Citation Report

List of articles citing

MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform

DOI: 10.1093/nar/gkf436
Nucleic Acids Research, 2002, 30, 3059-66.

Source: https://exaly.com/paper-pdf/34030440/citation-report.pdf
Version: 2024-04-27

#	Paper	IF	Citations
2256	The reactivity of hydrazine with photosystem II strongly depends on the redox state of the water oxidizing system. **1990**, 277, 141-6		40
2255	Kinesin-related genes from diplomonad, sponge, amphioxus, and cyclostomes: divergence pattern of kinesin family and evolution of giardial membrane-bounded organella. **2002**, 19, 1524-33		9
2254	Comparative analysis of ribosomal proteins in complete genomes: an example of reductive evolution at the domain scale. *Nucleic Acids Research*, **2002**, 30, 5382-90	20.1	254
2253	Amphioxus homologs of Go-coupled rhodopsin and peropsin having 11-cis- and all-trans-retinals as their chromophores. **2002**, 531, 525-8		90
2252	The CHAP domain: a large family of amidases including GSP amidase and peptidoglycan hydrolases. **2003**, 28, 234-7		182
2251	The TROVE module: a common element in Telomerase, Ro and Vault ribonucleoproteins. **2003**, 4, 49		21
2250	An overview of multiple sequence alignment. **2003**, Chapter 3, Unit 3.7		13
2249	Tcoffee@igs: A web server for computing, evaluating and combining multiple sequence alignments. *Nucleic Acids Research*, **2003**, 31, 3503-6	20.1	203
2248	Evolution of olfactory receptor genes in the human genome. **2003**, 100, 12235-40		196
2247	Systematic reverse genetic screening of T-DNA tagged genes in rice for functional genomic analyses: MADS-box genes as a test case. **2003**, 44, 1403-11		89
2246	Computing multiple sequence/structure alignments with the T-coffee package. **2004**, Chapter 3, Unit3.8		5
2245	Improved GA-based method for multiple protein sequence alignment.		1
2244	A Randomized Algorithm for Distance Matrix Calculations in Multiple Sequence Alignment. **2004**, 33-45		1
2243	Arabidopsis downy mildew resistance gene RPP27 encodes a receptor-like protein similar to CLAVATA2 and tomato Cf-9. **2004**, 135, 1100-12		47
2242	LEON: multiple aLignment Evaluation Of Neighbours. *Nucleic Acids Research*, **2004**, 32, 1298-307	20.1	20
2241	Local homology recognition and distance measures in linear time using compressed amino acid alphabets. *Nucleic Acids Research*, **2004**, 32, 380-5	20.1	80
2240	pyramus and thisbe: FGF genes that pattern the mesoderm of Drosophila embryos. **2004**, 18, 687-99		135

2239	The structure of chondroitin B lyase complexed with glycosaminoglycan oligosaccharides unravels a calcium-dependent catalytic machinery. **2004**, 279, 32882-96		76
2238	Bistable UV pigment in the lamprey pineal. **2004**, 101, 6687-91		117
2237	Type I MADS-box genes have experienced faster birth-and-death evolution than type II MADS-box genes in angiosperms. **2004**, 101, 1910-5		164
2236	The ASTRAL Compendium in 2004. *Nucleic Acids Research*, **2004**, 32, D189-92	20.1	433
2235	Suillus bovinus glutamine synthetase gene organization, transcription and enzyme activities in the Scots pine mycorrhizosphere developed on forest humus. **2004**, 164, 389-399		4
2234	Novel protein domains and motifs in the marine planctomycete Rhodopirellula baltica. **2004**, 236, 333-340		24
2233	The PepSY domain: a regulator of peptidase activity in the microbial environment?. **2004**, 29, 169-72		55
2232	The Hotdog fold: wrapping up a superfamily of thioesterases and dehydratases. **2004**, 5, 109		137
2231	MUSCLE: a multiple sequence alignment method with reduced time and space complexity. **2004**, 5, 113		5401
2230	Gapped alignment of protein sequence motifs through Monte Carlo optimization of a hidden Markov model. **2004**, 5, 157		28
2229	Benchmarking tools for the alignment of functional noncoding DNA. **2004**, 5, 6		85
2228	Characterization of GhRac1 GTPase expressed in developing cotton (Gossypium hirsutum L.) fibers. **2004**, 1679, 214-21		27
2227	In silico analysis of the sigma54-dependent enhancer-binding proteins in Pirellula species strain 1. **2004**, 230, 215-25		16
2226	Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-coded genes. **2004**, 2, 3		84
2225	Chloroplast phylogeny indicates that bryophytes are monophyletic. **2004**, 21, 1813-9		95
2224	MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research*, **2004**, 32, 1792-7	20.1	27137
2223	3DCoffee: combining protein sequences and structures within multiple sequence alignments. **2004**, 340, 385-95		271
2222	Peptidases, families, and clans. **2005**,		

2221	Pattern-constrained multiple polypeptide sequence alignment. **2005**, 29, 303-7	6
2220	Comprehensive survey of carapacial ridge-specific genes in turtle implies co-option of some regulatory genes in carapace evolution. **2005**, 7, 3-17	86
2219	The MukF subunit of Escherichia coli condensin: architecture and functional relationship to kleisins. **2005**, 24, 1921-30	61
2218	Fast fourier transform-based support vector machine for prediction of G-protein coupled receptor subfamilies. **2005**, 37, 759-66	12
2217	Cephalochordate melanopsin: evolutionary linkage between invertebrate visual cells and vertebrate photosensitive retinal ganglion cells. **2005**, 15, 1065-9	196
2216	Gjaerumia, a new genus in the Georgefischeriales (Ustilaginomycetes). **2005**, 109, 1250-8	14
2215	Analysis of the kinesin superfamily: insights into structure and function. **2005**, 15, 467-76	516
2214	Multiple sequence alignments. **2005**, 15, 261-6	80
2213	Kalign--an accurate and fast multiple sequence alignment algorithm. **2005**, 6, 298	476
2212	HmtDB, a human mitochondrial genomic resource based on variability studies supporting population genetics and biomedical research. **2005**, 6 Suppl 4, S4	46
2211	Hox code in embryos of Chinese soft-shelled turtle Pelodiscus sinensis correlates with the evolutionary innovation in the turtle. **2005**, 304, 107-18	38
2210	Two phylogenetically highly distinct beta-tubulin genes of the basidiomycete Suillus bovinus. **2005**, 47, 253-63	10
2209	Vanadium-dependent iodoperoxidases in Laminaria digitata, a novel biochemical function diverging from brown algal bromoperoxidases. **2005**, 10, 156-66	72
2208	Anther smuts of Caryophyllaceae: Molecular characters indicate host-dependent species delimitation. **2005**, 4, 225-238	64
2207	Randomized and parallel algorithms for distance matrix calculations in multiple sequence alignment. **2005**, 19, 351-9	3
2206	BAliBASE 3.0: latest developments of the multiple sequence alignment benchmark. **2005**, 61, 127-36	279
2205	Correspondence of function and phylogeny of ABC proteins based on an automated analysis of 20 model protein data sets. **2005**, 61, 888-99	19
2204	A study of archaeal enzymes involved in polar lipid synthesis linking amino acid sequence information, genomic contexts and lipid composition. **2005**, 1, 399-410	42

2203	The G5 domain: a potential N-acetylglucosamine recognition domain involved in biofilm formation. **2005**, 21, 1301-3		68
2202	Traffic of genetic information between segmental duplications flanking the typical 22q11.2 deletion in velo-cardio-facial syndrome/DiGeorge syndrome. **2005**, 15, 1487-95		26
2201	Mind the gaps: progress in progressive alignment. **2005**, 102, 10411-2		17
2200	An algorithm for progressive multiple alignment of sequences with insertions. **2005**, 102, 10557-62		699
2199	Evaluation of iterative alignment algorithms for multiple alignment. **2005**, 21, 1408-14		41
2198	Normal sexual development and fertility in testatin knockout mice. **2005**, 25, 4892-902		16
2197	Functional analysis of Avr9/Cf-9 rapidly elicited genes identifies a protein kinase, ACIK1, that is essential for full Cf-9-dependent disease resistance in tomato. **2005**, 17, 295-310		137
2196	Natural selection drives recurrent formation of activating killer cell immunoglobulin-like receptor and Ly49 from inhibitory homologues. **2005**, 201, 1319-32		187
2195	MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Research*, **2005**, 33, 511-8	20.1	3394
2194	Characterization of MADS-box genes in charophycean green algae and its implication for the evolution of MADS-box genes. **2005**, 102, 2436-41		93
2193	Clathrin heavy and light chain isoforms originated by independent mechanisms of gene duplication during chordate evolution. **2005**, 102, 7209-14		50
2192	The Chlamydophila abortus genome sequence reveals an array of variable proteins that contribute to interspecies variation. **2005**, 15, 629-40		144
2191	ProbCons: Probabilistic consistency-based multiple sequence alignment. **2005**, 15, 330-40		811
2190	Evolutionary dynamics of olfactory receptor genes in fishes and tetrapods. **2005**, 102, 6039-44		238
2189	Phylogenomic analysis of the receptor-like proteins of rice and Arabidopsis. **2005**, 138, 611-23		168
2188	Integrating reptilian herpesviruses into the family herpesviridae. **2005**, 79, 725-31		102
2187	Detection of subunit interfacial modifications by tracing the evolution of clamp-loader complex. **2005**, 18, 139-45		1
2186	Automatic assessment of alignment quality. *Nucleic Acids Research*, **2005**, 33, 7120-8	20.1	102

2185	PRALINE: a multiple sequence alignment toolbox that integrates homology-extended and secondary structure information. *Nucleic Acids Research*, **2005**, 33, W289-94	20.1	359
2184	Sister group relationship of turtles to the bird-crocodilian clade revealed by nuclear DNA-coded proteins. **2005**, 22, 810-3		139
2183	Constructing Neighbor-Joining phylogenetic trees with reduced redundancy computation. **2005**,		0
2182	Comparative evolutionary analysis of olfactory receptor gene clusters between humans and mice. **2005**, 346, 13-21		91
2181	Evolution of vomeronasal-type odorant receptor genes in the zebrafish genome. **2005**, 362, 19-28		22
2180	Xenopus CENP-A assembly into chromatin requires base excision repair proteins. **2005**, 4, 760-72		28
2179	Multiple alignment through protein secondary-structure information. **2005**, 4, 207-11		1
2178	Two threatened coexisting indigenous conifer species in the dry Afromontane forests of Ethiopia are associated with distinct arbuscular mycorrhizal fungal communities. **2006**, 84, 1617-1627		22
2177	Partitioned optimization algorithms for multiple sequence alignment. **2006**,		16
2176	The root endophytic fungus Piriformospora indica requires host cell death for proliferation during mutualistic symbiosis with barley. **2006**, 103, 18450-7		304
2175	Multiple sequence alignment for phylogenetic purposes. **2006**, 19, 479		113
2174	A statistical score for assessing the quality of multiple sequence alignments. **2006**, 7, 484		35
2173	M-Coffee: combining multiple sequence alignment methods with T-Coffee. *Nucleic Acids Research*, **2006**, 34, 1692-9	20.1	414
2172	DNA sequence comparisons of Ophiostoma spp., including Ophiostoma aurorae sp. nov., associated with pine bark beetles in South Africa. **2006**, 55, 269-77		47
2171	Phylogeny of the Quambalariaceae fam. nov., including important Eucalyptus pathogens in South Africa and Australia. **2006**, 55, 289-98		62
2170	Microthia, Holocryphia and Ursicollum, three new genera on Eucalyptus and Coccoloba for fungi previously known as Cryphonectria. **2006**, 55, 35-52		36
2169	Celoporthe dispersa gen. et sp. nov. from native Myrtales in South Africa. **2006**, 55, 255-67		25
2168	Origin and diversification of minisatellites derived from human Alu sequences. **2006**, 365, 21-6		14

(2005-2006)

2167	Analysis of cytoskeletal and motility proteins in the sea urchin genome assembly. **2006**, 300, 219-37	52
2166	The genomic repertoire for cell cycle control and DNA metabolism in S. purpuratus. **2006**, 300, 238-51	43
2165	Multiple Sequence Alignments: The Next Generation. **2006**, 46, 312-317	
2164	Establishment of hybrid-derived offspring populations in the Ohomopterus ground beetles through unidirectional hybridization. **2006**, 82, 232-50	2
2163	Two new pycnidial members of the Atractiellales: Basidiopycnis hyalina and Proceropycnis pinicola1. **2006**, 98, 637-649	11
2162	A phylogenetic hypothesis of Ustilaginomycotina based on multiple gene analyses and morphological data1. **2006**, 98, 906-916	72
2161	Ancestral sequence evolutionary trace and crystal structure analyses of alkaline alpha-amylase from Bacillus sp. KSM-1378 to clarify the alkaline adaptation process of proteins. **2007**, 66, 600-10	23
2160	Sebacinales form ectendomycorrhizas with Cavendishia nobilis, a member of the Andean clade of Ericaceae, in the mountain rain forest of southern Ecuador. **2006**, 169, 355-65	68
2159	Unique features of Myf-5 in turtles: nucleotide deletion, alternative splicing, and unusual expression pattern. **2006**, 8, 415-23	12
2158	New taxonomic concepts for the important forest pathogen Cryphonectria parasitica and related fungi. **2006**, 258, 161-72	20
2157	Extensive colonization of apples by smut anamorphs causes a new postharvest disorder. **2006**, 6, 63-76	24
2156	Cloning and expression analysis of takeout/JHBP family genes of silkworm, Bombyx mori. **2006**, 15, 245-51	28
2155	Time scale for cyclostome evolution inferred with a phylogenetic diagnosis of hagfish and lamprey cDNA sequences. **2006**, 23, 1053-64	151
2154	Intraspecific Relationship of Plasmopara halstedii Isolates Differing in Pathogenicity and Geographic Origin Based on ITS Sequence Data. **2006**, 114, 309-315	41
2153	cDNA-based gene mapping and GC3 profiling in the soft-shelled turtle suggest a chromosomal size-dependent GC bias shared by sauropsids. **2006**, 14, 187-202	37
2152	Classifying G protein-coupled receptors and nuclear receptors on the basis of protein power spectrum from fast Fourier transform. **2006**, 30, 397-402	92
2151	Functional analysis through site-directed mutations and phylogeny of the Candida albicans LYS1-encoded saccharopine dehydrogenase. **2006**, 275, 74-80	1
2150	Organic anion transporting polypeptides of the OATP/SLCO superfamily: identification of new members in nonmammalian species, comparative modeling and a potential transport mode. **2005**, 208, 213-27	107

2149	Horizontal gene transfer in aminoacyl-tRNA synthetases including leucine-specific subtypes. **2006**, 63, 437-47	18
2148	Novel lysine biosynthetic gene sequences (LYS1 and LYS5) used as PCR targets for the detection of the pathogenic Candida yeast. **2006**, 72, 416-20	3
2147	The simple-septate basidiomycetes: a synopsis. **2006**, 5, 41-66	132
2146	Molecular basis for the redox control of nuclear transport of the structural chromatin protein Hmgb1. **2006**, 312, 3526-38	143
2145	Multiple sequence alignment. **2006**, 16, 368-73	267
2144	A revision of Bremia graminicola. **2006**, 110, 646-56	31
2143	Phylogenetic analysis of nuclear small subunit rDNA sequences suggests that the endangered African Pencil Cedar, Juniperus procera, is associated with distinct members of Glomeraceae. **2006**, 110, 1059-69	42
2142	SinicView: a visualization environment for comparisons of multiple nucleotide sequence alignment tools. **2006**, 7, 103	13
2141	IsoSVM--distinguishing isoforms and paralogs on the protein level. **2006**, 7, 110	15
2140	MACSIMS: multiple alignment of complete sequences information management system. **2006**, 7, 318	32
2139	M-GCAT: interactively and efficiently constructing large-scale multiple genome comparison frameworks in closely related species. **2006**, 7, 433	64
2138	The accuracy of several multiple sequence alignment programs for proteins. **2006**, 7, 471	100
2137	State of the art: refinement of multiple sequence alignments. **2006**, 7, 499	7
2136	Improvement in accuracy of multiple sequence alignment using novel group-to-group sequence alignment algorithm with piecewise linear gap cost. **2006**, 7, 524	21
2135	Implications of molecular characters for the phylogeny of the Microbotryaceae (Basidiomycota: Urediniomycetes). **2006**, 6, 35	63
2134	Evolution and origin of vomeronasal-type odorant receptor gene repertoire in fishes. **2006**, 6, 76	45
2133	Comprehensive analysis of gene expression patterns of hedgehog-related genes. **2006**, 7, 280	60
2132	The repertoire of olfactory C family G protein-coupled receptors in zebrafish: candidate chemosensory receptors for amino acids. **2006**, 7, 309	71

2131	The hedgehog-related gene qua-1 is required for molting in Caenorhabditis elegans. **2006**, 235, 1469-81		32
2130	Phylogeny and genetic diversity of palolo worms (Palola, Eunicidae) from the tropical North Pacific and the Caribbean. **2006**, 210, 25-37		32
2129	Phytome: a platform for plant comparative genomics. *Nucleic Acids Research*, **2006**, 34, D724-30	20.1	30
2128	Refining multiple sequence alignments with conserved core regions. *Nucleic Acids Research*, **2006**, 34, 2598-606	20.1	27
2127	A novel mechanism of allosteric regulation of archaeal phosphoenolpyruvate carboxylase: a combined approach to structure-based alignment and model assessment. **2006**, 19, 409-19		10
2126	Metagenome Analyses. **2006**, 261-286		1
2125	The MPI Bioinformatics Toolkit for protein sequence analysis. *Nucleic Acids Research*, **2006**, 34, W335-9	20.1	233
2124	Two-phase Quantum based Evolutionary Algorithm for Multiple Sequence Alignments. **2006**,		3
2123	ACache: Using Caching to Improve the Performance of Multiple Sequence Alignments.		
2122	MT-ClustalW: multithreading multiple sequence alignment. **2006**,		19
2121	An Efficient Ant Colony Algorithm for Multiple Sequences Alignment. **2007**,		3
2120	G-protein Coupled Receptor Subfamilies Prediction Based on Nearest Neighbor Approach. **2007**,		
2119	Structural evidence for the evolution of xyloglucanase activity from xyloglucan endo-transglycosylases: biological implications for cell wall metabolism. **2007**, 19, 1947-63		178
2118	Consensus sequences improve PSI-BLAST through mimicking profile-profile alignments. *Nucleic Acids Research*, **2007**, 35, 2238-46	20.1	8
2117	Molecular characterization of water-selective AQP (EbAQP4) in hagfish: insight into ancestral origin of AQP4. **2007**, 292, R644-51		17
2116	Multiple alignment by aligning alignments. **2007**, 23, i559-68		172
2115	Detecting key structural features within highly recombined genes. **2007**, 3, e14		9
2114	Evolution of trace amine associated receptor (TAAR) gene family in vertebrates: lineage-specific expansions and degradations of a second class of vertebrate chemosensory receptors expressed in the olfactory epithelium. **2007**, 24, 2099-107		119

2113	PartTree: an algorithm to build an approximate tree from a large number of unaligned sequences. **2007**, 23, 372-4		81
2112	A simulated annealing algorithm for multiple sequence alignment with guaranteed accuracy. **2007**,		2
2111	A Reliable Metric for Quantifying Multiple Sequence Alignment. **2007**,		0
2110	Single- and Multi-objective phylogenetic analysis of primate evolution using a genetic algorithm. **2007**,		4
2109	An efficient algorithm for multiple sequence alignment based on ant colony optimisation and divide-and-conquer method. **2007**, 50, 617-626		5
2108	QOMA: quasi-optimal multiple alignment of protein sequences. **2007**, 23, 162-8		4
2107	INDELSCAN: a web server for comparative identification of species-specific and non-species-specific insertion/deletion events. *Nucleic Acids Research*, **2007**, 35, W633-8	20.1	4
2106	Episodes of natural selection shaped the interactions of IgA-Fc with FcalphaRI and bacterial decoy proteins. **2007**, 178, 7943-54		27
2105	Functional and phylogenetic properties of the pore-forming beta-barrel transporters of the Omp85 family. **2007**, 282, 1882-90		73
2104	A TolC-like protein is required for heterocyst development in Anabaena sp. strain PCC 7120. **2007**, 189, 7887-95		47
2103	Horizontal transfer of a nitrate assimilation gene cluster and ecological transitions in fungi: a phylogenetic study. **2007**, 2, e1097		106
2102	The GC Skew Index: A Measure of Genomic Compositional Asymmetry and the Degree of Replicational Selection. **2007**, 3, 117693430700300		13
2101	Molecular phylogenetics of the lizard genus Microlophus (squamata:tropiduridae): aligning and retrieving indel signal from nuclear introns. **2007**, 56, 776-97		40
2100	How do obligate parasites evolve? A multi-gene phylogenetic analysis of downy mildews. **2007**, 44, 105-22		114
2099	Diversification and adaptive evolution of putative sweet taste receptors in threespine stickleback. **2007**, 396, 170-9		29
2098	The evolutionary process of bioluminescence and aposematism in cantharoid beetles (Coleoptera: Elateroidea) inferred by the analysis of 18S ribosomal DNA. **2007**, 400, 104-13		37
2097	Multiple receptor-like kinase cDNAs from liverwort Marchantia polymorpha and two charophycean green algae, Closterium ehrenbergii and Nitella axillaris: Extensive gene duplications and gene shufflings in the early evolution of streptophytes. **2007**, 401, 135-44		37
2096	The structure of serine palmitoyltransferase; gateway to sphingolipid biosynthesis. **2007**, 370, 870-86		99

2095	Soil microbial community analysis using two-dimensional polyacrylamide gel electrophoresis of the bacterial ribosomal internal transcribed spacer regions. **2007**, 69, 256-67	22
2094	Antibodies to the superantigenic site of HIV-1 gp120: hydrolytic and binding activities of the light chain subunit. **2007**, 44, 2707-18	27
2093	Noise-reduction filtering for accurate detection of replication termini in bacterial genomes. **2007**, 581, 253-8	15
2092	Evolution of the gene families forming the Pax/Six regulatory network: isolation of genes from primitive animals and molecular phylogenetic analyses. **2007**, 581, 1639-43	34
2091	Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. **2007**, 56, 564-77	3133
2090	A New Dynamic Programming Algorithm for Multiple Sequence Alignment. **2007**, 52-61	1
2089	A New Alignment-Independent Algorithm for Clustering Protein Sequences. **2007**,	1
2088	QOMA2: Optimizing the alignment of many sequences. **2007**,	
2087	Alignment of Multiple Proteins with an Ensemble of Hidden Markov Models. **2007**,	3
2086	The crystal structure of cytochrome P460 of Nitrosomonas europaea reveals a novel cytochrome fold and heme-protein cross-link. **2007**, 46, 8340-9	39
2085	Intramolecular interaction between the DEP domain of RGS7 and the Gbeta5 subunit. **2007**, 46, 6859-70	30
2084	Clustal W and Clustal X version 2.0. **2007**, 23, 2947-8	21333
2083	Structure of SixA, a histidine protein phosphatase of the ArcB histidine-containing phosphotransfer domain in Escherichia coli. **2007**, 422, 288-304	7
2082	Taxonomy, nomenclature and phylogeny of three cladosporium-like hyphomycetes, Sorocybe resinae, Seifertia azaleae and the Hormoconis anamorph of Amorphotheca resinae. **2007**, 58, 235-45	35
2081	Isolation and Identification of the Causal Agent of Brown Stalk Rot, A New Disease of Maize in South Africa. **2007**, 91, 711-718	29
2080	Ophiostoma species (Ascomycetes: Ophiostomatales) associated with bark beetles (Coleoptera: Scolytinae) colonizing Pinus radiata in northern Spain. **2007**, 53, 756-67	58
2079	New methods for inferring population dynamics from microbial sequences. **2007**, 7, 24-43	17
2078	Ideal amino acid exchange forms for approximating substitution matrices. **2007**, 69, 379-93	11

2077	Changing story of the receptor for phosphatidylserine-dependent clearance of apoptotic cells. **2007**, 8, 465-9	26
2076	Notothrix halsei gen. n., sp. n., representative of a new family of freshwater cladocerans (Branchiopoda, Anomopoda) from SW Australia, with a discussion of ancestral traits and a preliminary molecular phylogeny of the order. **2007**, 36, 465-487	18
2075	Botryosphaeriaceae occurring on native Syzygium cordatum in South Africa and their potential threat to Eucalyptus. **2007**, 56, 624-636	78
2074	Identification of Legionella spp. by 19 European reference laboratories: results of the European Working Group for Legionella Infections External Quality Assessment Scheme using DNA sequencing of the macrophage infectivity potentiator gene and dedicated online tools. **2007**, 13, 1119-24	17
2073	Sebacinales are common mycorrhizal associates of Ericaceae. **2007**, 174, 864-878	171
2072	Detection and characterization of hepatitis B virus of anti-hepatitis B core antigen-reactive blood donors in Quebec with an in-house nucleic acid testing assay. **2007**, 47, 1794-802	35
2071	Dyneins across eukaryotes: a comparative genomic analysis. **2007**, 8, 1708-1721	215
2070	Progressive multiple sequence alignments from triplets. **2007**, 8, 254	15
2069	Identification of discriminative characteristics for clusters from biologic data with InforBIO software. **2007**, 8, 281	1
2068	CLUSS: clustering of protein sequences based on a new similarity measure. **2007**, 8, 286	39
2067	Assessing the ability of sequence-based methods to provide functional insight within membrane integral proteins: a case study analyzing the neurotransmitter/Na+ symporter family. **2007**, 8, 397	7
2066	Phylo-mLogo: an interactive and hierarchical multiple-logo visualization tool for alignment of many sequences. **2007**, 8, 63	20
2065	Automatic extraction of reliable regions from multiple sequence alignments. **2007**, 8 Suppl 5, S9	4
2064	Purifying selection in mitochondria, free-living and obligate intracellular proteobacteria. **2007**, 7, 17	23
2063	Evolutionary relationships among species of Puccinia and Uromyces (Pucciniaceae, Uredinales) inferred from partial protein coding gene phylogenies. **2007**, 111, 163-75	55
2062	Flamingomyces and Parvulago, new genera of marine smut fungi (Ustilaginomycotina). **2007**, 111, 1199-206	16
2061	The expanded cattle KIR genes are orthologous to the conserved single-copy KIR3DX1 gene of primates. **2007**, 59, 517-22	49
2060	Ectomycorrhiza-mediated repression of the high-affinity ammonium importer gene AmAMT2 in Amanita muscaria. **2007**, 51, 71-8	34

2059	Characteristics of a Plasmopara angustiterminalis isolate from Xanthium strumarium. **2007**, 119, 421-428	19
2058	Identification and developmental expression of two Tbx1/10-related genes in the agnathan Lethenteron japonicum. **2007**, 217, 691-7	19
2057	Fusarium mangiferae associated with mango malformation in the Sultanate of Oman. **2008**, 121, 195-199	28
2056	Molecular evolution of arthropod color vision deduced from multiple opsin genes of jumping spiders. **2008**, 66, 130-7	48
2055	A new species of Volvocisporium from Namibia, V. grewiae sp. nov. (Microstromatales, Ustilaginomycota). **2008**, 7, 1-5	5
2054	About the genus Thecaphora (Glomosporiaceae) and its new synonyms. **2008**, 7, 31-39	25
2053	Molecular phylogeny of equine herpesvirus 1 isolates from onager, zebra and Thomson's gazelle. **2008**, 153, 2297-302	14
2052	Cu/Zn superoxide dismutases in developing cotton fibers: evidence for an extracellular form. **2008**, 228, 281-92	39
2051	The BsaHI restriction-modification system: cloning, sequencing and analysis of conserved motifs. **2008**, 9, 48	8
2050	Calcineurin B-like domains in the large regulatory alpha/beta subunits of phosphorylase kinase. **2008**, 71, 1597-606	9
2049	Properties of recombinant Staphylococcus haemolyticus cystathionine beta-lyase (metC) and its potential role in the generation of volatile thiols in axillary malodor. **2008**, 5, 2372-85	20
2048	Towards the phylogeny of chafers (Sericini): analysis of alignment-variable sequences and the evolution of segment numbers in the antennal club. **2008**, 47, 783-98	46
2047	Molecular systematics of Volvocales (Chlorophyceae, Chlorophyta) based on exhaustive 18S rRNA phylogenetic analyses. **2008**, 48, 281-91	137
2046	Colonization and diversification of the spider genus Pholcus Walckenaer, 1805 (Araneae, Pholcidae) in the Macaronesian archipelagos: evidence for long-term occupancy yet rapid recent speciation. **2008**, 48, 596-614	27
2045	Evolution of a complex minisatellite DNA sequence. **2008**, 49, 488-94	5
2044	Pesotum australi sp. nov. and Ophiostoma quercus associated with Acacia mearnsii trees in Australia and Uganda, respectively. **2008**, 37, 406	12
2043	On the systematics and phylogeography of eight-barbel loaches of the genus Lefua (Cobitoidea: Nemacheilidae): mtDNA typing of L. pleskei. **2008**, 44, 817-825	11
2042	Patterns of praying mantis auditory system evolution based on morphological, molecular, neurophysiological, and behavioural data. **2008**, 94, 541-568	54

2041	Incorporation of gap characters and lineage-specific regions into phylogenetic analyses of gene families from divergent clades: an example from the kinesin superfamily across eukaryotes. **2008**, 24, 372-384	7
2040	Molecular analysis of the gut microbiota of identical twins with Crohn's disease. **2008**, 2, 716-27	354
2039	The virophage as a unique parasite of the giant mimivirus. **2008**, 455, 100-4	389
2038	Colonization of Sulfurovum sp. on the gill surfaces of Alvinocaris longirostris, a deep-sea hydrothermal vent shrimp. **2008**, 29, 106-114	27
2037	Identification and characterization of two trypanosome TFIIS proteins exhibiting particular domain architectures and differential nuclear localizations. **2008**, 69, 1121-36	19
2036	The gonadotropin receptors FSH-R and LH-R of Atlantic halibut (Hippoglossus hippoglossus), 1: isolation of multiple transcripts encoding full-length and truncated variants of FSH-R. **2008**, 156, 584-94	25
2035	Improved accuracy of multiple ncRNA alignment by incorporating structural information into a MAFFT-based framework. **2008**, 9, 212	434
2034	A new protein linear motif benchmark for multiple sequence alignment software. **2008**, 9, 213	20
2033	A tree-based conservation scoring method for short linear motifs in multiple alignments of protein sequences. **2008**, 9, 229	40
2032	Grammar-based distance in progressive multiple sequence alignment. **2008**, 9, 306	32
2031	A fast structural multiple alignment method for long RNA sequences. **2008**, 9, 33	80
2030	GenomeMatcher: a graphical user interface for DNA sequence comparison. **2008**, 9, 376	179
2029	An efficient genetic algorithm for structural RNA pairwise alignment and its application to non-coding RNA discovery in yeast. **2008**, 9, 521	6
2028	Searching for evolutionary distant RNA homologs within genomic sequences using partition function posterior probabilities. **2008**, 9, 61	9
2027	Molecular evolution of Cide family proteins: novel domain formation in early vertebrates and the subsequent divergence. **2008**, 8, 159	38
2026	Phylogenomics of plant genomes: a methodology for genome-wide searches for orthologs in plants. **2008**, 9, 183	16
2025	Insights and inferences about integron evolution from genomic data. **2008**, 9, 261	40
2024	The RHNumtS compilation: features and bioinformatics approaches to locate and quantify Human NumtS. **2008**, 9, 267	31

2023	Multiple protein sequence alignment. **2008**, 18, 382-6	54
2022	Cloning and developmental expression of kinesin superfamily7 (kif7) in the brackish medaka (Oryzias melastigma), a close relative of the Japanese medaka (Oryzias latipes). **2008**, 57, 425-32	9
2021	A standard operating procedure for phylogenetic inference (SOPPI) using (rRNA) marker genes. **2008**, 31, 251-7	71
2020	Phylogenetic relationships among species and genera of Lycoperdaceae based on ITS and LSU sequence data from north European taxa. **2008**, 112, 4-22	41
2019	Fourteen coprophilous species of Psathyrella identified in the Nordic countries using morphology and nuclear rDNA sequence data. **2008**, 112, 1165-85	50
2018	Anther smuts of Caryophyllaceae: molecular analyses reveal further new species. **2008**, 112, 1280-96	57
2017	Anther smut fungi on monocots. **2008**, 112, 1297-306	36
2016	Coevolution with higher taxonomic host groups within the Puccinia/Uromyces rust lineage obscured by host jumps. **2008**, 112, 1387-408	43
2015	Host specificity is linked to intraspecific variability in the genus Lamellodiscus (Monogenea). **2008**, 135, 607-16	31
2014	Multiple sequence alignment. **2008**, 452, 143-61	12
2013	Protein multiple sequence alignment. **2008**, 484, 379-413	47
2012	DNA topoisomerases: harnessing and constraining energy to govern chromosome topology. **2008**, 41, 41-101	344
2011	Multiple ancient origins of neoteny in Lycidae(Coleoptera): consequences for ecology and macroevolution. **2008**, 275, 2015-23	63
2010	Universal primers that amplify RNA from all three flavivirus subgroups. **2008**, 5, 16	49
2009	Stability of multiple alignments and phylogenetic trees: an analysis of ABC-transporter proteins family. **2008**, 3, 15	6
2008	DIALIGN-TX: greedy and progressive approaches for segment-based multiple sequence alignment. **2008**, 3, 6	178
2007	Picoeukaryotic sequences in the Sargasso sea metagenome. **2008**, 9, R5	31
2006	Detecting lateral genetic transfer : a phylogenetic approach. **2008**, 452, 457-69	22

2005	Methods for Analyzing Viral Evolution. **2008**, 165-204		5
2004	The MEROPS batch BLAST: a tool to detect peptidases and their non-peptidase homologues in a genome. **2008**, 90, 243-59		61
2003	Kank proteins: a new family of ankyrin-repeat domain-containing proteins. **2008**, 1780, 128-33		32
2002	Mutational analysis and a structural model of methyl-directed restriction enzyme Mrr. **2008**, 377, 862-6		11
2001	Orthologous gene of beetle luciferase in non-luminous click beetle, Agrypnus binodulus (Elateridae), encodes a fatty acyl-CoA synthetase. **2008**, 407, 169-75		13
2000	Phylogenomics reveals a new 'megagroup' including most photosynthetic eukaryotes. **2008**, 4, 366-9		208
1999	Segment-based multiple sequence alignment. **2008**, 24, i187-92		39
1998	RBT-I: A novel approach for solving the Multiple Sequence Alignment problem. **2008**,		1
1997	Sample-Align-D: A high performance Multiple Sequence Alignment system using phylogenetic sampling and domain decomposition. **2008**,		3
1996	Genetic diversity and phylogeography of the greater mouse-tailed bat Rhinopoma microphyllum (Br�nich, 1782) in the Levant. **2008**, 10, 207-212		9
1995	Clostridium acetobutylicum 8-oxoguanine DNA glycosylase (Ogg) differs from eukaryotic Oggs with respect to opposite base discrimination. **2008**, 47, 7626-36		19
1994	Characterization of polyketide metabolites from foliar endophytes of Picea glauca. **2008**, 71, 1393-8		66
1993	Performance comparison between k-tuple distance and four model-based distances in phylogenetic tree reconstruction. *Nucleic Acids Research*, **2008**, 36, e33	20.1	33
1992	Knowledge-based expert systems and a proof-of-concept case study for multiple sequence alignment construction and analysis. **2009**, 10, 11-23		12
1991	Taxonomy and phylogeny of new wood- and soil-inhabiting Sporothrix species in the Ophiostoma stenoceras-Sporothrix schenckii complex. **2008**, 100, 647-61		96
1990	Comparative genomics supports a deep evolutionary origin for the large, four-module transcriptional mediator complex. *Nucleic Acids Research*, **2008**, 36, 3993-4008	20.1	255
1989	Model-based prediction of sequence alignment quality. **2008**, 24, 2165-71		15
1988	How well does the HoT score reflect sequence alignment accuracy?. **2008**, 25, 1576-80		10

1987	Arthropod 7SK RNA. **2008**, 25, 1923-30		39
1986	Evolutionary analysis and molecular dissection of caveola biogenesis. **2008**, 121, 2075-86		91
1985	Retroposed SNOfall--a mammalian-wide comparison of platypus snoRNAs. **2008**, 18, 1005-10		53
1984	Identification and functional analysis of genes controlling biosynthesis of 2-methylisoborneol. **2008**, 105, 7422-7		168
1983	Mango: multiple alignment with N gapped oligos. **2008**, 6, 521-41		3
1982	Identification of a novel Babesia sp. from a sable antelope (Hippotragus niger Harris, 1838). **2008**, 46, 2247-51		69
1981	The cis-acting replication elements define human enterovirus and rhinovirus species. **2008**, 14, 1568-78		45
1980	Evolution of MDA-5/RIG-I-dependent innate immunity: independent evolution by domain grafting. **2008**, 105, 17040-5		63
1979	Jellyfish vision starts with cAMP signaling mediated by opsin-G(s) cascade. **2008**, 105, 15576-80		113
1978	Mariniflexile fucanivorans sp. nov., a marine member of the Flavobacteriaceae that degrades sulphated fucans from brown algae. **2008**, 58, 2107-13		30
1977	Evolutionary diversification of plant shikimate kinase gene duplicates. **2008**, 4, e1000292		32
1976	Bosque: integrated phylogenetic analysis software. **2008**, 24, 2539-41		43
1975	Kinesins are indispensable for interdigitation of phragmoplast microtubules in the moss Physcomitrella patens. **2008**, 20, 3094-106		71
1974	Characterization of an endoglucanase belonging to a new subfamily of glycoside hydrolase family 45 of the basidiomycete Phanerochaete chrysosporium. **2008**, 74, 5628-34		66
1973	Alignment uncertainty and genomic analysis. **2008**, 319, 473-6		286
1972	Arabidopsis TONNEAU1 proteins are essential for preprophase band formation and interact with centrin. **2008**, 20, 2146-59		138
1971	Structural and evolutionary classification of Type II restriction enzymes based on theoretical and experimental analyses. *Nucleic Acids Research*, **2008**, 36, 3552-69	20.1	88
1970	Molecular epidemiology of the African horse sickness virus S10 gene. **2008**, 89, 1159-1168		26

1969	Nucleus-encoded periplastid-targeted EFL in chlorarachniophytes. **2008**, 25, 1967-77	22
1968	Role of ampD homologs in overproduction of AmpC in clinical isolates of Pseudomonas aeruginosa. **2008**, 52, 3922-7	39
1967	Improvement in Speed and Accuracy of Multiple Sequence Alignment Program PRIME. **2008**, 1, 2-12	1
1966	Multiple sequence alignment using modified dynamic programming and particle swarm optimization. **2008**, 31, 659-673	10
1965	Strategies for reliable exploitation of evolutionary concepts in high throughput biology. **2008**, 4, 121-37	13
1964	Utility of computational methods to identify the apoptosis machinery in unicellular eukaryotes. **2008**, 2, 101-17	4
1963	Evolution of a domain conserved in microtubule-associated proteins of eukaryotes. **2008**, 1, 51-69	5
1962	A short guide to phylogeny reconstruction. **2008**, 53, 442-446	5
1961	Pattern of the divergence of olfactory receptor genes during tetrapod evolution. **2008**, 3, e2385	12
1960	Relaxation of selective constraints causes independent selenoprotein extinction in insect genomes. **2008**, 3, e2968	56
1959	Evolution of the G+C Content Frontier in the Rat Cytomegalovirus Genome. **2008**, 1, VRT.S1023	
1958	The phylogeny, biogeography and morphological evolution of Gaultheria (Ericaceae) from Australia and New Zealand. **2009**, 22, 229	14
1957	Fido, a novel AMPylation domain common to fic, doc, and AvrB. **2009**, 4, e5818	103
1956	Origin of saxitoxin biosynthetic genes in cyanobacteria. **2009**, 4, e5758	95
1955	Evidence for the concerted evolution between short linear protein motifs and their flanking regions. **2009**, 4, e6052	29
1954	Phylogenetic analysis of seven WRKY genes across the palm subtribe Attaleinae (Arecaceae) [corrected] identifies Syagrus as sister group of the coconut. **2009**, 4, e7353	53
1953	Groups without cultured representatives dominate eukaryotic picophytoplankton in the oligotrophic South East Pacific Ocean. **2009**, 4, e7657	129
1952	Genotypic characterization of CRF01_AE env genes derived from human immunodeficiency virus type 1-infected patients residing in central Thailand. **2009**, 25, 229-36	18

1951	Evidence of frequent introductions of Japanese encephalitis virus from south-east Asia and continental east Asia to Japan. **2009**, 90, 827-832	44
1950	Molecular and phenotypic characterization of three phylogenetic species discovered within the Neofisicoccum parvum/N. ribis complex. **2009**, 101, 636-47	51
1949	A JAK2 interdomain linker relays Epo receptor engagement signals to kinase activation. **2009**, 284, 26988-98	33
1948	Characterization of arrangement and expression of the T cell receptor gamma locus in the sandbar shark. **2009**, 106, 8591-6	48
1947	Comparative genomics reveal the mechanism of the parallel evolution of O157 and non-O157 enterohemorrhagic Escherichia coli. **2009**, 106, 17939-44	273
1946	A consistency-based consensus algorithm for de novo and reference-guided sequence assembly of short reads. **2009**, 25, 1118-24	24
1945	. **2009**,	
1944	Immunity or digestion: glucanase activity in a glucan-binding protein family from Lepidoptera. **2009** , 284, 2214-24	74
1943	Floral variation and floral genetics in basal angiosperms. **2009**, 96, 110-28	55
1942	Chimpanzees use more varied receptors and ligands than humans for inhibitory killer cell Ig-like receptor recognition of the MHC-C1 and MHC-C2 epitopes. **2009**, 182, 3628-37	45
1941	KIR2DS4 is a product of gene conversion with KIR3DL2 that introduced specificity for HLA-A*11 while diminishing avidity for HLA-C. **2009**, 206, 2557-72	186
1940	Large-scale phylogenomic analyses reveal that two enigmatic protist lineages, telonemia and centroheliozoa, are related to photosynthetic chromalveolates. **2009**, 1, 231-8	130
1939	A machine-learning approach reveals that alignment properties alone can accurately predict inference of lateral gene transfer from discordant phylogenies. **2009**, 26, 1931-9	10
1938	Ceratocystis larium sp. nov., a new species from Styrax benzoin wounds associated with incense harvesting in Indonesia. **2009**, 22, 75-82	18
1937	Taxonomy and evolutionary relationships within species of section Rimosae (Inocybe) based on ITS, LSU and mtSSU sequence data. **2009**, 23, 86-98	32
1936	Assessing phylogenetic motif models for predicting transcription factor binding sites. **2009**, 25, i339-47	13
1935	The family 6 carbohydrate-binding modules have coevolved with their appended catalytic modules toward similar substrate specificity. **2009**, 19, 615-23	31
1934	The evolutionary rates of eukaryotic RNA polymerases and of their transcription factors are affected by the level of concerted evolution of the genes they transcribe. **2009**, 26, 2515-20	11

1933	A novel system of polymorphic and diverse NK cell receptors in primates. **2009**, 5, e1000688		54
1932	Phylogenomics of unusual histone H2A Variants in Bdelloid rotifers. **2009**, 5, e1000401		19
1931	Distribution and phylogeny of light-oxygen-voltage-blue-light-signaling proteins in the three kingdoms of life. **2009**, 191, 7234-42		79
1930	Functional differentiation of tbf1 orthologues in fission and budding yeasts. **2009**, 8, 207-16		9
1929	Bioinformatics and functional analysis define four distinct groups of AlkB DNA-dioxygenases in bacteria. *Nucleic Acids Research*, **2009**, 37, 7124-36	20.1	27
1928	Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two novel clades. **2009**, 90, 2788-2797		65
1927	Novel cytomegaloviruses in free-ranging and captive great apes: phylogenetic evidence for bidirectional horizontal transmission. **2009**, 90, 2386-2394		36
1926	Rapid changes of mRNA-binding protein levels following glucose and 3-isobutyl-1-methylxanthine stimulation of insulinoma INS-1 cells. **2009**, 8, 393-408		11
1925	Evolutionary relationships among the Fusarium oxysporum f. sp. cubense vegetative compatibility groups. **2009**, 75, 4770-81		99
1924	Comparative sequence analysis of Mycobacterium leprae and the new leprosy-causing Mycobacterium lepromatosis. **2009**, 191, 6067-74		70
1923	Genotype-phenotype associations: substitution models to detect evolutionary associations between phenotypic variables and genotypic evolutionary rate. **2009**, 25, i94-100		26
1922	A short motif in Drosophila SECIS Binding Protein 2 provides differential binding affinity to SECIS RNA hairpins. *Nucleic Acids Research*, **2009**, 37, 2126-41	20.1	39
1921	Accurate and efficient reconstruction of deep phylogenies from structured RNAs. *Nucleic Acids Research*, **2009**, 37, 6184-93	20.1	95
1920	Community-level analysis of psbA gene sequences and irgarol tolerance in marine periphyton. **2009** , 75, 897-906		25
1919	The taxonomy of the Caloplaca citrina group (Teloschistaceae) in the Black Sea region; with contributions to the cryptic species concept in lichenology. **2009**, 41, 571-604		84
1918	Identification and classification of bcl genes and proteins of Bacillus cereus group organisms and their application in Bacillus anthracis detection and fingerprinting. **2009**, 75, 7163-72		34
1917	Dissection of CENP-C-directed centromere and kinetochore assembly. **2009**, 20, 4246-55		92
1916	Orthology, function and evolution of accessory gland proteins in the Drosophila repleta group. **2009**, 181, 235-45		26

1915	Phylogenetic ubiquity and shuffling of the bacterial RecBCD and AddAB recombination complexes. **2009**, 191, 5076-84	39
1914	Isolation of the anaerobic thermoacidophilic crenarchaeote Acidilobus saccharovorans sp. nov. and proposal of Acidilobales ord. nov., including Acidilobaceae fam. nov. and Caldisphaeraceae fam. nov. **2009**, 59, 3116-22	61
1913	The decay of the chromosomally encoded ccdO157 toxin-antitoxin system in the Escherichia coli species. **2009**, 181, 1557-66	37
1912	Haradamyces foliicola anam. gen. et sp. nov., a cause of zonate leaf blight disease in Cornus florida in Japan. **2009**, 113, 173-81	7
1911	Putative natural hybrid between Puccinia lagenophorae and an unknown rust fungus on Senecio madagascariensis in KwaZulu-Natal, South Africa. **2009**, 113, 725-36	25
1910	Multigene phylogeny of filamentous ambrosia fungi associated with ambrosia and bark beetles. **2009**, 113, 822-35	78
1909	Cystobasidiopsis nirenbergiae, a new agaricostilbomycete (Pucciniomycotina). **2009**, 113, 960-6	8
1908	Are the microcyclic rust species Puccinia melampodii and Puccinia xanthii conspecific?. **2009**, 113, 1271-82	16
1907	OrthoSelect: a protocol for selecting orthologous groups in phylogenomics. **2009**, 10, 219	20
1906	The B6 database: a tool for the description and classification of vitamin B6-dependent enzymatic activities and of the corresponding protein families. **2009**, 10, 273	179
1905	Analysis of the Rickettsia africae genome reveals that virulence acquisition in Rickettsia species may be explained by genome reduction. **2009**, 10, 166	95
1904	Complexity of the MSG gene family of Pneumocystis carinii. **2009**, 10, 367	28
1903	A comparison of reptilian and avian olfactory receptor gene repertoires: species-specific expansion of group gamma genes in birds. **2009**, 10, 446	51
1902	RBT-GA: a novel metaheuristic for solving the Multiple Sequence Alignment problem. **2009**, 10 Suppl 1, S10	34
1901	Bos taurus genome sequence reveals the assortment of immunoglobulin and surrogate light chain genes in domestic cattle. **2009**, 10, 22	25
1900	Phylogenetic analysis, subcellular localization, and expression patterns of RPD3/HDA1 family histone deacetylases in plants. **2009**, 9, 37	68
1899	Characterization of novel VP7, VP4, and VP6 genotypes of a previously untypeable group A rotavirus. **2009**, 385, 58-67	95
1898	Identification of angiotensinogen genes with unique and variable angiotensin sequences in chondrichthyans. **2009**, 161, 115-22	12

1897	Phylogeny of the CDC25 homology domain reveals rapid differentiation of Ras pathways between early animals and fungi. **2009**, 21, 1579-85	17
1896	Pathogenic or not? And if so, then how? Studying the effects of missense mutations using bioinformatics methods. **2009**, 30, 703-14	184
1895	Multiple sequence alignment algorithm based on a dispersion graph and ant colony algorithm. **2009**, 30, 2031-8	11
1894	Phylogenetic analyses of Japanese species of Phyllosticta sensu stricto. **2009**, 50, 291-302	26
1893	The perfect invader: a parthenogenic crayfish poses a new threat to Madagascar's freshwater biodiversity. **2009**, 11, 1475-1482	105
1892	Diverse Fusarium solani isolates colonise agricultural environments in Ethiopia. **2009**, 124, 369-378	16
1891	Defense by volatiles in leaf-mining insect larvae. **2009**, 35, 507-17	8
1890	The phylogeny and taxonomy of genera Cystoderma and Cystodermella (Agaricales) based on nuclear ITS and LSU sequences. **2009**, 8, 59-73	25
1889	Taxomomy, ecology and phylogenetic relationships of Bovista pusilla and B. limosa in North Europe. **2009**, 8, 289-299	5
1888	Arbuscular mycorrhizal fungal community structures differ between co-occurring tree species of dry Afromontane tropical forest, and their seedlings exhibit potential to trap isolates suited for reforestation. **2009**, 8, 317-328	30
1887	Diverse archaeal community of a bat guano pile in Domica Cave (Slovak Karst, Slovakia). **2009**, 54, 436-46	15
1886	ITS2 ribosomal DNA sequence variation of the bumblebee,Bombus ardens (hymenoptera: Apidae). **2009**, 31, 293-303	11
1885	The NfeD protein family and its conserved gene neighbours throughout prokaryotes: functional implications for stomatin-like proteins. **2009**, 69, 657-67	10
1884	Systematic structural studies of iron superoxide dismutases from human parasites and a statistical coupling analysis of metal binding specificity. **2009**, 77, 26-37	31
1883	Aphids acquired symbiotic genes via lateral gene transfer. **2009**, 7, 12	124
1882	Functional chloroplasts in metazoan cells - a unique evolutionary strategy in animal life. **2009**, 6, 28	108
1881	Pleistocene glaciation leaves deep signature on the freshwater crab Aegla alacalufi in Chilean Patagonia. **2009**, 18, 904-18	74
1880	Towards the definition of a core of microorganisms involved in anaerobic digestion of sludge. **2009**, 3, 700-14	584

1879	Subcellular homeostasis of phytohormone auxin is mediated by the ER-localized PIN5 transporter. **2009**, 459, 1136-40	383
1878	A Mek1-Mek2 heterodimer determines the strength and duration of the Erk signal. **2009**, 16, 294-303	128
1877	Phylogeny and systematic position of Zosterodasys (Ciliophora, Synhymeniida): a combined analysis of ciliate relationships using morphological and molecular data. **2009**, 56, 323-38	12
1876	The distribution of Elongation Factor-1 Alpha (EF-1alpha), Elongation Factor-Like (EFL), and a non-canonical genetic code in the ulvophyceae: discrete genetic characters support a consistent phylogenetic framework. **2009**, 56, 367-72	20
1875	Identification of the novel TRAPP associated protein Tca17. **2009**, 10, 713-23	37
1874	Differentiation of Debaryomyces hansenii and Candida famata by rRNA gene intergenic spacer fingerprinting and reassessment of phylogenetic relationships among D. hansenii, C. famata, D. fabryi, C. flareri (=D. subglobosus) and D. prosopidis: description of D. vietnamensis sp. nov. closely related to D. nepalensis. **2009**, 9, 641-62	45
1873	Phylogenetic relationships of the spider family Tetragnathidae (Araneae, Araneoidea) based on morphological and DNA sequence data. **2009**, 25, 109-146	64
1872	Reconstructing the origins of praying mantises (Dictyoptera, Mantodea): the roles of Gondwanan vicariance and morphological convergence. **2009**, 25, 468-514	116
1871	Use of stable isotope-labelled cells to identify active grazers of picocyanobacteria in ocean surface waters. **2009**, 11, 512-25	101
1870	A phylogenetic approach to detect selection on the target site of the antifouling compound irgarol in tolerant periphyton communities. **2009**, 11, 2065-77	10
1869	Deciphering the products of evolution at the species level: the need for an integrative taxonomy. **2009**, 38, 431-447	114
1868	'Glomus intraradices DAOM197198', a model fungus in arbuscular mycorrhiza research, is not Glomus intraradices. **2009**, 183, 1176-1187	215
1867	A data structure for representing multi-version texts online. **2009**, 67, 497-514	36
1866	Molecular cloning and phylogenetic analysis of Babesia orientalis heat shock protein 70. **2009**, 162, 183-91	20
1865	Multiple gene genealogies and phenotypic data reveal cryptic species of the Botryosphaeriaceae: a case study on the Neofusicoccum parvum/N. ribis complex. **2009**, 51, 259-68	77
1864	On the role of character loss in orbiniid phylogeny (Annelida): molecules vs. morphology. **2009**, 52, 57-69	22
1863	Marbleseeds are gromwells--systematics and evolution of Lithospermum and allies (Boraginaceae tribe Lithospermeae) based on molecular and morphological data. **2009**, 52, 755-68	58
1862	Slippery when wet: phylogeny and character evolution in the gelatinous cyanobacterial lichens (Peltigerales, Ascomycetes). **2009**, 53, 862-71	58

1861	A 454 sequencing approach for large scale phylogenomic analysis of the common emperor scorpion (Pandinus imperator). **2009**, 53, 826-34	74
1860	Changing from computing grid to knowledge grid in life-science grid. **2009**, 4, 1244-52	3
1859	Phylogeny and evolution of male genitalia within the praying mantis genus Tenodera (Mantodea:Mantidae). **2009**, 23, 409	11
1858	Functional roles of ubiquitin-like domain (ULD) and ubiquitin-binding domain (UBD) containing proteins. **2009**, 109, 1481-94	92
1857	Phylogenetic methods in natural product research. **2009**, 26, 1585-602	24
1856	Mechanical behavior of silk during the evolution of orb-web spinning spiders. **2009**, 10, 1904-10	46
1855	Transaldolase: from biochemistry to human disease. **2009**, 41, 1482-94	73
1854	Detection of circulating Asian H5N1 viruses by a newly established monoclonal antibody. **2009**, 378, 197-202	24
1853	Belowground ectomycorrhizal fungal communities respond to liming in three southern Swedish coniferous forest stands. **2009**, 257, 2217-2225	36
1852	Screening the V2R-type putative odorant receptor gene repertoire in bitterling Tanakia lanceolata. **2009**, 441, 74-9	4
1851	Phylogenetic construction of 17 bacterial phyla by new method and carefully selected orthologs. **2009**, 429, 59-64	16
1850	Evaluation of the effect of CpG hypermutability on human codon substitution. **2009**, 431, 18-22	12
1849	Diel changes in the expression of long wavelength-sensitive and ultraviolet-sensitive opsin genes in the Japanese firefly, Luciola cruciata. **2009**, 436, 66-70	15
1848	Occurrence of Can-SINEs and intron sequence evolution supports robust phylogeny of pinniped carnivores and their terrestrial relatives. **2009**, 448, 221-6	14
1847	The X-ray crystal structure of the phage lambda tail terminator protein reveals the biologically relevant hexameric ring structure and demonstrates a conserved mechanism of tail termination among diverse long-tailed phages. **2009**, 389, 938-51	46
1846	A new cloning system using a mutant esterase containing MCS as an indicator for gene cloning. **2009**, 77, 302-7	6
1845	Metagenomic study of the oral microbiota by Illumina high-throughput sequencing. **2009**, 79, 266-71	248
1844	Exploring the utility of an indel-rich, mitochondrial intergenic region as a molecular barcode for bamboo corals (Octocorallia: Isididae). **2009**, 2, 183-92	24

1843	Automatic Prediction of the Genetic Code. **2009**, 1125-1129	1
1842	Evolutionary convergence and nitrogen metabolism in Blattabacterium strain Bge, primary endosymbiont of the cockroach Blattella germanica. **2009**, 5, e1000721	101
1841	The human Ago2 MC region does not contain an eIF4E-like mRNA cap binding motif. **2009**, 4, 2	28
1840	Identification of a crenarchaeal orthologue of Elf1: implications for chromatin and transcription in Archaea. **2009**, 4, 24	19
1839	DNA Sequence Analysis. **2009**,	
1838	Hidden diversity in the non-caryophyllaceous plant-parasitic members of Microbotryum (Pucciniomycotina: Microbotryales). **2009**, 7, 297-306	31
1837	Modeling of glutamate GluR6 receptor and its interactions with novel noncompetitive antagonists. **2009**, 49, 1094-104	13
1836	Biological Feature Incorporated Alignment for Cross Species Analysis on Carbohydrate Binding Modules. **2009**,	1
1835	Geometric aspects of biological sequence comparison. **2009**, 16, 579-610	6
1834	Phylogeography of the flathead mullet Mugil cephalus in the north-west Pacific as inferred from the mtDNA control region. **2009**, 75, 393-407	17
1833	Phylogenetic support values are not necessarily informative: the case of the Serialia hypothesis (a mollusk phylogeny). **2009**, 6, 12	41
1832	Arabidopsis WUSCHEL is a bifunctional transcription factor that acts as a repressor in stem cell regulation and as an activator in floral patterning. **2009**, 21, 3493-505	213
1831	Multiple alignment of DNA sequences with MAFFT. **2009**, 537, 39-64	888
1830	Phylogenetic analysis of new Prasinoviruses (Phycodnaviridae) that infect the green unicellular algae Ostreococcus, Bathycoccus and Micromonas. **2009**, 1, 114-23	33
1829	PhyLIS: a simple GNU/Linux distribution for phylogenetics and phyloinformatics. **2009**, 5, 91-5	3
1828	Ophiostoma denticiliatum sp. nov. and other Ophiostoma species associated with the birch bark beetle in southern Norway. **2009**, 23, 9-15	21
1827	Roselliniella revealed as an overlooked genus of Hypocreales, with the description of a second species on parmelioid lichens. **2010**, 24, 12-7	13
1826	Ophiostoma spp. associated with pine- and spruce-infesting bark beetles in Finland and Russia. **2010**, 25, 72-93	49

1825	HIV-1 transmission after cessation of early antiretroviral therapy among men having sex with men. **2010**, 24, 1177-83	52
1824	Molecular phylogenies of figs and fig-pollinating wasps in the Ryukyu and Bonin (Ogasawara) islands, Japan. **2010**, 85, 177-92	14
1823	High-resolution cardiovascular function confirms functional orthology of myocardial contractility pathways in zebrafish. **2010**, 42, 300-9	56
1822	Alignment of multiple proteins with an ensemble of hidden Markov models. **2010**, 4, 60-71	5
1821	Identification and Pathogenicity of Chrysoporthe cubensis on Eucalyptus and Syzygium spp. in South China. **2010**, 94, 1143-1150	28
1820	Phylogenetic position of sponges from Chagatai and Tore-Khol lakes. **2010**, 46, 1471-1478	4
1819	Molecular systematics: A synthesis of the common methods and the state of knowledge. **2010**, 15, 311-41	35
1818	The Hydrocarbon-Degrading Oleaginous Yeast Yarrowia lipolytica. **2010**, 2111-2121	15
1817	Cryptometrion aestuescens gen. sp. nov. (Cryphonectriaceae) pathogenic to Eucalyptus in Indonesia. **2010**, 39, 161	21
1816	Potyviruses and the digital revolution. **2010**, 48, 205-23	195
1815	The phylogenetic position of Myxozoa: exploring conflicting signals in phylogenomic and ribosomal data sets. **2010**, 27, 2733-46	63
1814	Localization of eukaryote-specific ribosomal proteins in a 5.5-□cryo-EM map of the 80S eukaryotic ribosome. **2010**, 107, 19754-9	112
1813	Evolutionary relationships among scyphozoan jellyfish families based on complete taxon sampling and phylogenetic analyses of 18S and 28S ribosomal DNA. **2010**, 50, 436-55	56
1812	Small-scale diversity and succession of fungi in the detritusphere of rye residues. **2010**, 59, 130-40	56
1811	Identification and characterization of a protostome homologue of peropsin from a jumping spider. **2010**, 196, 51-9	42
1810	Kinetoplastid RNA editing ligases 1 and 2 exhibit different electrostatic properties. **2010**, 16, 61-76	3
1809	Phylogenetic relationships of true butterflies (Lepidoptera: Papilionoidea) inferred from COI, 16S rRNA and EF-1□sequences. **2010**, 30, 409-25	27
1808	Auxin-related gene families in abiotic stress response in Sorghum bicolor. **2010**, 10, 533-46	184

1807	Ogataea cecidiorum sp. nov., a methanol-assimilating yeast isolated from galls on willow leaves. **2010**, 98, 93-101	19
1806	Development and evaluation of a one-step real-time RT-PCR assay for universal detection of influenza A viruses from avian and mammal species. **2010**, 155, 665-73	40
1805	Association of an atypical alphasatellite with a bipartite New World begomovirus. **2010**, 155, 1843-7	69
1804	Phylogeny, Life History Evolution and Biogeography of the Rhinanthoid Orobanchaceae. **2010**, 45, 347-367	32
1803	Characterisation of synnematous bark beetle-associated fungi from China, including Graphium carbonarium sp. nov.. **2010**, 40, 75-88	21
1802	New Ceratocystis species infecting coffee, cacao, citrus and native trees in Colombia. **2010**, 40, 103-117	23
1801	Mycosphaerella podagrariae□ necrotrophic phytopathogen forming a special cellular interaction with its host Aegopodium podagraria. **2010**, 9, 49-56	2
1800	Taxonomy and pathogenicity of two novel Chrysoporthe species from Eucalyptus grandis and Syzygium guineense in Zambia. **2010**, 9, 379-393	18
1799	Phylogenetic relationships in genus Geopora (Pyronemataceae, Pezizales). **2010**, 9, 509-522	14
1798	The threatened plant intermediate wintergreen (Pyrola media) associates with a wide range of biotrophic fungi in native Scottish pine woods. **2010**, 19, 3963-3971	16
1797	Auxiliary electron transport pathways in chloroplasts of microalgae. **2010**, 106, 19-31	130
1796	Rapid Sequence Homology Assessment by Subsampling the Genome Space Using Difference Sets. **2010**, 56, 756-770	1
1795	Alignment method for spectrograms of DNA sequences. **2010**, 14, 3-9	
1794	Biodiversity of streptomycetes isolated from a succession sequence at a post-mining site and their evidence in Miocene lacustrine sediment. **2010**, 165, 594-608	10
1793	Pelagodinium gen. nov. and P. b□ comb. nov., a dinoflagellate symbiont of planktonic foraminifera. **2010**, 161, 385-99	60
1792	Development and optimisation of a duplex real-time reverse transcription quantitative PCR assay targeting the VP7 and NS2 genes of African horse sickness virus. **2010**, 167, 45-52	28
1791	MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. **2010**, 11, 10	46
1790	MISHIMA--a new method for high speed multiple alignment of nucleotide sequences of bacterial genome scale data. **2010**, 11, 142	16

1789	MTRAP: pairwise sequence alignment algorithm by a new measure based on transition probability between two consecutive pairs of residues. **2010**, 11, 235	8
1788	Automatic detection of anchor points for multiple sequence alignment. **2010**, 11, 445	4
1787	Reticular alignment: a progressive corner-cutting method for multiple sequence alignment. **2010**, 11, 570	11
1786	Patterns of kinesin evolution reveal a complex ancestral eukaryote with a multifunctional cytoskeleton. **2010**, 10, 110	98
1785	Unsuspected diversity of Niphargus amphipods in the chemoautotrophic cave ecosystem of Frasassi, central Italy. **2010**, 10, 171	41
1784	A phylogenetic mosaic plastid proteome and unusual plastid-targeting signals in the green-colored dinoflagellate Lepidodinium chlorophorum. **2010**, 10, 191	57
1783	Filoviruses are ancient and integrated into mammalian genomes. **2010**, 10, 193	126
1782	The worldwide holoparasitic Apodanthaceae confidently placed in the Cucurbitales by nuclear and mitochondrial gene trees. **2010**, 10, 219	27
1781	History of myxozoan character evolution on the basis of rDNA and EF-2 data. **2010**, 10, 228	92
1780	Phylogenetic analysis of ferlin genes reveals ancient eukaryotic origins. **2010**, 10, 231	39
1779	Mating system drives negative associations between morphological features in Schistosomatidae. **2010**, 10, 245	2
1778	Diversity of sponge mitochondrial introns revealed by cox 1 sequences of Tetillidae. **2010**, 10, 288	30
1777	Chlorophyll-binding proteins revisited--a multigenic family of light-harvesting and stress proteins from a brown algal perspective. **2010**, 10, 365	76
1776	Evolution of Rhizaria: new insights from phylogenomic analysis of uncultivated protists. **2010**, 10, 377	104
1775	Fast evolving 18S rRNA sequences from Solenogastres (Mollusca) resist standard PCR amplification and give new insights into mollusk substitution rate heterogeneity. **2010**, 10, 70	61
1774	Molecular evidence for a diverse green algal community growing in the hair of sloths and a specific association with Trichophilus welckeri (Chlorophyta, Ulvophyceae). **2010**, 10, 86	46
1773	Comparative genomics and proteomics of Helicobacter mustelae, an ulcerogenic and carcinogenic gastric pathogen. **2010**, 11, 164	31
1772	Study of inter- and intra-individual variations in the salivary microbiota. **2010**, 11, 523	167

1771	The venom composition of the parasitic wasp Chelonus inanitus resolved by combined expressed sequence tags analysis and proteomic approach. **2010**, 11, 693	80
1770	Genomic and neural analysis of the estradiol-synthetic pathway in the zebra finch. **2010**, 11, 46	24
1769	Family-level relationships of the spittlebugs and froghoppers (Hemiptera: Cicadomorpha: Cercopoidea). **2010**, 35, 393-415	52
1768	Isolation of a new heterolobosean amoeba from a rice field soil: Vrihiamoeba italica gen. nov., sp. nov. **2010**, 46, 164-70	10
1767	Arthropod phylogeny revisited, with a focus on crustacean relationships. **2010**, 39, 88-110	61
1766	Consolidation of glycosyl hydrolase family 30: a dual domain 4/7 hydrolase family consisting of two structurally distinct groups. **2010**, 584, 4435-41	97
1765	Transmission of lungworms of harbour porpoises and harbour seals: molecular tools determine potential vertebrate intermediate hosts. **2010**, 40, 845-53	40
1764	Myospora metanephrops (n. g., n. sp.) from marine lobsters and a proposal for erection of a new order and family (Crustaceacida; Myosporidae) in the Class Marinosporidia (Phylum Microsporidia). **2010**, 40, 1433-46	33
1763	Phylogenetic analysis of the haemagglutinin gene of current wild-type canine distemper viruses from South Africa: lineage Africa. **2010**, 143, 126-32	34
1762	First isolation of an H1N1 avian influenza virus from wild terrestrial non-migratory birds in Argentina. **2010**, 396, 76-84	21
1761	Viral encephalitis of tilapia larvae: primary characterization of a novel herpes-like virus. **2010**, 399, 239-47	34
1760	Glycoprotein gene sequence variation in rhesus monkey rhadinovirus. **2010**, 400, 175-86	19
1759	Computational analysis of human adenovirus serotype 18. **2010**, 404, 284-92	8
1758	Four p67 alleles identified in South African Theileria parva field samples. **2010**, 167, 244-54	23
1757	Evolution of Picornaviridae: an examination of phylogenetic relationships and cophylogeny. **2010**, 54, 995-1005	20
1756	Incongruence between molecular phylogeny and morphological classification in amphipod crustaceans: a case study of Antarctic lysianassoids. **2010**, 55, 202-209	43
1755	Molecular systematics of the bubblegum coral genera (Paragorgiidae, Octocorallia) and description of a new deep-sea species. **2010**, 55, 123-135	42
1754	Phylogenetic relationships within the lophophorate lineages (Ectoprocta, Brachiopoda and Phoronida). **2010**, 55, 1121-7	64

1753	Phylogeny of the bristle worm family Eunicidae (Eunicida, Annelida) and the phylogenetic utility of noncongruent 16S, COI and 18S in combined analyses. **2010**, 55, 660-76	56
1752	Conflicting signal within a single gene confounds syllid phylogeny (Syllidae, Annelida). **2010**, 55, 1128-38	12
1751	Phylogeny of entelegyne spiders: affinities of the family Penestomidae (NEW RANK), generic phylogeny of Eresidae, and asymmetric rates of change in spinning organ evolution (Araneae, Araneoidea, Entelegynae). **2010**, 55, 786-804	82
1750	Species boundaries and phylogenetic relationships between Atlanto-Mediterranean shallow-water and deep-sea coral associated Hexadella species (Porifera, Ianthellidae). **2010**, 56, 104-14	41
1749	A multilocus timescale for the origin of extant amphibians. **2010**, 56, 554-61	87
1748	Obtaining mtDNA genomes from next-generation transcriptome sequencing: a case study on the basal Passerida (Aves: Passeriformes) phylogeny. **2010**, 57, 466-70	36
1747	Molecular phylogeny of the genus Luzula DC. (Juncaceae, Monocotyledones) based on plastome and nuclear ribosomal regions: a case of incongruence, incomplete lineage sorting and hybridisation. **2010**, 57, 536-51	22
1746	Molecular phylogeny and evolutionary habitat transition of the flower bugs (Heteroptera: Anthocoridae). **2010**, 57, 1173-83	20
1745	Sequence embedding for fast construction of guide trees for multiple sequence alignment. **2010**, 5, 21	74
1744	A structural dissection of amino acid substitutions in helical transmembrane proteins. **2010**, 78, 2895-907	9
1743	HETEROCAPSA ARCTICA SUBSP. FRIGIDA SUBSP. NOV. (PERIDINIALES, DINOPHYCEAE)DESCRIPTION OF A NEW DINOFLAGELLATE AND ITS OCCURRENCE IN THE BALTIC SEA1. **2010**, 46, 751-762	10
1742	Detecting gene duplications in the human lineage. **2010**, 74, 555-65	5
1741	Potential link between plant and fungal distributions in a dipterocarp rainforest: community and phylogenetic structure of tropical ectomycorrhizal fungi across a plant and soil ecotone. **2010**, 185, 529-42	166
1740	DNA barcoding of arbuscular mycorrhizal fungi. **2010**, 187, 461-474	204
1739	Central and storage carbon metabolism of the brown alga Ectocarpus siliculosus: insights into the origin and evolution of storage carbohydrates in Eukaryotes. **2010**, 188, 67-81	129
1738	The cell wall polysaccharide metabolism of the brown alga Ectocarpus siliculosus. Insights into the evolution of extracellular matrix polysaccharides in Eukaryotes. **2010**, 188, 82-97	297
1737	Identification of a functional luciferase gene in the non-luminous diurnal firefly, Lucidina biplagiata. **2010**, 19, 737-43	8
1736	Multilocus analysis of honeyeaters (Aves: Meliphagidae) highlights spatio-temporal heterogeneity in the influence of biogeographic barriers in the Australian monsoonal zone. **2010**, 19, 2980-94	65

1735	Phylogenetic analysis of Bacteroidales 16S rRNA gene sequences from human and animal effluents and assessment of ruminant faecal pollution by real-time PCR. **2010**, 108, 974-984	81
1734	Multiple fossil calibrations, nuclear loci and mitochondrial genomes provide new insight into biogeography and divergence timing for true seals (Phocidae, Pinnipedia). **2010**, 37, 814-829	64
1733	When Thailand was an island □the phylogeny and biogeography of mite harvestmen (Opiliones, Cyphophthalmi, Stylocellidae) in Southeast Asia. **2010**, 37, 1114-1130	45
1732	Multiple periglacial refugia in the Patagonian steppe and post-glacial colonization of the Andes: the phylogeography of Calceolaria polyrhiza. **2010**, 37, no-no	15
1731	Gondwanan radiation of the Southern Hemisphere crayfishes (Decapoda: Parastacidae): evidence from fossils and molecules. **2010**, 37, 2275-2290	59
1730	An aqueous H+ permeation pathway in the voltage-gated proton channel Hv1. **2010**, 17, 869-875	131
1729	Identification and transcriptional analysis of trans-DCE-producing reductive dehalogenases in Dehalococcoides species. **2010**, 4, 1020-30	66
1728	Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota. **2010**, 464, 908-12	734
1727	Chemical phylogenetics of histone deacetylases. **2010**, 6, 238-243	564
1726	Evolutionary relationships among marine cercozoans as inferred from combined SSU and LSU rDNA sequences and polyubiquitin insertions. **2010**, 57, 518-27	12
1725	A multilocus approach to harvestman (Arachnida: Opiliones) phylogeny with emphasis on biogeography and the systematics of Laniatores. **2010**, 26, 408-437	95
1724	Recovering phylogenetic signal from frog mating calls. **2010**, 39, 141-154	45
1723	The Baikalian genus Rhyacodriloides in Europe: phylogenetic assessment of Rhyacodriloidinae subfam. n. within the Naididae (Annelida). **2010**, 39, 462-482	11
1722	Systematics of the snake genera Stenophis and Lycodryas from Madagascar and the Comoros. **2010**, 39, 426-435	8
1721	Phylogenetic relationships among species of the genus Oligoryzomys (Rodentia, Cricetidae) from Central and South America. **2010**, 39, 511-526	10
1720	Systematics of Andean gladiator frogs of the Hypsiboas pulchellus species group (Anura, Hylidae). **2010**, 39, 572-590	20
1719	Incongruent patterns of genetic connectivity among four ophiuroid species with differing coral host specificity on North Atlantic seamounts. **2010**, 31, 121-143	48
1718	Degeneration patterns of the olfactory receptor genes in sea snakes. **2010**, 23, 302-10	23

1717	Major clades and phylogenetic relationships between lichenized and non-lichenized lineages in Ostropales (Ascomycota: Lecanoromycetes). **2010**, 59, 1483-1494		67
1716	Phylogenomic analyses reveal the evolutionary origin of the inhibin alpha-subunit, a unique TGFbeta superfamily antagonist. **2010**, 5, e9457		10
1715	Validation of coevolving residue algorithms via pipeline sensitivity analysis: ELSC and OMES and ZNMI, oh my!. **2010**, 5, e10779		24
1714	Arabidopsis thaliana PGR7 encodes a conserved chloroplast protein that is necessary for efficient photosynthetic electron transport. **2010**, 5, e11688		15
1713	A gene in the process of endosymbiotic transfer. **2010**, 5, e13234		13
1712	Silkworm coatomers and their role in tube expansion of posterior silkgland. **2010**, 5, e13252		13
1711	Different patterns of evolution in the centromeric and telomeric regions of group A and B haplotypes of the human killer cell Ig-like receptor locus. **2010**, 5, e15115		173
1710	Genome-wide synteny through highly sensitive sequence alignment: Satsuma. **2010**, 26, 1145-51		157
1709	Sequence-based identification of Japanese Armillaria species using the elongation factor-1 alpha gene. **2010**, 102, 898-910		32
1708	Crystal structure of TtgV in complex with its DNA operator reveals a general model for cooperative DNA binding of tetrameric gene regulators. **2010**, 24, 2556-65		28
1707	Conserved and variable features of Gag structure and arrangement in immature retrovirus particles. **2010**, 84, 11729-36		51
1706	Dynamic coinfection with multiple viral subtypes in acute hepatitis C. **2010**, 202, 1770-9		28
1705	Increased activity of Diaphanous homolog 3 (DIAPH3)/diaphanous causes hearing defects in humans with auditory neuropathy and in Drosophila. **2010**, 107, 13396-401		80
1704	Character evolution in Hydrozoa (phylum Cnidaria). **2010**, 50, 456-72		67
1703	PicXAA: greedy probabilistic construction of maximum expected accuracy alignment of multiple sequences. *Nucleic Acids Research*, **2010**, 38, 4917-28	20.1	37
1702	Lymphocryptovirus phylogeny and the origins of Epstein-Barr virus. **2010**, 91, 630-42		60
1701	GC content-based pan-pox universal PCR assays for poxvirus detection. **2010**, 48, 268-76		72
1700	Differential gene retention in plastids of common recent origin. **2010**, 27, 1530-7		85

1699	Genome sequencing of recent clinical Chlamydia trachomatis strains identifies loci associated with tissue tropism and regions of apparent recombination. **2010**, 78, 2544-53		98
1698	The bivalve mollusc Mactra corallina: genetic evidence of existing sibling species. **2010**, 90, 633-644		10
1697	A quantum-inspired genetic algorithm based on probabilistic coding for multiple sequence alignment. **2010**, 8, 59-75		4
1696	Parallel evolution of opsin gene expression in African cichlid fishes. **2010**, 27, 2839-54		79
1695	EM-Coffee: An Improvement of M-Coffee. **2010**,		
1694	AlexSys: a knowledge-based expert system for multiple sequence alignment construction and analysis. *Nucleic Acids Research*, **2010**, 38, 6338-49	20.1	10
1693	Rangewide analysis of fungal associations in the fully mycoheterotrophic Corallorhiza striata complex (Orchidaceae) reveals extreme specificity on ectomycorrhizal Tomentella (Thelephoraceae) across North America. **2010**, 97, 628-43		38
1692	Natural hybridization in tropical spikerushes of Eleocharis subgenus Limnochloa (Cyperaceae): Evidence from morphology and DNA markers. **2010**, 97, 1229-40		10
1691	Caloplaca phlogina, a lichen with two facies; an example of infraspecific variability resulting in the description of a redundant species. **2010**, 42, 685-692		8
1690	YbdG in Escherichia coli is a threshold-setting mechanosensitive channel with MscM activity. **2010**, 107, 12664-9		77
1689	Reducing phylogenetic bias in correlated mutation analysis. **2010**, 23, 321-6		22
1688	Genomic, proteomic, and transcriptomic analysis of virulent and avirulent Rickettsia prowazekii reveals its adaptive mutation capabilities. **2010**, 20, 655-63		54
1687	Complete nucleotide sequence analysis of plasmids in strains of Staphylococcus aureus clone USA300 reveals a high level of identity among isolates with closely related core genome sequences. **2010**, 48, 4504-11		56
1686	Compositional heterogeneity and phylogenomic inference of metazoan relationships. **2010**, 27, 2095-104		68
1685	Comparative structural biology of eubacterial and archaeal oligosaccharyltransferases. **2010**, 285, 4941-50		77
1684	Parallelization of the MAFFT multiple sequence alignment program. **2010**, 26, 1899-900		551
1683	Different phylogenomic approaches to resolve the evolutionary relationships among model fish species. **2010**, 27, 2757-74		17
1682	Variability of Bartonella genotypes among small mammals in Spain. **2010**, 76, 8062-70		42

1681	RBT-Km: K-Means clustering for Multiple Sequence Alignment. **2010**,		
1680	New sequence alignment by a measure due to entangled correlation in two consecutive residues. **2010**,		0
1679	. **2010**,		1
1678	alns A searchable and filterable sequence alignment format. **2010**,		
1677	Characterization of three mnp genes of Fomitiporia mediterranea and report of additional class II peroxidases in the order hymenochaetales. **2010**, 76, 6431-40		27
1676	Opsin co-expression in Limulus photoreceptors: differential regulation by light and a circadian clock. **2010**, 213, 2589-601		36
1675	Evolution of anatomical and physiological specialization in the compound eyes of stomatopod crustaceans. **2010**, 213, 3473-86		48
1674	A small, variable, and irregular killer cell Ig-like receptor locus accompanies the absence of MHC-C and MHC-G in gibbons. **2010**, 184, 1379-91		36
1673	Evolutionary origin of a functional gonadotropin in the pituitary of the most primitive vertebrate, hagfish. **2010**, 107, 15832-7		48
1672	Evolutionary expansion and specialization of the PDZ domains. **2010**, 27, 1058-69		33
1671	Essential biological processes of an emerging pathogen: DNA replication, transcription, and cell division in Acinetobacter spp. **2010**, 74, 273-97		56
1670	Human and non-human primate genomes share hotspots of positive selection. **2010**, 6, e1000840		52
1669	Issues in bioinformatics benchmarking: the case study of multiple sequence alignment. *Nucleic Acids Research*, **2010**, 38, 7353-63	20.1	53
1668	Genome sequence of the pea aphid Acyrthosiphon pisum. **2010**, 8, e1000313		732
1667	Plasmodium falciparum erythrocyte membrane protein 1 diversity in seven genomes--divide and conquer. **2010**, 6, e1000933		245
1666	A comprehensive genome-wide map of autonomously replicating sequences in a naive genome. **2010**, 6, e1000946		41
1665	Demonstration of cross-protective vaccine immunity against an emerging pathogenic Ebolavirus Species. **2010**, 6, e1000904		94
1664	Structural basis of cell wall cleavage by a staphylococcal autolysin. **2010**, 6, e1000807		62

1663	Objective sequence-based subfamily classifications of mouse homeodomains reflect their in vitro DNA-binding preferences. *Nucleic Acids Research*, **2010**, 38, 7927-42	20.1	2
1662	Mycorrhizal symbionts of Pisonia grandis and P. sechellarum in Seychelles: identification of mycorrhizal fungi and description of new Tomentella species. **2010**, 102, 522-33		34
1661	Development and application of bovine and porcine oligonucleotide arrays with protein-based annotation. **2010**, 2010, 453638		7
1660	Feature-incorporated alignment based ligand-binding residue prediction for carbohydrate-binding modules. **2010**, 26, 1022-8		6
1659	Multi-objective pairwise RNA sequence alignment. **2010**, 26, 2383-90		25
1658	Re-examination of strains formerly assigned to Hyphopichia burtonii, the phylogeny of the genus Hyphopichia, and the description of Hyphopichia pseudoburtonii sp. nov. **2010**, 60, 2675-2680		18
1657	Phylogeographic analysis of the migration of Japanese encephalitis virus in Asia. **2010**, 5, 343-354		5
1656	A tile-based parallel Viterbi algorithm for biological sequence alignment on GPU with CUDA. **2010**,		1
1655	Co-existing ericaceous plant species in a subarctic mire community share fungal root endophytes. **2010**, 3, 205-214		40
1654	Species richness analysis and ITS rDNA phylogeny revealed the majority of cultivable foliar endophytes from beech (Fagus sylvatica). **2010**, 3, 366-378		54
1653	Molecules reject an opheliid affinity for Travisia (Annelida). **2010**, 8, 507-512		21
1652	Target promiscuity and heterogeneous effects of tarantula venom peptides affecting Na+ and K+ ion channels. **2010**, 285, 4130-4142		73
1651	Diversity of rock varnish bacterial communities from Black Canyon, New Mexico. **2010**, 115, n/a-n/a		53
1650	Using morphometrics, in situ observations and genetic characters to distinguish among commercially valuable Hawaiian black coral species; a redescription of Antipathes grandis Verrill, 1928 (Antipatharia:Antipathidae). **2010**, 24, 271		22
1649	Lack of hemocyanin in Oriental Plecoptera and multifunctionality of the protein in Larvae. **2010**, 44, 429-446		1
1648	The origins of eukaryotic-like proteins in Legionella pneumophila. **2010**, 300, 470-81		72
1647	The solution structure of the C-terminal Ig-like domain of the bacteriophage ▯tail tube protein. **2010**, 403, 468-79		39
1646	Systematics of Catenulifera (anamorphic Hyaloscyphaceae) with an assessment of the phylogenetic position of Phialophora hyalina. **2010**, 114, 396-409		19

1645	Characterization of luciferases and its paralogue in the Panamanian luminous click beetle Pyrophorus angustus: a click beetle luciferase lacks the fatty acyl-CoA synthetic activity. **2010**, 452, 1-6	17
1644	Peptidase inhibitors in the MEROPS database. **2010**, 92, 1463-83	52
1643	Characterization of arrangement and expression of the beta-2 microglobulin locus in the sandbar and nurse shark. **2010**, 34, 189-95	9
1642	Quantitative detection and typing of hepatitis D virus in human serum by real-time polymerase chain reaction and melting curve analysis. **2010**, 67, 172-9	15
1641	Aggregation of deamidated human betaB2-crystallin and incomplete rescue by alpha-crystallin chaperone. **2010**, 90, 688-98	22
1640	The genome of Naegleria gruberi illuminates early eukaryotic versatility. **2010**, 140, 631-42	346
1639	The monopolin complex crosslinks kinetochore components to regulate chromosome-microtubule attachments. **2010**, 142, 556-67	99
1638	Introducing the bacterial 'chromid': not a chromosome, not a plasmid. **2010**, 18, 141-8	249
1637	Phylogenetic relationships within the suborder Dermanyssina (Acari: Parasitiformes) and a test of dermanyssoid monophyly. **2010**, 36, 299-312	22
1636	The impact of rRNA secondary structure consideration in alignment and tree reconstruction: simulated data and a case study on the phylogeny of hexapods. **2010**, 27, 2507-21	44
1635	Computing multiple sequence/structure alignments with the T-coffee package. **2010**, Chapter 3, Unit 3.8.1-25	22
1634	A novel approach to multiple sequence alignment using hadoop data grids. **2010**,	12
1633	Stimulation of lignocellulosic biomass hydrolysis by proteins of glycoside hydrolase family 61: structure and function of a large, enigmatic family. **2010**, 49, 3305-16	597
1632	MSAProbs: multiple sequence alignment based on pair hidden Markov models and partition function posterior probabilities. **2010**, 26, 1958-64	170
1631	Identification and characterization of a luciferase isotype in the Japanese firefly, Luciola cruciata, involving in the dim glow of firefly eggs. **2010**, 49, 10788-95	26
1630	Characterization of kinesin-like proteins in silkworm posterior silk gland cells. **2010**, 20, 713-27	7
1629	Genome-wide classification and evolutionary analysis of the bHLH family of transcription factors in Arabidopsis, poplar, rice, moss, and algae. **2010**, 153, 1398-412	341
1628	A Visualization Quality Evaluation Method for Multiple Sequence Alignments. **2011**,	

1627	A Web-Based Phylogenetic Analysis for a Query Gene. **2011**,	
1626	The dawn of symbiosis between plants and fungi. **2011**, 7, 574-7	180
1625	Exploiting topological constraints to reveal buried sequence motifs in the membrane-bound N-linked oligosaccharyl transferases. **2011**, 50, 7557-67	29
1624	Mining human genome for novel purinergic P2Y receptors: a sequence analysis and molecular modeling approach. **2011**, 31, 75-84	3
1623	An efficient way of multiple sequence alignment. **2011**,	
1622	The anamorph genus Knufia and its phylogenetically allied species in Coniosporium, Sarcinomyces, and Phaeococcomyces. **2011**, 89, 523-536	43
1621	Interaction of diverse voltage sensor homologs with lipid bilayers revealed by self-assembly simulations. **2011**, 100, 875-84	11
1620	Five novel Wickerhamomyces- and Metschnikowia-related yeast species, Wickerhamomyces chaumierensis sp. nov., Candida pseudoflosculorum sp. nov., Candida danieliae sp. nov., Candida robnettiae sp. nov. and Candida eppingiae sp. nov., isolated from plants. **2011**, 61, 2015-2022	18
1619	Third lineage of rodent eimerians: morphology, phylogeny and re-description of Eimeria myoxi (Apicomplexa: Eimeriidae) from Eliomys quercinus (Rodentia: Gliridae). **2011**, 138, 1217-23	5
1618	The family Agaricaceae: phylogenies and two new white-spored genera. **2011**, 103, 494-509	47
1617	New records of the Cryphonectriaceae from southern Africa including Latruncellus aurorae gen. sp. nov. **2011**, 103, 554-69	26
1616	Taxonomy of Pluteus eugraptus and morphologically similar taxa. **2011**, 103, 646-55	7
1615	The Chp1-Tas3 core is a multifunctional platform critical for gene silencing by RITS. **2011**, 18, 1351-7	31
1614	Diversity of Stag Beetle-Associated Nematodes in Japan. **2011**, 40, 281-288	22
1613	Novel species of Celoporthe from Eucalyptus and Syzygium trees in China and Indonesia. **2011**, 103, 1384-410	29
1612	Towards Automated Phylogenomic Inference. **2011**, 205-215	
1611	In vitro Selection of DNA Aptamers to Glioblastoma Multiforme. **2011**, 2, 175-181	88
1610	Phylogenetic analysis of protein sequence data using the Randomized Axelerated Maximum Likelihood (RAXML) Program. **2011**, Chapter 19, Unit19.11	33

1609	Recent trends in molecular phylogenetic analysis: where to next?. **2011**, 102, 130-8	70
1608	A new classification of the long-horned caddisflies (Trichoptera: Leptoceridae) based on molecular data. **2011**, 11, 10	19
1607	Lafora disease E3-ubiquitin ligase malin is related to TRIM32 at both the phylogenetic and functional level. **2011**, 11, 225	16
1606	Geographic location and phylogeny are the main determinants of the size of the geographical range in aquatic beetles. **2011**, 11, 344	38
1605	FluReF, an automated flu virus reassortment finder based on phylogenetic trees. **2011**, 12 Suppl 2, S3	10
1604	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. **2011**, 7, 539	8587
1603	The Camaenid Species of the Kimberley Islands, Western Australia (Stylommatophora: Helicoidea). **2011**, 54, 203-406	38
1602	. **2011**, 59, 4210-4224	4
1601	The relationships of the enigmatic neogastropod Loxotaphrus (Cancellariidae). **2011**, 54, 115-124	2
1600	Selection of in silico drug screening results for G-protein-coupled receptors by using universal active probes. **2011**, 51, 2398-407	19
1599	Persicivirga ulvanivorans sp. nov., a marine member of the family Flavobacteriaceae that degrades ulvan from green algae. **2011**, 61, 1899-1905	35
1598	Molecular architecture of the transport channel of the nuclear pore complex. **2011**, 147, 590-602	87
1597	The intronome of budding yeasts. **2011**, 334, 662-70	47
1596	Evidence for high degrees of specialisation, evolutionary diversity, and morphological´distinctiveness in the genus Bremia. **2011**, 115, 102-11	29
1595	Phylogeny and intraspecific variation of the extreme xerophile, Xeromyces bisporus. **2011**, 115, 1100-11	22
1594	Species of Heterobasidion host a diverse pool of partitiviruses with global distribution and interspecies transmission. **2011**, 115, 1234-43	51
1593	Gymnodinium litoralis sp. nov. (Dinophyceae), a newly identified bloom-forming dinoflagellate from the NW Mediterranean Sea. **2011**, 12, 11-25	22
1592	Enzymatic characterization of Catalase from Bacillus anthracis and prediction of critical residues using information theoretic measure of Relative Entropy. **2011**, 411, 88-95	8

1591	Phylogenetic Relationships ofMuehlenbeckia,Fallopia, andReynoutria(Polygonaceae) Investigated with Chloroplast and Nuclear Sequence Data. **2011**, 172, 1053-1066	18
1590	Evolutionary implications of morphogenesis and molecular patterning of the blind gut in the planarian Schmidtea polychroa. **2011**, 352, 164-76	47
1589	The C. elegans nck-1 gene encodes two isoforms and is required for neuronal guidance. **2011**, 354, 55-66	9
1588	The enigma of the E326K mutation in acid β-glucocerebrosidase. **2011**, 104, 35-8	40
1587	Reconstructing intraordinal relationships in Lepidoptera using mitochondrial genome data with the description of two newly sequenced lycaenids, Spindasis takanonis and Protantigius superans (Lepidoptera: Lycaenidae). **2011**, 61, 436-45	113
1586	Reappraisal of the "Molecular phylogeny of Western Palaearctic Helicidae s.l. (Gastropoda: Stylommatophora)": when poor science meets GenBank. **2011**, 61, 914-23	26
1585	Nucleotide diversity and linkage disequilibrium of nine genes with putative effects on flowering time in perennial ryegrass (Lolium perenne L.). **2011**, 180, 228-37	30
1584	Comparative analysis of GT14/GT14-like gene family in Arabidopsis, Oryza, Populus, Sorghum and Vitis. **2011**, 181, 688-95	18
1583	Histaminergic signaling in the central nervous system of Daphnia and a role for it in the control of phototactic behavior. **2011**, 214, 1773-82	43
1582	Molecular and morphological analysis of the family Calonymphidae with a description of Calonympha chia sp. nov., Snyderella kirbyi sp. nov., Snyderella swezyae sp. nov. and Snyderella yamini sp. nov. **2011**, 61, 2547-2558	24
1581	Limitations of mitochondrial gene barcoding in Octocorallia. **2011**, 11, 19-31	176
1580	Detection of parasitizing coccidia and determination of host crane species, sex and genotype by faecal DNA analysis. **2011**, 11, 1033-44	6
1579	A molecular phylogeny of the Chalcidoidea (Hymenoptera). **2011**, 6, e27023	92
1578	References. **2011**, r1-r178	3
1577	An improved scoring method for protein residue conservation and multiple sequence alignment. **2011**, 10, 275-85	7
1576	Phylogenetic relationships and morphological diversity in Neotropical Heliotropium (Heliotropiaceae). **2011**, 60, 663-680	27
1575	Phylogeny of Polygoneae (Polygonaceae: Polygonoideae). **2011**, 60, 1653-1666	26
1574	The new FioreDB database provides comprehensive information on plant transcription factors and phenotypes induced by CRES-T in ornamental and model plants. **2011**, 28, 123-130	23

1573	Population genetic structure of the migratory rice leaf roller, Cnaphalocrocis medinalis (Lepidoptera: Pyralidae), inferred from the mitochondrial A+T-rich region and nuclear ITS2 sequences. **2011**, 10, 273-94	9
1572	Not All Larvae Stay Close to Home: Insights into Marine Population Connectivity with a Focus on the Brown Surgeonfish (). **2011**, 2011,	41
1571	Diversity and vertical distribution of microbial eukaryotes in the snow, sea ice and seawater near the north pole at the end of the polar night. **2011**, 2, 106	77
1570	Contrasting 5' and 3' evolutionary histories and frequent evolutionary convergence in Meis/hth gene structures. **2011**, 3, 551-64	15
1569	Advanced computational biology methods identify molecular switches for malignancy in an EGF mouse model of liver cancer. **2011**, 6, e17738	15
1568	□arrestin functionally regulates the non-bleaching pigment parapinopsin in lamprey pineal. **2011**, 6, e16402	17
1567	Phylogenetic relationships among NE Atlantic Plocamionida Topsent (1927) (Porifera, Poecilosclerida): under-estimated diversity in reef ecosystems. **2011**, 6, e16533	21
1566	A novel method of characterizing genetic sequences: genome space with biological distance and applications. **2011**, 6, e17293	60
1565	The contribution of coevolving residues to the stability of KDO8P synthase. **2011**, 6, e17459	13
1564	Plastid 16S rRNA gene diversity among eukaryotic picophytoplankton sorted by flow cytometry from the South Pacific Ocean. **2011**, 6, e18979	62
1563	Novel, divergent simian hemorrhagic fever viruses in a wild Ugandan red colobus monkey discovered using direct pyrosequencing. **2011**, 6, e19056	55
1562	Simulated atmospheric N deposition alters fungal community composition and suppresses ligninolytic gene expression in a northern hardwood forest. **2011**, 6, e20421	131
1561	Historical isolation versus recent long-distance connections between Europe and Africa in bifid toadflaxes (Linaria sect. Versicolores). **2011**, 6, e22234	48
1560	Evolutionary genomics implies a specific function of Ant4 in mammalian and anole lizard male germ cells. **2011**, 6, e23122	11
1559	Mariprofundus ferrooxydans PV-1 the first genome of a marine Fe(II) oxidizing Zetaproteobacterium. **2011**, 6, e25386	112
1558	Lepiota maculans, an Unusual Mushroom Rediscovered after 105 years. **2011**, 10, 267-274	5
1557	Comparative transcriptomics of Eastern African cichlid fishes shows signs of positive selection and a large contribution of untranslated regions to genetic diversity. **2011**, 3, 443-55	49
1556	A New Cryptic Species of Salamander, Genus Oedipina (Caudata: Plethodontidae), from Premontane Elevations in Northern Nicaragua, with Comments on the Systematic Status of the Nicaraguan Paratypes of O. pseudouniformis Brame, 1968. **2011**, 526, 1-16	1

1555	Increased polymorphism near low-complexity sequences across the genomes of Plasmodium falciparum isolates. **2011**, 3, 539-50	8
1554	Novel species of Calonectria associated with Eucalyptus leaf blight in Southeast China. **2011**, 26, 1-12	36
1553	The value of the D1/D2 and internal transcribed spacers (ITS) domains for the identification of yeast species belonging to the genus Yamadazyma. **2011**, 26, 40-6	30
1552	Why everlastings don’t last. **2011**, 26, 70-84	33
1551	Positive selection for gains of N-linked glycosylation sites in hemagglutinin during evolution of H3N2 human influenza A virus. **2011**, 86, 287-94	17
1550	Phylogeographic patterns and cryptic speciation across oceanographic barriers in South African intertidal fishes. **2011**, 24, 2505-19	34
1549	Discovery and structural characterization of a novel glycosidase family of marine origin. **2011**, 13, 1253-70	70
1548	Accurate analysis of prevalence of coccidiosis in individually identified wild cranes in inhabiting and migrating populations in Japan. **2011**, 13, 2876-87	12
1547	Highly co-ordinated var gene expression and switching in clinical Plasmodium falciparum isolates from non-immune malaria patients. **2011**, 13, 1397-409	24
1546	Phylogenetic relationships of Western Mediterranean subterranean Trechini groundbeetles (Coleoptera: Carabidae). **2011**, 40, 282-295	26
1545	Molecular phylogeny endorses the relationship between carnivorous and filter-feeding tunicates (Tunicata, Ascidiacea). **2011**, 40, 603-612	11
1544	Diplodia scrobiculata found in the southern hemisphere. **2011**, 41, 175-181	15
1543	Characterization of Botryosphaeriaceae from plantation-grown Eucalyptus species in South China. **2011**, 60, 739-751	52
1542	Root hair-specific expansins modulate root hair elongation in rice. **2011**, 66, 725-34	110
1541	Fungal community composition and function after long-term exposure of northern forests to elevated atmospheric CO2 and tropospheric O3. **2011**, 17, 2184-2195	37
1540	Is sexual selection driving diversification of the bioluminescent ponyfishes (Teleostei: Leiognathidae)?. **2011**, 20, 2818-34	16
1539	Signatures of selection and sex-specific expression variation of a novel duplicate during the evolution of the Drosophila desaturase gene family. **2011**, 20, 3617-30	15
1538	Stage-specific requirement for Isa1 and Isa2 proteins in the mitochondrion of Trypanosoma brucei and heterologous rescue by human and Blastocystis orthologues. **2011**, 81, 1403-18	33

1537	Differentiating between effects of invasion and diversity: impacts of aboveground plant communities on belowground fungal communities. **2011**, 189, 526-35	25
1536	The N-terminal region of the bacterial DNA polymerase PolC features a pair of domains, both distantly related to domain V of the DNA polymerase III □subunit. **2011**, 278, 3109-18	4
1535	Identification of the Vibrio parahaemolyticus type III secretion system 2-associated chaperone VocC for the T3SS2-specific effector VopC. **2011**, 324, 156-64	13
1534	Elevational gradients in phylogenetic structure of ant communities reveal the interplay of biotic and abiotic constraints on diversity. **2011**, 34, 364-371	145
1533	Speciation and dispersal along continental coastlines and island arcs in the Indo-West Pacific turbinid gastropod genus Lunella. **2011**, 65, 1752-71	32
1532	Monophyletic origin of brood care in damselfishes. **2011**, 59, 245-8	13
1531	Molecular phylogenetics of Linaceae with complete generic sampling and data from two plastid genes. **2011**, 165, 64-83	23
1530	Morphology to the rescue: molecular data and the signal of morphological characters in combined phylogenetic analyses-a case study from mysmenid spiders (Araneae, Mysmenidae), with comments on the evolution of web architecture. **2011**, 27, 278-330	47
1529	Inference of phylogenetic relationships within Fabriciidae (Sabellida, Annelida) using molecular and morphological data. **2011**, 27, 356-379	14
1528	An extraordinary new genus of spiders from Western Australia with an expanded hypothesis on the phylogeny of Tetragnathidae (Araneae). **2011**, 161, 735-768	20
1527	Morphological and ecological uniformity in the funnel-mouthed tadpoles of Malagasy litter frogs, subgenus Chonomantis. **2011**, 162, 149-183	18
1526	Sequence diversity and novelty of natural assemblages of picoeukaryotes from the Indian Ocean. **2011**, 5, 184-95	36
1525	Evolution and metabolic significance of the urea cycle in photosynthetic diatoms. **2011**, 473, 203-7	321
1524	Musumecia gen. nov. in the Tricholomatoid clade (Basidiomycota, Agaricales) related to Pseudoclitocybe. **2011**, 29, 734-740	10
1523	Tracing protein evolution through ancestral structures of fish galectin. **2011**, 19, 711-21	13
1522	Leishmania donovani encodes a functional enzyme involved in vitamin C biosynthesis: arabino-1,4-lactone oxidase. **2011**, 180, 76-85	14
1521	Xanthidae MacLeay, 1838 (Decapoda: Brachyura: Xanthoidea) systematics: A multi-gene approach with support from adult and zoeal morphology. **2011**, 250, 407-448	33
1520	A new wilt and die-back disease of Acacia mangium associated with Ceratocystis manginecans and C. acaciivora sp. nov. in Indonesia. **2011**, 77, 292-304	94

1519	Long-distance transport, vacuolar sequestration, tolerance, and transcriptional responses induced by cadmium and arsenic. **2011**, 14, 554-62	272
1518	Molecular identification of sequestered diatom chloroplasts and kleptoplastidy in foraminifera. **2011**, 162, 394-404	66
1517	Emerging diversity within chrysophytes, choanoflagellates and bicosoecids based on molecular surveys. **2011**, 162, 435-48	88
1516	Analyses of genes encoding Theileria parva p104 and polymorphic immunodominant molecule (PIM) reveal evidence of the presence of cattle-type alleles in the South African T. parva population. **2011**, 181, 120-30	9
1515	MSACompro: protein multiple sequence alignment using predicted secondary structure, solvent accessibility, and residue-residue contacts. **2011**, 12, 472	20
1514	Potential pitfalls of modelling ribosomal RNA data in phylogenetic tree reconstruction: evidence from case studies in the Metazoa. **2011**, 11, 146	31
1513	The phylogenomic analysis of the anaphase promoting complex and its targets points to complex and modern-like control of the cell cycle in the last common ancestor of eukaryotes. **2011**, 11, 265	23
1512	Cleaning up the 'Bigmessidae': molecular phylogeny of scleractinian corals from Faviidae, Merulinidae, Pectiniidae and Trachyphylliidae. **2011**, 11, 37	77
1511	The complete mitochondrial genome of Flustra foliacea (Ectoprocta, Cheilostomata) - compositional bias affects phylogenetic analyses of lophotrochozoan relationships. **2011**, 12, 572	20
1510	Matching dimorphic sexes and immature stages with adults: resolving the systematics of the Bekilya group of Malagasy assassin bugs (Hemiptera: Reduviidae: Peiratinae). **2011**, 36, 115-138	13
1509	Molecular and chemical characters to evaluate species status of two cuckoo bumblebees: Bombus barbutellus and Bombus maxillosus (Hymenoptera, Apidae, Bombini). **2011**, 36, 453-469	31
1508	Molecular phylogenetics of Braconidae (Hymenoptera: Ichneumonoidea), based on multiple nuclear genes, and implications for classification. **2011**, 36, 549-572	94
1507	Comparison of linear gap penalties and profile-based variable gap penalties in profile-profile alignments. **2011**, 35, 308-18	5
1506	Bendigoles D-F, bioactive sterols from the marine sponge-derived Actinomadura sp. SBMs009. **2011**, 19, 6570-5	42
1505	The diversity of Terfezia desert truffles: new species and a highly variable species complex with intrasporocarpic nrDNA ITS heterogeneity. **2011**, 103, 841-53	36
1504	Systematics and ecology of the caecilian Crotaphatrema lamottei (Nussbaum) (Amphibia: Gymnophiona: Scolecomorphidae). **2011**, 45, 827-841	9
1503	The 18S and 28S rDNA identity and phylogeny of the common lotic chrysophyte Hydrurus foetidus. **2011**, 46, 282-291	35
1502	Parmelia sulcata (Ascomycota: Parmeliaceae), a sympatric monophyletic species complex. **2011**, 43, 585-601	46

1501	The Caloplaca crenulatella species complex; its intricate taxonomy and description of a new species. **2011**, 43, 467-481	14
1500	Methods for sequence-structure alignment. **2012**, 857, 55-82	5
1499	Paternal leakage of mitochondrial DNA in experimental crosses of populations of the potato cyst nematode Globodera pallida. **2011**, 139, 1509-19	9
1498	Spongiforma squarepantsii, a new species of gasteroid bolete from Borneo. **2011**, 103, 1119-23	16
1497	Evolutionary dynamics of spliceosomal intron revealed by in silico analyses of the P-Type ATPase superfamily genes. **2011**, 38, 2285-93	4
1496	The genome of Oryctes rhinoceros nudivirus provides novel insight into the evolution of nuclear arthropod-specific large circular double-stranded DNA viruses. **2011**, 42, 444-56	49
1495	Mannitol-1-phosphate dehydrogenase activity in Ectocarpus siliculosus, a key role for mannitol synthesis in brown algae. **2011**, 233, 261-73	48
1494	A novel gammaherpesvirus isolated from a black-tailed prairie dog (Cynomys ludovicianus). **2011**, 156, 1835-40	1
1493	Occurrence of a silicatein gene in glass sponges (Hexactinellida: Porifera). **2011**, 13, 810-9	18
1492	Bioactivity, chemical profiling, and 16S rRNA-based phylogeny of Pseudoalteromonas strains collected on a global research cruise. **2011**, 13, 1062-73	70
1491	Molecular phylogenetic analyses of Tofieldiaceae (Alismatales): family circumscription and intergeneric relationships. **2011**, 124, 349-57	14
1490	Ophiocordyceps pulvinata sp. nov., a pathogen with a reduced stroma. **2011**, 52, 39-47	23
1489	DNA sequence variation of the tobacco cutworm, Spodoptera litura (Lepidoptera: Noctuidae), determined by mitochondrial A+T-rich region and nuclear ITS2 sequences. **2011**, 49, 760-87	10
1488	Computational analysis of ligand recognition mechanisms by prostaglandin E2 (subtype 2) and D2 receptors. **2011**, 130, 1131-1143	
1487	Evolution of the TOR pathway. **2011**, 73, 209-20	90
1486	Cryptic diversity of Plasmopara viticola (Oomycota, Peronosporaceae) in North America. **2011**, 11, 3-7	22
1485	Four new Ceratocystis spp. associated with wounds on Eucalyptus, Schizolobium and Terminalia trees in Ecuador. **2011**, 46, 111-131	19
1484	New insights into relationships of lichen-forming Dothideomycetes. **2011**, 51, 155-162	57

1483	Phytophthora chrysanthemi sp. nov., a new species causing root rot of chrysanthemum in Japan. **2011**, 10, 21-31	25
1482	Taxonomy and phylogeny of Puccinia lagenophorae: a study using rDNA sequence data, morphological and host range features. **2011**, 10, 175-187	19
1481	Defining species in Tulasnella by correlating morphology and nrDNA ITS-5.8S sequence data of basidiomata from a tropical Andean forest. **2011**, 10, 229-238	27
1480	Recent outbreaks of downy mildew on grape ivy (Parthenocissus tricuspidata, Vitaceae) in Germany are caused by a new species of Plasmopara. **2011**, 10, 415-422	19
1479	Microarray estimation of genomic inter-strain variability in the genus Ectocarpus (Phaeophyceae). **2011**, 12, 2	18
1478	Incongruence between morphotypes and genetically delimited species in the coral genus Stylophora: phenotypic plasticity, morphological convergence, morphological stasis or interspecific hybridization?. **2011**, 11, 22	69
1477	The taming of an impossible child: a standardized all-in approach to the phylogeny of Hymenoptera using public database sequences. **2011**, 9, 55	50
1476	Mimivirus reveals Mre11/Rad50 fusion proteins with a sporadic distribution in eukaryotes, bacteria, viruses and plasmids. **2011**, 8, 427	13
1475	PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. **2011**, 12, 10	14
1474	More accurate recombination prediction in HIV-1 using a robust decoding algorithm for HMMs. **2011**, 12, 168	2
1473	Estimation of bacterial diversity using next generation sequencing of 16S rDNA: a comparison of different workflows. **2011**, 12, 473	47
1472	Homoplastic microinversions and the avian tree of life. **2011**, 11, 141	27
1471	Evolution of the mammalian lysozyme gene family. **2011**, 11, 166	42
1470	Phylogenomic analyses of malaria parasites and evolution of their exported proteins. **2011**, 11, 167	37
1469	A unique horizontal gene transfer event has provided the octocoral mitochondrial genome with an active mismatch repair gene that has potential for an unusual self-contained function. **2011**, 11, 228	68
1468	Early evolution of the biotin-dependent carboxylase family. **2011**, 11, 232	35
1467	Loss of genes for DNA recombination and repair in the reductive genome evolution of thioautotrophic symbionts of Calyptogena clams. **2011**, 11, 285	18
1466	Evolutionary maintenance of filovirus-like genes in bat genomes. **2011**, 11, 336	42

1465	Leucine-rich repeat receptor kinases are sporadically distributed in eukaryotic genomes. **2011**, 11, 367	35
1464	The origin of multicellularity in cyanobacteria. **2011**, 11, 45	175
1463	Molecular evolution of urea amidolyase and urea carboxylase in fungi. **2011**, 11, 80	43
1462	Plio-Pleistocene sea level and temperature fluctuations in the northwestern Pacific promoted speciation in the globally-distributed flathead mullet Mugil cephalus. **2011**, 11, 83	120
1461	Differential phylogenetic expansions in BAHD acyltransferases across five angiosperm taxa and evidence of divergent expression among Populus paralogues. **2011**, 12, 236	85
1460	Genome-level homology and phylogeny of Shewanella (Gammaproteobacteria: lteromonadales: Shewanellaceae). **2011**, 12, 237	31
1459	Unresolved orthology and peculiar coding sequence properties of lamprey genes: the KCNA gene family as test case. **2011**, 12, 325	52
1458	A codon substitution model that incorporates the effect of the GC contents, the gene density and the density of CpG islands of human chromosomes. **2011**, 12, 397	7
1457	Comparative analysis of information contents relevant to recognition of introns in many species. **2011**, 12, 45	28
1456	Parallel progressive multiple sequence alignment on reconfigurable meshes. **2011**, 12 Suppl 5, S4	4
1455	A multiple-template approach to protein threading. **2011**, 79, 1930-9	74
1454	Molecular characterization of hepatitis C virus genotype 4 sequences in HIV-coinfected patients from Argentina. **2011**, 83, 935-40	3
1453	Mutually exclusive expression of G□a and G□4 reveals diversification of taste receptor cells in zebrafish. **2011**, 519, 1616-29	30
1452	INTEGRATING COMPUTATIONAL PROTEIN FUNCTION PREDICTION INTO DRUG DISCOVERY INITIATIVES. **2011**, 72, 4-16	4
1451	Making new out of old: recycling and modification of an ancient protein translocation system during eukaryotic evolution. Mechanistic comparison and phylogenetic analysis of ERAD, SELMA and the peroxisomal importomer. **2011**, 33, 368-76	31
1450	The transaldolase family: new synthetic opportunities from an ancient enzyme scaffold. **2011**, 12, 1454-74	38
1449	Purification and characterization of tributyltin-binding protein of tiger puffer, Takifugu rubripes. **2011**, 153, 17-23	7
1448	The role of swine as "mixing vessel" for interspecies transmission of the influenza A subtype H1N1: a simultaneous Bayesian inference of phylogeny and ancestral hosts. **2011**, 11, 437-41	25

1447	Assessing divergence time of Spirulida and Sepiida (Cephalopoda) based on hemocyanin sequences. **2011**, 58, 390-4	26
1446	The mitochondrial genome of Bacillus stick insects (Phasmatodea) and the phylogeny of orthopteroid insects. **2011**, 58, 304-16	33
1445	Late Miocene diversification of the genus Hydrochus (Coleoptera, Hydrochidae) in the west Mediterranean area. **2011**, 59, 377-85	22
1444	Molecular systematics of caeciliid caecilians (Amphibia: Gymnophiona) of the Western Ghats, India. **2011**, 59, 698-707	16
1443	Molecular phylogeny of the nutmeg shells (Neogastropoda, Cancellariidae). **2011**, 59, 685-97	11
1442	Evolutionary history of Lissotriton helveticus: multilocus assessment of ancestral vs. recent colonization of the Iberian Peninsula. **2011**, 60, 170-82	43
1441	Multi-gene analysis provides a well-supported phylogeny of Rosales. **2011**, 60, 21-8	64
1440	The phylogeny of monkey beetles based on mitochondrial and ribosomal RNA genes (Coleoptera: Scarabaeidae: Hopliini). **2011**, 60, 408-15	26
1439	Phylogeny and character evolution in the jelly fungi (Tremellomycetes, Basidiomycota, Fungi). **2011** , 61, 12-28	88
1438	Diversification in the Andes: age and origins of South American Heliotropium lineages (Heliotropiaceae, Boraginales). **2011**, 61, 90-102	46
1437	Identification and characterization of the Chlamydia trachomatis L2 S-adenosylmethionine transporter. **2011**, 2, e00051-11	16
1436	Evolution of the Ras-like small GTPases and their regulators. **2011**, 2, 4-16	44
1435	A domain-centric analysis of oomycete plant pathogen genomes reveals unique protein organization. **2011**, 155, 628-44	59
1434	Genes involved in convergent evolution of eusociality in bees. **2011**, 108, 7472-7	159
1433	Evolutionary sequence divergence predicts protein sub-cellular localization signals. **2011**,	
1432	Lasiodiplodia species associated with dying Euphorbia ingens in South Africa. **2011**, 73, 165-173	12
1431	Genomic differentiation between temperate and tropical Australian populations of Drosophila melanogaster. **2011**, 187, 245-60	170
1430	Sea urchin tube feet are photosensory organs that express a rhabdomeric-like opsin and PAX6. **2011**, 278, 3371-9	49

1429	Why do leafcutter bees cut leaves? New insights into the early evolution of bees. **2011**, 278, 3593-600		67
1428	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. **2011**, 27, 749-56		16
1427	Protein multiple sequence alignment by hybrid bio-inspired algorithms. *Nucleic Acids Research*, **2011**, 39, 1980-92	20.1	19
1426	Paleozoic origin of insect large dsDNA viruses. **2011**, 108, 15931-5		111
1425	Dynamic evolution of base composition: causes and consequences in avian phylogenomics. **2011**, 28, 2197-210		71
1424	Analysis of a new family of widely distributed metal-independent alpha-mannosidases provides unique insight into the processing of N-linked glycans. **2011**, 286, 15586-96		51
1423	Taxonomy and phylogeny of the Caloplaca cerina group in Europe. **2011**, 43, 113-135		36
1422	Computational analysis of DNA replicases in double-stranded DNA viruses: relationship with the genome size. *Nucleic Acids Research*, **2011**, 39, 8291-305	20.1	13
1421	Novel adenoviruses in wild primates: a high level of genetic diversity and evidence of zoonotic transmissions. **2011**, 85, 10774-84		76
1420	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. **2011**, 21, 634-41		84
1419	Molecular phylogeny reveals a core clade of Rhytismatales. **2011**, 103, 57-74		58
1418	Functional Evolution of BRCT Domains from Binding DNA to Protein. **2011**, 7, 87-97		14
1417	Evolution of antifreeze protein genes in the diatom genus fragilariopsis: evidence for horizontal gene transfer, gene duplication and episodic diversifying selection. **2011**, 7, 279-89		28
1416	Identification of potential conserved RNA secondary structure throughout influenza A coding regions. **2011**, 17, 991-1011		73
1415	Vahliellaceae, a new family of cyanobacterial lichens (Peltigerales, Ascomycetes). **2011**, 43, 67-72		20
1414	The enigmatic genome of Chara australis virus. **2011**, 92, 2679-2690		20
1413	Gradual disintegration of the floral symmetry gene network is implicated in the evolution of a wind-pollination syndrome. **2011**, 108, 2343-8		51
1412	The general definition of the p97/valosin-containing protein (VCP)-interacting motif (VIM) delineates a new family of p97 cofactors. **2011**, 286, 38670-38678		40

1411	Phylogenomics-based reconstruction of protozoan species tree. **2011**, 7, 107-21		5
1410	The Psb32 protein aids in repairing photodamaged photosystem II in the cyanobacterium Synechocystis 6803. **2011**, 4, 1052-61		16
1409	Although divergent in residues of the peptide binding site, conserved chimpanzee Patr-AL and polymorphic human HLA-A*02 have overlapping peptide-binding repertoires. **2011**, 186, 1575-88		19
1408	Identification, tissue distribution and orexigenic activity of neuropeptide F (NPF) in penaeid shrimp. **2011**, 214, 1386-96		43
1407	Native Americans experienced a strong population bottleneck coincident with European contact. **2011**, 108, 20444-8		86
1406	2'-O-ribose methylation of cap2 in human: function and evolution in a horizontally mobile family. *Nucleic Acids Research*, **2011**, 39, 4756-68	20.1	85
1405	Ecology of hemiepiphytism in fig species is based on evolutionary correlation of hydraulics and carbon economy. **2011**, 92, 2117-30		38
1404	A novel flucytosine-resistant yeast species, Candida pseudoaaseri, causes disease in a cancer patient. **2011**, 49, 4195-202		11
1403	Experimental Evidence for Microbially Mediated Carbonate Dissolution from the Saline Water Zone of the Edwards Aquifer, Central Texas. **2011**, 28, 313-327		14
1402	Diversification ofCeanothus(Rhamnaceae) in the California Floristic Province. **2011**, 172, 1137-1164		31
1401	A new species of Antherospora supports the systematic placement of its host plant. **2011**, 2, 135-42		19
1400	Acquisition of human-type receptor binding specificity by new H5N1 influenza virus sublineages during their emergence in birds in Egypt. **2011**, 7, e1002068		162
1399	Hidden conformations in protein structures. **2011**, 27, 1941-7		7
1398	Genome-wide detection of gene extinction in early mammalian evolution. **2011**, 3, 1449-62		25
1397	Molecular phylogenetic studies on the lichenicolous Xanthoriicola physciae reveal Antarctic rock-inhabiting fungi and Piedraia species among closest relatives in the Teratosphaeriaceae. **2011**, 2, 97-103		21
1396	Attenuation of the sensing capabilities of PhoQ in transition to obligate insect-bacterial association. **2011**, 7, e1002349		33
1395	Characterization of human immunodeficiency virus type 1 (HIV-1) diversity and tropism in 145 patients with primary HIV-1 infection. **2011**, 53, 1271-9		70
1394	Adding unaligned sequences into an existing alignment using MAFFT and LAST. **2012**, 28, 3144-6		142

1393	Structure and age jointly influence rates of protein evolution. **2012**, 8, e1002542	17
1392	The chordate proteome history database. **2012**, 8, 437-47	5
1391	Conjugal transfer of polychlorinated biphenyl/biphenyl degradation genes in Acidovorax sp. strain KKS102, which are located on an integrative and conjugative element. **2012**, 194, 4237-48	34
1390	GECA: a fast tool for gene evolution and conservation analysis in eukaryotic protein families. **2012**, 28, 1398-9	21
1389	Evolution and functional diversification of fructose bisphosphate aldolase genes in photosynthetic marine diatoms. **2012**, 29, 367-79	53
1388	Emerging roles for the influenza A virus nuclear export protein (NEP). **2012**, 8, e1003019	102
1387	Systematics of the Osteocephalusbuckleyi species complex (Anura, Hylidae) from Ecuador and Peru. **2012**, 1-52	20
1386	Shivasia gen. nov. for the Australasian smut Ustilago solida that historically shifted through five different genera. **2012**, 3, 143-54	13
1385	Description and phylogeny of Namalycastis jaya sp. n. (Polychaeta, Nereididae, Namanereidinae) from the southwest coast of India. **2012**, 31-43	7
1384	A unique protein phosphatase with kelch-like domains (PPKL) in Plasmodium modulates ookinete differentiation, motility and invasion. **2012**, 8, e1002948	54
1383	SMG-1 and mTORC1 act antagonistically to regulate response to injury and growth in planarians. **2012**, 8, e1002619	64
1382	Network evolution: rewiring and signatures of conservation in signaling. **2012**, 8, e1002411	27
1381	Gaps: an elusive source of phylogenetic information. **2012**, 61, 1075-82	13
1380	Mapping the phosphoproteome of influenza A and B viruses by mass spectrometry. **2012**, 8, e1002993	95
1379	Computer-based annotation of putative AraC/XylS-family transcription factors of known structure but unknown function. **2012**, 2012, 103132	11
1378	Afrocantharellus gen. stat. nov. is part of a rich diversity of African Cantharellaceae. **2012**, 3, 25-38	23
1377	Ceratocystis eucalypticola sp. nov. from Eucalyptus in South Africa and comparison to global isolates from this tree. **2012**, 3, 45-58	23
1376	Boletopsis nothofagi sp. nov. associated with Nothofagus in the Southern Hemisphere. **2012**, 3, 13-22	4

1375	Proteome-wide discovery of evolutionary conserved sequences in disordered regions. **2012**, 5, rs1		76
1374	Some like it hot: evolution and ecology of novel endosymbionts in bat flies of cave-roosting bats (hippoboscoidea, nycterophiliinae). **2012**, 78, 8639-49		20
1373	Bayesian estimation of bacterial community composition from 454 sequencing data. *Nucleic Acids Research*, **2012**, 40, 5240-9	20.1	22
1372	SR1--a small RNA with two remarkably conserved functions. *Nucleic Acids Research*, **2012**, 40, 11659-72	20.1	37
1371	Heterotrophic archaea contribute to carbon cycling in low-pH, suboxic biofilm communities. **2012**, 78, 8321-30		48
1370	Sequence shortening in the rodent ancestor. **2012**, 22, 478-85		16
1369	Ligand-binding properties and conformational dynamics of autolysin repeat domains in staphylococcal cell wall recognition. **2012**, 194, 3789-802		56
1368	Movement of DNA sequence recognition domains between non-orthologous proteins. *Nucleic Acids Research*, **2012**, 40, 9218-32	20.1	26
1367	CARNA--alignment of RNA structure ensembles. *Nucleic Acids Research*, **2012**, 40, W49-53	20.1	18
1366	Genomic comparison of Escherichia coli O104:H4 isolates from 2009 and 2011 reveals plasmid, and prophage heterogeneity, including shiga toxin encoding phage stx2. **2012**, 7, e48228		94
1365	An evolutionary network of genes present in the eukaryote common ancestor polls genomes on eukaryotic and mitochondrial origin. **2012**, 4, 466-85		104
1364	The Papillomavirus Episteme: a central resource for papillomavirus sequence data and analysis. *Nucleic Acids Research*, **2013**, 41, D571-8	20.1	151
1363	Universal amplification, next-generation sequencing, and assembly of HIV-1 genomes. **2012**, 50, 3838-44		96
1362	A novel aquaporin 3 in killifish (Fundulus heteroclitus) is not an arsenic channel. **2012**, 127, 101-9		10
1361	Biochemical and structural characterization of the complex agarolytic enzyme system from the marine bacterium Zobellia galactanivorans. **2012**, 287, 30571-84		85
1360	Characterization of squamate olfactory receptor genes and their transcripts by the high-throughput sequencing approach. **2012**, 4, 602-16		13
1359	Accurate extension of multiple sequence alignments using a phylogeny-aware graph algorithm. **2012**, 28, 1684-91		88
1358	Evolution of viral proteins originated de novo by overprinting. **2012**, 29, 3767-80		95

1357	Molecular cloning and pharmacological characterization of two novel GnRH receptors in the lamprey (Petromyzon marinus). **2012**, 153, 3345-56		17
1356	Comparative genomics of vancomycin-resistant Staphylococcus aureus strains and their positions within the clade most commonly associated with Methicillin-resistant S. aureus hospital-acquired infection in the United States. **2012**, 3,		97
1355	Tissue-specific alternative splicing of Tak1 is conserved in deuterostomes. **2012**, 29, 261-9		18
1354	Yeast communities of diverse Drosophila species: comparison of two symbiont groups in the same hosts. **2012**, 78, 7327-36		109
1353	The practical evaluation of DNA barcode efficacy. **2012**, 858, 365-77		9
1352	A dominant negative heterozygous G87R mutation in the zinc transporter, ZnT-2 (SLC30A2), results in transient neonatal zinc deficiency. **2012**, 287, 29348-61		72
1351	Fossil rhabdoviral sequences integrated into arthropod genomes: ontogeny, evolution, and potential functionality. **2012**, 29, 381-90		84
1350	Interactions between BRCA2 and RAD51 for promoting homologous recombination in Leishmania infantum. *Nucleic Acids Research*, **2012**, 40, 6570-84	20.1	25
1349	The plant proteome folding project: structure and positive selection in plant protein families. **2012**, 4, 360-71		13
1348	The trypanosomatid-specific N terminus of RPA2 is required for RNA polymerase I assembly, localization, and function. **2012**, 11, 662-72		9
1347	The human transporter associated with antigen processing: molecular models to describe peptide binding competent states. **2012**, 287, 28099-111		22
1346	Phylogenetic analysis of mitochondrial outer membrane βbarrel channels. **2012**, 4, 110-25		14
1345	Reconstruction of oomycete genome evolution identifies differences in evolutionary trajectories leading to present-day large gene families. **2012**, 4, 199-211		38
1344	Quality and quantity of data recovered from massively parallel sequencing: Examples in Asparagales and Poaceae. **2012**, 99, 330-48		95
1343	Molecular evolution in nonrecombining regions of the Drosophila melanogaster genome. **2012**, 4, 278-88		42
1342	Amino acid residues critical for the specificity for betaine aldehyde of the plant ALDH10 isoenzyme involved in the synthesis of glycine betaine. **2012**, 158, 1570-82		40
1341	Contrasting patterns of niche partitioning between two anaerobic terminal oxidizers of organic matter. **2012**, 6, 905-14		20
1340	Molecular identification of commercialized medicinal plants in southern Morocco. **2012**, 7, e39459		94

1339	Doing it in reverse: 3'-to-5' polymerization by the Thg1 superfamily. **2012**, 18, 886-99		47
1338	EvoluCode: Evolutionary Barcodes as a Unifying Framework for Multilevel Evolutionary Data. **2012**, 8, 61-77		3
1337	Evolution of Type II Antifreeze Protein Genes in Teleost Fish: A Complex Scenario Involving Lateral Gene Transfers and Episodic Directional Selection. **2012**, 8, 535-44		7
1336	An ancient genomic regulatory block conserved across bilaterians and its dismantling in tetrapods by retrogene replacement. **2012**, 22, 642-55		30
1335	Transcriptional Regulation of the Lignin Biosynthetic Pathway Revisited: New Players and Insights. **2012**, 61, 173-218		13
1334	Fungal Strategies for Lignin Degradation. **2012**, 61, 263-308		68
1333	Pathogenic and multidrug-resistant Escherichia fergusonii from broiler chicken. **2012**, 91, 512-25		39
1332	Absence of anthraquinone pigments is paraphyletic and a phylogenetically unreliable character in the Teloschistaceae. **2012**, 44, 401-418		16
1331	Quantifying homologous replacement of loci between haloarchaeal species. **2012**, 4, 1223-44		49
1330	PANTHER in 2013: modeling the evolution of gene function, and other gene attributes, in the context of phylogenetic trees. *Nucleic Acids Research*, **2013**, 41, D377-86	20.1	1204
1329	A novel congenital myasthenic syndrome due to decreased acetylcholine receptor ion-channel conductance. **2012**, 135, 1070-80		15
1328	Conservation of two lineages of peroxisomal (Type I) 3-ketoacyl-CoA thiolases in land plants, specialization of the genes in Brassicaceae, and characterization of their expression in Arabidopsis thaliana. **2012**, 63, 6093-103		14
1327	DNA barcoding of Mycosphaerella species of quarantine importance to Europe. **2012**, 29, 101-15		62
1326	PhyloMarker□A Tool for Mining Phylogenetic Markers through Genome Comparison: Application of the Mouse Lemur (Genus Microcebus) Phylogeny. **2012**, 8, EBO.S9886		5
1325	Extensive diversity of intestinal trichomonads of non-human primates. **2012**, 139, 92-102		17
1324	The type III effector HsvG of the gall-forming Pantoea agglomerans mediates expression of the host gene HSVGT. **2012**, 25, 231-40		17
1323	Molecular phylogeny of tintinnid ciliates (Tintinnida, Ciliophora). **2012**, 163, 873-87		45
1322	Opsins in onychophora (velvet worms) suggest a single origin and subsequent diversification of visual pigments in arthropods. **2012**, 29, 3451-8		49

1321	Alignment methods: strategies, challenges, benchmarking, and comparative overview. **2012**, 855, 203-35	15
1320	Phylogeny, integration and expression of sigma virus-like genes in Drosophila. **2012**, 65, 251-8	28
1319	Life and death of deep-sea vents: bacterial diversity and ecosystem succession on inactive hydrothermal sulfides. **2012**, 3, e00279-11	95
1318	Genetic diversity of the dung beetle, Copris tripartitus (Coleoptera: Scarabaeidae), that is endangered in Korea. **2012**, 42, 247-261	11
1317	Roadmap for annotating transposable elements in eukaryote genomes. **2012**, 859, 53-68	12
1316	Phylogenetic placement of pelican spiders (Archaeidae, Araneae), with insight into evolution of the "neck" and predatory behaviours of the superfamily Palpimanoidea. **2012**, 28, 598-626	40
1315	Comparative analysis of mitochondrial genomes of Rhizophagus irregularis - syn. Glomus irregulare - reveals a polymorphism induced by variability generating elements. **2012**, 196, 1217-1227	45
1314	Microbiology of diverse acidic and non-acidic microhabitats within a sulfidic ore mine. **2012**, 16, 911-22	15
1313	Binding mechanism of metal?NTP substrates and stringent-response alarmones to bacterial DnaG-type primases. **2012**, 20, 1478-89	58
1312	A multi-locus phylogenetic evaluation of Diaporthe (Phomopsis). **2012**, 56, 157-171	136
1311	A new species of burrowing crayfish,Virilastacus jarai(Crustacea, Decapoda, Parastacidae) from central-southern Chile. **2012**, 125, 258-275	12
1310	Molecular systematics and evolution of the subgenusMesocarabusThomson, 1875 (Coleoptera: Carabidae:Carabus), based on mitochondrial and nuclear DNA. **2012**, 166, 787-804	14
1309	Epistasis as the primary factor in molecular evolution. **2012**, 490, 535-8	246
1308	Hypocrea britdaniae and H. foliicola: two remarkable new European species. **2012**, 104, 1213-21	12
1307	The awr gene family encodes a novel class of Ralstonia solanacearum type III effectors displaying virulence and avirulence activities. **2012**, 25, 941-53	49
1306	Additive multiple k-mer transcriptome of the keelworm Pomatoceros lamarckii (Annelida; Serpulidae) reveals annelid trochophore transcription factor cassette. **2012**, 222, 325-39	10
1305	Tomato dwarf leaf virus, a New World begomovirus infecting tomato in Argentina. **2012**, 157, 1975-80	9
1304	A comparative analysis of the factors promoting deer invasion. **2012**, 14, 2271-2281	6

1303	Small-molecule inhibition of BRDT for male contraception. **2012**, 150, 673-84	277
1302	Why is the molecular identification of the forensically important blowfly species Lucilia caesar and L. illustris (family Calliphoridae) so problematic?. **2012**, 223, 153-9	37
1301	Effects of UV radiation on the taxonomic composition of natural bacterioplankton communities from Bah�a Enga�o (Patagonia, Argentina). **2012**, 117, 171-8	17
1300	Novel structural features of xylanase A1 from Paenibacillus sp. JDR-2. **2012**, 180, 303-11	9
1299	Diversity, evolution and molecular systematics of the Psalteriomonadidae, the main lineage of anaerobic/microaerophilic heteroloboseans (excavata: discoba). **2012**, 163, 807-31	28
1298	Genomic analysis of bovine herpesvirus type 4 (BoHV-4) from Argentina: high genetic variability and novel phylogenetic groups. **2012**, 160, 1-8	20
1297	Cloning and characterization of histone deacetylase from Babesia bovis. **2012**, 190, 423-33	4
1296	Characterisation of retroviruses in the horse genome and their transcriptional activity via transcriptome sequencing. **2012**, 433, 55-63	14
1295	Association between hTERT activation by HPV E6 proteins and oncogenic risk. **2012**, 433, 216-9	42
1294	Fusarium circinatum and pitch canker of Pinus in Colombia. **2012**, 41, 483-491	30
1293	Gazar virus Y, a new member of the celery mosaic virus group of potyviruses, isolated from carrots in Egypt. **2012**, 41, 529-534	0
1292	First report of Fusarium oxysporum f. sp. radicis-lycopersici in South Africa. **2012**, 7, 29-32	1
1291	Vibrio caribbeanicus sp. nov., isolated from the marine sponge Scleritoderma cyanea. **2012**, 62, 1736-1743	34
1290	The taxonomic status of Trichophyton quinckeanum and T. interdigitale revisited: a multigene phylogenetic approach. **2012**, 50, 871-82	39
1289	Maximal path based conflict resolution approach in multiple homologous gene list alignment. **2012**,	
1288	. **2012**,	
1287	Evidence for N-glycan shielding of antigenic sites during evolution of human influenza A virus hemagglutinin. **2012**, 86, 3446-51	56
1286	Past connection of the upper reaches of a Lake Tanganyika tributary with the upper Congo drainage suggested by genetic data of riverine cichlid fishes. **2012**, 47, 182-186	5

1285	Optimization of multiple sequence alignment methodologies using a multiobjective evolutionary algorithm based on NSGA-II. **2012**,	6
1284	A genome-wide view of transcription factor gene diversity in chordate evolution: less gene loss in amphioxus?. **2012**, 11, 177-86	34
1283	A standardized reanalysis of molecular phylogenetic hypotheses of Gobioidei. **2012**, 10, 375-390	22
1282	Genomic characterization of a newly discovered coronavirus associated with acute respiratory distress syndrome in humans. **2012**, 3,	632
1281	BpMatch: an efficient algorithm for a segmental analysis of genomic sequences. **2012**, 9, 1120-7	3
1280	Determination of gene point mutations by application of higher order central moments Preliminary research. **2012**,	
1279	Computational enzyme design approaches with significant biological outcomes: progress and challenges. **2012**, 2, e201209007	14
1278	Phosphorylation of yeast transcription factors correlates with the evolution of novel sequence and function. **2012**, 11, 261-8	6
1277	Digital genotyping of avian influenza viruses of H7 subtype detected in central Europe in 2007-2011. **2012**, 165, 126-33	11
1276	Phylogenetic relationships elucidate colonization patterns in the intertidal grazers Osilinus Philippi, 1847 and Phorcus Risso, 1826 (Gastropoda: Trochidae) in the northeastern Atlantic Ocean and Mediterranean Sea. **2012**, 62, 35-45	38
1275	Evolution of arid zone birds in Australia: leapfrog distribution patterns and mesic-arid connections in quail-thrush (Cinclosoma, Cinclosomatidae). **2012**, 62, 286-95	19
1274	Exploring diversity in cryptorhynchine weevils (Coleoptera) using distance-, character- and tree-based species delineation. **2012**, 63, 1-14	43
1273	Molecular phylogeny of the phylum Gastrotricha: new data brings together molecules and morphology. **2012**, 63, 208-12	13
1272	Molecular phylogenetics and historical biogeography of the west-palearctic common toads (Bufo bufo species complex). **2012**, 63, 113-30	65
1271	Complex evolution in Arundinarieae (Poaceae: Bambusoideae): incongruence between plastid and nuclear GBSSI gene phylogenies. **2012**, 63, 777-97	66
1270	Brunfelsia (Solanaceae): a genus evenly divided between South America and radiations on Cuba and other Antillean islands. **2012**, 64, 1-11	31
1269	Phylogenetic analysis of ticks (Acari: Ixodida) using mitochondrial genomes and nuclear rRNA genes indicates that the genus Amblyomma is polyphyletic. **2012**, 64, 45-55	65
1268	Molecular phylogeny of Aphyocharacinae (Characiformes, Characidae) with morphological diagnoses for the subfamily and recognized genera. **2012**, 64, 297-307	19

1267	A multilocus perspective on the speciation history of a North American aridland toad (Anaxyrus punctatus). **2012**, 64, 393-400	17
1266	Reticulate evolution on a global scale: a nuclear phylogeny for New World Dryopteris (Dryopteridaceae). **2012**, 64, 563-81	44
1265	Phylogenetic relatedness predicts priority effects in nectar yeast communities. **2012**, 279, 749-58	175
1264	Detection and identification of Theileria infection in sika deer (Cervus nippon) in China. **2012**, 98, 598-603	17
1263	The genus Cladosporium. **2012**, 72, 1-401	345
1262	Geographic homogeneity and high gene flow of the pear psylla, Cacopsylla pyricola (Hemiptera: Psyllidae), detected by mitochondrial COI gene and nuclear ribosomal internal transcribed spacer 2. **2012**, 16, 145-153	7
1261	From Amazonia to the Atlantic forest: molecular phylogeny of Phyzelaphryninae frogs reveals unexpected diversity and a striking biogeographic pattern emphasizing conservation challenges. **2012**, 65, 547-61	96
1260	Ribosomal DNA distribution and a genus-wide phylogeny reveal patterns of chromosomal evolution in Alstroemeria (Alstroemeriaceae). **2012**, 99, 1501-12	25
1259	Lifestyle transitions in plant pathogenic Colletotrichum fungi deciphered by genome and transcriptome analyses. **2012**, 44, 1060-5	564
1258	Horizontal Gene Transfer in Influenza Strain Generation: A Comparative Evolutionary Study. **2012**, 213-222	
1257	Leucosporidium drummii sp. nov., a member of the Microbotryomycetes isolated from soil. **2012**, 62, 728-734	16
1256	Experimental design in phylogenetics: testing predictions from expected information. **2012**, 61, 661-74	11
1255	A Revision of Species Diversity in the Neotropical GenusOreobates(Anura: Strabomantidae), with the Description of Three New Species from the Amazonian Slopes of the Andes. **2012**, 3752, 1-55	26
1254	Identification of novel glutathione transferases in Echinococcus granulosus. An evolutionary perspective. **2012**, 123, 208-16	8
1253	Description of complete mitochondrial genome of the black-veined white, Aporia crataegi (Lepidoptera: Papilionoidea), and comparison to papilionoid species. **2012**, 15, 331-341	31
1252	A phylogenetic analysis of normal modes evolution in enzymes and its relationship to enzyme function. **2012**, 422, 442-59	18
1251	The plant heat stress transcription factor (Hsf) family: structure, function and evolution. **2012**, 1819, 104-19	544
1250	ParaAT: a parallel tool for constructing multiple protein-coding DNA alignments. **2012**, 419, 779-81	147

1249	Genomic and morphological evidence converge to resolve the enigma of Strepsiptera. **2012**, 22, 1309-13	117
1248	Somatic hypermutation of TCR □V genes in the sandbar shark. **2012**, 37, 176-83	21
1247	B lymphopoiesis is characterized by pre-B cell marker gene expression in fetal cattle and declines in adults. **2012**, 37, 39-49	10
1246	The bovine genomic DNA sequence data reveal three IGHV subgroups, only one of which is functionally expressed. **2012**, 37, 457-61	15
1245	Genomic analyses of aminergic signaling systems (dopamine, octopamine and serotonin) in Daphnia pulex. **2012**, 7, 35-58	30
1244	Genomic analyses of gas (nitric oxide and carbon monoxide) and small molecule transmitter (acetylcholine, glutamate and GABA) signaling systems in Daphnia pulex. **2012**, 7, 124-60	17
1243	Premetazoan origin of the hippo signaling pathway. **2012**, 1, 13-20	81
1242	Microbotryum heliospermae, a new anther smut fungus parasitic on Heliosperma pusillum in the mountains of the European Alpine System. **2012**, 116, 185-95	28
1241	Patterns of fungal diversity in New Zealand Nothofagus forests. **2012**, 116, 401-12	16
1240	Both mating types in the heterothallic fungus Ophiostoma quercus contain MAT1-1 and MAT1-2 genes. **2012**, 116, 427-37	20
1239	A molecular phylogeny of thermophilic fungi. **2012**, 116, 489-502	91
1238	Characterisation of the gene cluster for l-rhamnose catabolism in the yeast Scheffersomyces (Pichia) stipitis. **2012**, 492, 177-85	25
1237	The global distribution and evolution of deoxyribonucleoside kinases in bacteria. **2012**, 492, 117-20	5
1236	The globally distributed genus Alexandrium: multifaceted roles in marine ecosystems and impacts on human health. **2012**, 14, 10-35	427
1235	Symbiont fidelity and the origin of species in fungus-growing ants. **2012**, 3, 840	43
1234	Revisiting the homology modeling of G-protein coupled receptors: □1-adrenoceptor as an example. **2012**, 8, 1686-93	6
1233	Studies of Physcomitrella patens reveal that ethylene-mediated submergence responses arose relatively early in land-plant evolution. **2012**, 72, 947-59	38
1232	Fast and robust multiple sequence alignment with phylogeny-aware gap placement. **2012**, 13, 129	14

1231	Surprising results on phylogenetic tree building methods based on molecular sequences. **2012**, 13, 148	7
1230	Comprehensive comparison of graph based multiple protein sequence alignment strategies. **2012**, 13, 64	5
1229	Molecules and fossils reveal punctuated diversification in Caribbean "faviid" corals. **2012**, 12, 123	14
1228	A multi-gene phylogeny of Cephalopoda supports convergent morphological evolution in association with multiple habitat shifts in the marine environment. **2012**, 12, 129	66
1227	New insights into family relationships within the avian superfamily Sylvioidea (Passeriformes) based on seven molecular markers. **2012**, 12, 157	40
1226	Extreme genetic diversity in the lizard Atlantolacerta andreanskyi (Werner, 1929): a montane cryptic species complex. **2012**, 12, 167	22
1225	Evidence for 5S rDNA horizontal transfer in the toadfish Halobatrachus didactylus (Schneider, 1801) based on the analysis of three multigene families. **2012**, 12, 201	20
1224	Winding up the molecular clock in the genus Carabus (Coleoptera: Carabidae): assessment of methodological decisions on rate and node age estimation. **2012**, 12, 40	89
1223	Molecular phylogeny of grunts (Teleostei, Haemulidae), with an emphasis on the ecology, evolution, and speciation history of new world species. **2012**, 12, 57	39
1222	Unique core genomes of the bacterial family vibrionaceae: insights into niche adaptation and speciation. **2012**, 13, 179	18
1221	A novel mutation causing nephronophthisis in the Lewis polycystic kidney rat localises to a conserved RCC1 domain in Nek8. **2012**, 13, 393	51
1220	Analysis of a comprehensive dataset of diversity generating retroelements generated by the program DiGReF. **2012**, 13, 430	22
1219	The origin of modern frogs (Neobatrachia) was accompanied by acceleration in mitochondrial and nuclear substitution rates. **2012**, 13, 626	44
1218	A novel method to discover fluoroquinolone antibiotic resistance (qnr) genes in fragmented nucleotide sequences. **2012**, 13, 695	20
1217	Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. **2012**, 12, 135	104
1216	Extensive remodeling of the Pseudomonas syringae pv. avellanae type III secretome associated with two independent host shifts onto hazelnut. **2012**, 12, 141	41
1215	Genome characterization and population genetic structure of the zoonotic pathogen, Streptococcus canis. **2012**, 12, 293	28
1214	Genome-scale identification of cell-wall related genes in Arabidopsis based on co-expression network analysis. **2012**, 12, 138	42

1213	Structural and molecular basis of interaction of HCV non-structural protein 5A with human casein kinase 1and PKR. **2012**, 12, 28	11
1212	Re-annotation of the CAZy genes of Trichoderma reesei and transcription in the presence of lignocellulosic substrates. **2012**, 11, 134	124
1211	Comparative genomic analysis of the DUF71/COG2102 family predicts roles in diphthamide biosynthesis and B12 salvage. **2012**, 7, 32	15
1210	Molecular characterization of the hexose transporter gene in benznidazole resistant and susceptible populations of Trypanosoma cruzi. **2012**, 5, 161	4
1209	Population-based analyses of Giardia duodenalis is consistent with the clonal assemblage structure. **2012**, 5, 168	19
1208	Parallel evolution of TCP and B-class genes in Commelinaceae flower bilateral symmetry. **2012**, 3, 6	43
1207	A new Neopaxillus species (Agaricomycetes) from the Dominican Republic and the status of Neopaxillus within the Agaricales. **2012**, 104, 138-47	9
1206	New teleomorph combinations in the entomopathogenic genus Metacordyceps. **2012**, 104, 182-97	62
1205	New species of Gondwanamyces from dying Euphorbia trees in South Africa. **2012**, 104, 574-84	11
1204	The phylogenetic position of Haasiella (Basidiomycota, Agaricomycetes) and the relationships between H. venustissima and H. splendidissima. **2012**, 104, 777-84	3
1203	Structure, mechanism, and evolution of Ero1 family enzymes. **2012**, 16, 790-9	71
1202	An ancient duplication of apple MYB transcription factors is responsible for novel red fruit-flesh phenotypes. **2013**, 161, 225-39	198
1201	The arbuscular mycorrhizal Paraglomus majewskii sp. nov. represents a distinct basal lineage in Glomeromycota. **2012**, 104, 148-56	38
1200	Is sociality required for the evolution of communicative complexity? Evidence weighed against alternative hypotheses in diverse taxonomic groups. **2012**, 367, 1811-28	34
1199	Sea level, topography and island diversity: phylogeography of the Puerto Rican Red-eyed Coqu Eleutherodactylus antillensis. **2012**, 21, 6033-52	12
1198	Spatial and temporal patterns of genetic variation in the widespread antitropical deep-sea coral Paragorgia arborea. **2012**, 21, 6053-67	42
1197	How lizards survived blizzards: phylogeography of the Liolaemus lineomaculatus group (Liolaemidae) reveals multiple breaks and refugia in southern Patagonia and their concordance with other codistributed taxa. **2012**, 21, 6068-85	44
1196	Molecular phylogenetics, species diversity, and biogeography of the Andean lizards of the genus Proctoporus (Squamata: Gymnophthalmidae). **2012**, 65, 953-64	23

1195	Identification of homologous gene sequences by PCR with degenerate primers. **2011**, 772, 245-56	8
1194	Antigenic analysis of highly pathogenic avian influenza virus H5N1 sublineages co-circulating in Egypt. **2012**, 93, 2215-2226	34
1193	The extensive bloom of alternate-stage Prymnesium polylepis (Haptophyta) in the Baltic Sea during autumn–spring 2007–2008. **2012**, 47, 310-320	12
1192	DNA sequence data reveal a subfamily-level divergence within Thamnophilidae (Aves: Passeriformes). **2012**, 65, 287-93	8
1191	Phylogenetic relationship and species delimitation of matsutake and allied species based on multilocus phylogeny and haplotype analyses. **2012**, 104, 1369-80	24
1190	A new Cortinarius of section Calochroi (Basidiomycota, Agaricomycetes) from Mediterranean Quercus woodlands (Italy). **2012**, 104, 1502-9	2
1189	Using protein-domain information for multiple sequence alignment. **2012**,	1
1188	FinIS: Improved in silico Finishing Using an Exact Quadratic Programming Formulation. **2012**, 314-325	14
1187	Transposable Element Annotation in Completely Sequenced Eukaryote Genomes. **2012**, 17-39	9
1186	Una especie nueva de rana venenosa de altura del género Excidobates (Dendrobatoidea: Dendrobatidae) de la Cordillera del Cóndor. **2012**, 52, 387-399	9
1185	Coarse woody debris retention in subalpine clearcuts affects ectomycorrhizal root tip community structure within fifteen years of harvest. **2012**, 60, 5-15	23
1184	Bacterial diversity of siliciclastic sediments in a Thalassia testudinum meadow and the implications for Lucinisca nassula chemosymbiosis. **2012**, 112, 153-161	9
1183	Endophytic fungi isolated from Khaya anthotheca in Ghana. **2012**, 5, 298-308	21
1182	The evolution of catalytic residues and enzyme mechanism within the bacterial nucleoside phosphorylase superfamily 1. **2012**, 510, 154-61	4
1181	Comparative aspects of polyglutamine binding domain in PQBP-1 among Vertebrata. **2012**, 511, 243-7	5
1180	Global alignment of molecular sequences via ancestral state reconstruction. **2012**, 122, 3852-3874	8
1179	Molecular and morphological identification of larval opecoelids (Digenea: Opecoelidae) parasitising prosobranch snails in a Western Mediterranean lagoon. **2012**, 61, 450-60	32
1178	Cryptic speciation in the mesopelagic environment: molecular phylogenetics of the lanternfish genus Benthosema. **2012**, 7, 7-10	7

1177	Convergent and divergent evolution of metabolism in sulfur-oxidizing symbionts and the role of horizontal gene transfer. **2012**, 15, 621-31	45
1176	The active stem cell specific expression of sponge Musashi homolog EflMsiA suggests its involvement in maintaining the stem cell state. **2012**, 129, 24-37	19
1175	Novel animal papillomavirus sequences and accurate phylogenetic placement. **2012**, 65, 883-91	19
1174	Construction and analysis of phylogenetic trees using DNA barcode data. **2012**, 858, 395-408	3
1173	Analytical approaches for DNA barcoding data □how to find a way for plants?. **2012**, 146, 805-813	31
1172	Acquisition of 1,000 eubacterial genes physiologically transformed a methanogen at the origin of Haloarchaea. **2012**, 109, 20537-42	180
1171	Bibliography. **2012**, 376-413	
1170	Species reassignment of Geotrichum bryndzae, Geotrichum phurueaensis, Geotrichum silvicola and Geotrichum vulgare based on phylogenetic analyses and mating compatibility. **2012**, 62, 3072-3080	14
1169	Aboveground Deadwood Deposition Supports Development of Soil Yeasts. **2012**, 4, 453-474	28
1168	Lepiota(Agaricales) in Northern Thailand-2LepiotaSectionLepiota. **2012**, 33, 25-42	8
1167	Life cycle completion of parasite Ascogregarina taiwanensis (Apicomplexa: Lecudinidae) in non-native host Ochlerotatus japonicus (Diptera: Culicidae). **2012**, 49, 1109-17	8
1166	Resurrection of endogenous retroviruses in antibody-deficient mice. **2012**, 491, 774-8	155
1165	Structural basis for microtubule binding and release by dynein. **2012**, 337, 1532-1536	124
1164	A Second Species of the Family Allophrynidae (Amphibia: Anura). **2012**, 3739, 1-17	5
1163	Opsin evolution in damselfish: convergence, reversal, and parallel evolution across tuning sites. **2012**, 75, 79-91	33
1162	Viequeamide A, a cytotoxic member of the kulolide superfamily of cyclic depsipeptides from a marine button cyanobacterium. **2012**, 75, 1560-70	52
1161	New weighting methods for phylogenetic tree reconstruction using multiple loci. **2012**, 75, 1-10	2
1160	Culture-free survey reveals diverse and distinctive fungal communities associated with developing figs (Ficus spp.) in Panama. **2012**, 64, 1073-84	22

1159	Ultrastructure, molecular phylogenetics, and chlorophyll a content of novel cyanobacterial symbionts in temperate sponges. **2012**, 64, 771-83	31
1158	Antarctic Tardigrada: a first step in understanding molecular operational taxonomic units (MOTUs) and biogeography of cryptic meiofauna. **2012**, 26, 526	32
1157	The tree alignment problem. **2012**, 13, 293	21
1156	Horizontal gene transfer of a chloroplast DnaJ-Fer protein to Thaumarchaeota and the evolutionary history of the DnaK chaperone system in Archaea. **2012**, 12, 226	34
1155	Massive expansion of the calpain gene family in unicellular eukaryotes. **2012**, 12, 193	30
1154	Unusual domain architecture of aminoacyl tRNA synthetases and their paralogs from Leishmania major. **2012**, 13, 621	32
1153	Improving N-terminal protein annotation of Plasmodium species based on signal peptide prediction of orthologous proteins. **2012**, 11, 375	3
1152	Distribution and properties of the genes encoding the biosynthesis of the bacterial cofactor, pyrroloquinoline quinone. **2012**, 51, 2265-75	80
1151	Accounting for alignment uncertainty in phylogenomics. **2012**, 7, e30288	127
1150	Transient expression of hemagglutinin antigen from low pathogenic avian influenza A (H7N7) in Nicotiana benthamiana. **2012**, 7, e33010	27
1149	The origin and evolutionary history of HIV-1 subtype C in Senegal. **2012**, 7, e33579	18
1148	The molecular mechanism of action of the CR6261-Azichromycin combination found through computational analysis. **2012**, 7, e37790	1
1147	mPSQed: a software for the design of multiplex pyrosequencing assays. **2012**, 7, e38140	6
1146	Deep-sea origin and in-situ diversification of chrysogorgiid octocorals. **2012**, 7, e38357	37
1145	Image correlation method for DNA sequence alignment. **2012**, 7, e39221	8
1144	The development of three long universal nuclear protein-coding locus markers and their application to osteichthyan phylogenetics with nested PCR. **2012**, 7, e39256	21
1143	Phylogeny and biogeography of the carnivorous plant family Sarraceniaceae. **2012**, 7, e39291	33
1142	Compensatory evolution of net-charge in influenza A virus hemagglutinin. **2012**, 7, e40422	27

1141	Two unique ligand-binding clamps of Rhizopus oryzae starch binding domain for helical structure disruption of amylose. **2012**, 7, e41131	8
1140	Unveiling trophic functions of uncultured protist taxa by incubation experiments in the brackish Baltic Sea. **2012**, 7, e41970	26
1139	Island evolution and systematic revision of Comoran snakes: why and when subspecies still make sense. **2012**, 7, e42970	39
1138	Unique features of odorant-binding proteins of the parasitoid wasp Nasonia vitripennis revealed by genome annotation and comparative analyses. **2012**, 7, e43034	48
1137	Reverse taxonomy for elucidating diversity of insect-associated nematodes: a case study with termites. **2012**, 7, e43865	26
1136	The first record of a trans-oceanic sister-group relationship between obligate vertebrate troglobites. **2012**, 7, e44083	39
1135	Characterization of cDNAs encoding serine proteases and their transcriptional responses to Cry1Ab protoxin in the gut of Ostrinia nubilalis larvae. **2012**, 7, e44090	13
1134	Groundtruthing next-gen sequencing for microbial ecology-biases and errors in community structure estimates from PCR amplicon pyrosequencing. **2012**, 7, e44224	126
1133	Investigating embryonic expression patterns and evolution of AHI1 and CEP290 genes, implicated in Joubert syndrome. **2012**, 7, e44975	14
1132	Transcriptome sequencing and annotation for the Jamaican fruit bat (Artibeus jamaicensis). **2012**, 7, e48472	53
1131	Conquered from the deep sea? A new deep-sea isopod species from the Antarctic shelf shows pattern of recent colonization. **2012**, 7, e49354	31
1130	Molecular evolution and structural features of IRAK family members. **2012**, 7, e49771	31
1129	Computational prediction of protein-protein interactions in Leishmania predicted proteomes. **2012**, 7, e51304	26
1128	Genetic variability among complete human respiratory syncytial virus subgroup A genomes: bridging molecular evolutionary dynamics and epidemiology. **2012**, 7, e51439	62
1127	Phylogenetic Analysis of the Thylakoid ATP/ADP Carrier Reveals New Insights into Its Function Restricted to Green Plants. **2011**, 2, 110	9
1126	Protein Phylogenetic Analysis of Ca(2+)/cation Antiporters and Insights into their Evolution in Plants. **2012**, 3, 1	330
1125	The Maize PIN Gene Family of Auxin Transporters. **2012**, 3, 16	78
1124	Re-Evaluation of the PBAN Receptor Molecule: Characterization of PBANR Variants Expressed in the Pheromone Glands of Moths. **2012**, 3, 6	30

1123	Evolutionary Analysis of Functional Divergence among Chemokine Receptors, Decoy Receptors, and Viral Receptors. **2012**, 3, 264	9
1122	BrassiBase: Tools and biological resources to study characters and traits in the BrassicaceaeVersion 1.1. **2012**, 61, 1001-1009	56
1121	References. **2012**, 337-348	
1120	Molecular phylogenetics and historical biogeography of the MeiogyneFitzalania clade (Annonaceae): Generic paraphyly and late MiocenePliocene diversification in Australasia and the Pacific. **2012**, 61, 559-575	29
1119	A case study of intragenomic ITS variation in bryophytes: Assessment of gene flow and role of polyploidy in the origin of European taxa of the Tortula muralis (Musci: Pottiaceae) complex. **2012**, 61, 709-720	28
1118	Pruning the polyphyletic genus Polyalthia (Annonaceae) and resurrecting the genus Monoon. **2012**, 61, 1021-1039	29
1117	Hepatitis E virus genotype 3 in wild rats, United States. **2012**, 18, 1268-73	68
1116	Youwanjela, a new genus of land snail from the Kimberley, Western Australia (Eupulmonata, Camaenidae). **2012**, 88, 25-31	8
1115	Cysteine-rich domains related to Frizzled receptors and Hedgehog-interacting proteins. **2012**, 21, 1172-84	27
1114	Yeast communities in Sphagnum phyllosphere along the temperature-moisture ecocline in the boreal forest-swamp ecosystem and description of Candida sphagnicola sp. nov. **2012**, 102, 29-43	34
1113	Phylogenetic placement of lichenicolous Phoma species in the Phaeosphaeriaceae (Pleosporales, Dothideomycetes). **2012**, 55, 195-213	41
1112	Collodictyon--an ancient lineage in the tree of eukaryotes. **2012**, 29, 1557-68	75
1111	An early-branching microbialite cyanobacterium forms intracellular carbonates. **2012**, 336, 459-62	164
1110	The TvPirin gene is necessary for haustorium development in the parasitic plant Triphysaria versicolor. **2012**, 158, 1046-53	19
1109	Two new European species from the heterogeneous Caloplaca holocarpa group (Teloschistaceae). **2012**, 44, 73-89	17
1108	Host jumping onto close relatives and across kingdoms by Tyrannicordyceps (Clavicipitaceae) gen. nov. and Ustilaginoidea_(Clavicipitaceae). **2012**, 99, 552-61	56
1107	Multigene phylogeny and taxonomy of the genus Melanconiella (Diaporthales). **2012**, 57, 1-44	51
1106	Lepidostroma vilgalysii, a new basidiolichen from the New World. **2012**, 11, 827-833	14

1105	Phylogenetic relationships within the Opisthokonta based on phylogenomic analyses of conserved single-copy protein domains. **2012**, 29, 531-44	133
1104	Phylogenetic assessment of filoviruses: how many lineages of Marburg virus?. **2012**, 2, 1826-33	10
1103	Genetic analysis. **2012**, 865, 207-27	1
1102	A practical guide for the computational selection of residues to be experimentally characterized in protein families. **2012**, 13, 329-36	9
1101	Diversity and structure of soil bacterial communities associated with vultures in an African savanna. **2012**, 3, art47	17
1100	A distinct lineage of influenza A virus from bats. **2012**, 109, 4269-74	741
1099	Who's who? Allocation of carbonyl reductase isoenzymes from Candida parapsilosis by combining bio- and computational chemistry. **2012**, 13, 803-9	22
1098	Reference genome sequence of the model plant Setaria. **2012**, 30, 555-61	573
1097	Relaxed genetic constraint is ancestral to the evolution of phenotypic plasticity. **2012**, 52, 16-30	42
1096	Phylogeny and spatio-temporal distribution of European Pectinidae (Mollusca: Bivalvia). **2012**, 10, 233-242	10
1095	Association mapping in sunflower for Sclerotinia Head Rot resistance. **2012**, 12, 93	38
1094	PhyLAT: a phylogenetic local alignment tool. **2012**, 28, 1336-44	5
1093	Genome research in the cloud. **2012**, 16, 422-8	14
1092	Stable establishment of cotyledon identity during embryogenesis in Arabidopsis by ANGUSTIFOLIA3 and HANABA TARANU. **2012**, 139, 2436-46	46
1091	Tremella diploschistina (Tremellales, Basidiomycota, Fungi), a new lichenicolous species growing on Diploschistes. **2012**, 44, 321-332	21
1090	Phylogeny of Cidaroida (Echinodermata: Echinoidea) based on mitochondrial and nuclear markers. **2012**, 12, 155-165	7
1089	Evidence of animal mtDNA recombination between divergent populations of the potato cyst nematode Globodera pallida. **2012**, 140, 19-29	8
1088	Multiple Copies of Genes Encoding XEGIPs are Harbored in an 85-kB Region of the Potato Genome. **2012**, 30, 1040-1046	7

1087	Phylogenetic relationships of the anoplocephaline cestodes of Australasian marsupials and resurrection of the genus Wallabicestus Schmidt, 1975. **2012**, 82, 49-63	10
1086	Genetic structure of Pacific Flyway avian influenza viruses is shaped by geographic location, host species, and sampling period. **2012**, 44, 415-28	8
1085	Exobasidium darwinii, a new Hawaiian species infecting endemic Vaccinium reticulatum in Haleakala National Park. **2012**, 11, 361-371	11
1084	Molecular prey identification in wild Octopus vulgaris paralarvae. **2012**, 159, 1335-1345	53
1083	Geographic specific coral-associated ammonia-oxidizing archaea in the northern Gulf of Eilat (Red Sea). **2012**, 64, 18-24	15
1082	Flowers as islands: spatial distribution of nectar-inhabiting microfungi among plants of Mimulus aurantiacus, a hummingbird-pollinated shrub. **2012**, 63, 711-8	118
1081	Phylogenetic position and taxonomy of three heterocytous cyanobacteria dominating the littoral of deglaciated lakes, James Ross Island, Antarctica. **2012**, 35, 759-774	23
1080	Comparison of wintertime eukaryotic community from sea ice and open water in the Baltic Sea, based on sequencing of the 18S rRNA gene. **2012**, 35, 875-889	47
1079	Analysis of the PKR-eIF2alpha phosphorylation homology domain (PePHD) of hepatitis C virus genotype 1 in HIV-coinfected patients by ultra-deep pyrosequencing and its relationship to responses to pegylated interferon-ribavirin treatment. **2012**, 157, 703-11	13
1078	Structure-based functional inference of hypothetical proteins from Mycoplasma hyopneumoniae. **2012**, 18, 1917-25	12
1077	Nematode cys-loop GABA receptors: biological function, pharmacology and sites of action for anthelmintics. **2012**, 12, 3-12	15
1076	Phylogenetic investigation of the genus Raoiella (Prostigmata: Tenuipalpidae): diversity, distribution, and world invasions. **2012**, 57, 257-69	17
1075	Nuclear DNA from the extinct Passenger Pigeon (Ectopistes migratorius) confirms a single origin of New World pigeons. **2012**, 194, 52-7	13
1074	Genetic and phylogenetic evidence for misidentification of Vibrio species within the Harveyi clade. **2012**, 54, 160-5	34
1073	Phylogenetic relationships of the Rhacophorus everetti-group and implications for the evolution of reproductive modes in Philautus (Amphibia: Anura: Rhacophoridae). **2012**, 41, 29-46	17
1072	454-sequencing reveals stochastic local reassembly and high disturbance tolerance within arbuscular mycorrhizal fungal communities. **2012**, 100, 151-160	110
1071	Molecular phylogeny of the plant bugs (Heteroptera: Miridae) and the evolution of feeding habits. **2012**, 28, 50-79	42
1070	A specific mix of generalists: bacterial symbionts in Mediterranean Ircinia spp. **2012**, 79, 619-37	63

1069	Conservation of structure and mechanism within the transaldolase enzyme family. **2012**, 279, 766-78	12
1068	A molecular and ultrastructural description of Spathidiopsis buddenbrocki and the phylogenetic position of the family Placidae (Ciliophora). **2012**, 59, 67-79	5
1067	Complete nucleotide sequence and organization of the mitochondrial genome of eri-silkworm, Samia cynthia ricini (Lepidoptera: Saturniidae). **2012**, 15, 162-173	62
1066	Phylogeny and evolution of the Piroplasmida as inferred from 18S rRNA sequences. **2012**, 42, 353-63	86
1065	Yeast cytochrome c oxidase: a model system to study mitochondrial forms of the haem-copper oxidase superfamily. **2012**, 1817, 620-8	45
1064	MOLECULAR EVOLUTION OF GLUTAMINE SYNTHETASE II AND III IN THE CHROMALVEOLATES(1). **2012**, 48, 768-83	3
1063	Amino acid screening based on structural modeling identifies critical residues for the function, ion selectivity and structure of Arabidopsis MTP1. **2012**, 279, 2339-56	38
1062	Molecular mechanism of the allosteric enhancement of the umami taste sensation. **2012**, 279, 3112-20	66
1061	Deoxyribonucleoside kinases in two aquatic bacteria with high specificity for thymidine and deoxyadenosine. **2012**, 331, 120-7	6
1060	High Performance Multiple Sequence Alignment System for Pyrosequencing Reads from Multiple Reference Genomes. **2012**, 72, 83-93	8
1059	Biodiversity of avian trypanosomes. **2012**, 12, 102-12	26
1058	Phylogenetic analyses of a combined data set suggest that the Attheya lineage is the closest living relative of the pennate diatoms (Bacillariophyceae). **2012**, 163, 252-62	20
1057	Phylogenetic position of Lophomonas striata B□schli (Parabasalia) from the hindgut of the cockroach Periplaneta americana. **2012**, 163, 274-83	19
1056	Phylogenetic relationships of Mongolian Babesia bovis isolates based on the merozoite surface antigen (MSA)-1, MSA-2b, and MSA-2c genes. **2012**, 184, 309-16	30
1055	Occurrence of Theileria and Babesia species in water buffalo (Bubalus babalis, Linnaeus, 1758) in the Hubei province, South China. **2012**, 186, 490-6	42
1054	Population structure of a novel putative mycovirus infecting the conifer root-rot fungus Heterobasidion annosum sensu lato. **2012**, 422, 366-76	51
1053	Systematics and evolution of syllids (Annelida, Syllidae). **2012**, 28, 234-250	49
1052	Molecular phylogeny of the New World Dipsadidae (Serpentes: Colubroidea): a reappraisal. **2012**, 28, 437-459	67

1051	A revision of Nereimyra (Psamathini, Hesionidae, Aciculata, Annelida). **2012**, 164, 36-51	4
1050	Branching out: a remarkable new branching syllid (Annelida) living in a Petrosia sponge (Porifera: Demospongiae). **2012**, 164, 481-497	16
1049	A partial revision of Gyptis (Gyptini, Ophiodrominae, Hesionidae, Aciculata, Annelida), with descriptions of a new tribe, a new genus and five new species. **2012**, 165, 471-494	6
1048	Cryptic diversity within the Moroccan endemic day geckos Quedenfeldtia (Squamata: Gekkonidae): a multidisciplinary approach using genetic, morphological and ecological data. **2012**, 106, 828-850	24
1047	Two decades of describing the unseen majority of aquatic microbial diversity. **2012**, 21, 1878-96	147
1046	Parallel phylogeographic structure in ecologically similar sympatric sister taxa. **2012**, 21, 987-1004	42
1045	Mycoheterotrophic interactions are not limited to a narrow phylogenetic range of arbuscular mycorrhizal fungi. **2012**, 21, 1524-32	48
1044	Model-based comparisons of phylogeographic scenarios resolve the intraspecific divergence of cactophilic Drosophila mojavensis. **2012**, 21, 3293-307	32
1043	BAR expressolog identification: expression profile similarity ranking of homologous genes in plant species. **2012**, 71, 1038-50	78
1042	Functional convergence of microbes associated with temperate marine sponges. **2012**, 14, 1224-39	101
1041	Characterization of the first alginolytic operons in a marine bacterium: from their emergence in marine Flavobacteriia to their independent transfers to marine Proteobacteria and human gut Bacteroides. **2012**, 14, 2379-94	128
1040	A global molecular phylogeny of 147 periwinkle species (Gastropoda, Littorininae). **2012**, 41, 125-136	45
1039	Morphology, phylogeny and taxonomy of South American bothropoid pitvipers (Serpentes, Viperidae). **2012**, 41, 109-124	65
1038	Forgotten in the ocean: systematics, biogeography and evolution of the Trachylepis skinks of the Socotra Archipelago. **2012**, 41, 346-362	30
1037	Advances in molecular systematics of the vetigastropod superfamily Trochoidea. **2012**, 41, 571-595	36
1036	Cenozoic evolution of Muricidae (Mollusca, Neogastropoda) in the Southern Ocean, with the description of a new subfamily. **2012**, 41, 596-616	18
1035	Evolutionary history of the genus Tarentola (Gekkota: Phyllodactylidae) from the Mediterranean Basin, estimated using multilocus sequence data. **2012**, 12, 14	29
1034	The phenylalanine ammonia lyase (PAL) gene family shows a gymnosperm-specific lineage. **2012**, 13 Suppl 3, S1	51

1033	Cellular, biochemical, and molecular characterization of nitric oxide synthase expressed in the nervous system of the prosobranch Stramonita haemastoma (Gastropoda, Neogastropoda). **2012**, 520, 364-83	9
1032	A clustering phenomenon among HCV-1a strains among patients coinfected with HIV from Buenos Aires, Argentina. **2012**, 84, 570-81	5
1031	Melanoxa, a new genus in the Urocystidales (Ustilaginomycotina). **2012**, 11, 149-158	12
1030	Colipila, a new genus in the Helotiales. **2012**, 11, 201-214	3
1029	Phylogeography of the marine interstitial nemertean Ototyphlonemertes parmula (Nemertea, Hoplonemertea) reveals cryptic diversity and high dispersal potential. **2012**, 159, 661-674	18
1028	Comparative genomic analysis of the proteasome β5t subunit gene: implications for the origin and evolution of thymoproteasomes. **2012**, 64, 49-58	25
1027	Culturable microorganisms associated with Sishen iron ore and their potential roles in biobeneficiation. **2012**, 28, 1057-70	14
1026	Identification and characterization of a bacteria-like sequence in the genome of some Silene species. **2012**, 56, 247-253	
1025	Ceratocystis species, including two new species associated with nitidulid beetles, on eucalypts in Australia. **2012**, 101, 217-41	28
1024	Morphological and molecular development of the eyes during embryogenesis of the freshwater planarian Schmidtea polychroa. **2012**, 222, 45-54	22
1023	Genetic and phylogenetic evidence for horizontal gene transfer among ecologically disparate groups of marine Vibrio. **2013**, 29, 46-64	2
1022	Phylogenetic analysis of Deladenus nematodes parasitizing northeastern North American Sirex species. **2013**, 113, 177-83	24
1021	Bacterial feeding, Leishmania infection and distinct infection routes induce differential defensin expression in Lutzomyia longipalpis. **2013**, 6, 12	39
1020	Striking structural dynamism and nucleotide sequence variation of the transposon Galileo in the genome of Drosophila mojavensis. **2013**, 4, 6	4
1019	Morphological and genetic analyses of xeniid soft coral diversity (Octocorallia; Alcyonacea). **2013**, 13, 135-150	8
1018	Polyporales genomes reveal the genetic architecture underlying tetrapolar and bipolar mating systems. **2013**, 105, 1374-90	33
1017	Endophytic Colletotrichum from tropical grasses with a new species C. endophytica. **2013**, 61, 107-115	43
1016	Global ITS diversity in the Sporothrix schenckii complex. **2013**, 66, 153	31

1015	First evidence of autotriploidization in sterlet (Acipenser ruthenus). **2013**, 54, 201-7	14
1014	Ammonia-oxidizing archaea and bacteria are structured by geography in biological soil crusts across North American arid lands. **2013**, 2, 9	45
1013	The Helvella lacunosa species complex in western North America: cryptic species, misapplied names and parasites. **2013**, 105, 1275-86	28
1012	Phylogenetic analysis and reconfiguration of genera in the cestode order Diphyllidea. **2013**, 43, 621-39	19
1011	Membrane environment imposes unique selection pressures on transmembrane domains of G protein-coupled receptors. **2013**, 76, 172-82	18
1010	Culturing bias in marine heterotrophic flagellates analyzed through seawater enrichment incubations. **2013**, 66, 489-99	19
1009	Regressive Evolution of Photosynthesis in the Roseobacter Clade. **2013**, 66, 385-405	14
1008	Characterization of the Mx and hepcidin genes in Epinephelus akaara asymptomatic carriers of the nervous necrosis virus. **2013**, 408-409, 175-183	9
1007	Phylogeny Reconstruction. **2013**,	
1006	Previously unknown and highly divergent ssDNA viruses populate the oceans. **2013**, 7, 2169-77	133
1005	Hagfish phylogeny and taxonomy, with description of the new genus Rubicundus (Craniata, Myxinidae). **2013**, 51, 296-307	18
1004	Molecular phylogeny of Elphidiidae (foraminifera). **2013**, 103, 1-14	23
1003	Molecular phylogenetics of Gobioidei and phylogenetic placement of European gobies. **2013**, 69, 619-33	112
1002	Molecular characterization of trophic ecology within an island radiation of insect herbivores (Curculionidae: Entiminae: Cratopus). **2013**, 22, 5441-55	28
1001	Mitogenomics at the base of Metazoa. **2013**, 69, 339-51	61
1000	Australasian sequestrate fungi 18: Solioccasus polychromus gen. & sp. nov., a richly colored, tropical to subtropical, hypogeous fungus. **2013**, 105, 888-95	22
999	Genomewide analysis of polysaccharides degrading enzymes in 11 white- and brown-rot Polyporales provides insight into mechanisms of wood decay. **2013**, 105, 1412-27	91
998	Effects of using coding potential, sequence conservation and mRNA structure conservation for predicting pyrrolysine containing genes. **2013**, 14, 118	3

997	Phylogeny and evolutionary history of glycogen synthase kinase 3/SHAGGY-like kinase genes in land plants. **2013**, 13, 143	15
996	Bayesian species delimitation reveals generalist and specialist parasitic wasps on Galerucella beetles (Chrysomelidae): sorting by herbivore or plant host. **2013**, 13, 92	30
995	Gene make-up: rapid and massive intron gains after horizontal transfer of a bacterial □-amylase gene to Basidiomycetes. **2013**, 13, 40	41
994	Evolution of microgastropods (Ellobioidea, Carychiidae): integrating taxonomic, phylogenetic and evolutionary hypotheses. **2013**, 13, 18	44
993	The complete mitochondrial genome of Solemya velum (Mollusca: Bivalvia) and its relationships with conchifera. **2013**, 14, 409	48
992	Recombinant structures expand and contract inter and intragenic diversification at the KIR locus. **2013**, 14, 89	53
991	High quality de novo sequencing and assembly of the Saccharomyces arboricolus genome. **2013**, 14, 69	59
990	Genomic and phenotypic characterization of in vitro-generated Chlamydia trachomatis recombinants. **2013**, 13, 142	42
989	Genome-level homology and phylogeny of Vibrionaceae (Gammaproteobacteria: Vibrionales) with three new complete genome sequences. **2013**, 13, 80	9
988	Mealybugs nested endosymbiosis: going into the 'matryoshka' system in Planococcus citri in depth. **2013**, 13, 74	32
987	The dual targeting ability of type II NAD(P)H dehydrogenases arose early in land plant evolution. **2013**, 13, 100	21
986	A structural role for the PHP domain in E. coli DNA polymerase III. **2013**, 13, 8	26
985	Phylogeny and taxonomy of poroid and lamellate genera in the Auriculariales (Basidiomycota). **2013**, 105, 1219-30	18
984	Phylogenetic analysis of the mitochondrial genomes and nuclear rRNA genes of ticks reveals a deep phylogenetic structure within the genus Haemaphysalis and further elucidates the polyphyly of the genus Amblyomma with respect to Amblyomma sphenodonti and Amblyomma elaphense. **2013**, 4, 265-74	53
983	A Molecular Phylogenetic Analysis of the Genus Dohrniphora (Diptera: Phoridae). **2013**, 106, 401-409	4
982	In vitro activity of novel in silico-developed antimicrobial peptides against a panel of bacterial pathogens. **2013**, 19, 554-65	15
981	Phylogenetic study of Cryptococcus laurentii mycocinogenic strains. **2013**, 12, 777-782	5
980	Description and affinities of a sequestrate Lepiota (Agaricaceae) from Australia. **2013**, 12, 525-532	12

979	Strobilomyces echinocephalus sp. nov. (Boletales) from south-western China, and a key to the genus Strobilomyces worldwide. **2013**, 12, 575-588	14
978	A new cryptic species in the genus Tubariomyces (Inocybaceae, Agaricales). **2013**, 12, 375-381	6
977	Little evidence for niche partitioning among ectomycorrhizal fungi on spruce seedlings planted in decayed wood versus mineral soil microsites. **2013**, 173, 1499-1511	13
976	TAC from Mycobacterium tuberculosis: a paradigm for stress-responsive toxin-antitoxin systems controlled by SecB-like chaperones. **2013**, 18, 129-35	29
975	Detection of photoactive siderophore biosynthetic genes in the marine environment. **2013**, 26, 507-16	13
974	Molecular data reveal cryptic lineages within the northeastern Atlantic and Mediterranean small mussel drills of theOcinebrina edwardsiicomplex (Mollusca: Gastropoda: Muricidae). **2013**, 169, 389-407	24
973	Pike and salmon as sister taxa: detailed intraclade resolution and divergence time estimation of Esociformes + Salmoniformes based on whole mitochondrial genome sequences. **2013**, 530, 57-65	39
972	In silico peptide-binding predictions of passerine MHC class I reveal similarities across distantly related species, suggesting convergence on the level of protein function. **2013**, 65, 299-311	10
971	Culture-independent sequence analysis of Chlamydia trachomatis in urogenital specimens identifies regions of recombination and in-patient sequence mutations. **2013**, 159, 2109-2117	28
970	Insights into the immuno-molecular biology of Angiostrongylus vasorum through transcriptomics--prospects for new interventions. **2013**, 31, 1486-500	16
969	Genetic analysis of the Australian whipbirds and wedgebills illuminates the evolution of their plumage and vocal diversity. **2013**, 113, 359-366	6
968	Developments in the taxonomy of silica-scaled chrysophytes ▯from morphological and ultrastructural to molecular approaches. **2013**, 31, 385-402	39
967	Metazoan innovation: from aromatic amino acids to extracellular signaling. **2013**, 45, 359-67	5
966	Kinesin-5: cross-bridging mechanism to targeted clinical therapy. **2013**, 531, 133-49	48
965	Integration of cytochromecoxidase I barcodes and geometric morphometrics to delimit species in the genusGnopharmia(Lepidoptera: Geometridae, Ennominae). **2013**, 169, 70-83	8
964	Evolution of Functional Genes in Cetaceans Driven by Natural Selection on a Phylogenetic and Population Level. **2013**, 40, 341-354	2
963	The Role of Aromatic-Aromatic Interactions in Strand-Strand Stabilization of ▯Sheets. **2013**, 425, 3522-35	22
962	Microcephaly thin corpus callosum intellectual disability syndrome caused by mutated TAF2. **2013**, 49, 411-416.e1	19

961	Parallel host range expansion in two unrelated cossid moths infesting Eucalyptus nitens on two continents. **2013**, 38, 112-116	6
960	Expansion of the antimicrobial peptide repertoire in the invasive ladybird Harmonia axyridis. **2013**, 280, 20122113	82
959	Reduction and expansion in microsporidian genome evolution: new insights from comparative genomics. **2013**, 5, 2285-303	74
958	Isolation of the MAT1-1 mating type idiomorph and evidence for selfing in the Chinese medicinal fungus Ophiocordyceps sinensis. **2013**, 117, 599-610	23
957	Guidance on the development and validation of diagnostic tests that depend on nucleic acid amplification and detection. **2013**, 56, 260-70	24
956	Genetic diversity within Theileria orientalis parasites detected in Sri Lankan cattle. **2013**, 4, 235-41	20
955	Diversimorbus metrosiderotis gen. et sp. nov. and three new species of Holocryphia (Cryphonectriaceae) associated with cankers on native Metrosideros angustifolia trees in South Africa. **2013**, 117, 289-310	18
954	The molecular prevalence and MSA-2b gene-based genetic diversity of Babesia bovis in dairy cattle in Thailand. **2013**, 197, 642-8	14
953	A knowledge-based multiple-sequence alignment algorithm. **2013**, 10, 884-96	4
952	Improved multiple sequence alignments using coupled pattern mining. **2013**, 10, 1098-112	3
951	Key innovations and island colonization as engines of evolutionary diversification: a comparative test with the Australasian diplodactyloid geckos. **2013**, 26, 2662-80	28
950	Application of nonspecific commercial AMF inocula results in poor mycorrhization in Camellia japonica L.. **2013**, 61, 63-76	17
949	The bacterial actin MamK: in vitro assembly behavior and filament architecture. **2013**, 288, 4265-77	52
948	Evolutionary origin of amino acid transporter families SLC32, SLC36 and SLC38 and physiological, pathological and therapeutic aspects. **2013**, 34, 571-85	97
947	Biochemical study of the extracellular aspartyl protease Eap1 from the phytopathogen fungus Sporisorium reilianum. **2013**, 92, 214-22	11
946	Discovery of a unique novel clade of mosquito-associated bunyaviruses. **2013**, 87, 12850-65	78
945	Phylogenies of central element proteins reveal the dynamic evolutionary history of the mammalian synaptonemal complex: ancient and recent components. **2013**, 195, 781-93	15
944	Prevalence of viral photosynthetic and capsid protein genes from cyanophages in two large and deep perialpine lakes. **2013**, 79, 7169-78	17

943	Optimizing multiple sequence alignments using a genetic algorithm based on three objectives: structural information, non-gaps percentage and totally conserved columns. **2013**, 29, 2112-21	36
942	Evaluating Multiple Sequence Alignments Using a LS-SVM Approach with a Heterogeneous Set of Biological Features. **2013**, 150-158	0
941	The evolution of complexity in the visual systems of stomatopods: insights from transcriptomics. **2013**, 53, 39-49	38
940	RNAi reveals the key role of Nervana 1 in cockroach oogenesis and embryo development. **2013**, 43, 178-88	10
939	NMDA receptor expression and C terminus structure in the rotifer Brachionus plicatilis and long-term potentiation across the Metazoa. **2013**, 13, 125-34	2
938	Corolla morphology influences diversification rates in bifid toadflaxes (Linaria sect. Versicolores). **2013**, 112, 1705-22	33
937	Crystal structure and computational characterization of the lytic polysaccharide monooxygenase GH61D from the Basidiomycota fungus Phanerochaete chrysosporium. **2013**, 288, 12828-39	131
936	A New Species ofAllophryne(Anura: Allophrynidae) from the Atlantic Rain Forest Biome of Eastern Brazil. **2013**, 69, 480-491	11
935	Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. **2013**, 164, 425-38	28
934	MICROTUBULE-ASSOCIATED PROTEIN65 is essential for maintenance of phragmoplast bipolarity and formation of the cell plate in Physcomitrella patens. **2013**, 25, 4479-92	38
933	Scalability and accuracy improvements of consistency-based multiple sequence alignment tools. **2013**,	4
932	Global survey on sequence characteristics of plant microRNA genes: Cis-regulatory SNPs in promoters and microRNA precursors. **2013**, 147, 445-450	3
931	Phylogeny of the cycads based on multiple single-copy nuclear genes: congruence of concatenated parsimony, likelihood and species tree inference methods. **2013**, 112, 1263-78	75
930	Elucidating the native sources of an invasive tree species, Acacia pycnantha, reveals unexpected native range diversity and structure. **2013**, 111, 895-904	15
929	Lineage-specific duplications of Muroidea Faim and Spag6 genes and atypical accelerated evolution of the parental Spag6 gene. **2013**, 77, 119-29	8
928	Integrative taxonomy of the freshwater worm Rhyacodrilus falciformis s.l. (Clitellata: Naididae), with the description of a new species. **2013**, 42, n/a-n/a	10
927	Making automated multiple alignments of very large numbers of protein sequences. **2013**, 29, 989-95	40
926	Less is more in mammalian phylogenomics: AT-rich genes minimize tree conflicts and unravel the root of placental mammals. **2013**, 30, 2134-44	131

925	Diversity and distribution of co-infecting Botryosphaeriaceae from Eucalyptus grandis and Syzygium cordatum in South Africa. **2013**, 84, 38-43	23
924	Contrasted evolution of the vomeronasal receptor repertoires in mammals and squamate reptiles. **2013**, 5, 389-401	42
923	How to describe a cryptic species? Practical challenges of molecular taxonomy. **2013**, 10, 59	194
922	Cydippid ctenophores in the coastal waters of Svalbard: is it only Mertensia ovum?. **2013**, 36, 1681-1686	7
921	Fast discovery and visualization of conserved regions in DNA sequences using quasi-alignment. **2013**, 14 Suppl 11, S2	1
920	Evidence for inter-specific recombination among the mitochondrial genomes of Fusarium species in the Gibberella fujikuroi complex. **2013**, 14, 605	28
919	Genome-wide analyses of Epstein-Barr virus reveal conserved RNA structures and a novel stable intronic sequence RNA. **2013**, 14, 543	53
918	Hidden diversity in Senegalese bats and associated findings in the systematics of the family Vespertilionidae. **2013**, 10, 48	21
917	Comparative genomics in acid mine drainage biofilm communities reveals metabolic and structural differentiation of co-occurring archaea. **2013**, 14, 485	75
916	Reductive evolution and the loss of PDC/PAS domains from the genus Staphylococcus. **2013**, 14, 524	10
915	A curious occurrence of Hazenia broadyi spec. nova in Antarctica and the review of the genus Hazenia (Ulotrichales, Chlorophyceae). **2013**, 36, 1281-1291	14
914	Transcriptomic and genomic evidence for Streptococcus agalactiae adaptation to the bovine environment. **2013**, 14, 920	31
913	Comparative inner ear transcriptome analysis between the Rickett's big-footed bats (Myotis ricketti) and the greater short-nosed fruit bats (Cynopterus sphinx). **2013**, 14, 916	18
912	A phylogenomic approach to bacterial subspecies classification: proof of concept in Mycobacterium abscessus. **2013**, 14, 879	17
911	Scent of a break-up: phylogeography and reproductive trait divergences in the red-tailed bumblebee (Bombus lapidarius). **2013**, 13, 263	46
910	New phylogenomic data support the monophyly of Lophophorata and an Ectoproct-Phoronid clade and indicate that Polyzoa and Kryptrochozoa are caused by systematic bias. **2013**, 13, 253	71
909	In silico characterization of the insect diapause-associated protein couch potato (CPO) in Calanus finmarchicus (Crustacea: Copepoda). **2013**, 8, 45-57	9
908	Phylogenetic status of insect parasitism in the subfamily Entaphelenchinae Nickle with description of Peraphelenchus orientalis n. sp. (Tylenchomorpha: Aphelenchoididae). **2013**, 99, 639-49	18

907	The evolutionary history of the order Antipatharia (Cnidaria: Anthozoa: Hexacorallia) as inferred from mitochondrial and nuclear DNA: implications for black coral taxonomy and systematics. **2013**, 169, 312-361	48
906	Phylogenetic analyses of endoparasitic Acanthocephala based on mitochondrial genomes suggest secondary loss of sensory organs. **2013**, 66, 182-9	40
905	Population genomic footprints of selection and associations with climate in natural populations of Arabidopsis halleri from the Alps. **2013**, 22, 5594-607	76
904	Sulcozoa revealed as a paraphyletic group in mitochondrial phylogenomics. **2013**, 69, 462-8	16
903	Diaporthe neotheicola, a new threat for kiwifruit in Greece. **2013**, 47, 35-40	10
902	Multiple origins for Hound's tongues (Cynoglossum L.) and Navel seeds (Omphalodes Mill.)--the phylogeny of the borage family (Boraginaceae s.str.). **2013**, 68, 604-18	58
901	A new clade, based on partial LSU rDNA sequences, of unarmoured dinoflagellates. **2013**, 164, 673-85	20
900	Advancing our understanding of the human microbiome using QIIME. **2013**, 531, 371-444	373
899	Determining an Ideal MSA Method for Constructing Phylogenetic Tree on DNA Dataset. **2013**,	0
898	Genomes of Stigonematalean cyanobacteria (subsection V) and the evolution of oxygenic photosynthesis from prokaryotes to plastids. **2013**, 5, 31-44	182
897	Phellinopsis helwingiae(Hymenochaetales, Basidiomycota), a New Species from China and a Brief Note onP. Junipericola. **2013**, 50, 408-412	4
896	Morphological and Molecular Characterization of a New Nearctic Species ofCalligraphaChevrolat, 1836 (Coleoptera: Chrysomelidae, Chrysomelinae) from Central Mexico. **2013**, 115, 369-391	4
895	Identification of contamination in the American type culture collection stock of human adenovirus type 8 by whole-genome sequencing. **2013**, 87, 1285-6	4
894	CUDA-MAFFT: Accelerating MAFFT on CUDA-enabled graphics hardware. **2013**,	1
893	Neural network based cloud computing platform for bioinformatics. **2013**,	4
892	Systematics and biogeography of the non-viny grape relativeLeea(Vitaceae). **2013**, 171, 354-376	13
891	Mitogenomics does not resolve deep molluscan relationships (yet?). **2013**, 69, 376-92	81
890	A method of alignment masking for refining the phylogenetic signal of multiple sequence alignments. **2013**, 30, 689-712	11

889	Molecular phylogeny and historical biogeography of the Anatolian lizard Apathya (Squamata, Lacertidae). **2013**, 66, 992-1001	47
888	Deep relationships of Rhizaria revealed by phylogenomics: a farewell to Haeckel's Radiolaria. **2013**, 67, 53-9	57
887	Comparative phylogeography of six herpetofauna species in Cyprus: late Miocene to Pleistocene colonization routes. **2013**, 108, 619-635	30
886	A phylogenetic analysis of the megadiverse Chalcidoidea (Hymenoptera). **2013**, 29, 466-542	135
885	Evolution of Archamoebae: morphological and molecular evidence for pelobionts including Rhizomastix, Entamoeba, Iodamoeba, and Endolimax. **2013**, 164, 380-410	37
884	Xerombrophila crystallifera, a new genus and species in the Helotiales. **2013**, 12, 475-488	3
883	Mazaedium evolution in the Ascomycota (Fungi) and the classification of mazaediate groups of formerly unclear relationship. **2013**, 29, 296-308	53
882	A serious canker disease caused by Immersiporthe knoxdaviesiana gen. et sp. nov. (Cryphonectriaceae) on native Rapanea melanophloeos in South Africa. **2013**, 62, 667-678	17
881	Phylogeny of Chaetonotidae and other Paucitubulatina (Gastrotricha: Chaetonotida) and the colonization of aquatic ecosystems. **2013**, 42, 88-105	39
880	Genetic exchanges of inteins between prasinoviruses (phycodnaviridae). **2013**, 67, 18-33	13
879	Saccharomyces cerevisiae Env7 is a novel serine/threonine kinase 16-related protein kinase and negatively regulates organelle fusion at the lysosomal vacuole. **2013**, 33, 526-42	10
878	Molecular phylogeny of North American Branchiobdellida (Annelida: Clitellata). **2013**, 66, 30-42	23
877	RNA secondary structure, an important bioinformatics tool to enhance multiple sequence alignment: a case study (Sordariomycetes, Fungi). **2013**, 12, 305-319	11
876	Contrasting phylogenetic patterns of anther smuts (Pucciniomycotina: Microbotryum) reflect phylogenetic patterns of their caryophyllaceous hosts. **2013**, 13, 111-126	19
875	Phylogeny and character evolution in the bee-assassins (Insecta: Heteroptera: Reduviidae). **2013**, 66, 283-302	11
874	Evolution of complementary nucleotides in 5' and 3' untranslated regions of influenza A virus genomic segments. **2013**, 13, 175-9	12
873	Genetic characterization and barcoding of taxa in the genus Wolffia Horkel ex Schleid. (Lemnaceae) as revealed by two plastidic markers and amplified fragment length polymorphism (AFLP). **2013**, 237, 1-13	34
872	Characterization of CCDC28B reveals its role in ciliogenesis and provides insight to understand its modifier effect on Bardet-Biedl syndrome. **2013**, 132, 91-105	29

871	The identification of concerted convergence in insect heads corroborates palaeoptera. **2013**, 62, 250-63		25
870	Molecular epidemiology of Theileria annulata and identification of 18S rRNA gene and ITS regions sequences variants in apparently healthy buffaloes and cattle in Pakistan. **2013**, 13, 124-32		20
869	Prevalence and genetic diversity of equine piroplasms in Tov province, Mongolia. **2013**, 16, 178-85		54
868	The variability of the large genomic segment of □ahy□a orthobunyavirus and an all-atom exploration of its anti-viral drug resistance. **2013**, 20, 304-11		8
867	Genetic diversity of merozoite surface antigens in Babesia bovis detected from Sri Lankan cattle. **2013**, 19, 134-40		20
866	Isolation and characterization of human breast cancer cells with SOX2 promoter activity. **2013**, 437, 205-11		28
865	Immunotherapy of CD30-expressing lymphoma using a highly stable ssDNA aptamer. **2013**, 34, 8909-17		61
864	Characterization of cys-loop receptor genes involved in inhibitory amine neurotransmission in parasitic and free living nematodes. **2013**, 62, 599-605		14
863	Characterisation of a functional allatotropin receptor in the bumblebee, Bombus terrestris (Hymenoptera, Apidae). **2013**, 193, 193-200		16
862	Tracking a refined eIF4E-binding motif reveals Angel1 as a new partner of eIF4E. *Nucleic Acids Research*, **2013**, 41, 7783-92	20.1	17
861	Diversification rates have declined in the Malagasy herpetofauna. **2013**, 280, 20131109		23
860	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. **2013**, 23, 1235-47		166
859	Sizing up Septoria. **2013**, 75, 307-90		207
858	Fungal host specificity is not a bottleneck for the germination of Pyroleae species (Ericaceae) in a Bavarian forest. **2013**, 22, 1473-81		25
857	Spatiotemporal seed development analysis provides insight into primary dormancy induction and evolution of the Lepidium delay of germination1 genes. **2013**, 161, 1903-17		17
856	A new approach to species delimitation in Septoria. **2013**, 75, 213-305		73
855	Genomic characterization of Felis catus papillomavirus-3: a novel papillomavirus detected in a feline Bowenoid in situ carcinoma. **2013**, 165, 319-25		37
854	Expression and characterization of the calcium-activated photoprotein from the ctenophore Bathocyroe fosteri: insights into light-sensitive photoproteins. **2013**, 431, 360-6		26

853	Microbial effects on the release and attenuation of arsenic in the shallow subsurface of a natural geochemical anomaly. **2013**, 180, 84-91	17
852	The complete mitochondrial genome of Biston panterinaria (Lepidoptera: Geometridae), with phylogenetic utility of mitochondrial genome in the Lepidoptera. **2013**, 515, 349-58	50
851	Application of a new informatics tool for contamination screening in the HIV sequencing laboratory. **2013**, 57, 249-53	5
850	Mass spectrometric characterization of the neuropeptidome of the ghost crab Ocypode ceratophthalma (Brachyura, Ocypodidae). **2013**, 184, 22-34	27
849	The E4 protein; structure, function and patterns of expression. **2013**, 445, 80-98	118
848	Prevalence and genetic variation of salivary gland hypertrophy virus in wild populations of the tsetse fly Glossina pallidipes from southern and eastern Africa. **2013**, 112 Suppl, S123-32	16
847	The phylogenetic placement of hypocrealean insect pathogens in the genus Polycephalomyces: an application of One Fungus One Name. **2013**, 117, 611-22	55
846	Evolutionary plasticity in coccidia - striking morphological similarity of unrelated coccidia (apicomplexa) from related hosts: Eimeria spp. from African and Asian Pangolins (Mammalia: Pholidota). **2013**, 164, 470-81	5
845	Phylogenetic position of the ectomycorrhizal basidiomycete Tricholoma dulciolens in relation to species of Tricholoma that produce matsutake mushrooms. **2013**, 54, 438-443	10
844	A comparison of microbial communities in deep-sea polymetallic nodules and the surrounding sediments in the Pacific Ocean. **2013**, 79, 40-49	41
843	Development of EMA-2 recombinant antigen based enzyme-linked immunosorbent assay for seroprevalence studies of Theileria equi infection in Indian equine population. **2013**, 198, 10-7	14
842	Expression of sulfatases in Rhodopirellula baltica and the diversity of sulfatases in the genus Rhodopirellula. **2013**, 9, 51-61	93
841	The evolutionary origins of chordate hematopoiesis and vertebrate endothelia. **2013**, 375, 182-92	39
840	Sea star populations diverge by positive selection at a sperm-egg compatibility locus. **2013**, 3, 640-54	17
839	Host range evolution in a selected group of osmiine bees (Hymenoptera: Megachilidae): the Boraginaceae-Fabaceae paradox. **2013**, 108, 35-54	25
838	Investigating the evolution of Lantaneae (Verbenaceae) using multiple loci. **2013**, 171, 103-119	17
837	Molecular phylogeny of the bee genusHoplitis(Megachilidae: Osmiini) - how does nesting biology affect biogeography?. **2013**, 167, 28-42	15
836	Precipitation rather than temperature influenced the phylogeography of the endemic shrub Anarthrophyllum desideratum in the Patagonian steppe. **2013**, 40, 168-182	29

835	A Phylogeny of Toadflaxes (LinariaMill.) Based on Nuclear Internal Transcribed Spacer Sequences: Systematic and Evolutionary Consequences. **2013**, 174, 234-249	30
834	Sequencing and annotation of the Ophiostoma ulmi genome. **2013**, 14, 162	34
833	Phylogeny and biogeography of the Poecilia sphenops species complex (Actinopterygii, Poeciliidae) in Central America. **2013**, 66, 1011-26	37
832	Phylogeny of the Lobariaceae (lichenized Ascomycota: Peltigerales), with a reappraisal of the genus Lobariella. **2013**, 45, 203-263	66
831	A phylogeny of the highly diverse cup-fungus family Pyronemataceae (Pezizomycetes, Ascomycota) clarifies relationships and evolution of selected life history traits. **2013**, 67, 311-35	63
830	Bayesian inference of phylogeny, morphology and range evolution reveals a complex evolutionary history in St. John’s wort (Hypericum). **2013**, 67, 379-403	54
829	Genetic relationships between Oeneis urda and O. mongolica (Nymphalidae: Lepidoptera). **2013**, 43, 85-100	3
828	Overview of tomato (Solanum lycopersicum) candidate pathogen recognition genes reveals important Solanum R locus dynamics. **2013**, 197, 223-237	66
827	Phylogenetic relationships of Cochlodinium polykrikoides Margalef (Gymnodiniales, Dinophyceae) from the Mediterranean Sea and the implications of its global biogeography. **2013**, 25, 39-46	24
826	The complex colonization history of nocturnal geckos (Paroedura) in the Comoros Archipelago. **2013**, 42, 135-150	13
825	Structural basis and SAR for G007-LK, a lead stage 1,2,4-triazole based specific tankyrase 1/2 inhibitor. **2013**, 56, 3012-23	90
824	What stabilizes close arginine pairing in proteins?. **2013**, 15, 5844-53	30
823	Taxonomy and pathogenicity of Ceratocystis species on Eucalyptus trees in South China, including C. chinaeucensis sp. nov.. **2013**, 58, 267-279	33
822	Environmental barcoding of the ectomycorrhizal fungal genus Cortinarius. **2013**, 58, 299-310	18
821	Molecular phylogeny of black fungus gnats (Diptera: Sciaroidea: Sciaridae) and the evolution of larval habitats. **2013**, 66, 833-46	37
820	Two apparently unrelated groups of symbiotic annelids, Nautiliniellidae and Calamyzidae (Phyllodocida, Annelida), are a clade of derived chrysopetalid polychaetes. **2013**, 29, 610-628	12
819	Sphaerospora sensu stricto: taxonomy, diversity and evolution of a unique lineage of myxosporeans (Myxozoa). **2013**, 68, 93-105	43
818	Phylodynamics analysis of canine parvovirus in Uruguay: evidence of two successive invasions by different variants. **2013**, 158, 1133-41	33

817	Phylogenetic relationships of the mycoheterotrophic genus Voyria and the implications for the biogeographic history of Gentianaceae. **2013**, 100, 712-21	28
816	Distinct but Closely Related Sebacinales form Mycorrhizae with Coexisting Ericaceae and Orchidaceae in a Neotropical Mountain Area. **2013**, 81-105	4
815	Genome-assisted development of nuclear intergenic sequence markers for entomopathogenic fungi of the Metarhizium anisopliae species complex. **2013**, 13, 210-7	41
814	Peptidergic signaling in Calanus finmarchicus (Crustacea, Copepoda): in silico identification of putative peptide hormones and their receptors using a de novo assembled transcriptome. **2013**, 187, 117-35	65
813	Species delineation in the tree pathogen genus Celoporthe (Cryphonectriaceae) in southern Africa. **2013**, 105, 297-311	9
812	Diversification in a biodiversity hotspot--the evolution of Southeast Asian rhacophorid tree frogs on Borneo (Amphibia: Anura: Rhacophoridae). **2013**, 68, 567-81	16
811	Genomes of the class Erysipelotrichia clarify the firmicute origin of the class Mollicutes. **2013**, 63, 2727-2741	31
810	Chalicogloea cavernicola gen. nov., sp. nov. (Chroococcales, Cyanobacteria), from low-light aerophytic environments: combined molecular, phenotypic and ecological criteria. **2013**, 63, 2326-2333	14
809	A survey of host range genes in poxvirus genomes. **2013**, 14, 406-25	68
808	Detection of positive selection eliminating effects of structural constraints in hemagglutinin of H3N2 human influenza A virus. **2013**, 16, 93-8	4
807	Phylogeny, biogeography and systematics of hydrothermal vent and methane seep Amphisamytha (Ampharetidae, Annelida), with descriptions of three new species. **2013**, 11, 35-65	41
806	Two new Antarctic Ophryotrocha (Annelida: Dorvilleidae) described from shallow-water whale bones. **2013**, 36, 1031-1045	25
805	An updated phylogeny of Anisoptera including formal convergence analysis of morphological characters. **2013**, 38, 474-490	31
804	Congruence between distribution modelling and phylogeographical analyses reveals Quaternary survival of a toadflax species (Linaria elegans) in oceanic climate areas of a mountain ring range. **2013**, 198, 1274-1289	31
803	The architecture of Trypanosoma brucei tubulin-binding cofactor B and implications for function. **2013**, 280, 3270-80	5
802	Quaternary refugia in southwestern Iran: insights from two sympatric moth species (Insecta, Lepidoptera). **2013**, 13, 409-423	30
801	Arsenite oxidase gene diversity among Chloroflexi and Proteobacteria from El Tatio Geyser Field, Chile. **2013**, 83, 745-56	44
800	Ostreopexin: a hemopexin fold protein from the oyster mushroom, Pleurotus ostreatus. **2013**, 1834, 1468-73	2

799	Cyathostoma (Cyathostoma) phenisci Baudet, 1937 (Nematoda: Syngamidae), a parasite of respiratory tract of African penguin Spheniscus demersus: morphological and molecular characterisation with some ecological and veterinary notes. **2013**, 62, 416-22	11
798	Analysis of DNA repair and protection in the Tardigrade Ramazzottius varieornatus and Hypsibius dujardini after exposure to UVC radiation. **2013**, 8, e64793	53
797	Prediction of the protein components of a putative Calanus finmarchicus (Crustacea, Copepoda) circadian signaling system using a de novo assembled transcriptome. **2013**, 8, 165-93	28
796	Phylogeny of salmonids (salmoniformes: Salmonidae) and its molecular dating: Analysis of mtDNA data. **2013**, 49, 623-637	28
795	What do we know about the transient receptor potential vanilloid 2 (TRPV2) ion channel?. **2013**, 280, 5471-87	105
794	Comparative analysis of cation/proton antiporter superfamily in plants. **2013**, 521, 245-51	22
793	Pelagic Oxygen Minimum Zone Microbial Communities. **2013**, 113-122	12
792	A new species and a new record of Diatrypaceae from Panama. **2013**, 105, 681-8	11
791	Comparative characterization of the virulence gene clusters (lipooligosaccharide [LOS] and capsular polysaccharide [CPS]) for Campylobacter coli, Campylobacter jejuni subsp. jejuni and related Campylobacter species. **2013**, 14, 200-13	31
790	Preserving the evolutionary history of freshwater biota in Iberian National Parks. **2013**, 162, 116-126	26
789	A comprehensive analysis of bilaterian mitochondrial genomes and phylogeny. **2013**, 69, 352-64	140
788	Biogeography of scorpions in the Pseudouroctonus minimus complex (Vaejovidae) from south-western North America: implications of ecological specialization for pre-Quaternary diversification. **2013**, 40, 1850-1860	27
787	Description of the tadpoles of two Cameroonian frogs, Leptodactylodon axillaris and L. perreti (Anura: Arthroleptidae). **2013**, 62, 28-39	4
786	Origins, evolution, and diversification of cleptoparasitic lineages in long-tongued bees. **2013**, 67, 2982-98	21
785	Diversity and species boundaries in floricolous downy mildews. **2013**, 12, 321-329	14
784	Phylogenetic relationships of Microdontinae (Diptera: Syrphidae) based on molecular and morphological characters. **2013**, 38, 661-688	25
783	An introduction to sequence similarity ("homology") searching. **2013**, Chapter 3, Unit3.1	308
782	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. **2013**, 499, 74-8	563

781	High local genetic diversity of canine parvovirus from Ecuador. **2013**, 166, 214-9	34
780	A taxonomic revision and species delimitation of the genus Purpuraria Enderlein, 1929 (Orthoptera: Pamphagidae) using an integrative approach. **2013**, 51, 173-186	6
779	The role of the potato (Solanum tuberosum) CCD8 gene in stolon and tuber development. **2013**, 198, 1108-1120	51
778	Phylogenetic overview of the Boletineae. **2013**, 117, 479-511	109
777	Phylogenetic relationships and biogeography of Pseudoxiphophorus (Teleostei: Poeciliidae) based on mitochondrial and nuclear genes. **2013**, 66, 80-90	21
776	Introduction. **2013**, li-liv	8
775	Elongation factor-1�a putative single-copy nuclear gene, has divergent sets of paralogs in an arachnid. **2013**, 68, 471-81	11
774	OTULIN antagonizes LUBAC signaling by specifically hydrolyzing Met1-linked polyubiquitin. **2013**, 153, 1312-26	304
773	Genetic introgression and hybridization in Antillean freshwater turtles (Trachemys) revealed by coalescent analyses of mitochondrial and cloned nuclear markers. **2013**, 67, 176-87	34
772	Mutualism and asexual reproduction influence recognition genes in a fungal symbiont. **2013**, 117, 439-50	2
771	Evolutionary patterns of the mitochondrial genome in the Moorish gecko, Tarentola mauritanica. **2013**, 512, 166-73	3
770	Lipid exposure prediction enhances the inference of rotational angles of transmembrane helices. **2013**, 14, 304	8
769	Human introductions create opportunities for intra-specific hybridization in an alien lizard. **2013**, 15, 1101-1112	19
768	Sequence Classification of Protein Families: Pfam and other Resources. **2013**, 25-36	1
767	Unusual Species Distribution and Horizontal Transfer of Peptidases. **2013**, 285-314	
766	Automatic phylogenetic classification of bacterial beta-lactamase sequences including structural and antibiotic substrate preference information. **2013**, 11, 1343011	
765	Identification of the ubiquitin-like domain of midnolin as a new glucokinase interaction partner. **2013**, 288, 35824-39	26
764	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. **2013**, 7, 2315-29	118

763	Patterns of population structure for inshore bottlenose dolphins along the eastern United States. **2013**, 104, 765-78	21
762	A genomics approach to deciphering lignin biosynthesis in switchgrass. **2013**, 25, 4342-61	80
761	The teleomorph state of Candida deformans Langeron & Guerra and description of Yarrowia yakushimensis comb. nov. **2013**, 103, 1023-8	27
760	Primary symbiont of the ancient scale insect family Coelostomidiidae exhibits strict cophylogenetic patterns. **2013**, 61, 77-91	9
759	Nyctiphanes couchii as intermediate host for Rhadinorhynchus sp. (Acanthocephala, Echinorhynchidae) from NW Iberian Peninsula waters. **2013**, 105, 9-20	21
758	Prediction of protein phosphorylation sites by support vector machines. **2013**,	
757	Differential modes of MHC class IIB gene evolution in cichlid fishes. **2013**, 65, 795-809	8
756	oskaracts with the transcription factor Creb to regulate long-term memory in crickets.	0
755	Evolutionary Analysis of Placental Orthologues Reveals Two Ancient DNA Virus Integrations.	0
754	Glacial Legacies: Microbial Communities of Antarctic Refugia. **2022**, 11, 1440	0
753	Revisiting Papillomavirus Taxonomy: A Proposal for Updating the Current Classification in Line with Evolutionary Evidence. **2022**, 14, 2308	1
752	Conservation priorities for global marine biodiversity across multiple dimensions.	0
751	Tripartite Symbiotic Digestion of Lignocellulose in the Digestive System of a Fungus-Growing Termite.	0
750	Construction of a transposase accessible chromatin landscape reveals chromatin state of repeat elements and potential causal variant for complex traits in pigs. **2022**, 13,	0
749	Crop management shapes the diversity and activity of DNA and RNA viruses in the rhizosphere. **2022**, 10,	0
748	Characterization of Mycobacterium salfingeri sp. nov.: A novel nontuberculous mycobacteria isolated from a human wound infection. 13,	0
747	The evolution and polymorphism of mono-amino acid repeats in androgen receptor and their regulatory role in health and disease. 9,	0
746	Taxonomic assessment of deep-sea decapod crustaceans collected from polymetallic nodule fields of the East Pacific Ocean using an integrative approach. **2022**, 52,	0

745	Soil Microbiome Influences on Seedling Establishment and Growth of Prosopis chilensis and Prosopis tamarugo from Northern Chile. **2022**, 11, 2717	0
744	Sodium acetate/sodium butyrate alleviates lipopolysaccharide-induced diarrhea in mice via regulating the gut microbiota, inflammatory cytokines, antioxidant levels, and NLRP3/Caspase-1 signaling. 13,	0
743	Intrinsic protein disorder uncouples affinity from binding specificity. **2022**, 31,	2
742	Multiple T6SSs, Mobile Auxiliary Modules, and Effectors Revealed in a Systematic Analysis of the Vibrio parahaemolyticus Pan-Genome.	0
741	Akhania, a new genus for Salsola daghestanica, Caroxylon canescens and C. carpathum (Salsoloideae, Chenopodiaceae, Amaranthaceae). 211, 45-61	0
740	Dissecting an island radiation: systematic revision of endemic land snails on Lord Howe Island (Gastropoda: Stylommatophora: Microcystidae).	0
739	Macrobiotus rebecchii sp. nov.: A New Limno-Terrestrial and Hermaphroditic Tardigrade from Kyrgyzstan. **2022**, 12, 2906	0
738	Creating De Novo Overlapped Genes. **2023**, 95-120	0
737	Structure-based screening for functional non-coding RNAs in fission yeast identifies a factor repressing untimely initiation of sexual differentiation.	0
736	Unraveling the Gut Microbiome of the Genus Herichthys (Pisces: Cichlidae): What Can We Learn from Museum Specimens? **2022**, 79,	0
735	The identity ofArgyria lacteella(Fabricius, 1794) (Lepidoptera, Pyraloidea, Crambinae), synonyms, and related species using morphology and DNA capture in type specimens.	0
734	Assessing SARS-CoV-2 evolution through the analysis of emerging mutations.	0
733	Effect of the soil and the landrace rootstock genotype on Hass avocado's rhizosphere bacterial communities.	0
732	The Changes of Microbial Communities and Key Metabolites after Early Bursaphelenchus xylophilus Invasion of Pinus massoniana. **2022**, 11, 2849	0
731	Moderate intakes of soluble corn fibre or inulin do not cause gastrointestinal discomfort and are well tolerated in healthy children. 1-12	0
730	Complete mitochondrial genomes of Boiga kraepelini and Hebius craspedogaster (Reptilia, Squamata, Colubridae) and their phylogenetic implications. 1124, 191-206	0
729	A chromosome-scale assembly ofBrassica carinata(BBCC) accession HC20 containing resistance to multiple pathogens and an early generation assessment of introgressions intoB. juncea(AABB).	1
728	Housekeeping gene gyrA, a potential molecular marker for Bacillus ecology study. **2022**, 12,	1

727	Multiple origins, one evolutionary trajectory: gradual evolution characterizes distinct lineages of allotetraploid Brachypodium.	2
726	Development and validation of two environmental DNA assays for American Eel (Anguilla rostrata).	0
725	Impact of Early Pandemic SARS-CoV-2 Lineages Replacement with the Variant of Concern P.1 (Gamma) in Western Bahia, Brazil. **2022**, 14, 2314	1
724	A new species of crayfish of the genus Cherax from Indonesian New Guinea (Crustacea, Decapoda, Parastacidae). **2022**, 98, 411-425	0
723	The wtf meiotic driver gene family has unexpectedly persisted for over 100 million years. 11,	1
722	Diploid Chromosome-level Reference Genome and Population Genomic Analyses Provide Insights into Gypenoside Biosynthesis and Demographic Evolution of Gynostemma pentaphyllum (Cucurbitaceae).	0
721	Genomic Changes During the Evolution of theCoxiellaGenus Along the Parasitism-Mutualism Continuum.	0
720	ICEscreen: a tool to detect Firmicute ICEs and IMEs, isolated or enclosed in composite structures. **2022**, 4,	2
719	Novel Borrelia Genotypes from Brazil Indicate a New Group of Borrelia spp. Associated with South American Bats.	0
718	Diversities in the Gut Microbial Patterns in Patients with Atherosclerotic Cardiovascular Diseases and Certain Heart Failure Phenotypes. **2022**, 10, 2762	0
717	Gene recruitments and dismissals in the argonaut genome provide insights into pelagic lifestyle adaptation and shell-like eggcase reacquisition.	1
716	Genome-scale analysis of Arabidopsis splicing-related protein kinase families reveals roles in abiotic stress adaptation. **2022**, 22,	0
715	Antiviral function and viral antagonism of the rapidly evolving dynein activating adapter NINL. 11,	0
714	Canine Distemper Virus in Autochtonous and Imported Dogs, Southern Italy (2014�2021). **2022**, 12, 2852	1
713	Translation and natural selection of micropeptides from long non-canonical RNAs. **2022**, 13,	0
712	Mathematical Approach to Protein Sequence Comparison Based on Physiochemical Properties. **2022**, 7, 39446-39455	0
711	Infection with a Recently Discovered Gammaherpesvirus Variant in European Badgers, Meles meles, is Associated with Higher Relative Viral Loads in Blood. **2022**, 11, 1154	0
710	Time-course Biofilm Formation and Presence of Antibiotic Resistance Genes on Everyday Plastic Items Deployed in River Waters. **2022**, 130271	0

709	A new cryptic species of land snail from the Northern Territory, Australia (Stylommatophora, Camaenidae, Parglogenia). **2022**, 98, 427-433	0
708	Diversity of the Bambusicolous Fungus Apiospora in Korea: Discovery of New Apiospora Species. 1-15	0
707	Two new stipitate species of Phylloporia (Basidiomycota, Hymenochaetaceae) from Chamela Biology Station, U.N.A.M. in Jalisco, Mexico. 359-375	0
706	Ancestral sequence reconstruction as a tool to study the evolution of wood decaying fungi. 3,	0
705	Spatially explicit phylogeographical reconstruction sheds light on the history of the forest cover in the Congo Basin.	0
704	Molecular characteristics of a coxsackievirus A12 strain in Zhejiang of China, 2019. **2022**, 19,	0
703	Categorizing 161 plant mitochondrial group II introns into 29 families of related paralogues finds only limited links between intron mobility and intron-borne maturases.	0
702	Thermal Endurance by a Hot-Spring-Dwelling Phylogenetic Relative of the Mesophilic Paracoccus.	0
701	Bioinformatics approaches for classification and investigation of the evolution of the Na/K-ATPase alpha-subunit. **2022**, 22,	0
700	Plastic leachates impair picophytoplankton and dramatically reshape the marine microbiome. **2022**, 10,	0
699	First Report of Wenzhou sobemo-like virus 4 in Aedes albopictus (Diptera: Culicidae) in Latin America. **2022**, 14, 2341	0
698	Ancestral SARS-CoV-2 driven antibody repertoire diversity in an unvaccinated individual correlates with expanded neutralization breadth.	0
697	Genomic Characterisation of Canis Familiaris Papillomavirus Type 24, a Novel Papillomavirus Associated with Extensive Pigmented Plaque Formation in a Pug Dog. **2022**, 14, 2357	0
696	Evolutionary Responses of a Reef-building Coral to Climate Change at the End of the Last Glacial Maximum. **2022**, 39,	0
695	Cecum microbiome and metabolism characteristics of Silky Fowl and White Leghorn chicken in late laying stages. 13,	0
694	Description of Ruehmaphelenchus kuroshioi n. sp. and R. interjectus n. sp. (Tylenchomorpha: Aphelenchoididae) isolated from ambrosia beetles, Euwallacea spp. (Scolytinae), from Japan. **2022**, 1-24	0
693	Complete functional analysis of type IV pilus components of a reemergent plant pathogen reveals neofunctionalization of paralog genes.	0
692	The Parapoynx stagnalis Nucleopolyhedrovirus (PastNPV), a Divergent Member of the Alphabaculovirus Group I Clade, Encodes a Homolog of Ran GTPase. **2022**, 14, 2289	0

691	Genomic epidemiology of the rotavirus G2P[4] strains in coastal Kenya pre- and post-rotavirus vaccine introduction, 2012 2018.	0
690	Genome Evolution of a Symbiont Population for Pathogen Defence in Honeybees.	0
689	Two new species ofCrocusseriesScardicifrom the Western Balkans.	0
688	A new class of polymorphic T6SS effectors and tethers.	1
687	Neolithic genomic data from Southern France showcase intensified interactions with hunter-gatherer communities. **2022**, 105387	0
686	Gene family expansions in Antarctic winged midge as a strategy for adaptation to cold environments. **2022**, 12,	0
685	Variation in plant Toll/Interleukin-1 receptor domain protein dependence on ENHANCED DISEASE SUSCEPTIBILITY 1.	1
684	An expanded arsenal of immune systems that protect bacteria from phages. **2022**,	2
683	Dissemination of metaldehyde catabolic pathways is driven by mobile genetic elements in Proteobacteria. **2022**, 8,	0
682	Divergent functions of two clades of flavodoxin in diatoms mitigate oxidative stress and iron limitation.	0
681	Asgard ESCRT-III and VPS4 reveal conserved chromatin binding properties of the ESCRT machinery.	1
680	Multi-phenotype analysis for enhanced classification of 11 herpes simplex virus 1 strains. **2022**, 103,	0
679	Life-history traits drive spatial genetic structuring in Dinaric cave spiders. 10,	0
678	Genetic diversity and evolutionary convergence of cryptic SARS- CoV-2 lineages detected via wastewater sequencing. **2022**, 18, e1010636	1
677	The chloroplast genome of the Iris japonica Thunberg (Butterfly flower) reveals the genomic and evolutionary characteristics of Iris species. **2022**, 7, 1776-1782	0
676	The complete chloroplast genome of Rhododendron shanii W.P. Fang (Ericaceae), a endemic plant from the Southern Dabie Mountains of China. **2022**, 7, 1787-1788	0
675	Logistic Regression-Guided Identification of Cofactor Specificity-Contributing Residues in Enzyme with Sequence Datasets Partitioned by Catalytic Properties.	0
674	Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation.	0

673	The fifth family of the true crickets (Insecta: Orthoptera: Ensifera: Grylloidea), Oecanthidae defin. nov.: phylogenetic relationships and divergence times.	0
672	Pseudomonas californiensis sp. nov. and Pseudomonas quasicaspiana sp. nov., isolated from ornamental crops in California. **2022**, 72,	0
671	Genetic diversity and variation in antimicrobial-resistance determinants of non-serotype 2 Streptococcus suis isolates from healthy pigs. **2022**, 8,	0
670	The composition and natural variation of the skin microbiota in healthy Australian cattle.	0
669	Biogeographical events, not cospeciation, might be the main drivers in the historical association between Noctiliostrebla species (Streblidae) and their bulldog bat hosts.	0
668	Complex host/symbiont integration of a multi-partner symbiotic system in the eusocial aphid Ceratovacuna japonica. **2022**, 105478	0
667	Blue turns to grey - Palaeogenomic insights into the evolutionary history and extinction of the blue antelope (Hippotragus leucophaeus).	0
666	Impact of host age on viral and bacterial communities in a waterbird population.	0
665	Soil properties rather than plant diversity mediate the response of soil bacterial community to N and P additions in an alpine meadow. 13,	0
664	Extensive recombination-driven coronavirus diversification expands the pool of potential pandemic pathogens.	0
663	H2S responsive PEGylated poly (lipoic acid) with ciprofloxacin for targeted therapy of Salmonella. **2022**, 351, 896-906	0
662	Antigenic Characterization and Pandemic Risk Assessment of North American H1 Influenza A Viruses Circulating in Swine.	0
661	Not just for the birds: Spiders as natural enemies of spruce budworm (Choristoneura fumiferana , Clem.).	0
660	Responsiveness to pulmonary rehabilitation in people with COPD is associated with changes in microbiota.	0
659	Multiple lineages of monkeypox virus detected in the United States, 2021�2022. **2022**, 378, 560-565	7
658	Methanotrophy by a Mycobacterium species that dominates a cave microbial ecosystem.	0
657	First rhyncaphytoptine mite (Eriophyoidea, Diptilomiopidae) parasitizing American hazelnut (Corylus americana): molecular identification, confocal microscopy, and phylogenetic position.	1
656	A western representative of an eastern clade: Phylogeographic history of the gypsum-associated plant Nepeta hispanica. **2022**, 57, 125699	0

655	Multiple Sequence Alignment based on deep Q network with negative feedback policy. **2022**, 101, 107780	0
654	Detection at high prevalence of newlavirus (protoparvovirus) in the carcasses of red foxes. **2023**, 323, 198971	0
653	Genome-wide analysis of the CSN genes in land plants and their expression under various abiotic stress and phytohormone conditions in rice. **2023**, 850, 146905	0
652	Gut microbiota impairment following graphene oxide exposure is associated to physiological alterations in Xenopus laevis tadpoles. **2023**, 857, 159515	0
651	Mitogenome of a monotypic genus, Oliotius Kottelat, 2013 (Cypriniformes: Cyprinidae): Genomic characterization and phylogenetic position. **2023**, 851, 147035	1
650	In silico study identifies peptide inhibitors that negate the effect of non-synonymous mutations in major drug targets of SARS-CoV-2 variants. 1-11	0
649	An RFX transcription factor regulated ciliogenesis in the progenitors of choanoflagellates and animals.	0
648	Chromosome-scale genome assembly of the African giant pouched rat (Cricetomys ansorgei) and evolutionary analysis reveals evidence of olfactory specialization. **2022**, 114, 110521	0
647	Is the Intergenic Region of Aedes aegypti Totivirus a Recombination Hotspot?. **2022**, 14, 2467	0
646	Swiss public health measures associated with reduced SARS-CoV-2 transmission using genome data.	0
645	Australian native Glycine clandestina seed microbiota hosts a more diverse bacterial community than the domesticated soybean Glycine max. **2022**, 17,	0
644	Initiation of speciation across multiple dimensions in a rock-restricted, tropical lizard.	1
643	Building a foundation for gene family analysis in Rosaceae genomes with a novel workflow: A case study in Pyrus architecture genes. 13,	0
642	Asplenium pseudocapillipes (Aspleniaceae), a New Fern Species from South Korea. **2022**, 11, 3089	0
641	Long-read genome assemblies reveals acis-regulatory landscape associated with phenotypic divergence in two sisterSinipercafishes.	0
640	Hypo-Osmoregulatory Roles of Vasotocinergic and Isotocinergic Systems in the Intestines of Two European Sea Bass Lineages. **2022**, 23, 13636	0
639	Characterization and phylogenetic analysis of the complete mitochondrial genome of Aythya marila.	0
638	Complete Mitogenome of Oreolalax Omeimontis Reveals Phylogenetic Status and Novel Gene Arrangement of Archaeobatrachia. **2022**, 13, 2089	0

637	Multilocus evidence provides insight into the demographic history and asymmetrical gene flow between Ostrinia furnacalis and Ostrinia nubilalis (Lepidoptera: Crambidae) in the Yili area, Xinjiang, China. **2022**, 12,	0
636	On Classification and Taxonomy of Coronaviruses (Riboviria, Nidovirales, Coronaviridae) with Special Focus on Severe Acute Respiratory Syndrome-Related Coronavirus 2 (SARS-CoV-2). **2022**, 17, 289-311	0
635	The complete chloroplast genome sequences of eight Orostachys species: Comparative analysis and assessment of phylogenetic relationships. **2022**, 17, e0277486	0
634	Reconstitution of an N-AChR from Brugia malayi an evolved change in acetylcholine receptor accessory protein requirements in filarial parasites. **2022**, 18, e1010962	0
633	An image cryptography method in highly error-prone DNA storage channel.	0
632	Gene family evolution and natural selection signatures in Datura spp. (Solanaceae). 10,	0
631	Structures of the Ndc80 complex and its interactions at the yeast kinetochore-microtubule interface.	1
630	Effect of a Novel E3 Probiotics Formula on the Gut Microbiome in Atopic Dermatitis Patients: A Pilot Study. **2022**, 10, 2904	0
629	A 40 % paddy surface soil organic carbon increase after 5-year no-tillage is linked with shifts in soil bacterial composition and functions. **2022**, 160206	0
628	Evolutionary gain and loss of a plant pattern-recognition receptor for HAMP recognition. 11,	1
627	Penicillium polonicum a new isolate obtained from Cerrado soil as a source of carbohydrate-active enzymes produced in response to sugarcane bagasse. **2022**, 12,	0
626	Characterization of a xylanase belonging to the glycoside hydrolase family 5 subfamily 35 from Paenibacillus sp. H2C.	0
625	Design principles of caveolins across metazoa and beyond.	0
624	First record of sponge-associated deep-sea polychaete (Polynoidae: Bathymoorea) on the ultraslow-spreading Southwest Indian Ridge. **2022**, 103923	0
623	Microbiome diversity and metabolic capacity determines the trophic ecology of the holobiont in Caribbean sponges. **2022**, 2,	1
622	Plastid phylogenomic insights into relationships, divergence, and evolution of Apiales. **2022**, 256,	0
621	Genome-wide mutational analysis of Chikungunya strains from 2016 to 2017 outbreak of central India: An attempt to elucidate the immunological basis for outbreak. **2022**, 8, e11400	0
620	Insights into Genomic Evolution and the Potential Genetic Basis of Klebsiella variicola subsp. variicola ZH07 Reveal Its Potential for Plant Growth Promotion and Autotoxin Degradation.	0

619	Pseudomonas aegrilactucae sp. nov. and Pseudomonas morbosilactucae sp. nov., pathogens causing bacterial rot of lettuce in Japan. **2022**, 72,	0
618	Monogeneans and chubs: ancient host-parasite system under the looking glass. **2022**, 107667	0
617	Cross-generational bacterial strain transfer to an infant after fecal microbiota transplantation to a pregnant patient: a case report. **2022**, 10,	0
616	Prevalence, Infection Intensity and Molecular Diagnosis of Mixed Infections with Metastrongylus spp. (Metastrongylidae) in Wild Boars in Uzbekistan. **2022**, 11, 1316	0
615	Integrative taxonomy helps to revise systematics and questions the purported cosmopolitan nature of the type species within the genus Diaforobiotus (Eutardigrada: Richtersiusidae).	0
614	Identification of a 17▯estradiol-degrading Microbacterium hominis SJTG1 With High Adaptability and Characterization of the Genes for Estrogen Degradation. **2022**, 130371	0
613	Large clones of pre-existing T cells drive early immunity against SARS-COV-2 and LCMV infection.	0
612	Phylogenomics reveals deep relationships and diversification within phylactolaemate bryozoans. **2022**, 289,	1
611	The red seaweed Asparagopsis taxiformis genome and integrative -omics analysis.	1
610	Co-evolving pairs of complementary nucleotide sequence regions containing compensatory divergences and polymorphisms in rotavirus genomes. **2022**, 29, 101709	0
609	Colonic innate immune defenses and microbiota alterations in acute swine dysentery. **2022**, 173, 105873	0
608	Comparative analyses of the complete mitochondrial genomes of two southern African endemic guitarfish, Acroteriobatus annulatus and A. blochii. **2022**, 223, 1094-1106	0
607	Exposure to diesel exhaust alters the functional metagenomic composition of the airway microbiome in former smokers. **2022**, 114826	0
606	Exploring new antiviral targets for influenza and COVID-19: Mapping promising hot spots in viral RNA polymerases. **2022**,	0
605	A widespread group of large plasmids in methanotrophic Methanoperedens archaea. **2022**, 13,	1
604	Sequencing of Camelina neglecta, a diploid progenitor of the hexaploid oilseed Camelina sativa.	0
603	Vibrio parahaemolyticusT6SS2 effector repertoires.	0
602	Characterization of the Chloroplast Genome Structure of Gueldenstaedtia verna (Papilionoideae) and Comparative Analyses among IRLC Species. **2022**, 13, 1942	0

601	Characterizing a century of genetic diversity and contemporary antigenic diversity of N1 neuraminidase in IAV from North American swine.	1
600	Population genomics reveals mechanisms and dynamics of de novo proto-gene emergence in Drosophila melanogaster.	0
599	An integrative study of Pannaria hookeri (Ascomycota lichenized) from Argentina and the update of the taxon circumscription based on specimens from the Northern and Southern Hemispheres. 36,	0
598	First description of archaeal communities in carbonate-rich seafloor and subseafloor sediments from the Southwestern Atlantic slope. **2022**, 70,	2
597	CUTIS-SEQ, a flexible bilocus sequence typing scheme that provides high resolution of Cutibacterium acnes strains across all subspecies. **2023**, 79, 102671	0
596	Genomic organization and gene evolution of two warm temperature acclimation proteins (Wap65s) of Micropterus salmoides and their responses to temperature and bacterial/viral infections. **2023**, 227, 340-353	0
595	Structural and functional analyses of chitinolytic enzymes in the nacreous layer of Pinctada fucata. **2023**, 191, 108780	0
594	Xenobiotic-induced ribosomal stress compromises dysbiotic gut barrier aging: A one health perspective. **2023**, 59, 102565	0
593	Analysis of SARS-CoV-2 genomic surveillance data during the Delta and Omicron waves at a Saudi tertiary referral hospital. **2023**, 16, 171-181	0
592	Molecular epidemiology of Trichophyton infections among canines from Northern India. **2023**, 33, 101352	0
591	Structural evolution of an amphibian-specific globin: A computational evolutionary biochemistry approach. **2023**, 45, 101055	0
590	Response of a temperate coral to temperature stress: A comparison of populations across sites. **2023**, 560, 151863	0
589	Habitat matters: The role of spore bank fungi in early seedling establishment of Florida slash pines. **2023**, 62, 101210	0
588	Prediction and verification of glycosyltransferase activity by bioinformatics analysis and protein engineering. **2023**, 4, 101905	0
587	Characterisation of the photosynthetic complexes from the marine gammaproteobacterium Congregibacter litoralis KT71. **2023**, 1864, 148946	0
586	Diversity in Expression Biases of Lineage-Specific Genes During Development and Anhydrobiosis Among Tardigrade Species. **2022**, 18, 117693432211402	0
585	Towards Privacy-Preserving Computation on Gene: Construct Covid-19 Phylogenetic Tree using Homomorphic Encryption. **2022**,	0
584	Piglet cardiopulmonary bypass induces intestinal dysbiosis and barrier dysfunction associated with systemic inflammation.	0

583	Host translation machinery is not a barrier to phages that infect both CPR and non-CPR bacteria.	0
582	Human Alu elements promote the establishment and enhancement of piRNA-protein-coding gene targeting relationships.	0
581	Selective isolation of Arctic marine actinobacteria and a down-scaled fermentation and extraction strategy for identifying bioactive compounds. 13,	0
580	Comparative analyses of three complete Primula mitogenomes with insights into mitogenome size variation in Ericales. **2022**, 23,	0
579	Carnivore protoparvovirus 1 (CPV-2 and FPV) Circulating in Wild Carnivores and in Puppies Illegally Imported into North-Eastern Italy. **2022**, 14, 2612	0
578	Assessment of the phylogenetic relationships within the spondylidine branch of Spondylidinae (Coleoptera, Cerambycidae). **2022**, 1-31	0
577	Kazak mitochondrial genomes provide insights into the human population history of Central Eurasia. **2022**, 17, e0277771	0
576	Climate Relicts: Asian Scorpion Family Pseudochactidae Survived Miocene Aridification in Caves of the Annamite Mountains. **2022**, 6,	0
575	A further step towards the characterisation of Terebellides (Annelida, Trichobranchidae) diversity in the Northeast Atlantic, with the description of a new species. 1132, 85-126	0
574	Molecular characterization and phylogenetic analysis of Argas persicus (Oken, 1818) (Acari: Argasidae) from domestic birds in eastern Algeria.	0
573	Characteristic alterations of gut microbiota in uncontrolled gout. **2022**, 60, 1178-1190	2
572	The compact genome of Caenorhabditis niphades n. sp., isolated from a wood-boring weevil, Niphades variegatus. **2022**, 23,	0
571	Throughput screening of Bacillus subtilis strains that abundantly secrete surfactin in vitro identifies effective probiotic candidates. **2022**, 17, e0277412	0
570	The virome of the invasive Asian bush mosquitoAedes japonicusin Europe.	0
569	The association of hyperketonemia with fecal and rumen microbiota at time of diagnosis in a case-control cohort of early lactation cows. **2022**, 18,	0
568	Whole-genome scanning reveals environmental selection mechanisms that shape diversity in populations of the epipelagic diatom Chaetoceros. **2022**, 20, e3001893	0
567	Phylogenomics and the flowering plant tree of life.	1
566	Identification of Novel Bile Salt-Tolerant Genes in Lactobacillus Using Comparative Genomics and Its Application in the Rapid Screening of Tolerant Strains. **2022**, 10, 2371	1

565	Phylogeny of the asexual lineage Murrayidae (Macrobiotoidea, Eutardigrada) with the description of. **2022**, 36, 1099-1117	0
564	Changes in soil properties and the phoD-harboring bacteria of the alfalfa field in response to phosphite treatment. 13,	0
563	Deep Learning for Predicting 16S rRNA Copy Number.	0
562	Homoplasy in shells discombobulated the taxonomy: revision of the larger helicarionid land snails of northern Queensland, Australia (Stylommatophora: Helicarionidae). **2022**, 56, 1727-1799	0
561	Untying the Gordian knot of plastid phylogenomic conflict: A case from ferns. 13,	0
560	Horizontal transfer of tRNA genes to mitochondrial plasmids facilitates gene loss from fungal mitochondrial DNA.	0
559	Community phylogeny and spatial scale affect phylogenetic diversity metrics in a species-rich rainforest in Borneo. **2022**, 12,	0
558	Ribosomal RNA operons define a central functional compartment in the Streptomyces chromosome. **2022**, 50, 11654-11669	0
557	A new Paleogene fossil and a new dataset for waterfowl (Aves: Anseriformes) clarify phylogeny, ecological evolution, and avian evolution at the K-Pg Boundary.	0
556	Evolution and regulation of microbial secondary metabolism. 11,	0
555	Development of Single Nucleotide Polymorphism Markers for the Autotetraploid Scaphirhynchus Sturgeons (Acipenseriformes).	0
554	Effect of probiotics for regulation of inflammatory response in radiation-induced enteritis.	0
553	A multivalent nucleoside-modified mRNA vaccine against all known influenza virus subtypes. **2022**, 378, 899-904	4
552	Improving orthologous signal and model fit in datasets addressing the root of the animal phylogeny.	0
551	Detection and Characterization of a Novel Picornavirus in European Badger (Meles meles). **2022**, 9, 645	0
550	Identifying magnetosome-associated genes in the extended CtrA regulon in Magnetospirillum magneticum AMB-1 using a combinational approach.	0
549	Reviving and characterizing three species of dinoflagellate cysts dormant for about 70 years in the East China Sea: Biecheleria brevisulcata, Biecheleriopsis adriatica, and Scrippsiella donghaienis.	0
548	Acetylation of nuclear receptors in health and disease: an update.	0

547 Assembly of 43 diverse human Y chromosomes reveals extensive complexity and variation. ○

546 Snf2 Proteins Are Required to Generate Gamete Pronuclei in Tetrahymena thermophila. **2022**, 10, 2426 ○

545 SPLACE: A tool to automatically SPLit, Align, and ConcatenatE genes for phylogenomic inference of several organisms. 2, ○

544 Dismantling and reorganising Pseudomonas marginalis sensu lato. ○

543 Detecting Horizontal Transfer of Transposons. **2023**, 45-62 ○

542 Analysis of a Dengue Virus Outbreak in Rosso, Senegal 2021. **2022**, 7, 420 ○

541 Machine learning assisted ligand binding energy prediction forin silicogenerated glycosyl hydrolase enzyme combinatorial mutant library. ○

540 Root-Zone Restriction Regulates Soil Factors and Bacterial Community Assembly of Grapevine. **2022**, 23, 15628 ○

539 Two New Uromunna Species (Isopoda: Asellota: Munnidae) from the Korean Peninsula and Their Phylogenetic Position within Munnoid Groups. **2023**, 15, 20 ○

538 Small-sporedAlternariaspp. (sectionAlternaria) are common pathogens on wild tomato species. ○

537 Massive sequencing of the V3–V4 hypervariable region of bronchoalveolar lavage from patients with COVID-19 and VAP reveals the collapse of the pulmonary microbiota. **2022**, 71, ○

536 Bacterial diversity across four drinking water distribution systems in Croatia: impacts of water management practices and disinfection by-products. **2022**, 99, ○

535 Deep divergence and genomic diversification of gut symbionts of neotropical stingless bees. ○

534 Experimental and computational analysis of the ancestry of an evolutionary young enzyme from histidine biosynthesis. ○

533 Epidemiological and Genomic Analysis of a Large SARS-CoV-2 Outbreak in a Long-Term Care Facility in Catalonia, Spain. **2022**, 7, ○

532 Tracing the First Days of the SARS-CoV-2 Pandemic in Greece and the Role of the First Imported Group of Travelers. **2022**, 10, ○

531 Identification and characterization of novel lineage 1 Powassan virus strains in New York State. **2023**, 12, ○

530 How elevated nitrogen load affects bacterial community structure and nitrogen cycling services in coastal water. 13, ○

529	Microsporidians (Microsporidia) parasitic on mosquitoes (Culicidae) in central Europe are often multi-host species. **2022**, 107873	0
528	Cuticle chemistry drives the development of diffraction gratings on the surface of Hibiscus trionum petals. **2022**, 32, 5323-5334.e6	0
527	Micronutrient Biosynthesis Potential of Spontaneous Grain Fermentation Microbiomes. **2022**, 19, 16621	0
526	The composition and function of the soil microbial community and its driving factors before and after cultivation of Panax ginseng in farmland of different ages. **2022**, 145, 109748	0
525	Investigating graph neural network for RNA structural embedding.	0
524	Conserved Double Translation Initiation Site for □160p53 Protein Hints at Isoform□ Key Role in Mammalian Physiology. **2022**, 23, 15844	0
523	Fine-mapping and comparative genomic analysis reveal the gene composition at the S and Z self-incompatibility loci in grasses.	0
522	Forest Gaps Modulate the Composition and Co-Occurrence Network of Soil Bacterial Community in Larix principis-rupprechtii Mayr Plantation. **2023**, 13, 38	0
521	Comprehensive profiling of antibody responses to the human anellome using programmable phage display. **2022**, 41, 111754	0
520	Assembly and Annotation of Red Spruce (Picea rubens) Chloroplast Genome, Identification of Simple Sequence Repeats, and Phylogenetic Analysis in Picea. **2022**, 23, 15243	0
519	Micro-fractionation shows microbial community changes in soil particles below 20 □m. 10,	0
518	Comparing T cell receptor repertoires using optimal transport. **2022**, 18, e1010681	0
517	Atmospheric hydrogen oxidation extends to the domain archaea.	0
516	A metabarcoding framework for wild bee assessment in Luxembourg. 94, 215-246	0
515	Multiplex detection of meningitis and encephalitis pathogens: A study from laboratory to clinic. 13,	0
514	Targeted single-cell genomics reveals novel host adaptation strategies of the symbiotic bacteria Endozoicomonas in Acropora tenuis coral. **2022**, 10,	0
513	Rapid molecular diversification and homogenization of clustered major ampullate silk genes in Argiope garden spiders. **2022**, 18, e1010537	0
512	Heritability of tomato rhizobacteria resistant to Ralstonia solanacearum. **2022**, 10,	1

511	Pan-kinome of Legionella expanded by a bioinformatics survey. **2022**, 12,	1
510	Global soil metagenomics reveals ubiquitous yet previously-hidden predominance ofDeltaproteobacteriain nitrogen-fixing microbiome.	0
509	The Hercules pseudoscorpions from Madagascar: A systematic study of Feaellidae (Pseudoscorpiones: Feaelloidea) highlights regional endemism and diversity in one of the □hottest□ biodiversity hotspots. 80, 649-691	0
508	Out of Asia? Expansion of Eurasian Lyme borreliosis causing genospecies display unique evolutionary trajectories.	0
507	A chromosome-level genome assembly reveals genomic characteristics of the American mink (Neogale vison). **2022**, 5,	0
506	Specific Enriched Acinetobacter in Camellia Weevil Gut Facilitate the Degradation of Tea Saponin: Inferred from Bacterial Genomic and Transcriptomic Analyses. **2022**, 10,	0
505	An application of morphological analysis and DNA barcoding to identify Ipnops from the Clarion-Clipperton Zone (CCZ) as I. meadi Nielsen, 1966 with notes on other species of the genus (Aulopiformes: Ipnopidae). **2022**, 52,	0
504	Deep photoautotrophic prokaryotes contribute substantially to carbon dynamics in oxygen-deficient waters in a permanently redox-stratified freshwater lake.	0
503	A refined characterization of large-scale genomic differences in the first complete human genome.	0
502	The unheeded existence of the tubular greens: molecular analyses reveal the distribution of a new Ulva species (Ulvophyceae, Chlorophyta), Ulva capillata sp. nov. in the Atlantic-Baltic Sea transect.	0
501	Conjectures and refutations: Species diversity and phylogeny of Australoheros from coastal rivers of southern South America (Teleostei: Cichlidae). **2022**, 17, e0261027	0
500	DNA Authentication and Chemical Analysis of Psilocybe Mushrooms Reveal Widespread Misdeterminations in Fungaria and Inconsistencies in Metabolites. **2022**, 88,	0
499	Dietary supplementation with Mexican foods, Opuntia ficus indica, Theobroma cacao, and Acheta domesticus: Improving obesogenic and microbiota features in obese mice. 9,	0
498	The bacteria of Yangtze finless porpoise (Neophocaena asiaeorientalis asiaeorientalis) are site-specific and distinct from freshwater environment. 13,	0
497	Maternal Mycobiome, but Not Antibiotics, Alters Fungal Community Structure in Neonatal Piglets. **2022**, 88,	0
496	Mapping HPV 16 Sub-Lineages in Anal Cancer and Implications for Disease Outcomes. **2022**, 12, 3222	0
495	Abyssal fauna of polymetallic nodule exploration areas, eastern Clarion-Clipperton Zone, central Pacific Ocean: Amphinomidae and Euphrosinidae (Annelida, Amphinomida). 1137, 33-74	0
494	Key amino acid position 272 in neuraminidase determines the replication and virulence of H5N6 avian influenza virus in mammals. **2022**, 25, 105693	0

493	Molecular characterization of circulating Dengue virus 2 during an outbreak in Northern Senegal's Saint-Louis region in 2018. **2023**, 95,	0
492	Comparison of bacterial community structure in PM2.5 during hazy and non-hazy periods in Guilin, South China.	0
491	Network Science and Group Fusion Similarity-Based Searching to Explore the Chemical Space of Antiparasitic Peptides. **2022**, 7, 46012-46036	1
490	Analysis of the ARTIC V4 and V4.1 SARS-CoV-2 primers and their impact on the detection of Omicron BA.1 and BA.2 lineage defining mutations.	0
489	Kombuchas from Green and Black Tea Modulate the Gut Microbiota and Improve the Intestinal Health of Wistar Rats Fed a High-Fat High-Fructose Diet. **2022**, 14, 5234	1
488	Genomic epidemiology of SARS-CoV-2 in Cambodia, January 2020 to February 2021.	0
487	New Insights into Lymphocystis Disease Virus Genome Diversity. **2022**, 14, 2741	1
486	Dynamic Monitoring of Changes in Fecal Flora of Giant Pandas in Mice: Co-Occurrence Network Reconstruction.	0
485	Crop rotation increases root biomass and promotes the correlation of soil dissolved carbon with the microbial community in the rhizosphere. 10,	0
484	Molecular determinants of inhibition of UCP1-mediated respiratory uncoupling.	0
483	Changes of bacterial communities in restored Phragmites australis wetlands indicated the improvement of soil in the Yellow River Delta.	0
482	A highly quality genome sequence of Penicillium oxalicum species isolated from the root of Ixora chinensis in Vietnam.	0
481	Ecological and evolutionary patterns of virus-host interactions throughout a grassland soil depth profile.	0
480	Dissimilatory iron reduction contributes to anaerobic mineralization of sediment in a shallow transboundary lake. **2022**,	0
479	Jack of all trades: Genome assembly of Wild Jack and comparative genomics of Artocarpus. 13,	0
478	The Macrobiotus persimilis-polonicus complex (Eutardigrada, Macrobiotidae), another example of problematic species identification, with the description of four new species.	0
477	A Novel Trichothecene Toxin Phenotype Associated with Horizontal Gene Transfer and a Change in Gene Function in Fusarium. **2023**, 15, 12	0
476	Candida khanbhaisp. nov., a new clinically relevant yeast within theCandida haemuloniispecies complex.	0

475	Building Quantitative Bridges between Dynamics and Sequences of SARS-CoV-2 Main Protease and a Diverse Set of Thirty-Two Proteins.	0
474	A new eyeless species of Nereis (Annelida, Nereididae) from deep-sea sediments of the northern South China Sea. 1134, 23-37	0
473	The novel compound heterozygous rare variants may impact positively selected regions of TUBGCP6, a microcephaly associated gene. 10,	0
472	Two canonically aerobic foraminifera express distinct peroxisomal and mitochondrial metabolisms. 9,	0
471	Phylogenomics and the first higher taxonomy of Placozoa, an ancient and enigmatic animal phylum. 10,	0
470	Carotene suppresses cancer cachexia by regulating the adipose tissue metabolism and gut microbiota dysregulation. **2022**, 109248	0
469	Phylogenomics of the psychoactive mushroom genusPsilocybeand evolution of the psilocybin biosynthetic gene cluster.	0
468	Unsupervised outlier detection applied to SARS-CoV-2 nucleotide sequences can identify sequences of common variants and other variants of interest. **2022**, 23,	0
467	Detection of A-to-I microRNA editing with miRmedon reveals widespread co-editing of mature microRNA in the human brain.	0
466	Molecular characterization of a novel Victorivirus (Gharbivirales: Totiviridae) infecting Metarhizium anisopliae.	0
465	To explore strange new worlds the diversification in Tremella caloplacae was linked to the adaptive radiation of the Teloschistaceae. **2022**, 107680	0
464	Antimicrobial Activity of Tannic Acid In Vitro and Its Protective Effect on Mice against Clostridioides difficile.	0
463	Epizootic Haemorrhagic Disease Virus Serotype 8 in Tunisia, 2021. **2023**, 15, 16	0
462	Whole genome analysis of clouded leopard species reveals an ancient divergence and distinct demographic histories. **2022**, 25, 105647	0
461	The gut microbiota and depressive symptoms across ethnic groups. **2022**, 13,	1
460	Phylogenetic Position of Centroglossa and Dunstervillea (Ornithocephalus Clade: Oncidiinae: Orchidaceae) Based on Molecular and Morphological Data. **2022**, 47, 927-937	0
459	The complete mitochondrial genome of Coccotorus beijingensis Lin et Li, 1990 (Coleoptera, Curculionidae, Curculioninae, Anthonomini) and its phylogenetic implications. 10,	0
458	Compact Cas9d and HEARO enzymes for genome editing discovered from uncultivated microbes. **2022**, 13,	0

457	Discovery and functional characterization of neuropeptides in crinoid echinoderms. 16,	0
456	Response to the detection of an exotic fungal pathogen, Fusarium commune, in a Pinus radiata production nursery in Australia. 1-12	1
455	Microbiome-mediated fructose depletion restricts murine gut colonization by vancomycin-resistant Enterococcus. **2022**, 13,	0
454	Climate warming triggers the emergence of native viruses in Iberian amphibians. **2022**, 25, 105541	0
453	A New Endemic Species of Loasa ser. Macrospermae (Loasaceae) from Northern Chile. **2022**, 47, 1065-1079	0
452	WiChR, a highly potassium-selective channelrhodopsin for low-light one- and two-photon inhibition of excitable cells. **2022**, 8,	1
451	Expression and function of an S1-type nuclease in the digestive fluid of a sundew Drosera adelae.	0
450	Reekeekee- and roodoodooviruses, two different Microviridae clades constituted by the smallest DNA phages.	0
449	A morphological basis for path dependent evolution of visual systems.	0
448	Rapid detection of DNA and RNA shrimp viruses using CRISPR-based diagnostics.	0
447	Using axenic and gnotobiotic insects to examine the role of different microbes on the development and reproduction of the kissing bug Rhodnius prolixus (Hemiptera: Reduviidae).	0
446	Identification of Genetic Markers for the Detection of Bacillus thuringiensis Strains of Interest for Food Safety. **2022**, 11, 3924	0
445	Complete mitochondrial genome of Appasus japonicus Vuillefroy, 1864 (Hemiptera: Belostomatidae). **2022**, 7, 2048-2050	0
444	Identification of a conserved maxicircle and unique minicircles as part of the mitochondrial genome of Leishmania martiniquensis strain PCM3 in Thailand. **2022**, 15,	0
443	Additional Taxonomic Information for Lamproglena hemprichii (Copepoda: Lernaeidae) Based on Scanning Electron Microscopy and Genetic Characterization, Alongside Some Aspects of Its Ecology. **2022**, 40,	0
442	Complete chloroplast genome sequence of Adenostemma madurense (Asteraceae). **2023**,	0
441	Wild emmer wheat, the progenitor of modern bread wheat, exhibits great diversity in the VERNALIZATION1 gene. 13,	0
440	Complete mitochondrial genome of Macromia manchurica Asahina, 1964 (Odonata: Macromiidae). **2023**, 8, 10-12	0

439	Evolutionary dynamics of sex-biased gene expression in a young XY system: Insights from the brown alga genus Fucus.	0
438	The nucleoprotein of influenza A virus inhibits the innate immune response by inducing mitophagy. 1-18	0
437	Genome Update for Pseudomonas fluorescens Isolate SBW25.	0
436	Genome-wide association and RNA-seq analyses identify loci for pod orientation in rapeseed (Brassica napus). 13,	0
435	Genome-scale angiosperm phylogenies based on nuclear, plastome, and mitochondrial datasets.	0
434	Characterization of the complete chloroplast genome of the important herbal medicinal plant, Thymus quinquecostatus (Lamiaceae). **2023**,	0
433	Rapid Identification of Relevant Microbial Strains by Identifying Multiple Marker Single Nucleotide Polymorphisms via Amplicon Sequencing: Epidemic Monkeypox Virus as a Proof of Concept.	0
432	Mechanism of Enhancing Pyrazines in Daqu via Inoculating Bacillus licheniformis with Strains Specificity. **2023**, 12, 304	0
431	Heritable maize microbiomes contribute to local adaptation and host stress resilience.	0
430	Exploring the mechanism of regulating the microbial community and metabolizing trait in Chinese Baijiu fermentation via Huizao. **2023**, 174, 114445	0
429	HIV and SARS-CoV-2 infection in postpartum Kenyan women and their infants. **2023**, 18, e0278675	0
428	Improving Orthologous Signal and Model Fit in Datasets Addressing the Root of the Animal Phylogeny. **2023**, 40,	0
427	Cryptic, sibling or neither of the two? Integrative species delimitation of Psylliodes flea beetles with overlapping ranges.	0
426	Emergence of an Auxin Sensing Domain in Plant-Associated Bacteria.	0
425	Mosquito vector competence for dengue is modulated by insect-specific viruses. **2023**, 8, 135-149	0
424	The BacteriophagePhage-Inducible Chromosomal Island Arms Race Designs an Interkingdom Inhibitor of dUTPases.	0
423	The submandibular and sublingual glands maintain oral microbial homeostasis through multiple antimicrobial proteins. 12,	0
422	Into the darkness of the microbial dark matter in situ activities through expression profiles of Patescibacteria populations. 13,	0

421	The gestational membrane microbiome in the presence or absence of intraamniotic infection. **2023**, 100837	0
420	Influence of structural features and feruloylation on fermentability and ability to modulate gut microbiota of arabinoxylan in in vitro fermentation. 13,	0
419	Biased mutations and gene losses underlying diploidization of the tetraploid broomcorn millet genome.	0
418	Cosmopolitan abyssal lineages? A systematic study of East Pacific deep-sea squat lobsters (Decapoda: Galatheoidea: Munidopsidae). **2023**, 37, 14	0
417	The DNA Phosphorothioation Restriction-Modification System Influences the Antimicrobial Resistance of Pathogenic Bacteria.	0
416	Overexpression of Liriodenron´WOX5 in Arabidopsis Leads to Ectopic Flower Formation and Altered Root Morphology. **2023**, 24, 906	0
415	Rapid and Flexible RT-qPCR Surveillance Platforms To Detect SARS-CoV-2 Mutations.	0
414	Endophytic fungi related to the ash dieback causal agent encode signatures of pathogenicity on European ash.	0
413	Genomic Analysis of the Suspicious SARS-CoV-2 Sequences in the Public Sequencing Database.	0
412	Microbiome and hydraulic performance changes of drinking water biofilters during disruptive events-media replacement, lake diatom bloom, and chlorination.	0
411	The role of the gut microbiota in patients with Kleefstra syndrome.	0
410	Domestic Cat Hepadnavirus: Molecular Epidemiology and Phylogeny in Cats in Hong Kong. **2023**, 15, 150	0
409	A novel picorna-like virus identified in the cotton boll weevil Anthonomus grandis (Coleoptera: Curculionidae). **2023**, 168,	0
408	Diversity and prevalence of type VI secretion system effectors in clinical Pseudomonas aeruginosa isolates. 13,	0
407	Haemosporidians in Non-Passerine Birds of Colombia: An Overview of the Last 20 Years of Research. **2023**, 15, 57	0
406	Modular transcriptional responses to environmental changes.	0
405	Distribution and Prevalence of Theileria orientalis Genotypes in Adult Lactating Dairy Cows in South West Region of Western Australia. **2023**, 12, 125	0
404	Variability in Nutrient Use by Orchid Mycorrhizal Fungi in Two Medium Types. **2023**, 9, 88	0

403	Chromosome genome assembly for the meagre, Argyrosomus regius, reveals species adaptations and sciaenid sex-related locus evolution. 13,	0
402	Assembly, annotation, and comparative analysis of Ipomoea chloroplast genomes provide insights into the parasitic characteristics of Cuscuta species. 13,	0
401	Effects of access to feed, water, and a competitive exclusion product in the hatcher on some immune traits and gut development in broiler chickens.	0
400	Complex multiple introductions drive fall armyworm invasions into Asia and Australia. **2023**, 13,	0
399	Effects of Five Consecutive Years of Fallow Tillage on Soil Microbial Community Structure and Winter Wheat Yield. **2023**, 13, 224	0
398	Blood parasites (Trypanosoma, Leucocytozoon, Haemoproteus) in the Eurasian sparrowhawk (Accipiter nisus): diversity, incidence and persistence of infection at the individual level. **2023**, 16,	0
397	Evolutionary analysis of p38 stress-activated kinases in unicellular relatives of animals suggests an ancestral function in osmotic stress. **2023**, 13,	0
396	Microbiome variation correlates with the insecticide susceptibility in different geographic strains of a significant agricultural pest, Nilaparvata lugens. **2023**, 9,	0
395	Evolutionary rate of SARS-CoV-2 increases during zoonotic infection of farmed mink.	1
394	Utilizing evolutionary conservation to detect deleterious mutations and improve genomic prediction in cassava. 13,	0
393	Inflammatory Responses Induced by the Monophasic Variant of Salmonella Typhimurium in Pigs Play a Role in the High Shedder Phenotype and Fecal Microbiota Composition.	2
392	Large-scale analyses of angiosperm Flowering Locus T genes reveal duplication and functional divergence in monocots. 13,	0
391	Grain, Gluten, and Dietary Fiber Intake Influence Gut Microbial Diversity: Data from the Food and Microbiome Longitudinal Investigation. **2023**, 3, 43-53	0
390	Geography and elevation as drivers of cloacal microbiome assemblages of a passerine bird distributed across Sulawesi, Indonesia. **2023**, 5,	0
389	Growth stage and nitrate limiting response of NRT2 and NAR2 gene families of bread wheat, and complementation and retrieval of nitrate uptake of atnrt2.1 mutant by a wheat NRT2 gene. **2023**, 207, 105205	0
388	Alteration of the organic wheat rhizobiome and enzyme activities by reduced tillage and diversified crop rotation. **2023**, 144, 126726	0
387	Insights into the evolutionary history and taxonomic status of Sinopteris (Pteridaceae). **2023**, 180, 107672	0
386	Mitochondrial characteristics of the powdery mildew genus Erysiphe revealed an extraordinary evolution in protein-coding genes. **2023**, 230, 123153	0

385	Conductive carrier promotes synchronous biofilm formation and granulation of anammox bacteria. **2023**, 447, 130754	0
384	Divergent responses of phoD- and pqqC-harbouring bacterial communities across soil aggregates to long fertilization practices. **2023**, 228, 105634	0
383	Molecular characterization and functional analysis of peroxiredoxin 3 (NdPrx3) from Neocaridina denticulata sinensis. **2023**, 4, 100081	0
382	An Enhanced Web-based Tools for Multiple Sequence Alignment: A Comparative Approach. **2022**,	0
381	The First Snake Venom KTS/Disintegrins-Integrin Interactions Using Bioinformatics Approaches. **2023**, 28, 325	0
380	Gut Microbiota Signature of Obese Adults Across Different Classifications. Volume 15, 3933-3947	1
379	First faunistic investigation of semiterrestrial tardigrade fauna of North-West Russia using the method of DNA barcoding. **2022**, 19, 452-474	0
378	Detection and Characterization of Feline Calicivirus Associated with Paw and Mouth Disease. **2023**, 13, 65	0
377	Whole Genome Sequencing of SARS-CoV-2 in Cats and Dogs in South Korea in 2021. **2023**, 10, 6	0
376	Prevalence of Hepatitis E Virus (HEV) in Feral and Farmed Wild Boars in Xinjiang, Northwest China. **2023**, 15, 78	0
375	Microbial rewilding in the gut microbiomes of captive ring-tailed lemurs (Lemur catta) in Madagascar. **2022**, 12,	0
374	Complete chloroplast genome sequence of <i>Clematis calcicola</i> (Ranunculaceae), a species endemic to Korea. **2022**, 52, 262-268	0
373	Screening of Antibacterial Activity of Some Resupinate Fungi, Reveal Gloeocystidiellum lojanense sp. nov. (Russulales) against E. coli from Ecuador. **2023**, 9, 54	0
372	Sabahia polypodii gen. et sp. nov. (Hemiptera: Cicadellidae: Evacantihinae) and its Phylogenetic Position within the Nirvanini Tribe. **2022**, 70, 151-162	0
371	Gut microbiota mediates positive effects of liraglutide on dyslipidemia in mice fed a high-fat diet. 9,	0
370	Low-elevation warm-edge Fagus crenata populations in the core of the species range are glacial relicts with high conservation value.	0
369	Coalescent-Based Species Delimitation in Herbaceous Bamboos (Bambusoideae, Olyreae) from Eastern Brazil: Implications for Taxonomy and Conservation in a Group with Weak Morphological Divergence Coupled with Low Genetic Diversity. **2023**, 12, 107	0
368	Multiple Sequence Alignment. **2022**, 85-101	0

367	Accurate and fast graph-based pangenome annotation and clustering with ggCaller.	0
366	Invasive Californian death caps develop mushrooms unisexually and bisexually.	1
365	Four New Species of Torula (Torulaceae, Pleosporales) from Sichuan, China. **2023**, 9, 150	0
364	Multiple pathways of SARS-CoV-2 nosocomial transmission uncovered by integrated genomic and epidemiological analyses during the second wave of the COVID-19 pandemic in the UK. 12,	0
363	Big diversity in a small hotspot: two new species of Leptophlebiidae (Insecta, Ephemeroptera) from New Caledonia. 1143, 71-88	0
362	Strain Tracking with Uncertainty Quantification.	0
361	Complete chloroplast genomes provide insights into evolution and phylogeny of Zingiber (Zingiberaceae). **2023**, 24,	0
360	An integrated approach to explore the monophyletic status of the cosmopolitan genus Hexabathynella (Crustacea, Bathynellacea, Parabathynellidae): two new species from Rottnest Island (Wadjemup), Western Australia. **2023**, 21,	0
359	Molecular screening of Amblyomma species (Acari: Ixodidae) in Egypt, with first report of the snake tick Amblyomma latum Koch, 1844.	0
358	Deciphering the genetic basis of silkworm cocoon colors provides new insights into biological coloration and phenotypic diversification.	0
357	The Chromosome-Scale Genomes of Exserohilum rostratum and Bipolaris zeicola Pathogenic Fungi Causing Rice Spikelet Rot Disease. **2023**, 9, 177	0
356	Genome and Transcriptome Analysis of Ascochyta pisi Provides Insights into the Pathogenesis of Ascochyta Blight of Pea.	0
355	The Gynandropsis gynandra genome provides insights into whole-genome duplications and the evolution of C4 photosynthesis in Cleomaceae.	0
354	SeqPanther: Sequence manipulation and mutation statistics toolset.	0
353	Isolation and infection cycle of a polinton-like virus virophage in an abundant marine alga. **2023**, 8, 332-346	0
352	MOTIFS IN SARS-COV-2 EVOLUTION.	0
351	Tandem repeats in giant archaeal Borg elements undergo rapid evolution and create new intrinsically disordered regions in proteins. **2023**, 21, e3001980	0
350	Effects of the Long-Term Continuous Cropping of Yongfeng Yam on the Bacterial Community and Function in the Rhizospheric Soil. **2023**, 11, 274	0

349	MBPD: A multiple bacterial pathogen detection pipeline for One Health practices.	1
348	A comprehensive survey of coronaviral main protease active site diversity in 3D: Identifying and analyzing drug discovery targets in search of broad specificity inhibitors for the next coronavirus pandemic.	0
347	Antibiotic hyper-resistance in a class I aminoacyl-tRNA synthetase with altered active site signature motif.	0
346	Comparison of gut microbiota between immigrant and native populations of the Silver-eared Mesia (Leiothrix argentauris) living in mining area. 14,	0
345	Chromosome-Level Genome Assembly of Herpetospermum pedunculosum (Cucurbitaceae). **2023**, 15,	0
344	HIV-PULSE: A long-read sequencing assay for high-throughput near full-length HIV-1 proviral genome characterization.	0
343	Rare ribosomal RNA sequences from archaea stabilize the bacterial ribosome.	0
342	Museum specimens of a landlocked pinniped reveal recent loss of genetic diversity and unexpected population connections. **2023**, 13,	0
341	A SARS-CoV-2 full genome sequence of the B.1.1 lineage sheds light on viral evolution in Sicily in late 2020. 11,	0
340	Comparative Analyses Reveal the Genetic Mechanism of Ambergris Production in the Sperm Whale Based on the Chromosome-Level Genome. **2023**, 13, 361	0
339	Phylogenetics and phylogeography ofEuphorbia canariensisreveal an extreme Canarian-Asian disjunction and limited inter-island colonization.	0
338	Phylogeny and cross-regulation of the YjjM and LeuO transcription factors translated as multiple protein forms from one gene in Escherichia coli. **2023**, 18, 1-14	0
337	Using environmental DNA to investigate avian interactions with flowering plants.	0
336	Population genetic analysis of the microsporidium Ordospora colligata reveals the role of natural selection and phylogeography on its extremely compact and reduced genome.	0
335	The complete mitochondrial genome of Cuspidaria undata (Bivalvia, Anomalodesmata, Cuspidariidae). **2023**, 8, 157-160	0
334	Evolutionary transcriptomics reveals longevity mostly driven by polygenic and indirect selection in mammals.	0
333	Complex scaffold remodeling in plant triterpene biosynthesis. **2023**, 379, 361-368	2
332	The Evolution of Local Energetic Frustration in Protein Families.	0

331	Methanocaldococcus lauensis sp. nov., a novel deep-sea hydrothermal vent hyperthermophilic methanogen. **2023**, 73,	o
330	Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater. **2023**, 13,	o
329	Host Tree and Geography Induce Metabolic Shifts in the Epiphytic Liverwort Radula complanata. **2023**, 12, 571	o
328	Gut microbiota of skywalker hoolock gibbons (Hoolock tianxing) from different habitats and in captivity:́Implications for gibbon health.	o
327	Archival wild-type poliovirus 1 infected central nervous system tissues of the pre-vaccination era in Switzerland reveal a distinct virus genotype.	o
326	Traditional taxonomy underestimates the number of species of Bokermannohyla (Amphibia: Anura: Hylidae) diverging in the mountains of southeastern Brazil since the Miocene. **2023**, 21,	o
325	Ecological Dynamics of Broad- and Narrow-Host-Range Viruses Infecting the Bloom-Forming Toxic Cyanobacterium Microcystis aeruginosa.	o
324	Different response of arbuscular mycorrhizal fungal communities in soil and Elymus nutans roots to long-term warming in alpine meadow.	o
323	Correlated evolution of social organization and lifespan in mammals. **2023**, 14,	o
322	Morphology and phylogenetic position of three anaerobic ciliates from the classes Odontostomatea and Muranotrichea (Ciliophora).	o
321	High Throughput Reproducible Literate Phylogenetic Analysis. **2022**,	o
320	The mitochondrial genome ofIsognomon nucleusand mitogenomics of pteriomorphia (Bivalvia: Autobranchia). **2023**, 89,	o
319	Agta hunter‐gatherer oral microbiomes are shaped by contact network structure. **2023**, 5,	o
318	Field Use of Protective Bacteriophages against Pectinolytic Bacteria of Potato. **2023**, 11, 620	o
317	Genomic adaptation of giant viruses in polar oceans.	o
316	SALON ontology for the formal description of sequence alignments. **2023**, 24,	o
315	P2X7 Receptor Modulation of the Gut Microbiota and the Inflammasome Determines the Severity of Toxoplasma gondii-Induced Ileitis. **2023**, 11, 555	o
314	Evolutionary Patterns of the Chloroplast Genome in Vanilloid Orchids (Vanilloideae, Orchidaceae). **2023**, 24, 3808	o

313	A bat MERS-like coronavirus circulates in pangolins and utilizes human DPP4 and host proteases for cell entry. **2023**, 186, 850-863.e16	0
312	Phylogenetic relationships of three rockfish: Sebastes melanops, Sebastes ciliatus and Sebastes variabilis (Scorpaeniformes, Scorpaenidae) based on complete mitochondrial genome sequences. 11,	0
311	Emergence and spread of two SARS-CoV-2 variants of interest in Nigeria. **2023**, 14,	1
310	Characterisation of the complete mitochondrial genome of Taraxacum mongolicum revealed five repeat-mediated recombinations.	0
309	The genome of Bacillus tequilensis EA-CB0015 sheds light into its epiphytic lifestyle and potential as a biocontrol agent. 14,	0
308	Maternal effects drive intestinal development beginning in the embryonic period on the basis of maternal immune and microbial transfer in chickens. **2023**, 11,	0
307	Telomerase RNA plays a major role in the completion of the life cycle in Ustilago maydis and shares conserved domains with other Ustilaginales. **2023**, 18, e0281251	0
306	Spatial-temporal expression analysis of lineage-restricted shell matrix proteins reveals shell field regionalization and distinct cell populations in the slipper snailCrepidula atrasolea.	0
305	Genome mining unveils a class of ribosomal peptides with two amino termini. **2023**, 14,	0
304	Deep Divergence and Genomic Diversification of Gut Symbionts of Neotropical Stingless Bees.	0
303	Cecal Microbial Succession and Its Apparent Association with Nutrient Metabolism in Broiler Chickens.	0
302	DNA Barcoding Data Reveal Important Overlooked Diversity of Cortinarius sensu lato (Agaricales, Basidiomycota) in the Romanian Carpathians. **2023**, 15, 553	0
301	Ancient Fish Lineages Illuminate Toll-Like Receptor Diversification in Early Vertebrate Evolution.	0
300	Evolution and Classification of Musaceae Based on Male Floral Morphology. **2023**, 12, 1602	0
299	Characterization of Phietavirus Henu 2 in the virome of individuals with acute gastroenteritis.	0
298	Elaphomyces castilloi (Elaphomycetaceae, Ascomycota) and Entoloma secotioides (Entolomataceae, Basidiomycota), two new sequestrate fungi from tropical montane cloud forest from south Mexico. 96, 127-142	0
297	COVID-19-Associated Pulmonary Aspergillosis Isolates Are Genomically Diverse but Similar to Each Other in Their Responses to Infection-Relevant Stresses. **2023**, 11,	1
296	Different Diet Energy Levels Alter Body Condition, Glucolipid Metabolism, Fecal Microbiota and Metabolites in Adult Beagle Dogs. **2023**, 13, 554	0

295	RNAi-mediated knockdown of two orphan G-protein coupled receptors reduces fecundity in the yellow fever mosquitoAedes aegypti.	0
294	The little skate genome and the evolutionary emergence of wing-like fins.	0
293	Characterization of atypical Mycoplasma anserisalpingitidis strains. **2023**, 280, 109722	0
292	Delineation of the complex microbial nitrogen-transformation network in an anammox-driven full-scale wastewater treatment plant. **2023**, 235, 119799	0
291	Antlers far and wide: Biomolecular identification of Scandinavian hair combs from Ribe, Denmark, 720▯00 CE. **2023**, 153, 105773	0
290	The role of inherited characteristics from parent materials in shaping bacterial communities in agricultural soils. **2023**, 433, 116455	0
289	Diversification and introgression in four chromosomal taxa of the Pearson▯ horseshoe bat (Rhinolophus pearsoni) group. **2023**, 183, 107784	0
288	Towards the accurate alignment of over a million protein sequences: Current state of the art. **2023**, 80, 102577	0
287	East Asian monsoon manipulates the richness and taxonomic composition of airborne bacteria over China coastal area. **2023**, 875, 162581	0
286	SARS-CoV-2 wastewater-based epidemiology in an enclosed compound: A 2.5-year survey to identify factors contributing to local community dissemination. **2023**, 875, 162466	0
285	Bacterial communities and toxin profiles of Ostreopsis (Dinophyceae) from the Pacific island of Okinawa, Japan. **2023**, 89, 125976	0
284	Polyethylene and polyvinyl chloride microplastics promote soil nitrification and alter the composition of key nitrogen functional bacterial groups. **2023**, 453, 131391	0
283	Organelle genomes of Indigofera amblyantha and Indigofera pseudotinctoria: comparative genome analysis, and intracellular gene transfer. **2023**, 198, 116674	0
282	Emergence of terpene chemical communication in insects: Evolutionary recruitment of isoprenoid metabolism. **2023**, 32,	0
281	Draft Genome Sequences of Two Dothideomycetes Strains, NU30 and NU200, Derived from the Marine Environment around Sugashima, Japan.	0
280	A Multiplexed, Tiled PCR Method for Rapid Whole-Genome Sequencing of Infectious Spleen and Kidney Necrosis Virus (ISKNV) in Tilapia. **2023**, 15, 965	0
279	First molecular evidence of Wolbachia occurrence in Amblyomma sculptum (Acari: Ixodidae). **2023**, 317, 109907	0
278	An improved method for determining frequency of multiple variants of SARS-CoV-2 in wastewater using qPCR assays. **2023**, 881, 163292	0

277	Two taxa of the genus Sticta (Peltigerales, Ascomycota), S. andina and S. scabrosa subsp. scabrosa, new to Bolivia confirmed by molecular data. **2022**, 67, 45-54	0
276	Rapid nitrification involving comammox and canonical Nitrospira at extreme pH in saline-alkaline lakes.	0
275	Expanding Acutuncus: Phylogenetics and morphological analyses reveal a considerably wider distribution for this tardigrade genus. **2023**, 180, 107707	0
274	Two residues determine nicotinic acetylcholine receptor requirement for RIC-3.	0
273	A New Webbing Aberoptus Species from South Africa Provides Insight in Silk Production in Gall Mites (Eriophyoidea). **2023**, 15, 151	0
272	SARS-CoV-2 variants-associated outbreaks of COVID-19 in a tertiary institution, North-Central Nigeria: Implications for epidemic control. **2023**, 18, e0280756	0
271	Candida khanbhaisp. nov., a new clinically relevant yeast within theCandida haemuloniispecies complex. **2023**, 61,	0
270	MAMMLE: A Framework for Phylogeny Estimation Based on Multiobjective Application-aware Multiple Sequence Alignment and Maximum Likelihood Ensemble. **2023**, 30, 245-249	0
269	PCR detection of Theileria equi and Babesia caballi in apparently healthy horses in Paraguay. **2023**, 39, 100835	0
268	Mechanistic and microbial ecological insights into the impacts of micro- and nano-´plastics on microbial reductive dehalogenation of organohalide pollutants. **2023**, 448, 130895	0
267	Co-circulation of dengue virus serotypes 1 and 3 in the Fatick region of senegal 2018. 2,	0
266	Microbiota-Associated HAF-EVs Regulate Monocytes by Triggering or Inhibiting Inflammasome Activation. **2023**, 24, 2527	0
265	Prevalence of Viral Frequency-Dependent Infection in Coastal Marine Prokaryotes Revealed Using Monthly Time Series Virome Analysis. **2023**, 8,	1
264	A New Species of Bisexual Milnesium (Eutardigrada: Apochela) Having Aberrant Claws from Innhovde, Dronning Maud Land, East Antarctica. **2023**, 40,	0
263	Microbiota composition in the lower respiratory tract is associated with severity in patients with acute respiratory distress by influenza. **2023**, 20,	1
262	Alphaviruses Detected in Mosquitoes in the North-Eastern Regions of South Africa, 2014 to 2018. **2023**, 15, 414	0
261	Bordetella bronchiseptica-Mediated Interference Prevents Influenza A Virus Replication in the Murine Nasal Cavity. **2023**, 11,	0
260	On distinguishing between canonical tRNA genes and tRNA gene fragments in prokaryotes. **2023**, 20, 48-58	0

259	Functional assignment of gut-specific archaeal proteins in the human gut microbiome.	0
258	HiMAP2 : Identifying phylogenetically informative genetic markers from diverse genomic resources.	0
257	Functionality of methane cycling microbiome during methane flux hot moments from riparian buffer systems. **2023**, 870, 161921	0
256	Targeting influenza A virus by splicing inhibitor herboxidiene reveals the importance of subtype-specific signatures around splice sites. **2023**, 30,	0
255	Epistasis between promoter activity and coding mutations shapes gene evolvability. **2023**, 9,	0
254	Application of EMD Combined with Deep Learning and Knowledge Graph in Bearing Fault.	0
253	Single-cell genomics reveals the divergent mitochondrial genomes of Retaria (Foraminifera and Radiolaria).	0
252	Host phylogeny and functional traits differentiate gut microbiomes in a diverse natural community of small mammals.	0
251	Rational identification of a high catalytic efficiency leucine dehydrogenase and process development for efficient synthesis of l -phenylglycine. 2200465	0
250	Insights into the Deep Phylogeny and Novel Gene Rearrangement of Mytiloidea from Complete Mitochondrial Genome.	0
249	Muc2-dependent microbial colonization of the jejunal mucus layer is diet sensitive and confers local resistance to enteric pathogen infection. **2023**, 42, 112084	0
248	Complete mitochondrial genome of a livebearing freshwater fish (Cyprinodontiformes: Poeciliidae): Poecilia parae. **2023**, 8, 215-219	0
247	The identity of Argyria lacteella (Fabricius, 1794) (Lepidoptera, Pyraloidea, Crambinae), synonyms, and related species revealed by morphology and DNA capture in type specimens. 1146, 1-42	0
246	Prebiotic mechanisms of resistant starches from dietary beans and pulses on gut microbiome and metabolic health in a humanized murine model of aging. 10,	0
245	Integrative taxonomy reveals new, widely distributed tardigrade species of the genus Paramacrobiotus (Eutardigrada: Macrobiotidae). **2023**, 13,	0
244	Adding context to the pneumococcal core genes using bioinformatic analysis of the intergenic pangenome of Streptococcus pneumoniae. 3,	0
243	The Ancestral Mitotic State: Closed Orthomitosis With Intranuclear Spindles in the Syncytial Last Eukaryotic Common Ancestor. **2023**, 15,	0
242	Woody encroachment affects multiple dimensions of ant diversity in a neotropical savanna.	0

241	Lack of neutralizing antibodies against the current circulating influenza viruses during the Omicron outbreak in Hong Kong.	0
240	Sediment microbial community structure associated to different ecological types of mangroves in Celestún, a coastal lagoon in the Yucatan Peninsula, Mexico. 11, e14587	0
239	Neutralization of SARS-CoV-2 BQ.1.1 and XBB.1.5 by Breakthrough Infection Sera from Previous and Current Waves in China.	0
238	Insights into the convergent evolution of fructan biosynthesis in angiosperms from the highly characteristic chicory genome. **2023**, 238, 1245-1262	0
237	Using Multiplex Amplicon PCR Technology to Efficiently and Timely Generate Rift Valley Fever Virus Sequence Data for Genomic Surveillance. **2023**, 15, 477	0
236	The dynamics of the microbiome in Ixodidae are shaped by tick ontogeny and pathogens in Sarawak, Malaysian Borneo. **2023**, 9,	0
235	Salinity determines performance, functional populations, and microbial ecology in consortia attenuating organohalide pollutants. **2023**, 17, 660-670	0
234	Propionylated high-amylose maize starch alleviates obesity by modulating gut microbiota in high-fat diet-fed mice. **2023**, 102, 105447	0
233	De-MISTED: Image-based classification of erroneous multiple sequence alignments using convolutional neural networks.	0
232	Molecular characterization of a novel victorivirus (order Ghabrivirales, family Totiviridae) infecting Metarhizium anisopliae. **2023**, 168,	0
231	Next-generation sequencing approach to investigate genome variability of Parapoxvirus in Canadian muskoxen (Ovibos moschatus). **2023**, 109, 105414	0
230	The genome of a vestimentiferan tubeworm (Ridgeia piscesae) provides insights into its adaptation to a deep-sea environment. **2023**, 24,	0
229	Complete functional analysis of type IV pilus components of a reemergent plant pathogen reveals neofunctionalization of paralog genes. **2023**, 19, e1011154	0
228	Minus-C subfamily has diverged from Classic odorant-binding proteins in honeybees. **2023**, 54,	0
227	Antioxidant enzymes that target hydrogen peroxide are conserved across the animal kingdom, from sponges to mammals. **2023**, 13,	0
226	Variation in mitogenome structural conformation in wild and cultivated lineages of sorghum corresponds with domestication history and plastome evolution. **2023**, 23,	1
225	Kinetics of the Antibody Response to Symptomatic SARS-CoV-2 Infection in Vaccinated and Unvaccinated Individuals in the Blinded Phase of the mRNA-1273 COVID-19 Vaccine Efficacy Trial. **2023**, 10,	0
224	Effect of probiotics for regulation of inflammatory response in radiation-induced enteritis.	0

223	Host phylogeny and ecological associations best explain Wolbachia host shifts in scale insects.	0
222	Genome-Wide Identification of G Protein-Coupled Receptors in Ciliated Eukaryotes. **2023**, 24, 3869	0
221	Kojic Acid Gene Clusters and the Transcriptional Activation Mechanism of Aspergillus flavus KojR on Expression of Clustered Genes. **2023**, 9, 259	0
220	A diverse repertoire of anti-defense systems is encoded in the leading region of plasmids.	0
219	De Novo Assembly and Characterization of the Transcriptome of an Omnivorous Camel Cricket (Tachycines meditationis). **2023**, 24, 4005	0
218	Amazonian birds in more dynamic habitats have less population genetic structure and higher gene flow.	0
217	TCNformer Model for Photovoltaic Power Prediction. **2023**, 13, 2593	0
216	Using PhyloSuite for molecular phylogeny and tree-based analyses. **2023**, 2,	0
215	Analysis of 3.5 million SARS-CoV-2 sequences reveals unique mutational trends with consistent nucleotide and codon frequencies. **2023**, 20,	0
214	Resolving the Sticta fuliginosa Morphodeme (Lichenized Ascomycota: Peltigeraceae) in Northwestern North America. **2023**, 126,	0
213	A needle in a haystack: A new metabarcoding approach to survey diversity at the species level of Arcellinida (Amoebozoa: Tubulinea).	0
212	Mutual information networks reveal evolutionary relationships within the influenza A virus polymerase.	0
211	Ticks and Rickettsiae Associated with Wild Animals Sold in Bush Meat Markets in Cameroon. **2023**, 12, 348	0
210	Hazardous potential evaluation of biochar exposure on mice through analyses of gut-microbiome and fatty acids in brain. **2023**, 461, 142006	0
209	Whole-Genome Comparison Reveals Structural Variations behind Heading Leaf Trait in Brassica oleracea. **2023**, 24, 4063	0
208	Characterization of the nearly complete mitochondrial genome of ochraceous darkies, Euphaea ochracea Selys, 1859 (Odonata: Zygoptera: Euphaeidae) and phylogenetic analysis. **2023**, 8, 292-296	0
207	Vibrio parahaemolyticus T6SS2 effector repertoires. **2023**, 15,	0
206	Community Characteristics of Soil Ectomycorrhizal Fungi under Different Forests in the Sandy Areas of Northeastern China.	0

205	Histone deacetylase OsHDA706 increases salt tolerance via H4K5/K8 deacetylation of OsPP2C49 in rice.	0
204	Phylogeography of Ramalina ́farinacea (Lichenized Fungi, Ascomycota) in the Mediterranean Basin, Europe, and Macaronesia. **2023**, 15, 310	0
203	Thaxterogaster carneus (Cortinariaceae), a new species of Thaxterogaster sect. Vibratiles , from coniferous forests of Kashmir Himalaya, India.	0
202	Bacterial origins of thymidylate metabolism in Asgard archaea and Eukarya. **2023**, 14,	0
201	ARBUSCULAR MYCORRHIZA-INDUCED KINASES AMK8 and AMK24 associate with the receptor-like kinase KINASE3 to regulate arbuscular mycorrhizal symbiosis inLotus japonicus.	0
200	Complete mitochondrial genomes of Lycosa grahami and Lycosa sp. (Araneae: Lycosidae): comparison within the family Lycosidae.	0
199	Prevalence, evolution, replication and transmission of H3N8 avian influenza viruses isolated from migratory birds in eastern China from 2017 to 2021. **2023**, 12,	0
198	Plerocercoids of Adenocephalus pacificus in Argentine hakes: Broad distribution, low zoonotic risk. **2023**, 391-393, 110142	0
197	Machado Joseph disease severity is linked with gut microbiota alterations in transgenic mice. **2023**, 179, 106051	0
196	A chromosome-level genome assembly for Erianthus fulvus provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. **2023**, 100562	0
195	Exploring the Astrovirome of Shellfish Matrices Using Nanopore Sequencing. **2023**, 10, 175	0
194	Giant proteins in a giant cell: Molecular basis of ultrafast Ca 2+ -dependent cell contraction. **2023**, 9,	0
193	The spatial patterns of diversity and their relationships with environments in rhizosphere microorganisms and host plants differ along elevational gradients. 14,	0
192	Novel Chaphamaparvovirus in Insectivorous Molossus molossus Bats, from the Brazilian Amazon Region. **2023**, 15, 606	0
191	Cover Crops Modulate the Response of Arbuscular Mycorrhizal Fungi to Water Supply: A Field Study in Corn. **2023**, 12, 1015	1
190	Discovery and Enzymatic Screening of Genome-Mined Microbial Levanases to Produce Second-Generation (2,6)-Fructooligosaccharides: Catalytic Properties. **2023**, 18, 465-475	0
189	Roadmap to the study of gene and protein phylogeny and evolutionA practical guide. **2023**, 18, e0279597	0
188	Function of the bacteriophage P2 baseplate central spike Apex domain in the infection process.	0

187	Draft Genome and Biological Characteristics of Fusarium solani and Fusarium oxysporum Causing Black Rot in Gastrodia elata. **2023**, 24, 4545	0
186	Six Additions to the Genus Periconia (Dothideomycetes: Periconiaceae) from Graminaceous Plants in China. **2023**, 9, 300	0
185	Genome-Wide Investigation of the NAC Transcription Factor Family in Apocynum venetum Revealed Their Synergistic Roles in Abiotic Stress Response and Trehalose Metabolism. **2023**, 24, 4578	0
184	Estimating number of European eel (Anguilla anguilla) individuals using environmental DNA and haplotype count in small rivers. **2023**, 13,	0
183	Gene conversion drives allelic dimorphism in two paralogous surface antigens of the malaria parasiteP. falciparum.	0
182	luxAgene fromEnhygromyxa salinaencodes a functional homodimeric luciferase.	0
181	DNA metabarcoding of trawling bycatch reveals diversity and distribution patterns of sharks and rays in the central Tyrrhenian Sea.	0
180	Lower viral evolutionary pressure under stable versus fluctuating conditions in subzero Arctic brines.	0
179	Beyond the Active Site: The addition of a remote loop reveals a new complex biological function for chitinase enzymes.	0
178	Molecular exploration of fossil eggshell uncovers hidden lineage of giant extinct bird. **2023**, 14,	0
177	Phototrophy by antenna-containing rhodopsin pumps in aquatic environments. **2023**, 615, 535-540	1
176	Zearalenone and Its Emerging Metabolites Promptly Affect the Rumen Microbiota in Holstein Cows Fed a Forage-Rich Diet. **2023**, 15, 185	0
175	Composition and evolution of the gut microbiota of growing puppies is impacted by their birth weight.	0
174	Evolution of the germline mutation rate across vertebrates. **2023**, 615, 285-291	1
173	Diversity and function of soybean rhizosphere microbiome under nature farming. 14,	0
172	Variety of rumen microbial populations involved in biohydrogenation related to individual milk fat percentage of dairy cows. 10,	0
171	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. **2023**, 186, 1279-1294.e19	0
170	Immunogenic Properties and Antigenic Similarity of Virus-like Particles Derived from Human Polyomaviruses. **2023**, 24, 4907	0

169	Phylogeny of the flea beetles (Galerucinae: Alticini) and the position of Aulacothorax elucidated through anchored phylogenomics (Coleoptera: Chrysomelidae: Alticini).	1
168	Tyrosyl-DNA phosphodiesterase 1 (TDP1) and SPRTN protease repair histone 3 and topoisomerase 1 DNA-protein crosslinks in vivo.	0
167	Genome biology and evolution of mating type loci in four cereal rust fungi.	0
166	Ophiotholia (Echinodermata: Ophiuroidea): A little-known deep-sea genus present in polymetallic nodule fields with the description of a new species. 10,	0
165	Lactobacillus gasseri LG-G12 Restores Gut Microbiota and Intestinal Health in Obesity Mice on Ceftriaxone Therapy. **2023**, 12, 1092	0
164	Sensing volatiles throughout the body: Geographic and tissue-specific olfactory receptor expression in the fig waspCeratosolen fusciceps.	0
163	Comparative transcriptomics reveals divergence in pathogen response gene families amongst twenty forest tree species.	0
162	Virus diversity and activity is driven by snowmelt and host dynamics in a high-altitude watershed soil ecosystem.	0
161	Risk potential of international fruit trade for viroid spreading - case study on hop viroids in Europe.	0
160	Two new species of Eleutherodactylus from western and central Mexico (Eleutherodactylus jamesdixoni sp. nov., Eleutherodactylus humboldti sp. nov.). 11, e14985	0
159	New records and species of deep-sea squat lobsters (Galatheoidea, Munidopsidae) from the Hawaiian Archipelago: an integrative approach using micro-CT and barcodes. 11, e14956	0
158	De novo assembly of a chromosome-level reference genome of the ornamental butterfly Sericinus montelus based on nanopore sequencing and Hi-C analysis. 14,	0
157	Evolution of mitogenomic gene order in Orthoptera.	0
156	Internal Translation of p53 Oncoproteins During Integrated Stress Response Confers Survival Advantage on Cancer Cells.	0
155	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. **2023**, 15, 699	0
154	Eelgrass (Zosteraspp.) associated phytomyxids are host-specific congeneric parasites and predominant eukaryotes in the eelgrass rhizosphere on a global scale.	0
153	Multiplexed Amplicon Sequencing Reveals High Sequence Diversity of Antibiotic Resistance Genes in Québec Sewers.	0
152	Molecular Phylogeny of Cimicoidea (Heteroptera: Cimicomorpha) Revisited: Increased Taxon Sampling Reveals Evolution of Traumatic Insemination and Paragenitalia. **2023**, 14, 267	0

151	Opuntia setocarpa (Cactaceae, Opuntioideae): Phylogenetic Hypothesis and Notes. **2023**, 29,	0
150	Development of the oral resistome during the first decade of life. **2023**, 14,	0
149	Eventually tested: Phylogenetic position of Testechiniscus meridionalis (Murray, 1906) (Heterotardigrada) revealed. **2023**, 304, 49-60	0
148	Functional and regulatory diversification of circadian rhythmperiodgenes during the evolution of vertebrates.	0
147	Circulation of enterotoxigenic Escherichia coli (ETEC) isolates expressing CS23 from the environment to clinical settings.	0
146	Genome mining unveils a class of ribosomal peptides with two amino termini.	0
145	Genomic selection for agronomic traits in a winter wheat breeding program. **2023**, 136,	0
144	Uncovering the link between gut microbiome, highly processed food consumption and diet quality through bioinformatics methods.	0
143	SARS-CoV-2 Mutations Lead to a Decrease in the Number of Tissue-Specific MicroRNA-Binding Regions in the Lung. **2023**, 174, 527-532	0
142	Association of aberrant brain network dynamics with gut microbial composition uncovers disrupted brain‐gut‐microbiome interactions in irritable bowel syndrome: Preliminary findings.	0
141	Comammox Nitrospira and Ammonia-Oxidizing Archaea Are Dominant Ammonia Oxidizers in Sediments of an Acid Mine Lake Containing High Ammonium Concentrations. **2023**, 89,	0
140	There and Back Again: The Unexpected Journeys of Metridium de Blainville, 1824 between the Old Oceans and throughout the Modern World. 000-000	0
139	Disentangling the Functional Role of Fungi in Cold Seep Sediment. **2023**, 11,	0
138	PML and PML-like exonucleases restrict retrotransposons in jawed vertebrates.	0
137	Endoparasitic Gall Mites: Two New Novophytoptus Species (Eriophyoidea, Phytoptidae) from Southern African Sedges (Cyperaceae, Carex) and New Hypotheses on the Phylogeny of Novophytoptines. **2023**, 15, 416	0
136	Genomic and clinical case characterisation of Staphylococcus haemolyticus isolated from dogs and cats in the United States, including strains with high-level mupirocin tolerance.	0
135	Categorizing 161 plant (streptophyte) mitochondrial group II introns into 29 families of related paralogues finds only limited links between intron mobility and intron-borne maturases. **2023**, 23,	0
134	Postbiotics from Pichia kudriavzevii promote intestinal health performance through regulation of Limosilactobacillus reuteri in weaned piglets.	0

133	The tropical cookbook: Termite diet and phylogenetics□over geographical origin□drive the microbiome and functional genetic structure of nests. 14,	0
132	Zobellia alginoliquefacienssp. nov., a new flavobacteria isolated from the epibiota of the brown algaEricaria zosteroides(C.Agardh) Molinari & Guiry 2020.	0
131	Deciphering the global spread of canine rabies virus in the modern era.	0
130	Fibre fermentation and pig faecal microbiota composition are affected by the interaction between sugarcane fibre and (poly)phenols in vitro. **2023**, 74, 219-233	0
129	The Complete Mitochondrial Genome of Box Tree Moth Cydalima perspectalis and Insights into Phylogenetics in Pyraloidea. **2023**, 13, 1045	0
128	Ubiquitous, B12-dependent virioplankton utilizing ribonucleotide triphosphate reductase demonstrate interseasonal dynamics and associate with a diverse range of bacterial hosts in the pelagic ocean.	0
127	The origin and structural evolution ofde novogenes inDrosophila.	0
126	Characterization of the l-arabinofuranose-specific GafABCD ABC transporter essential for l-arabinose-dependent growth of the lignocellulose-degrading bacterium Shewanella sp. ANA-3. **2023**, 169,	0
125	Duplicate transcription factorsGT1andVRS1regulate branching and fertile flower number in maize andBrachypodium distachyon.	0
124	Bioinformatic and Statistical Analysis of Microbiome Data. **2023**, 183-229	0
123	Distribution characteristics of oral microbiota and its relationship with intestinal microbiota in patients with type 2 diabetes mellitus. 14,	0
122	Identification of the Coding-Complete Genome Sequence of a Novel Cytorhabdovirus in Tilia cordata Showing Extensive Leaf Chloroses. **2023**, 12,	0
121	Bifidobacterium mellis sp. nov., isolated from the honey stomach of the honey bee Apis mellifera. **2023**, 73,	0
120	Determinants of Total and Active Microbial Communities Associated with Cyanobacterial Aggregates in a Eutrophic Lake.	0
119	De novogenomic analysis ofEnterobacter asburiaeEBRJ12, a plant growth-promoting rhizobacteria isolated from the rhizosphere ofPhaseolus vulgarisL. **2023**, 134,	0
118	Comprehensive molecular characterization of complete mitogenome assemblies of 33 Eimeria isolates infecting domestic chickens. **2023**, 16,	0
117	Evolution of chemosensory and detoxification gene families across herbivorous Drosophilidae.	0
116	Growing gender disparity in HIV infection in Africa: sources and policy implications.	0

115	Effects of Eimeria acervulina infection on the luminal and mucosal microbiota of the duodenum and jejunum in broiler chickens. 14,	0
114	Mucosa-Associated Oscillospira sp. Is Related to Intestinal Stricture and Post-Operative Disease Course in Crohn’s Disease. **2023**, 11, 794	0
113	Single-Cell Genomics Reveals the Divergent Mitochondrial Genomes of Retaria (Foraminifera and Radiolaria).	0
112	Meta-Transcriptomic Analysis Reveals Novel RNA Viruses in Hippocampus erectus. **2023**, 15, 772	0
111	An efficient diazotroph-derived nitrogen transfer pathway in coral reef system. **2023**, 68, 963-981	0
110	Isolation and molecular characterization of Fusarium species (Fungi, Ascomycota) from unhatched eggs of Caretta caretta in Tuscany (Italy). 747-755	0
109	Identification of selective sweeps in bacteria.	0
108	Evidence of Zelkova carpinifolia as a potential host of Tuber uncinatum in Hyrcanian temperate forests.	0
107	Contingency, Repeatability and Predictability in the Evolution of a Prokaryotic Pangenome.	0
106	Detection of Selected Canine Viruses in Nigerian Free-Ranging Dogs Traded for Meat Consumption. **2023**, 13, 1119	0
105	Effect of natural weed and Siratro cover crop on soil fungal diversity in a banana cropping system in southwestern China. 14,	0
104	Pilot study of a comprehensive resource estimation method from environmental DNA using universal D-loop amplification primers. **2023**, 23,	0
103	From primordial clocks to circadian oscillators. **2023**, 616, 183-189	0
102	Evolutionary differences in gene loss and pseudogenization among mycoheterotrophic orchids in the tribe Vanilleae (subfamily Vanilloideae). 14,	0
101	Ancestral SARS-CoV-2-Driven Antibody Repertoire Diversity in an Unvaccinated Individual Correlates with Expanded Neutralization Breadth. **2023**, 11,	0
100	Coccoloba-associated xerocomoid boletes (Boletaceae) from the Caribbean and Mexico: Tropicoboletus ruborculus gen. et comb. nov., revision of Xerocomus coccolobae, phylogenetic assessment of Singerocomus guadelupae comb. nov., and type studies of Xerocomus caeruleonigrescens, X. cuneipes, and X. pseudoboletinus var. pini-caribaeae. **2023**, 22,	0
99	Discovery of a novel bacterial class with the capacity to drive sulfur cycling and microbiome structure in a paleo-ocean analog.	0
98	Metabarcoding and Metabolomics Reveal the Effect of the Invasive Alien Tree Miconia calvescens DC. on Soil Diversity on the Tropical Island of Mo’orea (French Polynesia). **2023**, 11, 832	0

97	Reverse vaccinology-based identification of a novel surface lipoprotein that is an effective vaccine antigen against bovine infections caused by Pasteurella multocida. **2023**, 19, e1011249	0
96	Dispersal-Limited Symbionts Exhibit Unexpectedly Wide Variation in Host Specificity.	0
95	The genomic landscape of reference genomes of cultivated human gut bacteria. **2023**, 14,	0
94	Genomic analysis of Vibrio harveyi strain PH1009, a potential multi-drug resistant pathogen due to acquisition of toxin genes. **2023**, 9, e14926	0
93	Evidence for adaptive evolution towards high magnetic sensitivity of potential magnetoreceptor in songbirds.	0
92	Structural Modeling and Functional Evaluation of Pectate Lyase Protein from Prunus armeniaca.	0
91	A high-resolution melt curve toolkit to identify lineage-defining SARS-CoV-2 mutations. **2023**, 13,	0
90	Comparative genome and phylogenetic analysis revealed the complex mitochondrial genome and phylogenetic position of Conopomorpha sinensis Bradley. **2023**, 13,	0
89	Non-structural genes of novel lemur adenoviruses reveal codivergence of virus and host. **2023**, 9,	0
88	A Cold Case of Equine Influenza Disentangled with Nanopore Sequencing. **2023**, 13, 1153	0
87	The North Asian Genus Kolhymamnicola Starobogatov and Budnikova 1976 (Gastropoda: Amnicolidae), Its Extended Diagnosis, Distribution, and Taxonomic Relationships. **2023**, 15, 483	0
86	Sequential viral introductions and spread of BA.1 drove the Omicron wave across Pakistani provinces.	0
85	A recombinant porcine reproductive and respiratory syndrome virus type 2 field strain derived from two PRRSV-2-modified live virus vaccines. 10,	0
84	A widespread bacterial mobile genetic element encodes weapons against phages, bacteria, and eukaryotes.	0
83	Phylogenomics and Biogeography of the Mammilloid Clade Revealed an Intricate Evolutionary History Arose in the Mexican Plateau. **2023**, 12, 512	1
82	Gut bacteria influence Blastocystis sp. phenotypes and may trigger pathogenicity. **2023**, 17, e0011170	0
81	Evidence of Zelkova carpinifolia as a potential host of Tuber uncinatum in Hyrcanian temperate forests.	0
80	k-mer-based GWAS enhances the discovery of causal variants and candidate genes in soybean.	0

79	Human seven-□strand (METTL) methyltransferases - conquering the universe of protein lysine methylation. **2023**, 104661	0
78	Gut microbial features and dietary fiber intake predict gut microbiota response to resistant starch supplementation.	0
77	Mechanistic and evolutionary insights into isoform-specific □supercharging□in DCLK family kinases.	0
76	Eelgrass (Zostera spp.) associated phytomyxids are host-specific congeneric parasites and predominant eukaryotes in the eelgrass rhizosphere on a global scale.	0
75	Prevalence and Homology of the Pneumococcal Serine-Rich Repeat Protein at the Global Scale.	0
74	miRNA binding pressure channels evolution of SARS-CoV-2 genomes.	0
73	The oldest case of paedomorphosis in rove beetles and description of a new genus of Paederinae from Cretaceous amber (Coleoptera: Staphylinidae). **2023**, 13,	0
72	Tracing the Origin of Genotype II African Swine Fever Virus in China by Genomic Epidemiology Analysis. **2023**, 2023, 1-14	0
71	Target-capture probes for phylogenomics of the Caenogastropoda.	0
70	Structural basis for activation of glutaminase.	0
69	A Novel E3 Probiotics Formula Restored Gut Dysbiosis and Remodelled Gut Microbial Network and Microbiome Dysbiosis Index (MDI) in Southern Chinese Adult Psoriasis Patients. **2023**, 24, 6571	0
68	Molecular evolution, diversification, and expression assessment of MADS gene family in Setaria italica, Setaria viridis, and Panicum virgatum.	0
67	Oral supplementation of nicotinamide riboside alters intestinal microbial composition in rats and mice, but not humans. **2023**, 9,	0
66	What is Salvinia molesta (Salviniaceae)? Determining the maternal progenitor and genetic diversity of the clonal invasive fern giant salvinia.	0
65	Similar Ones Are Not Related and Vice Versa□New Dendronotus Taxa (Nudibranchia: Dendronotidae) from the North Atlantic Ocean Provide a Platform for Discussion of Global Marine Biodiversity Patterns □ **2023**, 15, 504	0
64	Resolving the phylogeny of Thladiantha (Cucurbitaceae) with three different targeted-capture pipelines.	0
63	Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation. **2023**, 24,	0
62	Comparative genomics of <i>Viola selkirkii</i> and <i>V. ulleungdoensis</i> (Violaceae). **2023**, 53, 38-46	0

61	In defense of Apocynaceae: inference on evolution of pyrrolizidine alkaloids from evolution of an enzyme in their biosynthetic pathway, homospermidine synthase.	0
60	Sulfur, sterol and trehalose metabolism in the deep-sea hydrocarbon seep tubeworm Lamellibrachia luymesi. **2023**, 24,	0
59	Spontaneously Produced Lysogenic Phages Are an Important Component of the Soybean Bradyrhizobium Mobilome.	0
58	Gut Bacterial Communities in HIV-Infected Individuals with Metabolic Syndrome: Effects of the Therapy with Integrase Strand Transfer Inhibitor-Based and Protease Inhibitor-Based Regimens. **2023**, 11, 951	0
57	Texas microfungi: on the taxonomic placement of Flosculomyces floridaensis in Zygosporiaceae. **2022**, 137, 521-536	0
56	Comparative Phylogenomics and Phylotranscriptomics Provide Insights into the Genetic Complexity of Nitrogen Fixing Root Nodule Symbiosis.	0
55	Experimental Factors Influence Diversity Metrics of the Gut Microbiome in Laboratory Mice.	0
54	Morphology and phylogeny revealed Tomophagus cattienensis (Ganodermataceae) as a new record for India.	0
53	▯46p53 is a new p53 isoform that responds to DNA damage and regulates tumour growth.	0
52	Complete Genome of Rose Myrtle, Rhodomyrtus tomentosa, and Its Population Genetics in Thai Peninsula. **2023**, 12, 1582	0
51	An evolutionary paradox on threadsnakes: Phenotypic and molecular evidence reveal a new and remarkably polymorphic species of Siagonodon (Serpentes: Leptotyphlopidae: Epictinae) from Amazonia. 73, 345-366	0
50	High-throughput identification of prefusion-stabilizing mutations in SARS-CoV-2 spike. **2023**, 14,	0
49	Profiles of oral microbiome associated with nasogastric tube feeding. **2023**, 15,	0
48	ATP synthase evolution on a cross-braced dated tree of life.	0
47	Comparing the bacterial composition, succession and assembly patterns in plastisphere and kitchen waste composting with PLA/PBAT blends. **2023**, 131405	0
46	High-quality chromosome-level genome assembly of the plant bug Pachypeltis micranthus provides insights into the availability of Mikania micrantha control.	0
45	Analysis of SARS-CoV-2 Recombinant Lineages XBC and XBC.1 in the Philippines and Evidence for Delta-Omicron Co-infection as a Potential Origin.	0
44	Novel Putative Tymoviridae-like Virus Isolated from Culex Mosquitoes in Colombia. **2023**, 15, 953	0

43 Phylogenetic relationship and comparative analysis of the main Bupleuri Radix species in China. 11, e15157 o

42 Conserved intramolecular networks in GDAP1 are closely connected to CMT-linked mutations and protein stability. **2023**, 18, e0284532 o

41 First Study of Ascaris lumbricoides from the Semiwild Population of the Sumatran Orangutan Pongo abelii in the Context of Morphological Description and Molecular Phylogeny. **2023**, 13, 1016 o

40 Complex Networks Analyses of Antibiofilm Peptides: An Emerging Tool for Next-Generation Antimicrobials' Discovery. **2023**, 12, 747 o

39 A´new extremophile ostracod crustacean from the Movile Cave sulfidic chemoautotrophic ecosystem in Romania. **2023**, 13, o

38 Genetic Characterization of Raspberry Bushy Dwarf Virus Isolated from Red Raspberry in Kazakhstan. **2023**, 15, 975 o

37 HMMerge: an Ensemble Method for Multiple Sequence Alignment. o

36 Uniparental Inheritance and Recombination as Strategies to Avoid Competition and Combat Muller's Ratchet among Mitochondria in Natural Populations of the Fungus Amanita phalloides. **2023**, 9, 476 o

35 Y-linked copy number polymorphism of target of rapamycin (TOR) is associated with sexual size dimorphism in seed beetles. o

34 Characterization of the complete mitochondrial genomes of five hard ticks and phylogenetic implications. o

33 Novelties in Macrofungi of the Tropical Montane Cloud Forest in Mexico. **2023**, 9, 477 o

32 Single Copies of the 5S rRNA Inserted into 45S rDNA Intergenic Spacers in the Genomes of Nototheniidae (Perciformes, Actinopterygii). **2023**, 24, 7376 o

31 Identification and expression analysis of heat shock protein family genes of gall fly (Procecidochares utilis) under temperature stress. o

30 The Complete Chloroplast Genomes of Gynostemma Reveal the Phylogenetic Relationships of Species within the Genus. **2023**, 14, 929 o

29 Effects of non-protein nitrogen on buffel grass fiber and ruminal bacterial composition in sheep. **2023**, 105237 o

28 Viruses of sulfur oxidizing phototrophs encode genes for pigment, carbon, and sulfur metabolisms. **2023**, 4, o

27 Comparison of phylogenetic and taxonomic diversity of pitcher plant bogs in Georgia's Coastal Plain. o

26 Sociobiome - Individual and neighborhood socioeconomic status influence the gut microbiome in a multi-ethnic population in the US. o

25	An image cryptography method by highly error-prone DNA storage channel. 11,	0
24	Vaccination of SARS-CoV-2-infected individuals expands a broad range of clonally diverse affinity-matured B cell lineages. **2023**, 14,	0
23	Onthodiplogaster japonica n. gen., n. sp. (Rhabditida: Diplogastridae) isolated from Onthophagus sp. (Coleoptera: Scarabaeidae) from Japan. **2023**, 13,	0
22	Genetic characterization of a group of commercial African timber species: From genomics to barcoding. **2023**, 18, e0284732	0
21	Detection of G3 human-like rotavirus in institutionalized dogs from Brazil.	0
20	CO1 barcodes resolve an asymmetric biphyletic clade for Diabrotica undecimpunctata subspecies and provide nucleotide variants for differentiation from related lineages using real-time PCR. 3,	0
19	Analysis of genome instability and implications for the consequent phenotype in Plasmodium falciparum containing mutated MSH2-1 (P513T). **2023**, 9,	0
18	Isoperla riverae, a new stonefly species from the southeast Nearctic, with notes on sympatric species including the larval description of Isoperla lenati Szczytko & Kondratieff, 2015 (Plecoptera: Perlodidae). **2023**, 5270, 437-470	0
17	Field scale biodegradation of total petroleum hydrocarbons and soil restoration by Ecopiles: microbiological analysis of the process. 14,	0
16	Revisiting the phylogeny of the family Miridae (Heteroptera: Cimicomorpha), with updated insights into its origin and life history evolution. **2023**, 107796	0
15	Analysis of the ARTIC V4 and V4.1 SARS-CoV-2 primers and their impact on the detection of Omicron BA.1 and BA.2 lineage-defining mutations. **2023**, 9,	0
14	Epidemiologic and Clinical Characteristics of Human Bocavirus Infection in Children with or without Acute Gastroenteritis in Acre, Northern Brazil. **2023**, 15, 1024	0
13	A burst of genomic innovation at the origin of placental mammals mediated embryo implantation. **2023**, 6,	0
12	Genetic breaks caused by ancient forest fragmentation: phylogeography of Staudtia kamerunensis (Myristicaceae) reveals distinct clusters in the Congo Basin. **2023**, 19,	0
11	Enterobacter pseudoroggenkampii sp. nov. carrying quinolone-resistant gene qnrE recovered from clinical samples in China.	0
10	Evolution of stridulatory mechanisms: vibroacoustic communication may be common in leaf-footed bugs and allies (Heteroptera: Coreoidea). **2023**, 10,	0
9	Longitudinal Analysis of the Impacts of Urogenital Schistosomiasis on the Gut microbiota of Adolescents in Nigeria.	0
8	De novo transcriptomes of six calanoid copepods (Crustacea): a resource for the discovery of novel genes. **2023**, 10,	0

7	Comparative analysis of dioecious Amaranthus plastomes and phylogenomic implications within Amaranthaceae s.s.. **2023**, 23,	0
6	Ancestral genome reconstruction enhances transposable element annotation by identifying degenerate integrants.	0
5	Near-Complete Genome Sequence of White Spot Syndrome Virus Infecting Cultivated Shrimp (Penaeus vannamei) in Peru.	0
4	Full-spectrum HIV drug resistance mutation detection by high-resolution complete pol gene sequencing. **2023**, 164, 105491	0
3	Phylogenetic and Evolutionary Analysis of Plant Small RNA 2?-O-Methyltransferase (HEN1) Protein Family.	0
2	Humaria setimarginata (Pyronemataceae, Ascomycota), una nueva especie de México. **2023**,	0
1	Comparative Genome Analysis of Old World and New World TYLCV Reveals a Biasness toward Highly Variable Amino Acids in Coat Protein. **2023**, 12, 1995	0