov. and Listeria rustica sp. nov., isolated from agricultural water and natural environments. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	54
2345	Reenacting the Birth of a Function: Functional Divergence of HIUases and Transthyretins as Inferred by Evolutionary and Biophysical Studies. Journal of Molecular Evolution, 2021, 89, 370-383.	0.8	1
2346	Galanin isoforms by alternative splicing: Structure, expression, and immunohistochemical location in the gonads of European sea bass. General and Comparative Endocrinology, 2021, 305, 113730.	0.8	4
2347	Phylogeny Validation for Some Egyptian Brassicaceae Endemic Species. Arab Universities Journal of Agricultural Sciences, 2021, .	0.0	0
2348	A natural symbiotic bacterium drives mosquito refractoriness to Plasmodium infection via secretion of an antimalarial lipase. Nature Microbiology, 2021, 6, 806-817.	5.9	44
2350	Molecular Characterisation of Soybean Osmotins and Their Involvement in Drought Stress Response. Frontiers in Genetics, 2021, 12, 632685.	1.1	5
2351	Multiple Infiltration and Cross-Species Transmission of Foamy Viruses across the Paleozoic to the Cenozoic Era. Journal of Virology, 2021, 95, e0048421.	1.5	7

#	Article	IF	Citations
2352	Contingency and chance erase necessity in the experimental evolution of ancestral proteins. ELife, 2021, 10, .	2.8	30
2353	Comparative mitochondrial genomics of sponge-dwelling snapping shrimps in the genus Synalpheus: Exploring differences between eusocial and non-eusocial species and insights into phylogenetic relationships in caridean shrimps. Gene, 2021, 786, 145624.	1.0	1
2355	Helastic: On combining threshold-based and Serverless elasticity approaches for optimizing the execution of bioinformatics applications. Journal of Computational Science, 2021, 53, 101407.	1.5	4
2356	Genomic and transcriptomic analyses reveal metabolic complementarity between whiteflies and their symbionts. Insect Science, 2022, 29, 539-549.	1.5	9
2357	Characterization of the complete mitochondrial genome of the swine kidney worm Stephanurus dentatus (Nematoda: Syngamidae) and phylogenetic implications. Veterinary Parasitology, 2021, 295, 109475.	0.7	4
2358	Genomic and Experimental Investigations of Auriscalpium and Strobilurus Fungi Reveal New Insights into Pinecone Decomposition. Journal of Fungi (Basel, Switzerland), 2021, 7, 679.	1.5	1
2359	Genome-wide identification and analysis of NOD-like receptors and their potential roles in response to Edwardsiella tarda infection in black rockfish (Sebastes schlegelii). Aquaculture, 2021, 541, 736803.	1.7	12
2362	Lamprey lecticans link new vertebrate genes to the origin and elaboration of vertebrate tissues. Developmental Biology, 2021, 476, 282-293.	0.9	5
2363	The Archean origin of oxygenic photosynthesis and extant cyanobacterial lineages. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210675.	1.2	48
2364	Phylogeny and subcellular localization analyses reveal distinctions in monocot and eudicot class IV acyl-CoA-binding proteins. Planta, 2021, 254, 71.	1.6	4
2365	Identification of Chicken Transglutaminase 1 and In Situ Localization of Transglutaminase Activity in Avian Skin and Esophagus. Genes, 2021, 12, 1565.	1.0	4
2366	Reassessing the evolution of the 1-deoxy-D-xylulose 5-phosphate synthase family suggests a possible novel function for the DXS class 3 proteins. Plant Science, 2021, 310, 110960.	1.7	9
2367	Novel Fusari- and Toti-like Viruses, with Probable Different Origins, in the Plant Pathogenic Oomycete Globisporangium ultimum. Viruses, 2021, 13, 1931.	1.5	5
2368	HES and Mox genes are expressed during early mesoderm formation in a mollusk with putative ancestral features. Scientific Reports, 2021, 11, 18030.	1.6	1
2369	Description of four Millepora spp. transcriptomes and their potential to delimit the Caribbean fire coral species. Marine Genomics, 2021, 59, 100863.	0.4	0
2370	The complete mitochondrial genome of the Honduran white bat Ectophylla alba (Allen 1982) (Chiroptera: Phyllostomidae). Gene, 2021, 802, 145868.	1.0	7
2371	CC chemokines and their receptors in black rockfish (Sebastes schlegelii): Characterization, evolutionary analysis, and expression patterns after Aeromonas Salmonicida infection. Aquaculture, 2022, 546, 737377.	1.7	8
2372	Integrative multiomics analysis of Premolis semirufa caterpillar venom in the search for molecules leading to a joint disease. Scientific Reports, 2021, 11, 1995.	1.6	2

#	Article	IF	Citations
2373	Phylogenetic analysis of the caspase family in bivalves: implications for programmed cell death, immune response and development. BMC Genomics, 2021, 22, 80.	1.2	26
2374	Large-Scale Multiple Sequence Alignment and Phylogeny Estimation. Computational Biology, 2013, , 85-146.	0.1	14
2375	Phylogenetic Model Evaluation. Methods in Molecular Biology, 2008, 452, 331-364.	0.4	54
2376	Large-Scale Multiple Sequence Alignment and Tree Estimation Using SATÃ©. Methods in Molecular Biology, 2014, 1079, 219-244.	0.4	18
2377	Identification of Distinctive Variants of the Olive Pollen Allergen Ole e 5 (Cu,Zn Superoxide) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Tc Science, 2015, , 460-470.	1.0	2
2378	Characterization of hydroxymethylpyrimidine phosphate kinase from mesophilic and thermophilic bacteria and structural insights into their differential thermal stability. Archives of Biochemistry and Biophysics, 2020, 688, 108389.	1.4	6
2379	Comparative mitochondrial genome analysis of Spilarctia subcarnea and other noctuid insects. International Journal of Biological Macromolecules, 2018, 107, 121-128.	3.6	25
2380	BMP signaling plays a role in anterior-neural/head development, but not organizer activity, in the gastropod Crepidula fornicata. Developmental Biology, 2020, 463, 135-157.	0.9	20
2381	Probabilistic models and their impact on the accuracy of reconstructed ancestral protein sequences. , 2007, , 43-57.		6
2382	Codon models applied to the study of fungal genomes. , 2012, , 164-186.		2
2383	Aliterella atlantica gen. nov., sp. nov., and Aliterella antarctica sp. nov., novel members of coccoid Cyanobacteria. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2853-2861.	0.8	36
2384	Multigenetic characterization of â€˜Candidatus Xenohaliotis californiensisâ€™. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 42-49.	0.8	10
2385	Mixta gen. nov., a new genus in the Erwiniaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1396-1407.	0.8	53
2386	Evidence confirming the phylogenetic position of Anaplasma centrale (ex Theiler 1911) Ristic and Kreier 1984. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2682-2691.	0.8	13
2387	An all-atom, active site exploration of antiviral drugs that target Flaviviridae polymerases. Journal of General Virology, 2016, 97, 2552-2565.	1.3	5
2388	New insights into reovirus evolution: implications from a newly characterized mycoreovirus. Journal of General Virology, 2017, 98, 1132-1141.	1.3	9
2389	The discovery of Halictivirus resolves the Sinaivirus phylogeny. Journal of General Virology, 2017, 98, 2864-2875.	1.3	31
2390	Fish polyomaviruses belong to two distinct evolutionary lineages. Journal of General Virology, 2018, 99, 567-573.	1.3	19

#	Article	IF	Citations
2391	Linkage of the Nit1C gene cluster to bacterial cyanide assimilation as a nitrogen source. Microbiology (United Kingdom), 2018, 164, 956-968.	0.7	10
2392	Rat cytomegalovirus (RCMV) English isolate and a newly identified Berlin isolate share similarities with but are separate as an anciently diverged clade from Mouse CMV and the Maastricht isolate of RCMV. Journal of General Virology, 2015, 96, 1873-1882.	1.3	15
2393	Novel parvoviruses in reptiles and genome sequence of a lizard parvovirus shed light on Dependoparvovirus genus evolution. Journal of General Virology, 2015, 96, 2769-2779.	1.3	17
2394	Genetic diversity of simian lentivirus in wild De Brazza's monkeys (Cercopithecus neglectus) in Equatorial Africa. Journal of General Virology, 2010, 91, 1810-1816.	1.3	6
2395	Metagenomic identification of a novel anellovirus in Pacific harbor seal (Phoca vitulina richardsii) lung samples and its detection in samples from multiple years. Journal of General Virology, 2011, 92, 1318-1323.	1.3	61
2418	Crystal structure of an inferred ancestral bacterial pyruvate decarboxylase. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 179-186.	0.4	3
2419	Efficient SIVcpz replication in human lymphoid tissue requires viral matrix protein adaptation. Journal of Clinical Investigation, 2012, 122, 1644-1652.	3.9	44
2420	Hal: an Automated Pipeline for Phylogenetic Analyses of Genomic Data. PLOS Currents, 2011, 3, RRN1213.	1.4	65
2421	Building a Phylogenomic Pipeline for the Eukaryotic Tree of Life - Addressing Deep Phylogenies with Genome-Scale Data. PLOS Currents, 2014, 6, .	1.4	30
2422	MamO Is a Repurposed Serine Protease that Promotes Magnetite Biomineralization through Direct Transition Metal Binding in Magnetotactic Bacteria. PLoS Biology, 2016, 14, e1002402.	2.6	43
2423	Evolutionary and Functional Relationships in the Truncated Hemoglobin Family. PLoS Computational Biology, 2016, 12, e1004701.	1.5	36
2424	Consequences of Lineage-Specific Gene Loss on Functional Evolution of Surviving Paralogs: ALDH1A and Retinoic Acid Signaling in Vertebrate Genomes. PLoS Genetics, 2009, 5, e1000496.	1.5	69
2425	ROOT HAIR DEFECTIVE SIX-LIKE Class I Genes Promote Root Hair Development in the Grass Brachypodium distachyon. PLoS Genetics, 2016, 12, e1006211.	1.5	54
2426	Pre-Bilaterian Origins of the Hox Cluster and the Hox Code: Evidence from the Sea Anemone, Nematostella vectensis. PLoS ONE, 2007, 2, e153.	1.1	198
2427	Transient Receptor Potential Ion Channels Control Thermoregulatory Behaviour in Reptiles. PLoS ONE, 2007, 2, e281.	1.1	42
2428	A Post-Synaptic Scaffold at the Origin of the Animal Kingdom. PLoS ONE, 2007, 2, e506.	1.1	215
2429	Phylogenomics Reshuffles the Eukaryotic Supergroups. PLoS ONE, 2007, 2, e790.	1.1	352
2430	Early Evolution of Ionotropic GABA Receptors and Selective Regimes Acting on the Mammalian-Specific Theta and Epsilon Subunits. PLoS ONE, 2007, 2, e894.	1.1	18

#	Article	IF	Citations
2431	The Origins of Novel Protein Interactions during Animal Opsin Evolution. PLoS ONE, 2007, 2, e1054.	1.1	99
2432	Multigene Phylogeny of Choanozoa and the Origin of Animals. PLoS ONE, 2008, 3, e2098.	1.1	235
2433	Life-Cycle and Genome of OtV5, a Large DNA Virus of the Pelagic Marine Unicellular Green Alga Ostreococcus tauri. PLoS ONE, 2008, 3, e2250.	1.1	107
2434	EEF2 Analysis Challenges the Monophyly of Archaeplastida and Chromalveolata. PLoS ONE, 2008, 3, e2621.	1.1	57
2435	Seventeen New Complete mtDNA Sequences Reveal Extensive Mitochondrial Genome Evolution within the Demospongiae. PLoS ONE, 2008, 3, e2723.	1.1	122
2436	A Comparative Structural Bioinformatics Analysis of the Insulin Receptor Family Ectodomain Based on Phylogenetic Information. PLoS ONE, 2008, 3, e3667.	1.1	45
2437	A Hypothesis for the Evolution of Nuclear-Encoded, Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenase Genes in â€œChromalveolateâ€•Members. PLoS ONE, 2009, 4, e4737.	1.1	25
2438	Distribution and Phylogeny of EFL and EF-1Î± in Euglenozoa Suggest Ancestral Co-Occurrence Followed by Differential Loss. PLoS ONE, 2009, 4, e5162.	1.1	24
2439	Evolution of the B3 DNA Binding Superfamily: New Insights into REM Family Gene Diversification. PLoS ONE, 2009, 4, e5791.	1.1	128
2440	Solution Structure and Phylogenetics of Prod1, a Member of the Three-Finger Protein Superfamily Implicated in Salamander Limb Regeneration. PLoS ONE, 2009, 4, e7123.	1.1	62
2441	PALM: A Paralleled and Integrated Framework for Phylogenetic Inference with Automatic Likelihood Model Selectors. PLoS ONE, 2009, 4, e8116.	1.1	36
2442	The Mitochondrial Genome of the Entomoparasitic Green Alga Helicosporidium. PLoS ONE, 2010, 5, e8954.	1.1	46
2443	Phylogenomic Analysis of Marine Roseobacters. PLoS ONE, 2010, 5, e11604.	1.1	29
2444	Two Origins for the Gene Encoding Î±-Isopropylmalate Synthase in Fungi. PLoS ONE, 2010, 5, e11605.	1.1	16
2445	Two Lamprey Hedgehog Genes Share Non-Coding Regulatory Sequences and Expression Patterns with Gnathostome Hedgehogs. PLoS ONE, 2010, 5, e13332.	1.1	22
2446	Molecular Phylogeny Restores the Supra-Generic Subdivision of Homoscleromorph Sponges (Porifera,) Tj ETQq1 1 0.784314 rgBT /Ov	1.1	76
2447	Tracing the Origin of the Fungal Î±1 Domain Places Its Ancestor in the HMG-Box Superfamily: Implication for Fungal Mating-Type Evolution. PLoS ONE, 2010, 5, e15199.	1.1	93
2448	Molecular Phylogeny of the Astrophorida (Porifera, Demospongiaep) Reveals an Unexpected High Level of Spicule Homoplasy. PLoS ONE, 2011, 6, e18318.	1.1	74

#	Article	IF	Citations
2449	Origin of Secretin Receptor Precedes the Advent of Tetrapoda: Evidence on the Separated Origins of Secretin and Orexin. PLoS ONE, 2011, 6, e19384.	1.1	17
2450	Wolbachia Prophage DNA Adenine Methyltransferase Genes in Different Drosophila-Wolbachia Associations. PLoS ONE, 2011, 6, e19708.	1.1	27
2451	Comparative Genomics of the Mating-Type Loci of the Mushroom Flammulina velutipes Reveals Widespread Synteny and Recent Inversions. PLoS ONE, 2011, 6, e22249.	1.1	54
2452	The Vein Patterning 1 (VEP1) Gene Family Laterally Spread through an Ecological Network. PLoS ONE, 2011, 6, e22279.	1.1	16
2453	Diversification and Molecular Evolution of ATOH8, a Gene Encoding a bHLH Transcription Factor. PLoS ONE, 2011, 6, e23005.	1.1	24
2454	Comparative Analysis of Serine/Arginine-Rich Proteins across 27 Eukaryotes: Insights into Sub-Family Classification and Extent of Alternative Splicing. PLoS ONE, 2011, 6, e24542.	1.1	69
2455	Parallel Evolution of KCNQ4 in Echolocating Bats. PLoS ONE, 2011, 6, e26618.	1.1	39
2456	Phylogenetic and Complementation Analysis of a Single-Stranded DNA Binding Protein Family from Lactococcal Phages Indicates a Non-Bacterial Origin. PLoS ONE, 2011, 6, e26942.	1.1	8
2457	Interkingdom Gene Transfer of a Hybrid NPS/PKS from Bacteria to Filamentous Ascomycota. PLoS ONE, 2011, 6, e28231.	1.1	52
2458	Paleogene Radiation of a Plant Pathogenic Mushroom. PLoS ONE, 2011, 6, e28545.	1.1	31
2459	Incorporation of a Horizontally Transferred Gene into an Operon during Cnidarian Evolution. PLoS ONE, 2012, 7, e31643.	1.1	20
2460	Functional Desaturase Fads1 (Î”5) and Fads2 (Î”6) Orthologues Evolved before the Origin of Jawed Vertebrates. PLoS ONE, 2012, 7, e31950.	1.1	121
2461	Impact of Carnivory on Human Development and Evolution Revealed by a New Unifying Model of Weaning in Mammals. PLoS ONE, 2012, 7, e32452.	1.1	24
2462	Using Paleogenomics to Study the Evolution of Gene Families: Origin and Duplication History of the Relaxin Family Hormones and Their Receptors. PLoS ONE, 2012, 7, e32923.	1.1	50
2463	Molecular Evolution of the Neuropeptide S Receptor. PLoS ONE, 2012, 7, e34046.	1.1	20
2464	Multiple Episodes of Convergence in Genes of the Dim Light Vision Pathway in Bats. PLoS ONE, 2012, 7, e34564.	1.1	10
2465	Similar Genetic Mechanisms Underlie the Parallel Evolution of Floral Phenotypes. PLoS ONE, 2012, 7, e36033.	1.1	35
2466	Basal Jawed Vertebrate Phylogenomics Using Transcriptomic Data from Solexa Sequencing. PLoS ONE, 2012, 7, e36256.	1.1	27

#	Article	IF	Citations
2467	Skipping of Exons by Premature Termination of Transcription and Alternative Splicing within Intron-5 of the Sheep SCF Gene: A Novel Splice Variant. PLoS ONE, 2012, 7, e38657.	1.1	5
2468	Specific Evolution of F1-Like ATPases in Mycoplasmas. PLoS ONE, 2012, 7, e38793.	1.1	40
2469	Genes for the Major Structural Components of Thermotogales Speciesâ€™ Togas Revealed by Proteomic and Evolutionary Analyses of OmpA and OmpB Homologs. PLoS ONE, 2012, 7, e40236.	1.1	22
2470	Candidatus Sodalis melophagi sp. nov.: Phylogenetically Independent Comparative Model to the Tsetse Fly Symbiont Sodalis glossinidius. PLoS ONE, 2012, 7, e40354.	1.1	41
2471	Assessing Whether Alpha-Tubulin Sequences Are Suitable for Phylogenetic Reconstruction of Ciliophora with Insights into Its Evolution in Euplotids. PLoS ONE, 2012, 7, e40635.	1.1	30
2472	The Complete Mitochondrial Genome of Galba pervia (Gastropoda: Mollusca), an Intermediate Host Snail of Fasciola spp. PLoS ONE, 2012, 7, e42172.	1.1	33
2473	Phylogenomic Resolution of Paleozoic Divergences in Harvestmen (Arachnida, Opiliones) via Analysis of Next-Generation Transcriptome Data. PLoS ONE, 2012, 7, e42888.	1.1	57
2474	A Mitogenomic Re-Evaluation of the Bdelloid Phylogeny and Relationships among the Syndermata. PLoS ONE, 2012, 7, e43554.	1.1	17
2475	Agnathan VIP, PACAP and Their Receptors: Ancestral Origins of Today's Highly Diversified Forms. PLoS ONE, 2012, 7, e44691.	1.1	28
2476	The Protease Degrading Sperm Histones Post-Fertilization in Sea Urchin Eggs Is a Nuclear Cathepsin L That Is Further Required for Embryo Development. PLoS ONE, 2012, 7, e46850.	1.1	15
2477	Hyperdiversity of Genes Encoding Integral Light-Harvesting Proteins in the Dinoflagellate Symbiodinium sp. PLoS ONE, 2012, 7, e47456.	1.1	34
2478	Tick-Box for 3â€²-End Formation of Mitochondrial Transcripts in Ixodida, Basal Chelicerates and Drosophila. PLoS ONE, 2012, 7, e47538.	1.1	45
2479	Comparative Genomics of Neuroglobin Reveals Its Early Origins. PLoS ONE, 2012, 7, e47972.	1.1	27
2480	A Preliminary Molecular Phylogeny of Planthoppers (Hemiptera: Fulgoroidea) Based on Nuclear and Mitochondrial DNA Sequences. PLoS ONE, 2013, 8, e58400.	1.1	57
2481	Evolutionary Paths of the cAMP-Dependent Protein Kinase (PKA) Catalytic Subunits. PLoS ONE, 2013, 8, e60935.	1.1	46
2482	Phylogenetic Analyses of Novel Squamate Adenovirus Sequences in Wild-Caught Anolis Lizards. PLoS ONE, 2013, 8, e60977.	1.1	15
2483	Genetic Variants and Increased Expression of Parascaris equorum P-glycoprotein-11 in Populations with Decreased Ivermectin Susceptibility. PLoS ONE, 2013, 8, e61635.	1.1	61
2484	Ancestral Gene Organization in the Mitochondrial Genome of Thyridosmylus langii (McLachlan, 1870) (Neuroptera: Osmylidae) and Implications for Lacewing Evolution. PLoS ONE, 2013, 8, e62943.	1.1	30

#	Article	IF	Citations
2485	Evolution of and Horizontal Gene Transfer in the Endornavirus Genus. PLoS ONE, 2013, 8, e64270.	1.1	24
2486	Glycogen and Glucose Metabolism Are Essential for Early Embryonic Development of the Red Flour Beetle Tribolium castaneum. PLoS ONE, 2013, 8, e65125.	1.1	54
2487	Analysis of the Olive Fruit Fly Bactrocera oleae Transcriptome and Phylogenetic Classification of the Major Detoxification Gene Families. PLoS ONE, 2013, 8, e66533.	1.1	55
2488	A Novel C-Type Lysozyme from Mytilus galloprovincialis: Insight into Innate Immunity and Molecular Evolution of Invertebrate C-Type Lysozymes. PLoS ONE, 2013, 8, e67469.	1.1	20
2489	Evolution of the Plasma and Tissue Kallikreins, and Their Alternative Splicing Isoforms. PLoS ONE, 2013, 8, e68074.	1.1	40
2490	Expansion and Diversification of BTL Ring-H2 Ubiquitin Ligases in Angiosperms: Putative Rabring7/BCA2 Orthologs. PLoS ONE, 2013, 8, e72729.	1.1	12
2491	Protein Kinase C-Dependent Signaling Controls the Midgut Epithelial Barrier to Malaria Parasite Infection in Anopheline Mosquitoes. PLoS ONE, 2013, 8, e76535.	1.1	21
2492	A Molecular Evolution Approach to Study the Roles of Tropomyosin in Fission Yeast. PLoS ONE, 2013, 8, e76726.	1.1	12
2493	Pannexin1 Channel Proteins in the Zebrafish Retina Have Shared and Unique Properties. PLoS ONE, 2013, 8, e77722.	1.1	41
2494	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen Xanthomonas axonopodis pv. Manihotis Strain CIO151. PLoS ONE, 2013, 8, e79704.	1.1	42
2495	Mating Type Gene Homologues and Putative Sex Pheromone-Sensing Pathway in Arbuscular Mycorrhizal Fungi, a Presumably Asexual Plant Root Symbiont. PLoS ONE, 2013, 8, e80729.	1.1	40
2496	The Complete Mitochondrial Genomes of Two Octopods Cistopus chinensis and Cistopus taiwanicus: Revealing the Phylogenetic Position of the Genus Cistopus within the Order Octopoda. PLoS ONE, 2013, 8, e84216.	1.1	33
2497	Reconstructed Ancestral Myo-Inositol-3-Phosphate Synthases Indicate That Ancestors of the Thermococcales and Thermotoga Species Were More Thermophilic than Their Descendants. PLoS ONE, 2013, 8, e84300.	1.1	28
2498	High-Affinity Glucose Transport in Aspergillus nidulans Is Mediated by the Products of Two Related but Differentially Expressed Genes. PLoS ONE, 2014, 9, e94662.	1.1	22
2499	Evolution of Tertiary Structure of Viral RNA Dependent Polymerases. PLoS ONE, 2014, 9, e96070.	1.1	57
2500	De Novo Transcriptomes of a Mixotrophic and a Heterotrophic Ciliate from Marine Plankton. PLoS ONE, 2014, 9, e101418.	1.1	29
2501	Appearances Can Be Deceptive: Revealing a Hidden Viral Infection with Deep Sequencing in a Plant Quarantine Context. PLoS ONE, 2014, 9, e102945.	1.1	89
2502	Full Genome Characterization of the Culicoides-Borne Marsupial Orbiviruses: Wallal Virus, Mudjinbarry Virus and Warrego Viruses. PLoS ONE, 2014, 9, e108379.	1.1	9

#	Article	IF	Citations
2503	The Complete Mitochondrial Genomes of Six Species of Tetranychus Provide Insights into the Phylogeny and Evolution of Spider Mites. PLoS ONE, 2014, 9, e110625.	1.1	25
2504	The Timing of Timezyme Diversification in Vertebrates. PLoS ONE, 2014, 9, e112380.	1.1	26
2505	Analysis of the Na+/Ca2+ Exchanger Gene Family within the Phylum Nematoda. PLoS ONE, 2014, 9, e112841.	1.1	14
2506	Characterization of the Drosophila Group Ortholog to the Amino-Terminus of the Alpha-Thalassemia and Mental Retardation X-Linked (ATRX) Vertebrate Protein. PLoS ONE, 2014, 9, e113182.	1.1	10
2507	Intergenomic Comparisons Highlight Modularity of the Denitrification Pathway and Underpin the Importance of Community Structure for N2O Emissions. PLoS ONE, 2014, 9, e114118.	1.1	383
2508	New Insights into Flavivirus Evolution, Taxonomy and Biogeographic History, Extended by Analysis of Canonical and Alternative Coding Sequences. PLoS ONE, 2015, 10, e0117849.	1.1	139
2509	The Nuclear Receptors of Biomphalaria glabrata and Lottia gigantea: Implications for Developing New Model Organisms. PLoS ONE, 2015, 10, e0121259.	1.1	46
2510	Diversification, Evolution and Sub-Functionalization of 70kDa Heat-Shock Proteins in Two Sister Species of Antarctic Krill: Differences in Thermal Habitats, Responses and Implications under Climate Change. PLoS ONE, 2015, 10, e0121642.	1.1	38
2511	Glutathione S-Transferase (GST) Gene Diversity in the Crustacean Calanus finmarchicus â€“ Contributors to Cellular Detoxification. PLoS ONE, 2015, 10, e0123322.	1.1	53
2512	Candidatus Frankia Datiscae Dg1, the Actinobacterial Microsymbiont of Datisca glomerata, Expresses the Canonical nod Genes nodABC in Symbiosis with Its Host Plant. PLoS ONE, 2015, 10, e0127630.	1.1	131
2513	The Evolutionary History of MAPL (Mitochondria-Associated Protein Ligase) and Other Eukaryotic BAM/GIDE Domain Proteins. PLoS ONE, 2015, 10, e0128795.	1.1	2
2514	Functional Classification of Uncultured â€œCandidatus Caldiarchaeum subterraneumâ€•Using the Maple System. PLoS ONE, 2015, 10, e0132994.	1.1	29
2515	Phylogenetic Co-Occurrence of ExoR, ExoS, and ChvI, Components of the RSI Bacterial Invasion Switch, Suggests a Key Adaptive Mechanism Regulating the Transition between Free-Living and Host-Invading Phases in Rhizobiales. PLoS ONE, 2015, 10, e0135655.	1.1	23
2516	The Origin and Diversity of Cpt1 Genes in Vertebrate Species. PLoS ONE, 2015, 10, e0138447.	1.1	16
2517	Comparative Genomics of NAC Transcriptional Factors in Angiosperms: Implications for the Adaptation and Diversification of Flowering Plants. PLoS ONE, 2015, 10, e0141866.	1.1	43
2518	Evolution of Pentameric Ligand-Gated Ion Channels: Pro-Loop Receptors. PLoS ONE, 2016, 11, e0151934.	1.1	84
2519	Novel viruses in salivary glands of mosquitoes from sylvatic Cerrado, Midwestern Brazil. PLoS ONE, 2017, 12, e0187429.	1.1	34
2520	The effect of bio-irrigation by the polychaete Lanice conchilega on active denitrifiers: Distribution, diversity and composition of nosZ gene. PLoS ONE, 2018, 13, e0192391.	1.1	11

#	Article	IF	Citations
2521	Multispecies reconstructions uncover widespread conservation, and lineage-specific elaborations in eukaryotic mRNA metabolism. PLoS ONE, 2018, 13, e0192633.	1.1	20
2522	Evolution of CUT class homeobox genes: insights from the genome of the amphioxus, Branchiostoma floridae. International Journal of Developmental Biology, 2008, 52, 969-977.	0.3	9
2523	The complete mitochondrial genome of Pallisentis celatus (Acanthocephala) with phylogenetic analysis of acanthocephalans and rotifers. Folia Parasitologica, 2013, 60, 181-191.	0.7	18
2524	Inter and Intra Variation of Potato Yellow Vein Virus in Three Potato Species From Colombia. Revista Facultad Nacional De Agronomia Medellin, 2015, 68, 7387-7398.	0.2	5
2525	Transcriptomics analysis of Psidium cattleyanum Sabine (Myrtaceae) unveil potential genes involved in fruit pigmentation. Genetics and Molecular Biology, 2020, 43, e20190255.	0.6	8
2526	Genetic Basis of Hydrothermal Vent Adaptation in Bythograeidae Crabs: Insights from Adaptive Evolution of Mitochondrial Protein Coding Genes. Pakistan Journal of Zoology, 2019, 51, .	0.1	1
2527	Evolutionary history of the group formerly known as protists using a phylogenomics approach. Revista De La Academia Colombiana De Ciencias Exactas, Fisicas Y Naturales, 2016, 40, 147.	0.0	1
2529	Computational Design of Centralized HIV-1 Genes. Current HIV Research, 2010, 8, 613-621.	0.2	27
2530	Analysis of MBOAT family reveals the diversity of MBOAT1 amplification in Solanaceae. Archives of Biological Sciences, 2015, 67, 1349-1356.	0.2	1
2531	Haemagglutinin mutations and glycosylation changes shaped the 2012/13 influenza A(H3N2) epidemic, Houston, Texas. Eurosurveillance, 2015, 20, .	3.9	17
2532	Complete Mitochondrial Genomes of Two Pearl Oyster Species (Bivalvia: Pteriomorphia) Reveal Novel Gene Arrangements. Journal of Shellfish Research, 2018, 37, 1039.	0.3	7
2533	A Novel RNA Virus in the Parasitoid Wasp Lysiphlebus fabarum: Genomic Structure, Prevalence, and Transmission. Viruses, 2020, 12, 59.	1.5	7
2535	Phylogeny of major lineages of galliform birds (Aves: Galliformes) based on complete mitochondrial genomes. Genetics and Molecular Research, 2010, 9, 1625-1633.	0.3	58
2536	An Evolutionary Perspective on Human Cross-sensitivity to Tree Nut and Seed Allergens. Aliso, 2015, 33, 91-110.	0.4	3
2537	Classifying glycerol dehydratase by its functional residues and purifying selection in its evolution. Bioinformation, 2010, 5, 173-176.	0.2	1
2539	Recurrent loss of CenH3 is associated with independent transitions to holocentricity in insects. ELife, 2014, 3, .	2.8	174
2540	Ancestral resurrection reveals evolutionary mechanisms of kinase plasticity. ELife, 2014, 3, .	2.8	53
2541	A new class of cyclin dependent kinase in Chlamydomonas is required for coupling cell size to cell division. ELife, 2016, 5, e10767.	2.8	61

#	Article	IF	Citations
2542	A widely employed germ cell marker is an ancient disordered protein with reproductive functions in diverse eukaryotes. ELife, 2016, 5, .	2.8	56
2543	Ancient mechanisms for the evolution of the bicoid homeodomain's function in fly development. ELife, 2018, 7, .	2.8	28
2544	Efa6 protects axons and regulates their growth and branching by inhibiting microtubule polymerisation at the cortex. ELife, 2019, 8, .	2.8	25
2545	Breakdown of coevolution between symbiotic bacteriaWolbachiaand their filarial hosts. PeerJ, 2016, 4, e1840.	0.9	86
2546	The scavenger receptor repertoire in six cnidarian species and its putative role in cnidarian-dinoflagellate symbiosis. PeerJ, 2016, 4, e2692.	0.9	57
2547	The mitochondrial genomes of two walnut pests,Gastrolina depressa depressaandG.depressa thoracica(Coleoptera: Chrysomelidae), and phylogenetic analyses. PeerJ, 2018, 6, e4919.	0.9	11
2548	Molecular attributes and apoptosis-inducing activities of a putative serine protease isolated from Tiger Milk mushroom (Lignosus rhinocerus) sclerotium against breast cancer cellsin vitro. PeerJ, 2018, 6, e4940.	0.9	16
2549	Virus-host co-evolution under a modified nuclear genetic code. PeerJ, 2013, 1, e50.	0.9	27
2550	Structural models for the design of novel antiviral agents against Greek Goat Encephalitis. PeerJ, 2014, 2, e664.	0.9	24
2551	A holistic evolutionary and structural study offlaviviridaeprovides insights into the function and inhibition of HCV helicase. PeerJ, 2013, 1, e74.	0.9	28
2552	Conservation of transcriptional elements in the obligate symbiont of the whitefly Bemisia tabaci. PeerJ, 2019, 7, e7477.	0.9	6
2553	Widespread mitovirus sequences in plant genomes. PeerJ, 2015, 3, e876.	0.9	71
2554	OBAMA: OBAMA for Bayesian amino-acid model averaging. PeerJ, 2020, 8, e9460.	0.9	11
2555	Distribution of bacteriocin genes in the lineages of Lactiplantibacillus plantarum. Scientific Reports, 2021, 11, 20063.	1.6	15
2558	Accurate Selection of Models of Protein Evolution. Advances in Intelligent and Soft Computing, 2010, , 117-121.	0.2	0
2559	Estudio computacional de las relaciones evolutivas de los receptores ionotrÃ³picos NMDA, AMPA y kainato en cuatro especies de primates. Universitas Scientiarum, 2013, 15, 183.	0.2	1
2560	Molecular phylogeny of glass sponges (Porifera, Hexactinellida): increased taxon sampling and inclusion of the mitochondrial protein-coding gene, cytochrome oxidase subunit I. , 2011, , 11-20.		0
2561	The mitochondrial genome of stygobitic sponge Eunapius subterraneus: mtDNA is highly conserved in freshwater sponges. , 2011, , 49-59.		0

#	Article	IF	Citations
2562	Heuristic Algorithms for the Protein Model Assignment Problem. Lecture Notes in Computer Science, 2013, , 137-148.	1.0	1
2563	Phylogenetic analysis of subunit of the sulfite reductase gene from Colletotrichum lindemuthianum and fungi with different lifestyles. African Journal of Microbiology Research, 2014, 8, 1467-1473.	0.4	0
2564	Shared Memory and Hardware Utilizations for the Parallelization of Local Sequences Alignment using SW Algorithm: A Review. International Journal of Computer Applications, 2015, 115, 28-34.	0.2	0
2565	Transcriptome-Based Identification of a Seed Olive Legumin (11S Globulin). Characterization of Subunits, 3D Modelling and Molecular Assessment of Allergenicity. Lecture Notes in Computer Science, 2016, , 59-70.	1.0	0
2579	The Bitter Taste Receptor Genes of the Raccoon Dog (Nyctereutes procyonoides). Pakistan Journal of Zoology, 2018, 50, .	0.1	0
2596	Analysis of Adaptive Evolution and Coevolution ofrbcL Gene in the GenusHildenbrandia(Rhodophyta). Evolutionary Bioinformatics, 2020, 16, 117693432097786.	0.6	0
2597	Studies on the molecular biological peculiarities of bovine herpesvirus 4. Bulgarian Journal of Veterinary Medicine, 2020, 23, 411-423.	0.1	1
2602	The complete mitogenome of Lysmata vittata (Crustacea: Decapoda: Hippolytidae) with implication of phylogenomics and population genetics. PLoS ONE, 2021, 16, e0255547.	1.1	2
2604	Characterization and evolution of the cell cycle-associated mob domain-containing proteins in eukaryotes. Evolutionary Bioinformatics, 2007, 3, 121-58.	0.6	12
2607	The complete mitochondrial genome of the 'Zacatuche' Volcano rabbit (Romerolagus diazi), an endemic and endangered species from the Volcanic Belt of Central Mexico. Molecular Biology Reports, 2021, 49, 1141.	1.0	5
2608	The rhodopsin-retinochrome system for retinal re-isomerization predates the origin of cephalopod eyes. Bmc Ecology and Evolution, 2021, 21, 215.	0.7	7
2609	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. Microbiome, 2021, 9, 233.	4.9	53
2610	Characterizing the Complete Mitochondrial Genome of Arma custos and Picromerus lewisi (Hemiptera: Pentatomidae: Asopinae) and Conducting Phylogenetic Analysis. Journal of Insect Science, 2022, 22, .	0.6	8
2611	Characterization of the complete mitochondrial genome of the Atlantic seabob shrimpXiphopenaeus kroyeriHeller, 1862 (Decapoda: Dendrobranchiata: Penaeidae), with insights into the phylogeny of Penaeidae. Journal of Crustacean Biology, 2022, 42, .	0.3	2
2613	The complete mitochondrial genome of the spot prawn, Pandalus platyceros Brandt in von Middendorf, 1851 (Decapoda: Caridea: Pandalidae), assembled from linked-reads sequencing. Journal of Crustacean Biology, 2022, 42, .	0.3	4
2614	Survival and infectivity of second-stage root-knot nematode Meloidogyne incognita juveniles depend on lysosome-mediated lipolysis. Journal of Biological Chemistry, 2022, 298, 101637.	1.6	5
2615	A Pleiotropic Chemoreceptor Facilitates the Functional Coupling of Pheromone Production and Perception. SSRN Electronic Journal, 0, , .	0.4	0
2617	Comparative Mitochondrial Genome Analysis of Mamestra configurata (Lepidoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Phylogeny. Annals of the Entomological Society of America, 2022, 115, 304-313.	1.3	4

#	Article	IF	Citations
2618	Jingchuvirales : a New Taxonomical Framework for a Rapidly Expanding Order of Unusual Monjiviricete Viruses Broadly Distributed among Arthropod Subphyla. Applied and Environmental Microbiology, 2022, 88, AEM0195421.	1.4	16
2619	Complete mitochondrial genome of Idea leuconoe (Lepidoptera: Danaidae) and related phylogenetic analyses. Archives of Insect Biochemistry and Physiology, 2022, 111, e21868.	0.6	5
2620	Molecular cloning, antiserum preparation and expression analysis during head regeneration of Î±-crystallin type heat shock protein in. Journal of Genetics, 2018, 97, 911-924.	0.4	0
2621	Co-Infection of Peruvian Horse Sickness Virus and West Nile Virus Associated with Neurological Diseases in Horses from Brazil. SSRN Electronic Journal, 0, , .	0.4	0
2622	Isolation and Characterization of Novel Lytic Phages Infecting Multidrug-Resistant Escherichia coli. Microbiology Spectrum, 2022, 10, e0167821.	1.2	7
2623	Structures, evolutionary relationships and expression profiles of the tumour necrosis factor superfamily and their receptors in black rockfish (Sebastes schlegelii). Developmental and Comparative Immunology, 2022, 132, 104405.	1.0	0
2624	The evolution and competitive strategies of Akkermansia muciniphila in gut. Gut Microbes, 2022, 14, 2025017.	4.3	25
2626	A cytosolic pentatricopeptide repeat protein is essential for tapetal plastid development by regulating OsGLK1 transcript levels in rice. New Phytologist, 2022, 234, 1678-1695.	3.5	10
2627	A Comprehensive Analysis of Citrus Tristeza Variants of Bhutan and Across the World. Frontiers in Microbiology, 2022, 13, 797463.	1.5	5
2628	Evolution and Genetic Diversity of the Retroviral Envelope in Anamniotes. Journal of Virology, 2022, 96, e0207221.	1.5	4
2629	Genomic and transcriptomic evidence for the diverse adaptations of Synechococcus subclusters 5.2 and 5.3 to mesoscale eddies. New Phytologist, 2022, 233, 1828-1842.	3.5	4
2633	HIV Protease and Integrase Empirical Substitution Models of Evolution: Protein-Specific Models Outperform Generalist Models. Genes, 2022, 13, 61.	1.0	6
2634	RNA Viral Communities Are Structured by Host Plant Phylogeny in Oak and Conifer Leaves. Phytobiomes Journal, 2023, 7, 288-296.	1.4	2
2708	A Comprehensive Analysis of Fibrillar Collagens in Lamprey Suggests a Conserved Role in Vertebrate Musculoskeletal Evolution. Frontiers in Cell and Developmental Biology, 2022, 10, 809979.	1.8	2
2710	Resurrected Rubisco suggests uniform carbon isotope signatures over geologic time. Cell Reports, 2022, 39, 110726.	2.9	18
2711	Mitogenomics and mitochondrial gene phylogeny decipher the evolution ofSaccharomycotinayeasts. Genome Biology and Evolution, 2022, 14, .	1.1	8
2712	Origins of glycan selectivity in streptococcal Siglec-like adhesins suggest mechanisms of receptor adaptation. Nature Communications, 2022, 13, 2753.	5.8	4
2713	Genome-wide characterization of the Elovl gene family in Gymnocypris przewalskii and their potential roles in adaptation to cold temperature. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2022, 262, 110759.	0.7	6

#	Article	IF	Citations
2714	First genomic resource for an endangered neotropical mega-herbivore: the complete mitochondrial genome of the forest-dweller (Bairdâ€™s) tapir (Tapirus bairdii). PeerJ, 0, 10, e13440.	0.9	2
2715	Soil Collected in the Great Smoky Mountains National Park Yielded a Novel Listeria sensu stricto Species, L. swaminathanii. Microbiology Spectrum, 2022, 10, .	1.2	9
2717	In Silico Models on Algal Cultivation and Processing. Impact of Meat Consumption on Health and Environmental Sustainability, 2022, , 228-255.	0.4	0
2718	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. Nature Communications, 2022, 13, .	5.8	14
2719	Expression Patterns of Drosophila Melanogaster Glutathione Transferases. Insects, 2022, 13, 612.	1.0	7
2720	How candidate genes respond to aluminum toxicity in Citrus x limonia Osbeck?. Theoretical and Experimental Plant Physiology, 0, , .	1.1	1
2721	A mosaic of conserved and novel modes of gene expression and morphogenesis in mesoderm and muscle formation of a larval bivalve. Organisms Diversity and Evolution, 2022, 22, 893-913.	0.7	3
2722	The genome of the rice planthopper egg parasitoid wasps Anagrus nilaparvatae casts light on the chemo- and mechanosensation in parasitism. BMC Genomics, 2022, 23, .	1.2	5
2723	Tied up in knots: Untangling substrate recognition by the SPOUT methyltransferases. Journal of Biological Chemistry, 2022, 298, 102393.	1.6	12
2724	Expanding the environmental virome: Infection profile in a native rainforest tree species. Frontiers in Microbiology, 0, 13, .	1.5	2
2725	Genome-Based Analysis of Verticillium Polyketide Synthase Gene Clusters. Biology, 2022, 11, 1252.	1.3	2
2726	Current status of infection with infectious hypodermal and hematopoietic necrosis virus (IHHNV) in the Peruvian and Ecuadorian shrimp industry. PLoS ONE, 2022, 17, e0272456.	1.1	8
2727	Phylogenetic analysis based on single-copy orthologous proteins in highly variable chloroplast genomes of Corydalis. Scientific Reports, 2022, 12, .	1.6	1
2728	Genomic Analysis Reveals Adaptation of Vibrio campbellii to the Hadal Ocean. Applied and Environmental Microbiology, 2022, 88, .	1.4	5
2729	Impact of light wavelength on the transcriptome of Porphyridium cruentum and culture yield. Algal Research, 2022, 67, 102856.	2.4	3
2730	The complete mitochondrial genome of the roosterfish Nematistius pectoralis Gill 1862: Purifying selection in protein coding genes, organization of the control region, and insights into family-level phylogenomic relationships in the recently erected order Carangiformes. Gene, 2022, 845, 146847.	1.0	2
2731	The gastric proton pump in gobiid and mudskipper fishes. Evidence of stomach loss?. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 274, 111300.	0.8	2
2732	Comparative genomics and evolutionary analysis of plant CNGCs. Biology Methods and Protocols, 2022, 7, .	1.0	2

#	Article	IF	Citations
2733	An Evolutionary Framework of Acanthaceae Based on Transcriptomes and Genome Skims. Systematic Botany, 2022, 47, 716-728.	0.2	0
2734	RcgA and RcgR, Two Novel Proteins Involved in the Conjugative Transfer of Rhizobial Plasmids. MBio, 2022, 13, .	1.8	2
2735	Insights on KP4 Killer Toxin-like Proteins of Fusarium Species in Interspecific Interactions. Journal of Fungi (Basel, Switzerland), 2022, 8, 968.	1.5	3
2737	Detecting signals of adaptive evolution in grape plastomes with a focus on the Cretaceousâ€“Palaeogene (K/Pg) transition. Annals of Botany, 2022, 130, 965-980.	1.4	1
2738	Characterization and expression analysis of WRKY genes during leaf and corolla senescence of Petunia hybrida plants. Physiology and Molecular Biology of Plants, 2022, 28, 1765-1784.	1.4	3
2740	Phylogenomic and Evolutionary Analyses Reveal Diversifications of SET-Domain Proteins in Fungi. Journal of Fungi (Basel, Switzerland), 2022, 8, 1159.	1.5	0
2741	Dynamic evolution of transient receptor potential vanilloid (TRPV) ion channel family with numerous gene duplications and losses. Frontiers in Endocrinology, 0, 13, .	1.5	2
2742	Comparative analysis of codon usage of mitochondrial genomes provides evolutionary insights into reptiles. Gene, 2023, 851, 146999.	1.0	6
2743	Evolution of mitogen-activated protein kinase family and their immune function in Apostichopus japonicus. Developmental and Comparative Immunology, 2023, 139, 104586.	1.0	1
2745	Molecular evolution and structural analyses of proteins involved in metabolic pathways of volatile organic compounds in Petunia hybrida (Solanaceae). Genetics and Molecular Biology, 2023, 46, .	0.6	0
2746	Full-genome characterisation of a putative novel serotype of Yonaguni orbivirus isolated from cattle in Yunnan province, China. Virus Genes, 0, , .	0.7	1
2747	The evolution of plant proton pump regulation via the R domain may have facilitated plant terrestrialization. Communications Biology, 2022, 5, .	2.0	5
2749	Co-infection of Peruvian horse sickness virus and West Nile virus associated with neurological diseases in horses from Brazil. Heliyon, 2022, 8, e12097.	1.4	0
2750	The Phylogenetic Relationships of the Family Sciaenidae Based on Genome-Wide Data Analysis. Animals, 2022, 12, 3386.	1.0	0
2751	Host-symbiont interactions in Angomonas deanei include the evolution of a host-derived dynamin ring around the endosymbiont division site. Current Biology, 2023, 33, 28-40.e7.	1.8	8
2753	Mitochondrial genomes assembled from non-invasive eDNA metagenomic scat samples in the endangered Amur tiger ‹i›Panthera tigris altaica‹/i›. PeerJ, 0, 10, e14428.	0.9	2
2754	Topiary: Pruning the manual labor from ancestral sequence reconstruction. Protein Science, 2023, 32, .	3.1	6
2755	A small change with a twist ending - a single residue in EGF-CFC drives Bilaterian asymmetry. Molecular Biology and Evolution, 0, , .	3.5	2

#	Article	IF	Citations
2756	The for gene as one of the drivers of foraging variations in a parasitic wasp. Molecular Ecology, 0, , .	2.0	0
2757	Comparative analysis of mitochondrial genomes reveals family-specific architectures and molecular features in scorpions (Arthropoda: Arachnida: Scorpiones). Gene, 2023, 859, 147189.	1.0	1
2758	A pleiotropic chemoreceptor facilitates the production and perception of mating pheromones. IScience, 2023, 26, 105882.	1.9	3
2759	Identification of Cartilaginous Fish Endogenous Foamy Virus Rooting to Vertebrate Counterparts. Journal of Virology, 2023, 97, .	1.5	1
2760	Genetic Characterization of DH13M98, Umatilla Virus, Isolated from Culex tritaeniorhynchus Giles in Yunnan Province, China. Vector-Borne and Zoonotic Diseases, 2023, 23, 35-43.	0.6	1
2761	Multicopper oxidases with laccase-ferroxidase activity: Classification and study of ferroxidase activity determinants in a member from Heterobasidion annosum s. l.. Computational and Structural Biotechnology Journal, 2023, 21, 1041-1053.	1.9	3
2762	The Rosetta Stone Hypothesis-Based Interaction of the Tumor Suppressor Proteins Nit1 and Fhit. Cells, 2023, 12, 353.	1.8	0
2763	Sequencing and analysis of the complete mitochondrial genomes of Toona sinensis and Toona ciliata reveal evolutionary features of Toona. BMC Genomics, 2023, 24, .	1.2	5
2764	Influence of substitution model selection on protein phylogenetic tree reconstruction. Gene, 2023, 865, 147336.	1.0	2
2765	The mitochondrial genomes of big-eared bats, Macrotus waterhousii and Macrotus californicus (Chiroptera: Phyllostomidae: Macrotinae). Gene, 2023, 863, 147295.	1.0	0
2766	Mitochondrial Genome of â€œSpotted Numbfishâ€•Narcine timlei (Bloch & Schneider, 1801) and Phylogenetic Relationships among Order Torpediniformes. Journal of Applied Ichthyology, 2023, 2023, 1-8.	0.3	1
2768	Subspecies-level genome comparison of Lactobacillus delbrueckii. Scientific Reports, 2023, 13, .	1.6	7
2769	Roadmap to the study of gene and protein phylogeny and evolutionâ€”A practical guide. PLoS ONE, 2023, 18, e0279597.	1.1	4
2770	Transposon-derived transcription factors across metazoans. Frontiers in Cell and Developmental Biology, 0, 11, .	1.8	2
2771	Chromosome-level genome assembly of Phrynocephalus forsythii using third-generation DNA sequencing and Hi-C analysis. DNA Research, 2023, 30, .	1.5	0
2772	Genomic Insights into Niche Partitioning across Sediment Depth among Anaerobic Methane-Oxidizing Archaea in Global Methane Seeps. MSystems, 2023, 8, .	1.7	4
2773	Reverse vaccinology-based identification of a novel surface lipoprotein that is an effective vaccine antigen against bovine infections caused by Pasteurella multocida. PLoS Pathogens, 2023, 19, e1011249.	2.1	1
2774	The first genomic resource for the â€˜near threatenedâ€™ Neotropical otter Lontra longicaudis (Carnivora: Mustelidae): mitochondrial genome characterisation and insights into phylomitogenomic relationships in the family Mustelidae. Journal of Natural History, 2023, 57, 408-425.	0.2	1

#	Article	IF	Citations
2775	Deciphering the evolution of flavin-dependent monooxygenase stereoselectivity using ancestral sequence reconstruction. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	8
2776	Co-evolution of large inverted repeats and G-quadruplex DNA in fungal mitochondria may facilitate mitogenome stability: the case of Malassezia. Scientific Reports, 2023, 13, .	1.6	1
2808	In Silico Models on Algal Cultivation and Processing. , 2023, , 989-1016.		0