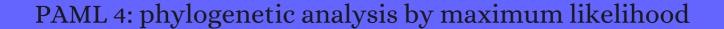
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2266	MORPH: probabilistic alignment combined with hidden Markov models of cis-regulatory modules. 2007 , 3, e216		34
2265	Evolutionary dynamics of introns in plastid-derived genes in plants: saturation nearly reached but slow intron gain continues. <i>Molecular Biology and Evolution</i> , 2008 , 25, 111-9	8.3	23
2264	Detecting groups of coevolving positions in a molecule: a clustering approach. 2007 , 7, 242		35
2263	Diversifying and purifying selection in the peptide binding region of DRB in mammals. 2008 , 66, 384-94		45
2262	Positive selection on HIV accessory proteins and the analysis of molecular adaptation after interspecies transmission. 2008 , 66, 598-604		6
2261	The evolutionary dynamics of human influenza B virus. 2008 , 66, 655-63		162
2260	Molecular evolution of the CPP-like gene family in plants: insights from comparative genomics of Arabidopsis and rice. 2008 , 67, 266-77		66
2259	Adaptive evolution of gamete-recognition proteins in birds. 2008, 67, 488-96		16
2258	Selection on an antimicrobial peptide defensin in ants. 2008 , 67, 643-52		37
2257	Evolution and regulation of the downstream gene of hypoxia-inducible factor-1alpha in naked carp (Gymnocypris przewalskii) from Lake Qinghai, China. 2008 , 67, 570-80		17
2256	Species-specific evolution of class I MHC genes in iguanas (order: Squamata; subfamily: Iguaninae). 2008 , 60, 371-82		16
2255	Recent allopolyploid origin of Zygosaccharomyces rouxii strain ATCC 42981. 2008 , 25, 449-56		62
2254	Hominoid seminal protein evolution and ancestral mating behavior. 2008 , 70, 939-48		30
2253	DNA evidence for a Paleocene origin of the Alcidae (Aves: Charadriiformes) in the Pacific and multiple dispersals across northern oceans. 2008 , 46, 430-45		41
2252	Relative rates of synonymous substitutions in the mitochondrial, chloroplast and nuclear genomes of seed plants. 2008 , 49, 827-31		237
2251	"Reverse ecology" and the power of population genomics. 2008 , 62, 2984-94		104
2250	An evolutionary expressed sequence tag analysis of Drosophila spermatheca genes. 2008 , 62, 2936-47		62

(2008-2008)

2249	The evolution of animal chemosensory receptor gene repertoires: roles of chance and necessity. 2008 , 9, 951-63	443
2248	Evolutionary history of the ancient cutinase family in five filamentous Ascomycetes reveals differential gene duplications and losses and in Magnaporthe grisea shows evidence of sub- and neo-functionalization. 2008 , 180, 711-721	27
2247	Comparative genomics and the study of evolution by natural selection. 2008 , 17, 4586-96	112
2246	Polymorphic MHC loci in an asexual fish, the amazon molly (Poecilia formosa; Poeciliidae). 2008 , 17, 5220-30	21
2245	IDEA: Interactive Display for Evolutionary Analyses. 2008 , 9, 524	19
2244	Consistent and contrasting properties of lineage-specific genes in the apicomplexan parasites Plasmodium and Theileria. 2008 , 8, 108	39
2243	Male-biased genes are overrepresented among novel Drosophila pseudoobscura sex-biased genes. 2008 , 8, 182	6
2242	High divergence in primate-specific duplicated regions: human and chimpanzee chorionic gonadotropin beta genes. 2008 , 8, 195	19
2241	An amphioxus orthologue of the estrogen receptor that does not bind estradiol: insights into estrogen receptor evolution. 2008 , 8, 219	58
2240	Molecular adaptation and expression evolution following duplication of genes for organellar ribosomal protein S13 in rosids. 2008 , 8, 25	10
2239	Non-homogeneous models of sequence evolution in the Bio++ suite of libraries and programs. 2008 , 8, 255	95
2238	Evolutionary history of the alpha2,8-sialyltransferase (ST8Sia) gene family: tandem duplications in early deuterostomes explain most of the diversity found in the vertebrate ST8Sia genes. 2008 , 8, 258	41
2237	Gene conversion and purifying selection of a placenta-specific ERV-V envelope gene during simian evolution. 2008 , 8, 266	23
2236	Unique genes in plants: specificities and conserved features throughout evolution. 2008 , 8, 280	29
2235	Evolutionary history of histone demethylase families: distinct evolutionary patterns suggest functional divergence. 2008 , 8, 294	58
2234	Divergent evolution and molecular adaptation in the Drosophila odorant-binding protein family: inferences from sequence variation at the OS-E and OS-F genes. 2008 , 8, 323	17
2233	The molecular evolution of four anti-malarial immune genes in the Anopheles gambiae species complex. 2008 , 8, 79	33
2232	An evolutionary and structural characterization of mammalian protein complex organization. 2008 , 9, 629	18

2231	The quest for adaptive evolution: a theoretical challenge in a maze of data. 2008 , 11, 110-5	11
2230	Empirical evaluation of a prior for Bayesian phylogenetic inference. 2008 , 363, 4031-9	14
2229	Did RNA editing in plant organellar genomes originate under natural selection or through genetic drift?. 2008 , 3, 43	50
2228	Occult hepatitis B infection: an evolutionary scenario. 2008 , 5, 146	34
2227	Comparative genomics of mutualistic viruses of Glyptapanteles parasitic wasps. 2008, 9, R183	89
2226	Chaetognath transcriptome reveals ancestral and unique features among bilaterians. 2008, 9, R94	52
2225	Comparative analysis of teleost fish genomes reveals preservation of different ancient clock duplicates in different fishes. 2008 , 1, 69-78	46
2224	The mitochondrial genome of Gyrodactylus derjavinoides (Platyhelminthes: Monogenea)a mitogenomic approach for Gyrodactylus species and strain identification. 2008 , 417, 27-34	49
2223	High rates of lateral gene transfer are not due to false diagnosis of gene absence. 2008, 421, 27-31	7
2222	Simple approach to reduce PCR artefact formation leads to reliable genotyping of MHC and other highly polymorphic lociimplications for evolutionary analysis. 2008 , 427, 117-23	130
2221	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. 2008 , 134, 416-26	405
2220	Selection on codon bias. 2008 , 42, 287-99	599
2219	Adaptive changes in the transcription factor HoxA-11 are essential for the evolution of pregnancy in mammals. 2008 , 105, 14928-33	73
2218	Comparative and evolutionary genomics of globin genes in fish. 2008 , 436, 511-38	5
2217	Natural selection on gene function drives the evolution of LTR retrotransposon families in the rice genome. 2009 , 19, 243-54	68
2216	Models of coding sequence evolution. 2009 , 10, 97-109	54
2215	Choosing BLAST options for better detection of orthologs as reciprocal best hits. 2008 , 24, 319-24	335
2214	Natural selection for nucleotide usage at synonymous and nonsynonymous sites in influenza A virus genes. 2008 , 82, 4938-45	21

2213	A dual origin of the Xist gene from a protein-coding gene and a set of transposable elements. 2008 , 3, e2521	129
2212	A captured viral interleukin 10 gene with cellular exon structure. 2008 , 89, 2447-2455	30
2211	Molecular evolution, functional variation, and proposed nomenclature of the gene family that includes sphingomyelinase D in sicariid spider venoms. <i>Molecular Biology and Evolution</i> , 2009 , 26, 547-66 ^{8.3}	85
2210	Recurrent tandem gene duplication gave rise to functionally divergent genes in Drosophila. Molecular Biology and Evolution, 2008, 25, 1451-8	29
2209	Uncorrected nucleotide bias in mtDNA can mimic the effects of positive Darwinian selection. Molecular Biology and Evolution, 2008, 25, 2521-4	16
2208	Comparing phylogenetic trees using a minimum weight perfect matching. 2008,	4
2207	xREI: a phylo-grammar visualization webserver. 2008 , 36, W65-9	2
2206	Null mutations in human and mouse orthologs frequently result in different phenotypes. 2008 , 105, 6987-92	182
2205	Genome-wide analyses of Geraniaceae plastid DNA reveal unprecedented patterns of increased nucleotide substitutions. 2008 , 105, 18424-9	121
2204	Evolution of an RNP assembly system: a minimal SMN complex facilitates formation of UsnRNPs in Drosophila melanogaster. 2008 , 105, 10045-50	75
2203	The promiscuous evolutionary history of the family Bromoviridae. 2008, 89, 1739-1747	39
2202	Bayesian inference of errors in ancient DNA caused by postmortem degradation. <i>Molecular Biology</i> and Evolution, 2008 , 25, 1503-11	16
2201	Building trees of algae: some advances in phylogenetic and evolutionary analysis. 2008 , 43, 229-252	42
2200	Evolutionary diversification of plant shikimate kinase gene duplicates. 2008 , 4, e1000292	32
2199	Evolutionary switch and genetic convergence on rbcL following the evolution of C4 photosynthesis. **Molecular Biology and Evolution, 2008 , 25, 2361-8 **Signal Revolution of C4 photosynthesis. **Signal Revolution of C4 photosynthesis.	102
2198	High-resolution mapping of expression-QTLs yields insight into human gene regulation. 2008 , 4, e1000214	456
2197	Population genomic analysis of strain variation in Leptospirillum group II bacteria involved in acid mine drainage formation. 2008 , 6, e177	106
2196	Molecular Evolution of the Herpesvirales. 2008, 447-475	12

2195	The subtelomere of Oryza sativa chromosome 3 short arm as a hot bed of new gene origination in rice. 2008 , 1, 839-50		31
2194	Adaptive evolution of 5'HoxD genes in the origin and diversification of the cetacean flipper. <i>Molecular Biology and Evolution</i> , 2009 , 26, 613-22	8.3	42
2193	Simulation of genomes: a review. 2008 , 9, 155-9		40
2192	Origin of primate orphan genes: a comparative genomics approach. <i>Molecular Biology and Evolution</i> , 2009 , 26, 603-12	8.3	169
2191	Elucidation of phenotypic adaptations: Molecular analyses of dim-light vision proteins in vertebrates. 2008 , 105, 13480-5		182
2190	Mutation-selection models of codon substitution and their use to estimate selective strengths on codon usage. <i>Molecular Biology and Evolution</i> , 2008 , 25, 568-79	8.3	220
2189	Large-scale reconstruction and phylogenetic analysis of metabolic environments. 2008 , 105, 14482-7		173
2188	Identification of ancient remains through genomic sequencing. 2008 , 18, 1347-53		46
2187	The population genetics of dN/dS. 2008 , 4, e1000304		547
2186	EnsemblCompara GeneTrees: Complete, duplication-aware phylogenetic trees in vertebrates. 2009 , 19, 327-35		836
2186 2185		8.3	836 47
2185	19, 327-35 Adaptive evolution in rodent seminal vesicle secretion proteins. <i>Molecular Biology and Evolution</i> ,	8.3	, in the second
2185	19, 327-35 Adaptive evolution in rodent seminal vesicle secretion proteins. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2301-10	8.3	47
2185 2184	19, 327-35 Adaptive evolution in rodent seminal vesicle secretion proteins. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2301-10 Adaptive functional divergence among triplicated alpha-globin genes in rodents. 2008 , 178, 1623-38 Calculating bootstrap probabilities of phylogeny using multilocus sequence data. <i>Molecular Biology</i>		47 26
2185 2184 2183	Adaptive evolution in rodent seminal vesicle secretion proteins. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2301-10 Adaptive functional divergence among triplicated alpha-globin genes in rodents. 2008 , 178, 1623-38 Calculating bootstrap probabilities of phylogeny using multilocus sequence data. <i>Molecular Biology and Evolution</i> , 2008 , 25, 960-71 Different strategies to persist: the pogo-like Lemi1 transposon produces miniature inverted-repeat		47 26 158
2185 2184 2183 2182	Adaptive evolution in rodent seminal vesicle secretion proteins. <i>Molecular Biology and Evolution</i> , 2008, 25, 2301-10 Adaptive functional divergence among triplicated alpha-globin genes in rodents. 2008, 178, 1623-38 Calculating bootstrap probabilities of phylogeny using multilocus sequence data. <i>Molecular Biology and Evolution</i> , 2008, 25, 960-71 Different strategies to persist: the pogo-like Lemi1 transposon produces miniature inverted-repeat transposable elements or typical defective elements in different plant genomes. 2008, 180, 83-92 Simulating DNA coding sequence evolution with EvolveAGene 3. <i>Molecular Biology and Evolution</i> ,	8.3	47 26 158
2185 2184 2183 2182 2181	Adaptive evolution in rodent seminal vesicle secretion proteins. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2301-10 Adaptive functional divergence among triplicated alpha-globin genes in rodents. 2008 , 178, 1623-38 Calculating bootstrap probabilities of phylogeny using multilocus sequence data. <i>Molecular Biology and Evolution</i> , 2008 , 25, 960-71 Different strategies to persist: the pogo-like Lemi1 transposon produces miniature inverted-repeat transposable elements or typical defective elements in different plant genomes. 2008 , 180, 83-92 Simulating DNA coding sequence evolution with EvolveAGene 3. <i>Molecular Biology and Evolution</i> , 2008 , 25, 688-95 An analysis of structural influences on selection in RNA genes. <i>Molecular Biology and Evolution</i> ,	8.3	47 26 158 17

2177	Efficient computation of the phylogenetic likelihood function on multi-gene alignments and multi-core architectures. 2008 , 363, 3977-84	76
2176	Positively selected sites on the surface glycoprotein (G) of infectious hematopoietic necrosis virus. 2008 , 89, 703-708	15
2175	Rapidly evolving mitochondrial genome and directional selection in mitochondrial genes in the parasitic wasp nasonia (hymenoptera: pteromalidae). <i>Molecular Biology and Evolution</i> , 2008 , 25, 2167-80 ^{8.3}	170
2174	Extremely intron-rich genes in the alveolate ancestors inferred with a flexible maximum-likelihood approach. <i>Molecular Biology and Evolution</i> , 2008 , 25, 903-11	44
2173	The origin and phylogeography of dog rabies virus. 2008 , 89, 2673-2681	165
2172	False-positive results obtained from the branch-site test of positive selection. 2008, 83, 331-8	22
2171	How to summarize estimates of ancestral divergence times. 2008 , 4, 75-95	21
2170	Evidence for positive selection in putative virulence factors within the Paracoccidioides brasiliensis species complex. 2008 , 2, e296	32
2169	Pilus operon evolution in Streptococcus pneumoniae is driven by positive selection and recombination. 2008 , 3, e3660	19
2168	Phylogenetic analyses: A toolbox expanding towards Bayesian methods. 2008 , 2008, 683509	5
2167	Evolution and survival on eutherian sex chromosomes. 2009 , 5, e1000568	58
2166	Exceptional diversity, non-random distribution, and rapid evolution of retroelements in the B73 maize genome. 2009 , 5, e1000732	266
2165	Molecular adaptation of rbcL in the heterophyllous aquatic plant Potamogeton. 2009, 4, e4633	42
2164	New genomic structure for prostate cancer specific gene PCA3 within BMCC1: implications for prostate cancer detection and progression. 2009 , 4, e4995	63
2163	Parallel loss of plastid introns and their maturase in the genus Cuscuta. 2009 , 4, e5982	44
2162	Evolutionary trends of A(H1N1) influenza virus hemagglutinin since 1918. 2009 , 4, e7789	60
2161	Rhodopsin molecular evolution in mammals inhabiting low light environments. 2009 , 4, e8326	42
2160	Evolvability of Chaperonin Substrate Proteins. 2009,	

2159 Novel determinants describe chaperonin substrate proteins. 2009,

2158	Accounting for molecular stochasticity in systematic revisions: species limits and phylogeny of Paroaria. 2009 ,	
2157	Load Balance in the Phylogenetic Likelihood Kernel. 2009,	9
2156	Positive Selection of Paclitaxel Biosynthetic Genes Detected at Both Nucleotide and Amino Acid Levels. 2009 ,	
2155	Horizontal gene transfer of an entire metabolic pathway between a eukaryotic alga and its DNA virus. 2009 , 19, 1441-9	107
2154	Adaptive evolution of young gene duplicates in mammals. 2009 , 19, 859-67	138
2153	The consequences of genetic drift for bacterial genome complexity. 2009 , 19, 1450-4	204
2152	Pathway evolution by horizontal transfer and positive selection is accommodated by relaxed negative selection upon upstream pathway genes in purple bacterial carotenoid biosynthesis. 2009 , 191, 7500-8	15
2151	Evidence for Positive Selection in Ser/Thr Protein Kinases (STKs) Genes of Trichodesmium erythraeum. 2009 ,	
2150	Reliabilities of identifying positive selection by the branch-site and the site-prediction methods. 2009 , 106, 6700-5	125
2149	The universal distribution of evolutionary rates of genes and distinct characteristics of eukaryotic genes of different apparent ages. 2009 , 106, 7273-80	160
2148	Signatures of natural selection are not uniform across genes of innate immune system, but purifying selection is the dominant signature. 2009 , 106, 7073-8	85
2147	Dynamic functional evolution of an odorant receptor for sex-steroid-derived odors in primates. 2009 , 106, 21247-51	34
2146	Formyl peptide receptors are candidate chemosensory receptors in the vomeronasal organ. 2009 , 106, 9842-7	177
2145	Distribution, diversity, evolution, and survival of Helitrons in the maize genome. 2009 , 106, 19922-7	122
2144	Response of gastric epithelial progenitors to Helicobacter pylori Isolates obtained from Swedish patients with chronic atrophic gastritis. 2009 , 284, 30383-94	22
2143	Evolutionary replacement of UV vision by violet vision in fish. 2009 , 106, 17457-62	28
2142	Rapid evolution of immune proteins in social insects. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1791-80 8.3	56

2141	Phylogenomics of C(4) photosynthesis in sedges (Cyperaceae): multiple appearances and genetic convergence. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1909-19	8.3	115
2140	Minimal effect of ectopic gene conversion among recent duplicates in four mammalian genomes. 2009 , 182, 615-22		38
2139	Learning to count: robust estimates for labeled distances between molecular sequences. <i>Molecular Biology and Evolution</i> , 2009 , 26, 801-14	8.3	78
2138	Population genomics of intron splicing in 38 Saccharomyces cerevisiae genome sequences. 2009 , 1, 466	-78	15
2137	Possible diversifying selection in the imprinted gene, MEDEA, in Arabidopsis. <i>Molecular Biology and Evolution</i> , 2009 , 26, 843-57	8.3	35
2136	Trends in prokaryotic evolution revealed by comparison of closely related bacterial and archaeal genomes. 2009 , 191, 65-73		107
2135	Genomic epidemiology of a dengue virus epidemic in urban Singapore. 2009 , 83, 4163-73		79
2134	Pervasive, genome-wide positive selection leading to functional divergence in the bacterial genus Campylobacter. 2009 , 19, 1224-32		55
2133	In planta expression screens of Phytophthora infestans RXLR effectors reveal diverse phenotypes, including activation of the Solanum bulbocastanum disease resistance protein Rpi-blb2. 2009 , 21, 2928-	-47	245
2132	Detecting species-site dependencies in large multiple sequence alignments. 2009 , 37, 5959-68		12
2131	Convergent evolution of metabolic roles in bacterial co-symbionts of insects. 2009 , 106, 15394-9		256
2130	Coevolution of interacting fertilization proteins. 2009 , 5, e1000570		107
2129	Patterns of variation in the evolution of carotenoid biosynthetic pathway enzymes of higher plants. 2009 , 100, 754-61		38
2128	Nucleotide and copy-number polymorphism at the odorant receptor genes Or22a and Or22b in Drosophila melanogaster. <i>Molecular Biology and Evolution</i> , 2009 , 26, 61-70	8.3	23
2127	Recent strong positive selection on Drosophila melanogaster HDAC6, a gene encoding a stress surveillance factor, as revealed by population genomic analysis. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1549-56	8.3	16
2126	Prolactin in the Afrotheria: characterization of genes encoding prolactin in elephant (Loxodonta africana), hyrax (Procavia capensis) and tenrec (Echinops telfairi). 2009 , 200, 233-40		3
2125	Phylogenetic relationships and molecular adaptation dynamics of human rhinoviruses. <i>Molecular Biology and Evolution</i> , 2009 , 26, 969-81	8.3	29
2124	Molecular evolution of GYPC: evidence for recent structural innovation and positive selection in humans. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2679-87	8.3	17

2123	Adaptive evolution of chloroplast genomes in ancestral grasses. 2009 , 4, 623-4	3
2122	When one plus one equals three: Biochemistry and bioinformatics combine to answer complex questions. 2009 , 3, 212-214	1
2121	Hormone-activated estrogen receptors in annelid invertebrates: implications for evolution and endocrine disruption. 2009 , 150, 1731-8	92
2120	Accurate estimation of gene evolutionary rates using XRATE, with an application to transmembrane proteins. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1715-21	7
2119	Molecular evolution and functional diversification of fatty acid desaturases after recurrent gene duplication in Drosophila. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1447-56	44
2118	Differential evolution of Human Immunodeficiency Virus type 1 Protease and Reverse Transcriptase genes between HAART-failing and nalle-treated individuals. 2009 , 7, 601-5	10
2117	Processing and population genetic analysis of multigenic datasets with ProSeq3 software. 2009 , 25, 3189-9	00 67
2116	mRNA retrotransposition coupled with 5' inversion as a possible source of new genes. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1405-20	9
2115	Evolution of regulatory sequences in 12 Drosophila species. 2009 , 5, e1000330	63
2114	Species-specific activity of HIV-1 Vpu and positive selection of tetherin transmembrane domain variants. 2009 , 5, e1000300	246
2113	Isolation and characterization of adenoviruses persistently shed from the gastrointestinal tract of non-human primates. 2009 , 5, e1000503	109
2112	Molecular evolutionary consequences of niche restriction in Francisella tularensis, a facultative intracellular pathogen. 2009 , 5, e1000472	103
2111	Molecular decay of the tooth gene Enamelin (ENAM) mirrors the loss of enamel in the fossil record of placental mammals. 2009 , 5, e1000634	107
2110	Identifying changes in selective constraints: host shifts in influenza. 2009 , 5, e1000564	83
2109	Predicting functional alternative splicing by measuring RNA selection pressure from multigenome alignments. 2009 , 5, e1000608	20
2108	Segregating YKU80 and TLC1 alleles underlying natural variation in telomere properties in wild yeast. 2009 , 5, e1000659	39
2107	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. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2515-20	11
2106	Nonlinear dynamics of nonsynonymous (dN) and synonymous (dS) substitution rates affects inference of selection. 2009 , 1, 308-19	75

2105	Evolution of mutation rates: phylogenomic analysis of the photolyase/cryptochrome family. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1143-53	8.3	62
2104	Genome-wide functional divergence after the symbiosis of proteobacteria with insects unraveled through a novel computational approach. 2009 , 5, e1000344		16
2103	Footprints of inversions at present and past pseudoautosomal boundaries in human sex chromosomes. 2009 , 1, 56-66		62
2102	Accelerated evolution of the Prdm9 speciation gene across diverse metazoan taxa. 2009 , 5, e1000753		203
2101	Temporal trails of natural selection in human mitogenomes. <i>Molecular Biology and Evolution</i> , 2009 , 26, 715-7	8.3	23
2100	Meiotic recombination generates rich diversity in NK cell receptor genes, alleles, and haplotypes. 2009 , 19, 757-69		87
2099	Evolutionary insights on C4 photosynthetic subtypes in grasses from genomics and phylogenetics. 2009 , 1, 221-30		53
2098	Investigating protein-coding sequence evolution with probabilistic codon substitution models. <i>Molecular Biology and Evolution</i> , 2009 , 26, 255-71	8.3	111
2097	A history of recurrent positive selection at the toll-like receptor 5 in primates. <i>Molecular Biology and Evolution</i> , 2009 , 26, 937-49	8.3	77
2096	Evolution of olfactory receptor genes in primates dominated by birth-and-death process. 2009 , 1, 258-0	64	31
2096	Evolution of olfactory receptor genes in primates dominated by birth-and-death process. 2009 , 1, 258-0. Hotspots of biased nucleotide substitutions in human genes. 2009 , 7, e26	54	31
2095		64	
2095	Hotspots of biased nucleotide substitutions in human genes. 2009 , 7, e26	64	118
2095 2094	Hotspots of biased nucleotide substitutions in human genes. 2009 , 7, e26 Phylogenomics of unusual histone H2A Variants in Bdelloid rotifers. 2009 , 5, e1000401 Death and resurrection of the human IRGM gene. 2009 , 5, e1000403 Evolution of C(4) phosphoenologyruvate carboxykinase in grasses, from genotype to phenotype.	8.3	118
2095 2094 2093	Hotspots of biased nucleotide substitutions in human genes. 2009 , 7, e26 Phylogenomics of unusual histone H2A Variants in Bdelloid rotifers. 2009 , 5, e1000401 Death and resurrection of the human IRGM gene. 2009 , 5, e1000403 Evolution of C(4) phosphoenolpyruvate carboxykinase in grasses, from genotype to phenotype.		1181975
2095 2094 2093 2092	Hotspots of biased nucleotide substitutions in human genes. 2009, 7, e26 Phylogenomics of unusual histone H2A Variants in Bdelloid rotifers. 2009, 5, e1000401 Death and resurrection of the human IRGM gene. 2009, 5, e1000403 Evolution of C(4) phosphoenolpyruvate carboxykinase in grasses, from genotype to phenotype. Molecular Biology and Evolution, 2009, 26, 357-65 Evolution of duplicated beta-globin genes and the structural basis of hemoglobin isoform differentiation in Mus. Molecular Biology and Evolution, 2009, 26, 2521-32 Comparative analysis between homoeologous genome segments of Brassica napus and its	8.3	118197554
2095 2094 2093 2092 2091	Hotspots of biased nucleotide substitutions in human genes. 2009, 7, e26 Phylogenomics of unusual histone H2A Variants in Bdelloid rotifers. 2009, 5, e1000401 Death and resurrection of the human IRGM gene. 2009, 5, e1000403 Evolution of C(4) phosphoenolpyruvate carboxykinase in grasses, from genotype to phenotype. Molecular Biology and Evolution, 2009, 26, 357-65 Evolution of duplicated beta-globin genes and the structural basis of hemoglobin isoform differentiation in Mus. Molecular Biology and Evolution, 2009, 26, 2521-32 Comparative analysis between homoeologous genome segments of Brassica napus and its progenitor species reveals extensive sequence-level divergence. 2009, 21, 1912-28	8.3	11819755427

2087	Novel cytomegaloviruses in free-ranging and captive great apes: phylogenetic evidence for bidirectional horizontal transmission. 2009 , 90, 2386-2394		36
2086	Proteomic discovery of previously unannotated, rapidly evolving seminal fluid genes in Drosophila. 2009 , 19, 886-96		114
2085	Genomic insights into the convergence and pathogenicity factors of Campylobacter jejuni and Campylobacter coli species. 2009 , 191, 5824-31		28
2084	Genotype-phenotype associations: substitution models to detect evolutionary associations between phenotypic variables and genotypic evolutionary rate. 2009 , 25, i94-100		26
2083	Response to Comment on "Human-Specific Gain of Function in a Developmental Enhancer". 2009 , 323, 714d-714d		8
2082	The smallest avian genomes are found in hummingbirds. 2009 , 276, 3753-7		38
2081	Sexual selection drives weak positive selection in protamine genes and high promoter divergence, enhancing sperm competitiveness. 2009 , 276, 2427-36		40
2080	Latitude, elevation and the tempo of molecular evolution in mammals. 2009 , 276, 3353-9		67
2079	Gourds afloat: a dated phylogeny reveals an Asian origin of the gourd family (Cucurbitaceae) and numerous oversea dispersal events. 2009 , 276, 843-51		205
2078	In defense of statistical methods for detecting positive selection. 2009 , 106, E95; author reply E96		34
2077	Comparative metagenomic analysis of a microbial community residing at a depth of 4,000 meters at station ALOHA in the North Pacific subtropical gyre. 2009 , 75, 5345-55		170
2076	Selectome: a database of positive selection. 2009 , 37, D404-7		32
2075	Statistical comparison of nucleotide, amino acid, and codon substitution models for evolutionary analysis of protein-coding sequences. 2009 , 58, 199-210		31
2074	Does gene translocation accelerate the evolution of laterally transferred genes?. 2009 , 182, 1365-75		11
2073	A recent adaptive transposable element insertion near highly conserved developmental loci in Drosophila melanogaster. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1949-61	8.3	52
2072	The decay of the chromosomally encoded ccdO157 toxin-antitoxin system in the Escherichia coli species. 2009 , 181, 1557-66		37
2071	Seven gene phylogeny of heterokonts. 2009 , 160, 191-204		100
2070	Weak functional constraints on phosphoproteomes. 2009 , 25, 193-7		222

2069	AIR: A batch-oriented web program package for construction of supermatrices ready for phylogenomic analyses. 2009 , 10, 357	180
2068	The mitochondrial genome structure of Xenoturbella bocki (phylum Xenoturbellida) is ancestral within the deuterostomes. 2009 , 9, 107	35
2067	Comparative mitochondrial genomics within and among species of killifish. 2009 , 9, 11	37
2066	A complex selection signature at the human AVPR1B gene. 2009 , 9, 123	8
2065	Independent inactivation of arginine decarboxylase genes by nonsense and missense mutations led to pseudogene formation in Chlamydia trachomatis serovar L2 and D strains. 2009 , 9, 166	13
2064	Evolution and functional divergence of NLRP genes in mammalian reproductive systems. 2009 , 9, 202	110
2063	Evolutionary dynamics of the LTR retrotransposons roo and rooA inferred from twelve complete Drosophila genomes. 2009 , 9, 205	14
2062	Evolutionary rate patterns of the Gibberellin pathway genes. 2009 , 9, 206	41
2061	Neogastropod phylogenetic relationships based on entire mitochondrial genomes. 2009 , 9, 210	95
2060	Phylogenetic inference under varying proportions of indel-induced alignment gaps. 2009 , 9, 211	54
2059	FoxO gene family evolution in vertebrates. 2009 , 9, 222	28
2058	Positive selection for the male functionality of a co-retroposed gene in the hominoids. 2009 , 9, 252	11
2057	Phylogenetic analysis of mitochondrial substitution rate variation in the angiosperm tribe Sileneae. 2009 , 9, 260	90
2056	Diverse MHC IIB allele repertoire increases parasite resistance and body condition in the Long-tailed giant rat (Leopoldamys sabanus). 2009 , 9, 269	44
2055	Statistical tests for natural selection on regulatory regions based on the strength of transcription factor binding sites. 2009 , 9, 286	17
2054	Evolution of the multifaceted eukaryotic akirin gene family. 2009 , 9, 34	72
2053	Molecular evolution of UCP1 and the evolutionary history of mammalian non-shivering thermogenesis. 2009 , 9, 4	63
2052	Expression and evolutionary divergence of the non-conventional olfactory receptor in four species of fig wasp associated with one species of fig. 2009 , 9, 43	16

2051	Evolution of the class C GPCR Venus flytrap modules involved positive selected functional divergence. 2009 , 9, 67	28
2050	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. 2009 , 9, 90	71
2049	A single origin of the photosynthetic organelle in different Paulinella lineages. 2009 , 9, 98	55
2048	IMGD: an integrated platform supporting comparative genomics and phylogenetics of insect mitochondrial genomes. 2009 , 10, 148	15
2047	Genome-wide identification and characterization of cytochrome P450 monooxygenase genes in the ciliate Tetrahymena thermophila. 2009 , 10, 208	27
2046	Complete sequence determination of a novel reptile iridovirus isolated from soft-shelled turtle and evolutionary analysis of Iridoviridae. 2009 , 10, 224	92
2045	Gene discovery using massively parallel pyrosequencing to develop ESTs for the flesh fly Sarcophaga crassipalpis. 2009 , 10, 234	102
2044	Divergence in function and expression of the NOD26-like intrinsic proteins in plants. 2009 , 10, 313	59
2043	Assessing the genomic evidence for conserved transcribed pseudogenes under selection. 2009 , 10, 435	56
2042	454 pyrosequencing based transcriptome analysis of Zygaena filipendulae with focus on genes involved in biosynthesis of cyanogenic glucosides. 2009 , 10, 574	55
2041	The mitochondrial genomes of sponges provide evidence for multiple invasions by Repetitive Hairpin-forming Elements (RHE). 2009 , 10, 591	36
2040	The expansion of amino-acid repeats is not associated to adaptive evolution in mammalian genes. 2009 , 10, 619	5
2039	Molecular evolution of the hyperthermophilic archaea of the Pyrococcus genus: analysis of adaptation to different environmental conditions. 2009 , 10, 639	22
2038	aes, the gene encoding the esterase B in Escherichia coli, is a powerful phylogenetic marker of the species. 2009 , 9, 273	9
2037	Phylogenetic analysis and molecular evolution of the dormancy associated MADS-box genes from peach. 2009 , 9, 81	67
2036	The cellulose synthase superfamily in fully sequenced plants and algae. 2009 , 9, 99	110
2035	An expanded clade of rodent Trim5 genes. 2009 , 385, 473-83	53
2034	Association between genomic heterogeneity of hepatitis B virus and intrauterine infection. 2009 , 387, 168-75	18

2033	Growth hormone and insulin-like growth factor of naked carp (Gymnocypris przewalskii) in Lake Qinghai: expression in different water environments. 2009 , 161, 400-6	23
2032	Evolution of opsin genes reveals a functional role of vision in the echolocating little brown bat (Myotis lucifugus). 2009 , 37, 154-161	18
2031	Diversifying selective pressure on influenza B virus hemagglutinin. 2009 , 81, 114-24	36
2030	Beta-keratins of the crocodilian epidermis: composition, structure, and phylogenetic relationships. 2009 , 312, 42-57	47
2029	Duplication of AP1 within the Spinacia oleracea L. AP1/FUL clade is followed by rapid amino acid and regulatory evolution. 2009 , 229, 507-21	17
2028	Expression diversity and evolutionary dynamics of rice duplicate genes. 2009 , 281, 483-93	35
2027	Genome-wide identification of NBS-encoding resistance genes in Brassica rapa. 2009 , 282, 617-31	114
2026	Increased constraints on MC4R during primate and human evolution. 2009 , 124, 633-47	22
2025	Genetically distinct strains of Cassava brown streak virus in the Lake Victoria basin and the Indian Ocean coastal area of East Africa. 2009 , 154, 353-9	91
2024	Positive selection drives the evolution of bat bitter taste receptor genes. 2009 , 47, 207-15	16
2023	Relaxed purifying selection of rhodopsin gene within a Chinese endemic cavefish genus Sinocyclocheilus (Pisces: Cypriniformes). 2009 , 624, 139-149	7
2022	Is Brightest Best? Testing the Hamilton-Zuk Hypothesis in Mandrills. 2009 , 30, 825-844	38
2021	Molecular evolution of paclitaxel biosynthetic genes TS and DBAT of Taxus species. 2009 , 135, 123-35	10
2020	Sequence signatures of a recent chromosomal rearrangement in Drosophila mojavensis. 2009 , 136, 5-11	11
2019	Comparative genomic analysis of teleost fish bmal genes. 2009 , 136, 149-61	32
2018	Evolution of the pili nut genus (Canarium L., Burseraceae) and its cultivated species. 2009 , 56, 765-781	15
2017	The selection pressure analysis of chicken anemia virus structural protein gene VP1. 2009 , 38, 259-62	6
2016	Molecular evolution of novel swine-origin A/H1N1 influenza viruses among and before human. 2009 , 39, 293-300	14

2015	Phylogenetic relationships and divergence times of the family Araucariaceae based on the DNA sequences of eight genes. 2009 , 54, 2648-2655	17
2014	Keeping the blood flowing-plasminogen activator genes and feeding behavior in vampire bats. 2009 , 96, 39-47	21
2013	Gene conversion and positive selection driving the evolution of the Caenorhabditis ssp. ZIM/HIM-8 protein family. 2009 , 68, 217-26	2
2012	Phylogenetic inference with weighted codon evolutionary distances. 2009 , 68, 377-92	5
2011	Characterization of the sperm molecule bindin in the sea urchin genus Paracentrotus. 2009 , 68, 366-76	18
2010	Correlation between Ka/Ks and Ks is related to substitution model and evolutionary lineage. 2009 , 68, 414-23	42
2009	Gene conversion among paralogs results in moderate false detection of positive selection using likelihood methods. 2009 , 68, 679-87	28
2008	Sequence polymorphism and evolution of three cetacean MHC genes. 2009 , 69, 260-75	20
2007	Phylogenetic analysis of the NEEP21/calcyon/P19 family of endocytic proteins: evidence for functional evolution in the vertebrate CNS. 2009 , 69, 319-32	14
2006	Distinct evolutionary patterns between two duplicated color vision genes within cyprinid fishes. 2009 , 69, 346-59	9
2005	Evolutionary history of an MHC gene in two leporid species: characterisation of Mhc-DQA in the European brown hare and comparison with the European rabbit. 2009 , 61, 131-44	27
2004	Identification and characterisation of a novel immune-type receptor (NITR) gene cluster in the European sea bass, Dicentrarchus labrax, reveals recurrent gene expansion and diversification by positive selection. 2009 , 61, 773-88	15
2003	Structural model of rho1 GABAC receptor based on evolutionary analysis: Testing of predicted protein-protein interactions involved in receptor assembly and function. 2009 , 18, 2371-83	16
2002	Base composition, selection, and phylogenetic significance of indels in the recombination activating gene-1 in vertebrates. 2009 , 6, 32	8
2001	Intronic regulatory elements determine the divergent expression patterns of AGAMOUS-LIKE6 subfamily members in Arabidopsis. 2009 , 59, 987-1000	61
2000	Elevation of Francisella philomiragia subsp. noatunensis Mikalsen et al. (2007) to Francisella noatunensis comb. nov. [syn. Francisella piscicida Ottem et al. (2008) syn. nov.] and characterization of Francisella noatunensis subsp. orientalis subsp. nov., two important fish pathogens. 2009 , 106, 1231-43	85
1999	Origin of Mediterranean insular endemics in the Boraginales: integrative evidence from molecular dating and ancestral area reconstruction. 2009 , 36, 1282-1296	75
1998	Hidden Wolbachia diversity in field populations of the European cherry fruit fly, Rhagoletis cerasi (Diptera, Tephritidae). 2009 , 18, 3816-30	85

1997	To see in different seas: spatial variation in the rhodopsin gene of the sand goby (Pomatoschistus minutus). 2009 , 18, 4227-39	45
1996	Complete mitochondrial DNA replacement in a Lake Tanganyika cichlid fish. 2009 , 18, 4240-55	79
1995	Adaptive evolution of interferon-gamma in Glire lineage and evidence for a recent selective sweep in Mus. m. domesticus. 2009 , 10, 297-308	4
1994	The dystrobrevin-binding protein 1 gene: features and networks. 2009 , 14, 18-29	93
1993	Protein kinase R reveals an evolutionary model for defeating viral mimicry. 2009, 457, 485-9	190
1992	Primate home range and GRIN2A, a receptor gene involved in neuronal plasticity: implications for the evolution of spatial memory. 2009 , 8, 435-41	6
1991	Phylogenetic origin of Phyllolobium with a further implication for diversification of Astragalus in China. 2009 , 51, 889-99	16
1990	Comparative genomic and population genetic analyses indicate highly porous genomes and high levels of gene flow between divergent helianthus species. 2009 , 63, 2061-75	96
1989	Slower tempo of microevolution in island birds: implications for conservation biology. 2009 , 63, 2275-87	33
1988	Deciphering and dating the red panda's ancestry and early adaptive radiation of Musteloidea. 2009 , 53, 907-22	109
1988		109
	Detecting positive selection in the budding yeast genome. 2009 , 22, 2430-7	
1987	53, 907-22 Detecting positive selection in the budding yeast genome. 2009 , 22, 2430-7 Timing of the functional diversification of alpha- and beta-adrenoceptors in fish and other	17
1987 1986	Detecting positive selection in the budding yeast genome. 2009 , 22, 2430-7 Timing of the functional diversification of alpha- and beta-adrenoceptors in fish and other vertebrates. 2009 , 1163, 343-7 ANALYSIS OF A PLASTID MULTIGENE DATA SET AND THE PHYLOGENETIC POSITION OF THE MARINE MACROALGA CAULERPA FILIFORMIS (CHLOROPHYTA)(1). 2009 , 45, 1206-12 Beta-keratins of turtle shell are glycine-proline-tyrosine rich proteins similar to those of	17 30
1987 1986 1985	Detecting positive selection in the budding yeast genome. 2009 , 22, 2430-7 Timing of the functional diversification of alpha- and beta-adrenoceptors in fish and other vertebrates. 2009 , 1163, 343-7 ANALYSIS OF A PLASTID MULTIGENE DATA SET AND THE PHYLOGENETIC POSITION OF THE MARINE MACROALGA CAULERPA FILIFORMIS (CHLOROPHYTA)(1). 2009 , 45, 1206-12 Beta-keratins of turtle shell are glycine-proline-tyrosine rich proteins similar to those of	17 30 23
1987 1986 1985 1984	Detecting positive selection in the budding yeast genome. 2009, 22, 2430-7 Timing of the functional diversification of alpha- and beta-adrenoceptors in fish and other vertebrates. 2009, 1163, 343-7 ANALYSIS OF A PLASTID MULTIGENE DATA SET AND THE PHYLOGENETIC POSITION OF THE MARINE MACROALGA CAULERPA FILIFORMIS (CHLOROPHYTA)(1). 2009, 45, 1206-12 Beta-keratins of turtle shell are glycine-proline-tyrosine rich proteins similar to those of crocodilians and birds. 2009, 214, 284-300 Evolutionary rates and timescale comparison of Chikungunya viruses inferred from the whole genome/E1 gene with special reference to the 2005-07 outbreak in the Indian subcontinent. 2009, 9, 16-23	17 30 23 55
1987 1986 1985 1984	Detecting positive selection in the budding yeast genome. 2009, 22, 2430-7 Timing of the functional diversification of alpha- and beta-adrenoceptors in fish and other vertebrates. 2009, 1163, 343-7 ANALYSIS OF A PLASTID MULTIGENE DATA SET AND THE PHYLOGENETIC POSITION OF THE MARINE MACROALGA CAULERPA FILIFORMIS (CHLOROPHYTA)(1). 2009, 45, 1206-12 Beta-keratins of turtle shell are glycine-proline-tyrosine rich proteins similar to those of crocodilians and birds. 2009, 214, 284-300 Evolutionary rates and timescale comparison of Chikungunya viruses inferred from the whole genome/E1 gene with special reference to the 2005-07 outbreak in the Indian subcontinent. 2009, 9, 16-23 Genetic characterization of type A foot-and-mouth disease virus 3A region in context of the	17 30 23 55 58
1987 1986 1985 1984 1983 1982	Detecting positive selection in the budding yeast genome. 2009, 22, 2430-7 Timing of the functional diversification of alpha- and beta-adrenoceptors in fish and other vertebrates. 2009, 1163, 343-7 ANALYSIS OF A PLASTID MULTIGENE DATA SET AND THE PHYLOGENETIC POSITION OF THE MARINE MACROALGA CAULERPA FILIFORMIS (CHLOROPHYTA)(1). 2009, 45, 1206-12 Beta-keratins of turtle shell are glycine-proline-tyrosine rich proteins similar to those of crocodilians and birds. 2009, 214, 284-300 Evolutionary rates and timescale comparison of Chikungunya viruses inferred from the whole genome/E1 gene with special reference to the 2005-07 outbreak in the Indian subcontinent. 2009, 9, 16-23 Genetic characterization of type A foot-and-mouth disease virus 3A region in context of the reemergence of VP359-deletion lineage in India. 2009, 9, 483-92 Rapidly evolving genes in pathogens: methods for detecting positive selection and examples	17 30 23 55 58

1979	MtZoa: a general mitochondrial amino acid substitutions model for animal evolutionary studies. 2009 , 52, 268-72	72
1978	The historical biogeography of the freshwater knifefishes using mitogenomic approaches: a mesozoic origin of the Asian notopterids (Actinopterygii: Osteoglossomorpha). 2009 , 51, 486-99	48
1977	Multiple colonisations of the western Indian Ocean by Pteropus fruit bats (Megachiroptera: Pteropodidae): the furthest islands were colonised first. 2009 , 51, 294-303	36
1976	A Pleistocene inter-tribal allopolyploidization event precedes the species radiation of Pachycladon (Brassicaceae) in New Zealand. 2009 , 51, 365-72	52
1975	Evolution and phylogenetic utility of the melanocortin-1 receptor gene (MC1R) in Cetartiodactyla. 2009 , 52, 550-7	17
1974	Accounting for molecular stochasticity in systematic revisions: species limits and phylogeny of Paroaria. 2009 , 53, 234-48	16
1973	The phylogenetic relationships of cynopterine fruit bats (Chiroptera: Pteropodidae: Cynopterinae). 2009 , 53, 772-83	11
1972	Analysis of the genetic variability of the mumps SH gene in viruses circulating in the UK between 1996 and 2005. 2009 , 9, 71-80	22
1971	Evolution of a novel phenolic pathway for pollen development. 2009 , 325, 1688-92	130
1970	A genome-wide in vitro bacterial-infection screen reveals human variation in the host response associated with inflammatory disease. 2009 , 85, 214-27	60
1969	Adaptive evolution of genes of archaea belonging to the genus Pyrococcus associated with adaptation to life under high-pressure conditions. 2009 , 425, 91-3	1
1968	Phylogenetic methods in natural product research. 2009 , 26, 1585-602	24
1967	Phytophthora infestans isolates lacking class I ipiO variants are virulent on Rpi-blb1 potato. 2009 , 22, 1535-45	99
1966	In This Issue. 2009 , 106, 8793-8794	78
1965	Molecular evolution and functional divergence of sulfate transporter gene family in plants. 2009,	
1964	Evolutionary analysis of orthologous cDNA sequences from cultured and symbiotic dinoflagellate symbionts of reef-building corals (Dinophyceae: Symbiodinium). 2009 , 4, 67-74	31
1963	Variations in the sequences of BMP2 imply different mechanisms for the evolution of morphological diversity in vertebrates. 2009 , 4, 100-4	1
1962	Differential spatio-temporal expression and functional diversification of the myogenic regulatory factors MyoD1 and MyoD2 in Atlantic halibut (Hippoglossus hippoglossus). 2009 , 154, 93-101	7

1961	Molecular systematics and evolution of the recently discovered "Parnassian" butterfly (Parnassius davydovi Churkin, 2006) and its allied species (Lepidoptera, Papilionidae). 2009 , 441, 80-8	12
1960	Evaluation of the effect of CpG hypermutability on human codon substitution. 2009 , 431, 18-22	12
1959	Evolutionary selection pressure of forkhead domain and functional divergence. 2009 , 432, 19-25	15
1958	The rapid evolution of signal peptides is mainly caused by relaxed selection on non-synonymous and synonymous sites. 2009 , 436, 8-11	30
1957	Identification of expressed transposable element insertions in the sequenced genome of Drosophila melanogaster. 2009 , 439, 55-62	19
1956	Characterization of a putative hsp70 pseudogene transcribed in protoscoleces and adult worms of Echinococcus granulosus. 2009 , 443, 1-11	8
1955	Fast, adaptive evolution at a bacterial host-resistance locus: the PFam54 gene array in Borrelia burgdorferi. 2009 , 445, 26-37	37
1954	Evolution of the Schlafen genes, a gene family associated with embryonic lethality, meiotic drive, immune processes and orthopoxvirus virulence. 2009 , 447, 1-11	68
1953	Origin and evolution of ubiquitin-conjugating enzymes from Guillardia theta nucleomorph to hominoid. 2009 , 447, 72-85	10
1952	New insulin-like growth factor (IGF)-precursor sequences from mammalian genomes: the molecular evolution of IGFs and associated peptides in primates. 2009 , 19, 12-23	58
1951	Identification of new meningococcal serogroup B surface antigens through a systematic analysis of neisserial genomes. 2009 , 28, 532-41	20
1950	Phylogeny and evolution of the NS1 and VP1/VP2 gene sequences from porcine parvovirus. 2009 , 140, 209-15	30
1949	Analysis of the leader proteinase (L(pro)) region of type A foot-and-mouth disease virus with due emphasis on phylogeny and evolution of the emerging VP3(59)-deletion lineage from India. 2009 , 141, 34-46	5
1948	Adaptive history of single copy genes highly expressed in the term human placenta. 2009 , 93, 33-41	22
1947	MtDNA GeneExtractor: a computer tool for mtDNA gene/region information extraction. 2009, 9, 36-40	1
1946	Murine NKG2D ligands: "double, double toil and trouble". 2009 , 46, 1011-9	34
1945	Recent relaxation of purifying selection on the tandem-repetitive early-stage histone H3 gene in brooding sea stars. 2009 , 2, 113-8	6
1944	Gamma-MYN: a new algorithm for estimating Ka and Ks with consideration of variable substitution rates. 2009 , 4, 20	60

1943	Divergent evolution and purifying selection of the flaA gene sequences in Aeromonas. 2009, 4, 23	7
1942	Inferring clocks when lacking rocks: the variable rates of molecular evolution in bacteria. 2009 , 4, 35	94
1941	Major histocompatibility complex Class II DRB exon-2 diversity of the Eurasian lynx (Lynx lynx) in China. 2009 , 43, 245-257	13
1940	Inferring selection in the Anopheles gambiae species complex: an example from immune-related serine protease inhibitors. 2009 , 8, 117	23
1939	Population genetics of fungal and oomycete effectors involved in gene-for-gene interactions. 2009 , 22, 371-80	104
1938	Genome-wide comparative analysis of the Brassica rapa gene space reveals genome shrinkage and differential loss of duplicated genes after whole genome triplication. 2009 , 10, R111	155
1937	The bovine lactation genome: insights into the evolution of mammalian milk. 2009 , 10, R43	143
1936	A Case Study of the Molecular Genetical Diagnosis of a Small African Elephant (Loxodontasp.) Nana Kept at Asahiyama Zoo. 2009 , 34, 171-177	1
1935	Evolution of AGL6-like MADS box genes in grasses (Poaceae): ovule expression is ancient and palea expression is new. 2009 , 21, 2591-605	68
1934	Evolutionary position of breviate amoebae and the primary eukaryote divergence. 2009 , 276, 597-604	72
1933	Relaxation of selective constraints on avian mitochondrial DNA following the degeneration of flight ability. 2009 , 19, 1760-5	114
1932	Histone genes of the razor clam Solen marginatus unveil new aspects of linker histone evolution in protostomes. 2009 , 52, 597-607	10
1931	Fossil and molecular evidence constrain scenarios for the early evolutionary and biogeographic history of hystricognathous rodents. 2009 , 106, 16722-7	64
1930	Molecular evolution and functional divergence of HAK potassium transporter gene family in rice (Oryza sativa L.). 2009 , 36, 161-72	51
1929	Adaptive evolution of rbcL in Conocephalum (Hepaticae, bryophytes). 2009 , 441, 169-75	25
1928	Successive radiations, not stasis, in the South American primate fauna. 2009 , 106, 5534-9	82
1927	The evolution of color vision in nocturnal mammals. 2009 , 106, 8980-5	175
1926	How do variable substitution rates influence Ka and Ks calculations?. 2009 , 7, 116-27	17

1925	Environmental, genomic and taxonomic perspectives on methanotrophic Verrucomicrobia. 2009 , 1, 293-306	335
1924	Experimental design in caecilian systematics: phylogenetic information of mitochondrial genomes and nuclear rag1. 2009 , 58, 425-38	26
1923	Evolution of primate orphan proteins. 2009 , 37, 778-82	21
1922	Evidence for an episodic model of protein sequence evolution. 2009 , 37, 783-6	14
1921	A secreted SPRY domain-containing protein (SPRYSEC) from the plant-parasitic nematode Globodera rostochiensis interacts with a CC-NB-LRR protein from a susceptible tomato. 2009 , 22, 330-40	86
1920	Detection, distribution, and genetic variability of European mountain ash ringspot-associated virus. 2009 , 99, 344-52	22
1919	Signal processing for metagenomics: extracting information from the soup. 2009 , 10, 493-510	23
1918	Chaperonin-dependent accelerated substitution rates in prokaryotes. 2010 , 2, 602-8	41
1917	The effect of chaperonin buffering on protein evolution. 2010 , 2, 609-19	59
1916	Analyses of nuclearly encoded mitochondrial genes suggest gene duplication as a mechanism for resolving intralocus sexually antagonistic conflict in Drosophila. 2010 , 2, 835-50	57
1915	Convergently recruited nuclear transport retrogenes are male biased in expression and evolving under positive selection in Drosophila. 2010 , 184, 1067-76	18
1914	Red algae lose key mitochondrial genes in response to becoming parasitic. 2010 , 2, 897-910	49
1913	Genome-wide influence of indel Substitutions on evolution of bacteria of the PVC superphylum, revealed using a novel computational method. 2010 , 2, 870-86	19
1912	Impact of extracellularity on the evolutionary rate of mammalian proteins. 2010 , 2, 39-43	38
1911	Phylogenetic Search Algorithms for Maximum Likelihood. 2010 , 547-577	3
1910	Impact of translational error-induced and error-free misfolding on the rate of protein evolution. 2010 , 6, 421	65
1909	Genome networks root the tree of life between prokaryotic domains. 2010 , 2, 379-92	70
1908	Diversity at the Mla powdery mildew resistance locus from cultivated barley reveals sites of positive selection. 2010 , 23, 497-509	123

1907	Evolution and regulation of the Lotus japonicus LysM receptor gene family. 2010 , 23, 510-21	91
1906	Molecular systematics: A synthesis of the common methods and the state of knowledge. 2010 , 15, 311-41	35
1905	Mutations in centrosomal protein CEP152 in primary microcephaly families linked to MCPH4. 2010 , 87, 40-51	163
1904	ALTER: program-oriented conversion of DNA and protein alignments. 2010 , 38, W14-8	265
1903	Mitochondrial genomic divergence in coelacanths (Latimeria): slow rate of evolution or recent speciation?. 2010 , 157, 2253-2262	12
1902	The evolution of fatty acid desaturases and cytochrome b5 in eukaryotes. 2010 , 233, 63-72	31
1901	Implications of the plastid genome sequence of typha (typhaceae, poales) for understanding genome evolution in poaceae. 2010 , 70, 149-66	138
1900	Lineage-specific duplication and loss of pepsinogen genes in hominoid evolution. 2010 , 70, 313-24	12
1899	Evolution of Conus peptide genes: duplication and positive selection in the A-superfamily. 2010 , 70, 190-202	49
1898	Recurrent emergence of catalytically inactive ornithine decarboxylase homologous forms that likely have regulatory function. 2010 , 70, 289-302	19
1897	Evolutionary dynamics of the 5S rDNA gene family in the mussel Mytilus: mixed effects of birth-and-death and concerted evolution. 2010 , 70, 413-26	33
1896	Rapid evolution of plethodontid modulating factor, a hypervariable salamander courtship pheromone, is driven by positive selection. 2010 , 70, 427-40	31
1895	Circadian input kinases and their homologs in cyanobacteria: evolutionary constraints versus architectural diversification. 2010 , 70, 453-65	17
1894	Testing for selection on synonymous sites in plant mitochondrial DNA: the role of codon bias and RNA editing. 2010 , 70, 479-91	32
1893	Molecular evolution of lepidopteran silk proteins: insights from the ghost moth, Hepialus californicus. 2010 , 70, 519-29	19
1892	Sequence polymorphism and geographical variation at a positively selected MHC-DRB gene in the finless porpoise (Neophocaena phocaenoides): implication for recent differentiation of the Yangtze finless porpoise?. 2010 , 71, 6-22	22
1891	Accelerated evolutionary rate of housekeeping genes in tunicates. 2010 , 71, 153-67	35
1890	Genes devoid of full-length transposable element insertions are involved in development and in the regulation of transcription in human and closely related species. 2010 , 71, 180-91	9

1889	Evolution of the Cinnamyl/Sinapyl Alcohol Dehydrogenase (CAD/SAD) gene family: the emergence of real lignin is associated with the origin of Bona Fide CAD. 2010 , 71, 202-18	52
1888	AVPR1A sequence variation in monogamous owl monkeys (Aotus azarai) and its implications for the evolution of platyrrhine social behavior. 2010 , 71, 279-97	21
1887	Evolution of dopamine-related systems: biosynthesis, degradation and receptors. 2010 , 71, 374-84	10
1886	Evolution of conserved non-coding sequences within the vertebrate Hox clusters through the two-round whole genome duplications revealed by phylogenetic footprinting analysis. 2010 , 71, 427-36	22
1885	Lineage pattern, trans-species polymorphism, and selection pressure among the major lineages of feline MHC-DRB peptide-binding region. 2010 , 62, 307-17	16
1884	MHC evolution in three salmonid species: a comparison between class II alpha and beta genes. 2010 , 62, 531-42	28
1883	MHC class I and MHC class II DRB gene variability in wild and captive Bengal tigers (Panthera tigris tigris). 2010 , 62, 667-79	24
1882	The CYP1D subfamily of genes in mammals and other vertebrates. 2010 , 21, 320-9	11
1881	Patterns of molecular evolution and predicted function in thaumatin-like proteins of Populus trichocarpa. 2010 , 232, 949-62	18
1880	Rapid evolution of a novel signalling mechanism by concerted duplication and divergence of a BMP ligand and its extracellular modulators. 2010 , 220, 235-50	25
1879	Genome-wide discovery of DNA polymorphism in Brassica rapa. 2010 , 283, 135-45	46
1878	Molecular evolution and positive Darwinian selection of the chloroplast maturase matK. 2010 , 123, 241-7	36
1877	Distribution of distances between topologies and its effect on detection of phylogenetic recombination. 2010 , 62, 145-159	3
1876	Adaptive evolution in the GAF domain of phytochromes in gymnosperms. 2010 , 48, 236-47	1
1875	Positive selection of the bat interferon alpha gene family. 2010 , 48, 840-6	15
1874	Positive selection signatures in the TLR7 family. 2010 , 32, 143-150	6
1873	Phenotype prediction of nonsynonymous single nucleotide polymorphisms in human phase II drug/xenobiotic metabolizing enzymes: perspectives on molecular evolution. 2010 , 53, 1252-62	17
1872	Complex positive selection pressures drive the evolution of HIV-1 with different co-receptor tropisms. 2010 , 53, 1204-14	O

1871 Adaptive evolution and structure modeling of rbcL gene in Ephedra. 2010 , 55, 2341-2346	4
1870 Physicochemical evolution and positive selection of the gymnosperm matK proteins. 2010 , 89, 81-9	4
1869 Complete genome sequence of an Argentinean isolate of Solenopsis invicta virus 3. 2010 , 40, 293-7	6
1868 Positive selection drives lactoferrin evolution in mammals. 2010 , 138, 757-62	12
1867 Drcd-1 related: a positively selected spermatogenesis retrogene in Drosophila. 2010 , 138, 925-37	17
1866 Molecular selection and functional divergence of HIF-Eproteins in vertebrates. 2010 , 138, 1241-50	3
1865 Malate dehydrogenase: a useful phylogenetic marker for the genus Aeromonas. 2010 , 33, 427-35	8
Evolutionary rates at codon sites may be used to align sequences and infer protein domain function. 2010 , 11, 151	5
1863 JCoDA: a tool for detecting evolutionary selection. 2010 , 11, 284	36
1862 GIGA: a simple, efficient algorithm for gene tree inference in the genomic age. 2010 , 11, 312	29
Trees on networks: resolving statistical patterns of phylogenetic similarities among interacting proteins. 2010 , 11, 470	3
1860 Towards realistic benchmarks for multiple alignments of non-coding sequences. 2010 , 11, 54	19
webPRANK: a phylogeny-aware multiple sequence aligner with interactive alignment browser. 2010 , 11, 579	267
Tubulin evolution in insects: gene duplication and subfunctionalization provide specialized isoforms in a functionally constrained gene family. 2010 , 10, 113	29
1857 Divergence of imprinted genes during mammalian evolution. 2010 , 10, 116	16
1856 Functional bias in molecular evolution rate of Arabidopsis thaliana. 2010 , 10, 125	13
1855 The molecular evolution of PL10 homologs. 2010 , 10, 127	19
1854 Molecular evolution of the duplicated TFIIAgamma genes in Oryzeae and its relatives. 2010 , 10, 128	9

1853	Evidence of positive selection at codon sites localized in extracellular domains of mammalian CC motif chemokine receptor proteins. 2010 , 10, 139	19
1852	Genomic organization and molecular phylogenies of the beta (beta) keratin multigene family in the chicken (Gallus gallus) and zebra finch (Taeniopygia guttata): implications for feather evolution. 2010 , 10, 148	54
1851	High amino acid diversity and positive selection at a putative coral immunity gene (tachylectin-2). 2010 , 10, 150	27
1850	The origin and evolution of ARGFX homeobox loci in mammalian radiation. 2010 , 10, 182	6
1849	Positive selection of HIV host factors and the evolution of lentivirus genes. 2010 , 10, 186	12
1848	A phylogenetic survey of myotubularin genes of eukaryotes: distribution, protein structure, evolution, and gene expression. 2010 , 10, 196	11
1847	Comparative analyses of the Conserved Oligomeric Golgi (COG) complex in vertebrates. 2010 , 10, 212	8
1846	A new lysozyme from the eastern oyster, Crassostrea virginica, and a possible evolutionary pathway for i-type lysozymes in bivalves from host defense to digestion. 2010 , 10, 213	44
1845	Diversifying selection and functional analysis of interleukin-4 suggests antagonism-driven evolution at receptor-binding interfaces. 2010 , 10, 223	16
1844	Identification, classification and evolution of owl monkeys (Aotus, Illiger 1811). 2010 , 10, 248	34
1843	Extensive loss of translational genes in the structurally dynamic mitochondrial genome of the angiosperm Silene latifolia. 2010 , 10, 274	78
1842	Molecular evolution and the role of oxidative stress in the expansion and functional diversification of cytosolic glutathione transferases. 2010 , 10, 281	59
1841	The evolutionary trajectory of mitochondrial carrier family during metazoan evolution. 2010, 10, 282	4
1840	Evidence for positive selection in the gene fruitless in Anastrepha fruit flies. 2010 , 10, 293	12
1839	Inferring nonneutral evolution from contrasting patterns of polymorphisms and divergences in different protein coding regions of enterovirus 71 circulating in Taiwan during 1998-2003. 2010 , 10, 294	9
1838	Unusual conservation among genes encoding small secreted salivary gland proteins from a gall midge. 2010 , 10, 296	43
1837	Mitochondrial genome evolution in fire ants (Hymenoptera: Formicidae). 2010 , 10, 300	44
1836	The evolution of vertebrate tetraspanins: gene loss, retention, and massive positive selection after whole genome duplications. 2010 , 10, 306	15

1835	Mutational dynamics of murine angiogenin duplicates. 2010 , 10, 310	4
1834	Are substitution rates and RNA editing correlated?. 2010 , 10, 349	27
1833	Next generation sequencing and analysis of a conserved transcriptome of New Zealand's kiwi. 2010 , 10, 387	12
1832	Evolution of plant RNA polymerase IV/V genes: evidence of subneofunctionalization of duplicated NRPD2/NRPE2-like paralogs in Viola (Violaceae). 2010 , 10, 45	19
1831	Lineage-specific positive selection at the merozoite surface protein 1 (msp1) locus of Plasmodium vivax and related simian malaria parasites. 2010 , 10, 52	18
1830	Two frequenins in Drosophila: unveiling the evolutionary history of an unusual neuronal calcium sensor (NCS) duplication. 2010 , 10, 54	12
1829	Chaperonin genes on the rise: new divergent classes and intense duplication in human and other vertebrate genomes. 2010 , 10, 64	21
1828	New insights into the evolution of subtilisin-like serine protease genes in Pezizomycotina. 2010 , 10, 68	52
1827	Genetic diversity, molecular phylogeny and selection evidence of the silkworm mitochondria implicated by complete resequencing of 41 genomes. 2010 , 10, 81	33
1826	Genomic analysis of expressed sequence tags in American black bear Ursus americanus. 2010 , 11, 201	15
1825	The ancient mammalian KRAB zinc finger gene cluster on human chromosome 8q24.3 illustrates principles of C2H2 zinc finger evolution associated with unique expression profiles in human tissues. 2010 , 11, 206	24
1824	Digital gene expression analysis of the zebra finch genome. 2010 , 11, 219	38
1823	Large genomic differences between the morphologically indistinguishable diplomonads Spironucleus barkhanus and Spironucleus salmonicida. 2010 , 11, 258	16
1822	Comparative analysis of secreted protein evolution using expressed sequence tags from four poplar leaf rusts (Melampsora spp.). 2010 , 11, 422	55
1821	Does the core circadian clock in the moss Physcomitrella patens (Bryophyta) comprise a single loop?. 2010 , 10, 109	49
1820	Genome-wide and molecular evolution analyses of the phospholipase D gene family in Poplar and Grape. 2010 , 10, 117	41
1819	Mechanisms of haplotype divergence at the RGA08 nucleotide-binding leucine-rich repeat gene locus in wild banana (Musa balbisiana). 2010 , 10, 149	17
1818	Structure and evolution of Apetala3, a sex-linked gene in Silene latifolia. 2010 , 10, 180	29

1817	Molecular analysis of phosphomannomutase (PMM) genes reveals a unique PMM duplication event in diverse Triticeae species and the main PMM isozymes in bread wheat tissues. 2010 , 10, 214	13
1816	Genome-wide investigation reveals high evolutionary rates in annual model plants. 2010 , 10, 242	36
1815	Functional divergence of the NIP III subgroup proteins involved altered selective constraints and positive selection. 2010 , 10, 256	18
1814	Genomic survey, characterization and expression profile analysis of the peptide transporter family in rice (Oryza sativa L.). 2010 , 10, 92	40
1813	Comparison of homoeolocus organisation in paired BAC clones from white clover (Trifolium repens L.) and microcolinearity with model legume species. 2010 , 10, 94	12
1812	The evolutionary rate variation among genes of HOG-signaling pathway in yeast genomes. 2010 , 5, 46	31
1811	Specialization of a Drosophila capping protein essential for the protection of sperm telomeres. 2010 , 20, 2090-9	32
1810	Positive selection on apoptosis related genes. 2010 , 584, 469-76	31
1809	Episodic sitewise positive selection on the signal recognition particle protein Ffh in Actinobacteria. 2010 , 584, 3975-8	
1808	Analysis of recombination and natural selection in human enterovirus 71. 2010 , 398, 251-61	53
1807	Evolutionary genomics of human intellectual disability. 2010 , 3, 52-63	6
1806	Class II DRB polymorphism and sequence diversity in two vesper bats in the genus Myotis. 2010 , 37, 401-5	13
1805	Allopatric divergence and regional range expansion of Juniperus sabina in China. 2010 , 48, 153-160	30
1804	Retracted: Evidence for duplicated Hox genes in polyploid Cyprinidae fish of common carp, crucian carp and silver crucian carp. 2010 , 314, i-xii	
1803	Speciation of polyploid Cyprinidae fish of common carp, crucian carp, and silver crucian carp derived from duplicated Hox genes. 2010 , 314, 445-56	17
1802	Species abundance patterns in an ecosystem simulation studied through Fisher logseries. 2010 , 18, 100-123	11
1801	Evolution of bacterial genes: evidences of positive Darwinian selection and fixation of base substitutions in virulence genes of Helicobacter pylori. 2010 , 10, 764-76	12
1800	Population genetic tests suggest that the epidemiologies of JCV and BKV are strikingly different. 2010 , 10, 397-403	5

1799	Detecting natural selection in RNA virus populations using sequence summary statistics. 2010 , 10, 421-30	21
1798	Evolution of TRIM5alpha B30.2 (SPRY) domain in New World primates. 2010 , 10, 246-53	9
1797	Phylogenetic inference of Indian malaria vectors from multilocus DNA sequences. 2010 , 10, 755-63	9
1796	Phylogeny and biogeography of the rice tribe (Oryzeae): evidence from combined analysis of 20 chloroplast fragments. 2010 , 54, 266-77	76
1795	Fast evolution of the retroprocessed mitochondrial rps3 gene in Conifer II and further evidence for the phylogeny of gymnosperms. 2010 , 54, 136-49	72
1794	High molecular diversity in the rhodopsin gene in closely related goby fishes: A role for visual pigments in adaptive speciation?. 2010 , 55, 689-98	35
1793	Phylogenomic and structural modeling analyses of the PsbP superfamily reveal multiple small segment additions in the evolution of photosystem II-associated PsbP protein in green plants. 2010 , 56, 176-86	35
1792	Speciation dynamics in the SE Asian tropics: Putting a time perspective on the phylogeny and biogeography of Sundaland tree squirrels, Sundasciurus. 2010 , 55, 711-20	42
1791	Supermatrix and species tree methods resolve phylogenetic relationships within the big cats, Panthera (Carnivora: Felidae). 2010 , 56, 64-76	53
1790	Congruence between nuclear and mitochondrial DNA: combination of multiple nuclear introns resolves a well-supported phylogeny of New World orioles (Icterus). 2010 , 56, 419-27	27
1789	The importance of taxon sampling in genomic studies: an example from the cyclooxygenases of teleost fishes. 2010 , 56, 451-5	9
1788	Evolutionary dynamics of the N1 neuraminidases of the main lineages of influenza A viruses. 2010 , 56, 526-35	11
1787	Molecular phylogenetic analyses of genus Crocodylus (Eusuchia, Crocodylia, Crocodylidae) and the taxonomic position of Crocodylus porosus. 2010 , 57, 393-402	36
1786	Phylogeny, biogeography, and host-plant association in the subfamily Apaturinae (Insecta: Lepidoptera: Nymphalidae) inferred from eight nuclear and seven mitochondrial genes. 2010 , 57, 1026-36	15
1785	Duplicate dmbx1 genes regulate progenitor cell cycle and differentiation during zebrafish midbrain and retinal development. 2010 , 10, 100	17
1784	Population dynamics of Neisseria gonorrhoeae in Shanghai, China: a comparative study. 2010 , 10, 13	18
1783	Bayesian random local clocks, or one rate to rule them all. 2010 , 8, 114	283
1782	Gene duplication and fragmentation in the zebra finch major histocompatibility complex. 2010 , 8, 29	106

1781	Asymmetric and non-uniform evolution of recently duplicated human genes. 2010 , 5, 54	19
1780	The ancient function of RB-E2F pathway: insights from its evolutionary history. 2010 , 5, 55	33
1779	Difference in larval type explains patterns of nonsynonymous substitutions in two ancient paralogs of the histone H3 gene in sea stars. 2010 , 12, 222-30	4
1778	AN UNRECOGNIZED ANCIENT LINEAGE OF GREEN PLANTS PERSISTS IN DEEP MARINE WATERS1. 2010 , 46, 1288-1295	32
1777	Specific resistances against Pseudomonas syringae effectors AvrB and AvrRpm1 have evolved differently in common bean (Phaseolus vulgaris), soybean (Glycine max), and Arabidopsis thaliana. 2010 , 187, 941-956	30
1776	Diversification and biogeography of Juniperus (Cupressaceae): variable diversification rates and multiple intercontinental dispersals. 2010 , 188, 254-72	168
1775	Promiscuity and the rate of molecular evolution at primate immunity genes. 2010 , 64, 2204-20	27
1774	Abrupt deceleration of molecular evolution linked to the origin of arborescence in ferns. 2010 , 64, 2786-92	33
1773	An integrative test of the dead-end hypothesis of selfing evolution in Triticeae (Poaceae). 2010 , 64, 2855-72	60
1772	Genome annotation and comparative analyses of the odorant-binding proteins and chemosensory proteins in the pea aphid Acyrthosiphon pisum. 2010 , 19 Suppl 2, 113-22	152
1771	Comparative analysis of nuclear tRNA genes of Nasonia vitripennis and other arthropods, and relationships to codon usage bias. 2010 , 19 Suppl 1, 49-58	24
1770	Molecular evolution of the thyrotrophin-releasing hormone precursor in vertebrates: insights from comparative genomics. 2010 , 22, 608-19	17
1769	Finding candidate genes under positive selection in Non-model species: examples of genes involved in host specialization in pathogens. 2010 , 19, 292-306	30
1768	Mining transcriptome sequences towards identifying adaptive single nucleotide polymorphisms in lake whitefish species pairs (Coregonus spp. Salmonidae). 2010 , 19 Suppl 1, 115-31	150
1767	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. 2010 , 19 Suppl 1, 266-76	97
1766	Rapid evolution and selection inferred from the transcriptomes of sympatric crater lake cichlid fishes. 2010 , 19 Suppl 1, 197-211	180
1765	Genetic divergence and assortative mating between colour morphs of the sea urchin Paracentrotus gaimardi. 2010 , 19, 484-93	18
1764	Spatial and temporal dynamics of rabies virus variants in big brown bat populations across Canada: footprints of an emerging zoonosis. 2010 , 19, 2120-36	30

1763	Molecular evidence of the survival of subterranean amphipods (Arthropoda) during Ice Age underneath glaciers in Iceland. 2010 , 19, 2516-30	32
1762	Evolutionary transitions in symbioses: dramatic reductions in bathymetric and geographic ranges of Zoanthidea coincide with loss of symbioses with invertebrates. 2010 , 19, 2587-98	33
1761	Molecular genetic analysis of virus isolates from wild and cultivated plants demonstrates that East Africa is a hotspot for the evolution and diversification of sweet potato feathery mottle virus. 2010 , 19, 3139-56	36
1760	Natural selection on PHYE by latitude in the Japanese archipelago: insight from locus specific phylogeographic structure in Arcterica nana (Ericaceae). 2010 , 19, 2779-91	21
1759	The anatomy of a 'suture zone' in Amazonian butterflies: a coalescent-based test for vicariant geographic divergence and speciation. 2010 , 19, 4283-301	46
1758	The transcriptomics of sympatric dwarf and normal lake whitefish (Coregonus clupeaformis spp., Salmonidae) divergence as revealed by next-generation sequencing. 2010 , 19, 5389-403	83
1757	Gondwanan radiation of the Southern Hemisphere crayfishes (Decapoda: Parastacidae): evidence from fossils and molecules. 2010 , 37, 2275-2290	59
1756	HipHop interacts with HOAP and HP1 to protect Drosophila telomeres in a sequence-independent manner. 2010 , 29, 819-29	70
1755	Contrasting patterns of selective constraints in nuclear-encoded genes of the oxidative phosphorylation pathway in holometabolous insects and their possible role in hybrid breakdown in Nasonia. 2010 , 104, 310-7	19
1754	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. 2010 , 105, 290-8	25
1753	Changes in Hox genes' structure and function during the evolution of the squamate body plan. 2010 , 464, 99-103	122
1752	Analysis of Drosophila TRPA1 reveals an ancient origin for human chemical nociception. 2010 , 464, 597-600	230
1751	Natural allelic variation underlying a major fitness trade-off in Arabidopsis thaliana. 2010 , 465, 632-6	273
1750	Sequence space and the ongoing expansion of the protein universe. 2010 , 465, 922-6	151
1749	Was the universal common ancestry proved?. 2010 , 468, E9; discussion E10	19
1748	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus Oryza. 2010 , 63, 430-42	43
1747	Human T cell epitopes of Mycobacterium tuberculosis are evolutionarily hyperconserved. 2010 , 42, 498-503	509
1746	Divergence times and colonization of the Canary Islands by Gallotia lizards. 2010 , 56, 747-57	81

1745	Diversification in subtropical mountains: phylogeography, Pleistocene demographic expansion, and evolution of polyphenic mandibles in Taiwanese stag beetle, Lucanus formosanus. 2010 , 57, 1149-61	20
1744	Molecular phylogeny and evolution of the Asian lineage of vole genus Microtus (Rodentia: Arvicolinae) inferred from mitochondrial cytochrome b sequence. 2010 , 99, 595-613	73
1743	Phylogeography of Parnassius apollo: hints on taxonomy and conservation of a vulnerable glacial butterfly invader. 2010 , 101, 169-183	36
1742	Phylogeographic structure in the gilgie (Decapoda: Parastacidae: Cherax quinquecarinatus): a south-western Australian freshwater crayfish. 2010 , 101, 385-402	6
1741	Holarctic phylogeography of the tundra shrew (Sorex tundrensis) based on mitochondrial genes. 2010 , 101, 721-746	21
1740	Energy and the tempo of evolution in amphibians. 2010 , 19, no-no	9
1739	Opposites attract: MHC-associated mate choice in a polygynous primate. 2010 , 23, 136-48	56
1738	Molecular evolutionary analysis of seminal receptacle sperm storage organ genes of Drosophila melanogaster. 2010 , 23, 1386-98	34
1737	The evolution of the repertoire and structure of G protein-coupled receptors. 5-31	
1736	. 2010,	20
1736 1735	. 2010, Introduction to Conservation Genetics. 539-594	20
1735		2 0
1735	Introduction to Conservation Genetics. 539-594	
1735 1734	Introduction to Conservation Genetics. 539-594 Recombination and its impact on the genome of the haplodiploid parasitoid wasp Nasonia. 2010, 5, e8597 Complete genome sequence and comparative metabolic profiling of the prototypical	54
1735 1734 1733	Introduction to Conservation Genetics. 539-594 Recombination and its impact on the genome of the haplodiploid parasitoid wasp Nasonia. 2010, 5, e8597 Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative Escherichia coli strain 042. 2010, 5, e8801 Anopheles immune genes and amino acid sites evolving under the effect of positive selection. 2010, 5, e8885	54 134
1735 1734 1733 1732	Introduction to Conservation Genetics. 539-594 Recombination and its impact on the genome of the haplodiploid parasitoid wasp Nasonia. 2010, 5, e8597 Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative Escherichia coli strain 042. 2010, 5, e8801 Anopheles immune genes and amino acid sites evolving under the effect of positive selection. 2010, 5, e8885	54 134 15
1735 1734 1733 1732	Introduction to Conservation Genetics. 539-594 Recombination and its impact on the genome of the haplodiploid parasitoid wasp Nasonia. 2010, 5, e8597 Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative Escherichia coli strain 042. 2010, 5, e8801 Anopheles immune genes and amino acid sites evolving under the effect of positive selection. 2010, 5, e8885 Atlantic cod piscidin and its diversification through positive selection. 2010, 5, e9501	54 134 15

1727	Antagonistic changes in sensitivity to antifungal drugs by mutations of an important ABC transporter gene in a fungal pathogen. 2010 , 5, e11309		13
1726	Molecular evolution of the primate antiviral restriction factor tetherin. 2010 , 5, e11904		20
1725	Evolutionary systems biology of amino acid biosynthetic cost in yeast. 2010 , 5, e11935		45
1724	A candidate subspecies discrimination system involving a vomeronasal receptor gene with different alleles fixed in M. m. domesticus and M. m. musculus. 2010 , 5, e12638		12
1723	Molecular evolution and functional divergence of the cytochrome P450 3 (CYP3) Family in Actinopterygii (ray-finned fish). 2010 , 5, e14276		23
1722	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
1721	EREM: Parameter Estimation and Ancestral Reconstruction by Expectation-Maximization Algorithm for a Probabilistic Model of Genomic Binary Characters Evolution. 2010 , 167408		6
1720	Genomic and population-level effects of gene conversion in caenorhabditis paralogs. 2010 , 1, 452-68		10
1719	Positive selection differs between protein secondary structure elements in Drosophila. 2010 , 2, 166-79		26
1718	Evolution of peroxisome proliferator-activated receptor gamma alternative splicing. 2010 , 2, 1334-43		2
1717	Extensive loss of RNA editing sites in rapidly evolving Silene mitochondrial genomes: selection vs. retroprocessing as the driving force. 2010 , 185, 1369-80		72
1716	Evolution of a distinct genomic domain in Drosophila: comparative analysis of the dot chromosome in Drosophila melanogaster and Drosophila virilis. 2010 , 185, 1519-34		25
1715	Evolution of the sweet taste receptor gene Tas1r2 in bats. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2642-50	8.3	67
1714	An effector-targeted protease contributes to defense against Phytophthora infestans and is under diversifying selection in natural hosts. 2010 , 154, 1794-804		121
1713	Genome-wide evidence for efficient positive and purifying selection in Capsella grandiflora, a plant species with a large effective population size. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1813-21	8.3	126
1712	Evolutionary dynamics of Clostridium difficile over short and long time scales. 2010 , 107, 7527-32		291
1711	Divergence of the mitochondrial genome structure in the apicomplexan parasites, Babesia and Theileria. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1107-16	8.3	82
1710	Lymphocryptovirus phylogeny and the origins of Epstein-Barr virus. 2010 , 91, 630-42		60

1709	Differential gene retention in plastids of common recent origin. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1530-7	,	85
1708	Localized hypermutation and associated gene losses in legume chloroplast genomes. 2010 , 20, 1700-10		168
1707	Tracing the temporal and spatial origins of island endemics in the Mediterranean region: a case study from the citrus family (Ruta L., Rutaceae). 2010 , 59, 705-22		70
1706	Comparative genomics and evolution of the alpha-defensin multigene family in primates. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2333-43		25
1705	Sequence-Based Analysis of Bacterial Population Structures. 2010 , 37-60		5
1704	Statistical Methods for Detecting the Presence of Natural Selection in Bacterial Populations. 2010 , 87-101		
1703	Molecular evolutionary analysis of cancer cell lines. 2010 , 9, 279-91		8
1702	Rooting the ribosomal tree of life. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1792-801		50
1701	Adaptive evolution of genes duplicated from the Drosophila pseudoobscura neo-X chromosome. Molecular Biology and Evolution, 2010 , 27, 1963-78	,	11
1700	H2A.Bbd: an X-chromosome-encoded histone involved in mammalian spermiogenesis. 2010 , 38, 1780-9		60
1699	A population genetics-based and phylogenetic approach to understanding the evolution of virulence in the genus Listeria. 2010 , 76, 6085-100		66
1698	Coalescent simulation of intracodon recombination. 2010 , 184, 429-37		55
1697	More reliable estimates of divergence times in Pan using complete mtDNA sequences and accounting for population structure. 2010 , 365, 3277-88		54
1696	Systemic factors dominate mammal protein evolution. 2010 , 277, 1403-8		17
1695	Hidden variability of floral homeotic B genes in Solanaceae provides a molecular basis for the evolution of novel functions. 2010 , 22, 2562-78		52
1694	Functional copies of the Mst77F gene on the Y chromosome of Drosophila melanogaster. 2010 , 184, 295-307		33
1693	Variation in the Neisseria meningitidis FadL-like protein: an evolutionary model for a relatively low-abundance surface antigen. 2010 , 156, 3596-3608		2
1692	Distinct hepatitis B virus dynamics in the immunotolerant and early immunoclearance phases. 2010 , 84, 3454-63		71

1691	Comparing genomes to computer operating systems in terms of the topology and evolution of their regulatory control networks. 2010 , 107, 9186-91		60
1690	Phylogenetic incongruence arising from fragmented speciation in enteric bacteria. 2010 , 107, 11453-8		53
1689	Gorgeous mosaic of mitochondrial genes created by horizontal transfer and gene conversion. 2010 , 107, 21576-81		74
1688	Degeneration of an intracellular ion channel in the primate lineage by relaxation of selective constraints. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2352-9	8.3	53
1687	Pseudogenization of the umami taste receptor gene Tas1r1 in the giant panda coincided with its dietary switch to bamboo. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2669-73	8.3	122
1686	Editor's Report. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2890-2891	8.3	
1685	A novel method to detect proteins evolving at correlated rates: identifying new functional relationships between coevolving proteins. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1152-61	8.3	33
1684	PANDITplus: toward better integration of evolutionary view on molecular sequences with supplementary bioinformatics resources. 2010 , 2, 1		6
1683	Protein E of Haemophilus influenzae is a ubiquitous highly conserved adhesin. 2010 , 201, 414-9		32
1682	A time line of the environmental genetics of the haptophytes. <i>Molecular Biology and Evolution</i> , 2010 , 27, 161-76	8.3	52
1681	Heterogeneous patterns of gene-expression diversification in mammalian gene duplicates. <i>Molecular Biology and Evolution</i> , 2010 , 27, 325-35	8.3	32
1680	Accelerated mutation accumulation in asexual lineages of a freshwater snail. <i>Molecular Biology and Evolution</i> , 2010 , 27, 954-63	8.3	88
1679	Accelerated evolution of PAK3- and PIM1-like kinase gene families in the zebra finch, Taeniopygia guttata. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1923-34	8.3	9
1678	An uncorrelated relaxed-clock analysis suggests an earlier origin for flowering plants. 2010 , 107, 5897-9	902	297
1677	Salt stress phenotypes in Listeria monocytogenes vary by genetic lineage and temperature. 2010 , 7, 1537-49		51
1676	Molecular cloning and characterization of the circumsporozoite protein gene of Plasmodium inui isolated from Formosan macaques (Macaca cyclopis) in Taiwan. 2010 , 96, 1145-51		
1675	Large-scale analysis of orthologs and paralogs under covarion-like and constant-but-different models of amino acid evolution. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2618-27	8.3	17
1674	Orthologous comparisons of the Hd1 region across genera reveal Hd1 gene lability within diploid Oryza species and disruptions to microsynteny in Sorghum. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2487-506	8.3	28

1673	Duplication of the class I cytosolic small heat shock protein gene and potential functional divergence revealed by sequence variations flanking the {alpha}-crystallin domain in the genus Rhododendron (Ericaceae). 2010 , 105, 57-69		6
1672	Two nonrecombining sympatric forms of the human malaria parasite Plasmodium ovale occur globally. 2010 , 201, 1544-50		235
1671	Nonallelic gene conversion in the genus Drosophila. 2010 , 185, 95-103		26
1670	Evolutionary relationships among primary endosymbionts of the mealybug subfamily phenacoccinae (hemiptera: Coccoidea: Pseudococcidae). 2010 , 76, 7521-5		48
1669	Extensive functional diversification of the Populus glutathione S-transferase supergene family. 2009 , 21, 3749-66		154
1668	Dramatic change in function and expression pattern of a gene duplicated by polyploidy created a paternal effect gene in the Brassicaceae. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2817-28	8.3	57
1667	Adaptation and constraint at Toll-like receptors in primates. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2172-86	8.3	130
1666	Evolution of an antifreeze protein by neofunctionalization under escape from adaptive conflict. 2010 , 107, 21593-8		87
1665	The molecular phylogeny of uterine serpins and its relationship to evolution of placentation. 2010 , 24, 526-37		12
1664	Evolutionary dynamics of rhodopsin type 2 opsins in vertebrates. <i>Molecular Biology and Evolution</i> , 2010 , 27, 133-41	8.3	12
1663	Sperm proteomics reveals intensified selection on mouse sperm membrane and acrosome genes. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1235-46	8.3	84
1662	Recombination yet inefficient selection along the Drosophila melanogaster subgroup's fourth chromosome. <i>Molecular Biology and Evolution</i> , 2010 , 27, 848-61	8.3	44
1661	First-order correct bootstrap support adjustments for splits that allow hypothesis testing when using maximum likelihood estimation. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1621-9	8.3	14
1660	Characterization of TRPC2, an essential genetic component of VNS chemoreception, provides insights into the evolution of pheromonal olfaction in secondary-adapted marine mammals. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1467-77	8.3	36
1659	Rapid likelihood analysis on large phylogenies using partial sampling of substitution histories. <i>Molecular Biology and Evolution</i> , 2010 , 27, 249-65	8.3	21
1658	A genomic survey of positive selection in Burkholderia pseudomallei provides insights into the evolution of accidental virulence. 2010 , 6, e1000845		91
1657	Parallel and convergent evolution of the dim-light vision gene RH1 in bats (Order: Chiroptera). 2010 , 5, e8838		28
1656	A more precise characterization of chaperonin substrates. 2010 , 26, 1685-9		22

1655	Maternal-fetal conflict: rapidly evolving proteins in the rodent placenta. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1221-5	8.3	36
1654	Profound differences in virus population genetics correspond to protection from CD4 decline resulting from feline lentivirus coinfection. 2010 , 2, 2663-80		5
1653	Whole-genome and chromosome evolution associated with host adaptation and speciation of the wheat pathogen Mycosphaerella graminicola. 2010 , 6, e1001189		106
1652	Adaptive evolution of digestive RNASE1 genes in leaf-eating monkeys revisited: new insights from ten additional colobines. <i>Molecular Biology and Evolution</i> , 2010 , 27, 121-31	8.3	23
1651	Divergence of recently duplicated M{gamma}-type MADS-box genes in Petunia. <i>Molecular Biology and Evolution</i> , 2010 , 27, 481-95	8.3	10
1650	Slip into something more functional: selection maintains ancient frameshifts in homopolymeric sequences. <i>Molecular Biology and Evolution</i> , 2010 , 27, 833-9	8.3	34
1649	Multi-platform next-generation sequencing of the domestic turkey (Meleagris gallopavo): genome assembly and analysis. 2010 , 8, e1000475		311
1648	Evolutionary trajectories of beta-lactamase CTX-M-1 cluster enzymes: predicting antibiotic resistance. 2010 , 6, e1000735		80
1647	Following tetraploidy in maize, a short deletion mechanism removed genes preferentially from one of the two homologs. 2010 , 8, e1000409		202
1646	Co-evolution of transcriptional silencing proteins and the DNA elements specifying their assembly. 2010 , 8, e1000550		32
1646 1645			32 117
	The extinction dynamics of bacterial pseudogenes. 2010 , 6, e1001050		
1645	2010, 8, e1000550 The extinction dynamics of bacterial pseudogenes. 2010, 6, e1001050 A global overview of the genetic and functional diversity in the Helicobacter pylori cag	8.3	117
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1645 1644 1643	The extinction dynamics of bacterial pseudogenes. 2010, 6, e1001050 A global overview of the genetic and functional diversity in the Helicobacter pylori cag pathogenicity island. 2010, 6, e1001069 Performance of relaxed-clock methods in estimating evolutionary divergence times and their credibility intervals. <i>Molecular Biology and Evolution</i> , 2010, 27, 1289-300 On the utility of short intron sequences as a reference for the detection of positive and negative selection in Drosophila. <i>Molecular Biology and Evolution</i> , 2010, 27, 1226-34 Pivotal Advance: Avian colony-stimulating factor 1 (CSF-1), interleukin-34 (IL-34), and CSF-1		117 152 73 87
1645 1644 1643 1642	The extinction dynamics of bacterial pseudogenes. 2010, 6, e1001050 A global overview of the genetic and functional diversity in the Helicobacter pylori cag pathogenicity island. 2010, 6, e1001069 Performance of relaxed-clock methods in estimating evolutionary divergence times and their credibility intervals. Molecular Biology and Evolution, 2010, 27, 1289-300 On the utility of short intron sequences as a reference for the detection of positive and negative selection in Drosophila. Molecular Biology and Evolution, 2010, 27, 1226-34 Pivotal Advance: Avian colony-stimulating factor 1 (CSF-1), interleukin-34 (IL-34), and CSF-1 receptor genes and gene products. 2010, 87, 753-64 Evolution of linked avirulence effectors in Leptosphaeria maculans is affected by genomic		117 152 73 87 136

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1637	Phylogenetics applied to genotype/phenotype association and selection analyses with sequence data from angptl4 in humans. 2010 , 11, 370-85		4
1636	The Trw type IV secretion system of Bartonella mediates host-specific adhesion to erythrocytes. 2010 , 6, e1000946		84
1635	The alpha glycerophosphate cycle in Drosophila melanogaster VI. structure and evolution of enzyme paralogs in the genus Drosophila. 2010 , 101, 225-34		9
1634	What makes an egg unique? Clues from evolutionary scenarios of egg-specific genes. 2010 , 83, 893-900		27
1633	Why genes evolve faster on secondary chromosomes in bacteria. 2010 , 6, e1000732		71
1632	Chromosomal redistribution of male-biased genes in mammalian evolution with two bursts of gene gain on the X chromosome. 2010 , 8, e1000494		131
1631	Adaptive divergence of ancient gene duplicates in the avian MHC class II beta. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2360-74	8.3	57
1630	A generation time effect on the rate of molecular evolution in invertebrates. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1173-80	8.3	151
1629	Bayesian dating of shallow phylogenies with a relaxed clock. 2010 , 59, 119-31		44
1628	Rapid proliferation of repetitive palindromic elements in mtDNA of the endemic Baikalian sponge Lubomirskia baicalensis. <i>Molecular Biology and Evolution</i> , 2010 , 27, 757-60	8.3	35
1627	The effect of insertions, deletions, and alignment errors on the branch-site test of positive selection. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2257-67	8.3	189
1626	Analysis of host-parasite incongruence in papillomavirus evolution using importance sampling. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1301-14	8.3	60
1625	Evolutionary rates and gene dispensability associate with replication timing in the archaeon Sulfolobus islandicus. 2010 , 2, 859-69		25
1624	The GMOD Drupal bioinformatic server framework. 2010 , 26, 3119-24		21
1623	The evolution of amastin surface glycoproteins in trypanosomatid parasites. <i>Molecular Biology and Evolution</i> , 2010 , 27, 33-45	8.3	69
1622	Robustness of ancestral sequence reconstruction to phylogenetic uncertainty. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1988-99	8.3	106
1621	Natural selection on cis and trans regulation in yeasts. 2010 , 20, 826-36		114
1620	Massive turnover of functional sequence in human and other mammalian genomes. 2010 , 20, 1335-43		76

1619	Functional conservation of DNA methylation in the pea aphid and the honeybee. 2010 , 2, 719-28		75
1618	Recombination and selection pressure in the ipomovirus sweet potato mild mottle virus (Potyviridae) in wild species and cultivated sweetpotato in the centre of evolution in East Africa. 2010 , 91, 1092-108		43
1617	The use of orthologous sequences to predict the impact of amino acid substitutions on protein function. 2010 , 6, e1000968		34
1616	Evolutionary analysis and expression profiling of zebra finch immune genes. 2010 , 2, 781-90		22
1615	On the diversity of malaria parasites in African apes and the origin of Plasmodium falciparum from Bonobos. 2010 , 6, e1000765		159
1614	Population-level variation of the preproricin gene contradicts expectation of neutral equilibrium for generalist plant defense toxins. 2010 , 55, 1475-83		4
1613	FPGA Acceleration of the phylogenetic likelihood function for Bayesian MCMC inference methods. 2010 , 11, 184		24
1612	Evolution of a cluster of innate immune genes (beta-defensins) along the ancestral lines of chicken and zebra finch. 2010 , 6, 3		46
1611	The position of gnetales among seed plants: overcoming pitfalls of chloroplast phylogenomics. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2855-63	8.3	69
1610	Myosin cross-reactive antigen of Streptococcus pyogenes M49 encodes a fatty acid double bond hydratase that plays a role in oleic acid detoxification and bacterial virulence. 2010 , 285, 10353-61		94
1609	Using DNA Sequence Diversity to Test for Selection in Silene. 2010 , 171, 1072-1082		1
1608	Genome-scale phylogenetic analyses of chikungunya virus reveal independent emergences of recent epidemics and various evolutionary rates. 2010 , 84, 6497-504		270
1607	Angiosperm genome comparisons reveal early polyploidy in the monocot lineage. 2010 , 107, 472-7		217
1606	Positions under positive selectionkey for selectivity and potency of scorpion alpha-toxins. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1025-34	8.3	64
1605	Use of phylogenetics in the molecular epidemiology and evolutionary studies of viral infections. 2010 , 47, 5-49		48
1604	Evolutionary origin and phylogeny of the modern holocephalans (Chondrichthyes: Chimaeriformes): a mitogenomic perspective. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2576-86	8.3	144
1603	Evolution of the nuclear-encoded cytochrome oxidase subunits in vertebrates. 2010 , 42, 76-84		25
1602	The neutral theory of molecular evolution in the genomic era. 2010 , 11, 265-89		152

1601	Lineage-specific differences in the amino acid substitution process. 2010 , 396, 1410-21	11
1600	Growth hormone-related genes from baboon (Papio hamadryas): Characterization, placental expression and evolutionary aspects. 2010 , 450, 1-7	4
1599	Phylogenesis of brain-derived neurotrophic factor (BDNF) in vertebrates. 2010 , 450, 85-93	36
1598	Genetic diversity of the Plasmodium vivax merozoite surface protein-5 locus from diverse geographic origins. 2010 , 456, 24-35	20
1597	Accelerated evolution of Fetuin-A (FETUA, also AHSG) is driven by positive Darwinian selection, not GC-biased gene conversion. 2010 , 463, 49-55	4
1596	MgC1q, a novel C1q-domain-containing protein involved in the immune response of Mytilus galloprovincialis. 2010 , 34, 926-34	81
1595	Sex in Penicillium: combined phylogenetic and experimental approaches. 2010 , 47, 693-706	35
1594	Watching the clock: studying variation in rates of molecular evolution between species. 2010 , 25, 495-503	133
1593	Identifying the confounding factors in resolving phylogenetic relationships in Vespertilionidae. 2010 , 91, 1435-1448	35
1592	Natural selection maintains the transcribed LTR retrotransposons in Nosema bombycis. 2010 , 37, 305-14	5
1591	Molecular and evolutionary analyses of formyl peptide receptors suggest the absence of VNO-specific FPRs in primates. 2010 , 37, 771-8	9
1590	Selection at the MHC class IIB locus across guppy (Poecilia reticulata) populations. 2010 , 104, 155-67	39
1589	Remarkably ancient balanced polymorphisms in a multi-locus gene network. 2010 , 464, 54-8	119
1588	Mutation rate is linked to diversification in birds. 2010 , 107, 20423-8	101
1587	Reconstructed ancestral sequences improve pathogen identification using resequencing DNA microarrays. 2010 , 5, e15243	5
1586	Functional differentiation of the glycosyltransferases that contribute to the chemical diversity of bioactive flavonol glycosides in grapevines (Vitis vinifera). 2010 , 22, 2856-71	112
1585	Comparative gene evolution in haemosporidian (apicomplexa) parasites of birds and mammals. Molecular Biology and Evolution, 2010 , 27, 537-42	27
1584	KaKs_Calculator 2.0: a toolkit incorporating gamma-series methods and sliding window strategies. 2010 , 8, 77-80	620

1583	BiDiBlast: comparative genomics pipeline for the PC. 2010 , 8, 135-8	1
1582	Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes. 2010 , 11, R72	191
1581	Molecular evolution of genes in avian genomes. 2010 , 11, R68	92
1580	Microsatellites in Brassica unigenes: relative abundance, marker design, and use in comparative physical mapping and genome analysis. 2010 , 53, 55-67	43
1579	The effect of recombination on the reconstruction of ancestral sequences. 2010 , 184, 1133-9	54
1578	An evaluation of phylogenetic informativeness profiles and the molecular phylogeny of diplazontinae (Hymenoptera, Ichneumonidae). 2010 , 59, 226-41	55
1577	Domain loss facilitates accelerated evolution and neofunctionalization of duplicate snake venom metalloproteinase toxin genes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2637-49	115
1576	H-bond network around retinal regulates the evolution of ultraviolet and violet vision. 2011 , 6, 775-80	24
1575	Accelerated evolution of CES7, a gene encoding a novel major urinary protein in the cat family. Molecular Biology and Evolution, 2011, 28, 911-20	8
1574	Genetic diversity of Potato virus Y infecting tobacco crops in China. 2011 , 101, 377-87	37
1573	Molecular evolution of candidate sour taste receptor gene PKD1L3 in mammals. 2011 , 54, 890-7	2
1572	Evolution and diverse roles of the CUP-SHAPED COTYLEDON genes in Arabidopsis leaf development. 2011 , 23, 54-68	128
1571	The Awesome Power of Yeast Evolutionary Genetics: New Genome Sequences and Strain Resources for the Saccharomyces sensu stricto Genus. 2011 , 1, 11-25	231
1570	Phylogenetic utility of nuclear introns in interfamilial relationships of Caniformia (order Carnivora). 2011 , 60, 175-87	36
1569	PhyloCSF: a comparative genomics method to distinguish protein coding and non-coding regions. 2011 , 27, i275-82	637
1568	The natural resistance-associated macrophage protein from the protozoan parasite Perkinsus marinus mediates iron uptake. 2011 , 50, 6340-55	15
1567	Genetic dissection of vitamin E biosynthesis in tomato. 2011 , 62, 3781-98	58
1566	Modeling High-Level Behavior Patterns for Precise Similarity Analysis of Software. 2011 ,	5

(2011-2011)

1565	Does positive selection drive transcription factor binding site turnover? A test with Drosophila cis-regulatory modules. 2011 , 7, e1002053	68
1564	Multiple invasions into freshwater by pufferfishes (teleostei: tetraodontidae): a mitogenomic perspective. 2011 , 6, e17410	55
1563	Multilocus Sequence Typing of Pathogens. 2011 , 503-521	4
1562	Network models of TEM Elactamase mutations coevolving under antibiotic selection show modular structure and anticipate evolutionary trajectories. 2011 , 7, e1002184	28
1561	Pseudogenization of the tooth gene enamelysin (MMP20) in the common ancestor of extant baleen whales. 2011 , 278, 993-1002	67
1560	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). 2011 , 11, 181	62
1559	Novel male-biased expression in paralogs of the aphid slimfast nutrient amino acid transporter expansion. 2011 , 11, 253	10
1558	Evolutionary relationships of the old world fruit bats (Chiroptera, Pteropodidae): another star phylogeny?. 2011 , 11, 281	45
1557	Expression level, cellular compartment and metabolic network position all influence the average selective constraint on mammalian enzymes. 2011 , 11, 89	19
1556	Genetic characterization of hantaviruses associated with sigmodontine rodents in an endemic area for hantavirus pulmonary syndrome in southern Brazil. 2011 , 11, 301-14	22
1555	Relaxed selection is a precursor to the evolution of phenotypic plasticity. 2011 , 108, 15936-41	111
1554	Bringing order to protein disorder through comparative genomics and genetic interactions. 2011 , 12, R14	105
1553	Comparative genomics of the social amoebae Dictyostelium discoideum and Dictyostelium purpureum. 2011 , 12, R20	117
1552	The monarch butterfly genome yields insights into long-distance migration. 2011 , 147, 1171-85	410
1551	Influenza C virus surveillance during the first influenza A (H1N1) 2009 pandemic wave in Catalonia, Spain. 2011 , 69, 419-27	26
1550	Six defensins from the triangle-shell pearl mussel Hyriopsis cumingii. 2011 , 31, 1232-8	15
1549	Evolutionary analysis of three gibberellin oxidase genes in rice, Arabidopsis, and soybean. 2011 , 473, 23-35	47
1548	Selected codon usage bias in members of the class Mollicutes. 2011 , 473, 110-8	5

1547	Molecular evolution of two duplicated CDPK genes CPK7 and CPK12 in grass species: a case study in wheat (Triticum aestivum L.). 2011 , 475, 94-103		17
1546	Complete mitochondrial genome sequences of three Crocodylus species and their comparison within the Order Crocodylia. 2011 , 478, 35-41		19
1545	Molecular evolution of the EGF-CFC protein family. 2011 , 482, 43-50		6
1544	Maximum likelihood analysis of mammalian p53 indicates the presence of positively selected sites and higher tumorigenic mutations in purifying sites. 2011 , 483, 29-35		8
1543	Unusual signatures of highly adaptable R-loci in closely-related Arabidopsis species. 2011 , 482, 24-33		21
1542	Sequence conservation among orthologous vomeronasal type 1 receptor-like (ora) genes does not support the differential tuning hypothesis in Salmonidae. 2011 , 485, 16-21		11
1541	Integrative analysis of transcriptome and genome indicates two potential genomic islands are associated with pathogenesis of Mycobacterium tuberculosis. 2011 , 489, 21-9		10
1540	Improved phylogenetic resolution of toxic and non-toxic Alexandrium strains using a concatenated rDNA approach. 2011 , 10, 676-688		46
1539	Structure and evolution of the Fusarium mating type locus: new insights from the Gibberellafujikuroi complex. 2011 , 48, 731-40		48
1538	Lipid-binding surfaces of membrane proteins: evidence from evolutionary and structural analysis. 2011 , 1808, 1092-102		63
1537	Dating primate divergences through an integrated analysis of palaeontological and molecular data. 2011 , 60, 16-31		155
1536	Molecular evolution and network-level analysis of the N-glycosylation metabolic pathway across primates. <i>Molecular Biology and Evolution</i> , 2011 , 28, 813-23	8.3	25
1535	Statistical properties of the branch-site test of positive selection. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1217-28	8.3	221
1534	Unlocking the barley genome by chromosomal and comparative genomics. 2011 , 23, 1249-63		390
1533	Sequence comparison between three geographically distinct Spodoptera frugiperda multiple nucleopolyhedrovirus isolates: Detecting positively selected genes. 2011 , 107, 33-42		32
1532	Markovian and non-Markovian protein sequence evolution: aggregated Markov process models. 2011 , 411, 910-23		16
1531	A computationally optimized broadly reactive antigen (COBRA) based H5N1 VLP vaccine elicits broadly reactive antibodies in mice and ferrets. 2011 , 29, 3043-54		115
1530	Comparative analysis of Gossypium and Vitis genomes indicates genome duplication specific to the Gossypium lineage. 2011 , 97, 313-20		18

1529	Origin and evolutionary analysis of the plant-specific TIFY transcription factor family. 2011, 98, 128-36	130
1528	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. 2011 , 19, 472-82	22
1527	Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. 2011, 108, 13212-7	131
1526	A Reconfigurable Processor for Phylogenetic Inference. 2011 ,	1
1525	Detecting signatures of positive selection in partial sequences generated on a large scale: pitfalls, procedures and resources. 2011 , 11 Suppl 1, 172-83	12
1524	Kakusan4 and Aminosan: two programs for comparing nonpartitioned, proportional and separate models for combined molecular phylogenetic analyses of multilocus sequence data. 2011 , 11, 914-21	464
1523	Searching for evidence of selection in avian DNA barcodes. 2011 , 11, 1045-55	24
1522	Museum genomics: low-cost and high-accuracy genetic data from historical specimens. 2011 , 11, 1082-92	89
1521	Computing Geodesic Distances in Tree Space. 2011 , 25, 1506-1529	23
1520	Substitution rate variation at human CpG sites correlates with non-CpG divergence, methylation level and GC content. 2011 , 12, R58	53
1519	Proteome-wide evidence for enhanced positive Darwinian selection within intrinsically disordered regions in proteins. 2011 , 12, R65	58
1518	A high-throughput venom-gland transcriptome for the Eastern Diamondback Rattlesnake (Crotalus adamanteus) and evidence for pervasive positive selection across toxin classes. 2011 , 57, 657-71	99
1517	Genomic data reject the hypothesis of a prosimian primate clade. 2011 , 61, 295-305	38
1516	Adaptive evolution of the vertebrate skeletal muscle sodium channel. 2011 , 34, 323-8	6
1515	Molecular and morphological description of a new species of Halisarca (Demospongiae: Halisarcida) from Mediterranean Sea and a redescription of the type species Halisarca dujardini. 2011 , 2768, 5	25
1514	Molecular evolution of two consecutive carotenoid cleavage dioxygenase genes in strigolactone biosynthesis in plants. 2011 , 10, 3664-73	8
1513	Phosphorylation network rewiring by gene duplication. 2011 , 7, 504	28
1512	Protein structural modularity and robustness are associated with evolvability. 2011 , 3, 456-75	27

1511 Evolutionary Biology and Drug Development. **2011**,

1510	Ancient antimicrobial peptides kill antibiotic-resistant pathogens: Australian mammals provide new options. 2011 , 6, e24030	61
1509	The first molecular phylogeny of Strepsiptera (Insecta) reveals an early burst of molecular evolution correlated with the transition to endoparasitism. 2011 , 6, e21206	28
1508	Complex interplay of evolutionary forces in the ladybird homeobox genes of Drosophila melanogaster. 2011 , 6, e22613	7
1507	Complete sequencing and pan-genomic analysis of Lactobacillus delbrueckii subsp. bulgaricus reveal its genetic basis for industrial yogurt production. 2011 , 6, e15964	66
1506	Phylogenetic comparison of F-Box (FBX) gene superfamily within the plant kingdom reveals divergent evolutionary histories indicative of genomic drift. 2011 , 6, e16219	93
1505	Odorant binding proteins of the red imported fire ant, Solenopsis invicta: an example of the problems facing the analysis of widely divergent proteins. 2011 , 6, e16289	35
1504	Molecular evolutionary analysis of ABCB5: the ancestral gene is a full transporter with potentially deleterious single nucleotide polymorphisms. 2011 , 6, e16318	21
1503	Vertebrate paralogous MEF2 genes: origin, conservation, and evolution. 2011 , 6, e17334	24
1502	Clues to evolution of the SERA multigene family in 18 Plasmodium species. 2011 , 6, e17775	34
1501	Change of positive selection pressure on HIV-1 envelope gene inferred by early and recent samples. 2011 , 6, e18630	20
1500	Two Theileria parva CD8 T cell antigen genes are more variable in buffalo than cattle parasites, but differ in pattern of sequence diversity. 2011 , 6, e19015	52
1499	Variation in the analysis of positively selected sites using nonsynonymous/synonymous rate ratios: an example using influenza virus. 2011 , 6, e19996	16
1498	Contrasting codon usage patterns and purifying selection at the mating locus in putatively asexual alternaria fungal species. 2011 , 6, e20083	15
1497	Identification of fast-evolving genes in the scleractinian coral Acropora using comparative EST analysis. 2011 , 6, e20140	18
1496	Host-pathogen o-methyltransferase similarity and its specific presence in highly virulent strains of Francisella tularensis suggests molecular mimicry. 2011 , 6, e20295	6
1495	Markov models of amino acid substitution to study proteins with intrinsically disordered regions. 2011 , 6, e20488	31
1494	MultiMSOAR 2.0: an accurate tool to identify ortholog groups among multiple genomes. 2011 , 6, e20892	15

1493	Adaptive evolution of the venom-targeted vWF protein in opossums that eat pitvipers. 2011, 6, e20997	57
1492	Expression and trans-specific polymorphism of self-incompatibility RNases in coffea (Rubiaceae). 2011 , 6, e21019	40
1491	LRR conservation mapping to predict functional sites within protein leucine-rich repeat domains. 2011 , 6, e21614	40
1490	Multiple nuclear gene phylogenetic analysis of the evolution of dioecy and sex chromosomes in the genus Silene. 2011 , 6, e21915	27
1489	Addressing inter-gene heterogeneity in maximum likelihood phylogenomic analysis: yeasts revisited. 2011 , 6, e22783	20
1488	Evolutionary genomics implies a specific function of Ant4 in mammalian and anole lizard male germ cells. 2011 , 6, e23122	11
1487	No evidence for natural selection on endogenous borna-like nucleoprotein elements after the divergence of Old World and New World monkeys. 2011 , 6, e24403	13
1486	Regional selection acting on the OFD1 gene family. 2011 , 6, e26195	7
1485	Evolutionary history of the vertebrate mitogen activated protein kinases family. 2011 , 6, e26999	44
1484	Molecular evolution of the transmembrane domains of G protein-coupled receptors. 2011 , 6, e27813	10
1483	Non-negative matrix factorization for learning alignment-specific models of protein evolution. 2011 , 6, e28898	8
1482	Comparative genomics of the anopheline glutathione S-transferase epsilon cluster. 2011 , 6, e29237	16
1481	Sexual selection halts the relaxation of protamine 2 among rodents. 2011 , 6, e29247	14
1480	Comparative genomic analysis of the Streptococcus dysgalactiae species group: gene content, molecular adaptation, and promoter evolution. 2011 , 3, 168-85	40
1479	Differential loss and retention of cytoglobin, myoglobin, and globin-E during the radiation of vertebrates. 2011 , 3, 588-600	57
1478	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
1477	Massive genomic decay in Serratia symbiotica, a recently evolved symbiont of aphids. 2011 , 3, 195-208	153
1476	The chloroplast genome of the green alga Schizomeris leibleinii (Chlorophyceae) provides evidence for bidirectional DNA replication from a single origin in the chaetophorales. 2011 , 3, 505-15	29

1475	Selection for translation efficiency on synonymous polymorphisms in recent human evolution. 2011 , 3, 749-61	37
1474	A very early-branching Staphylococcus aureus lineage lacking the carotenoid pigment staphyloxanthin. 2011 , 3, 881-95	119
1473	Significant selective constraint at 4-fold degenerate sites in the avian genome and its consequence for detection of positive selection. 2011 , 3, 1381-9	24
1472	Evolution of synonymous codon usage in Neurospora tetrasperma and Neurospora discreta. 2011 , 3, 332-43	31
1471	Evolution of the Max and Mlx networks in animals. 2011 , 3, 915-37	24
1470	Free energy calculations and binding analysis of two potential anti- influenza drugs with Polymerase basic protein-2 (PB2). 2011 , 18, 1002-9	5
1469	Genome sequences reveal divergence times of malaria parasite lineages. 2011 , 138, 1737-49	38
1468	Positive selection for gains of N-linked glycosylation sites in hemagglutinin during evolution of H3N2 human influenza A virus. 2011 , 86, 287-94	17
1467	454 Genome sequencing of Pseudoperonospora cubensis reveals effector proteins with a QXLR translocation motif. 2011 , 24, 543-53	73
1466	Population genetic analysis of Tomato spotted wilt virus on peanut in North Carolina and Virginia. 2011 , 101, 147-53	26
1465	Molecular Clock: Testing. 2011 ,	1
1464	Reptiles and mammals have differentially retained long conserved noncoding sequences from the amniote ancestor. 2011 , 3, 102-13	27
1463	Signature of selection on the rhodopsin gene in the marine radiation of American seven-spined gobies (Gobiidae, Gobiosomatini). 2011 , 24, 1618-25	6
1462	Genetic structure of marine Borrelia garinii and population admixture with the terrestrial cycle of Lyme borreliosis. 2011 , 13, 2453-67	46
1461	Rethinking the evolution of extant sub-Saharan African suids (Suidae, Artiodactyla). 2011 , 40, 327-335	34
1460	Testing fossil calibrations for vertebrate molecular trees. 2011 , 40, 538-543	12
1459	Association and evolutionary studies of the melatonin receptor 1B gene (MTNR1B) in the self-contained population of Sorbs from Germany. 2011 , 28, 1373-80	10
1458	Evolution of the YABBY gene family with emphasis on the basal eudicot Eschscholzia californica (Papaveraceae). 2012 , 14, 11-23	47

1457	Refugia and phylogeography of Taiwania in East Asia. 2011 , 38, 1992-2005	39
1456	Building bridges: formin1 of Arabidopsis forms a connection between the cell wall and the actin cytoskeleton. 2011 , 66, 354-65	95
1455	Relation of pretreatment sequence diversity in NS5A region of HCV genotype 1 with immune response between pegylated-INF/ribavirin therapy outcomes. 2011 , 18, 142-8	5
1454	Interpopulation patterns of divergence and selection across the transcriptome of the copepod Tigriopus californicus. 2011 , 20, 560-72	57
1453	Intraspecific specialization of the generalist parasitoid Cotesia sesamiae revealed by polyDNAvirus polymorphism and associated with different Wolbachia infection. 2011 , 20, 959-71	40
1452	An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the eIF4E resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. 2011 , 20, 3653-68	39
1451	Galega orientalis is more diverse than Galega officinalis in Caucasuswhole-genome AFLP analysis and phylogenetics of symbiosis-related genes. 2011 , 20, 4808-21	12
1450	Positive Darwinian selection in gamete recognition proteins of Strongylocentrotus sea urchins. 2011 , 20, 4968-82	31
1449	AQUATIC PLANT SPECIATION AFFECTED BY DIVERSIFYING SELECTION OF ORGANELLE DNA REGIONS(1). 2011 , 47, 999-1008	5
1448	The molecular basis for venation patterning of pigmentation and its effect on pollinator attraction in flowers of Antirrhinum. 2011 , 189, 602-15	127
1447	Investigation of the potential for triterpene synthesis in rice through genome mining and metabolic engineering. 2011 , 191, 432-448	37
1446	The evolution of RNA editing and pentatricopeptide repeat genes. 2011 , 191, 37-47	206
1445	Establishing a time-scale for plant evolution. 2011 , 192, 266-301	248
1444	Evolutionary history and complementary selective relaxation of the duplicated PI genes in grasses. 2011 , 53, 682-93	5
1443	Developmental decoupling of alternative phenotypes: insights from the transcriptomes of horn-polyphenic beetles. 2011 , 65, 231-45	70
1442	The local-clock permutation test: a simple test to compare rates of molecular evolution on phylogenetic trees. 2011 , 65, 606-11	12
1441	Complex evolutionary transitions and the significance of c(3)-c(4) intermediate forms of photosynthesis in Molluginaceae. 2011 , 65, 643-60	97
1440	Comparison of 16S rRNA and protein-coding genes as molecular markers for assessing microbial diversity (Bacteria and Archaea) in ecosystems. 2011 , 78, 617-28	43

1439	Unresolved molecular phylogenies of gibbons and siamangs (Family: Hylobatidae) based on mitochondrial, Y-linked, and X-linked loci indicate a rapid Miocene radiation or sudden vicariance event. 2011 , 58, 447-55	42
1438	Bayesian relaxed clock estimation of divergence times in foraminifera. 2011 , 61, 157-66	29
1437	The evolution of mitochondrial genomes in subterranean caviomorph rodents: adaptation against a background of purifying selection. 2011 , 61, 64-70	58
1436	Molecular phylogeny and evolution of the Perissodactyla. 2011 , 163, 1289-1303	73
1435	Multiple genetic divergences and population expansions of a Mediterranean sandfly, Phlebotomus ariasi, in Europe during the Pleistocene glacial cycles. 2011 , 106, 714-26	29
1434	Functional gametophytic self-incompatibility in a peripheral population of Solanum peruvianum (Solanaceae). 2011 , 107, 30-9	19
1433	MHC class II DRB diversity, selection pattern and population structure in a neotropical bat species, Noctilio albiventris. 2011 , 107, 115-26	22
1432	Molecular population genetics of the OBP83 genomic region in Drosophila subobscura and D. guanche: contrasting the effects of natural selection and gene arrangement expansion in the patterns of nucleotide variation. 2011 , 106, 191-201	10
1431	Molecular evolution of glycinin and Econglycinin gene families in soybean (Glycine max L. Merr.). 2011 , 106, 633-41	29
1430	Evidence of the accumulation of allele-specific non-synonymous substitutions in the young region of recombination suppression within the mating-type chromosomes of Neurospora tetrasperma. 2011 , 107, 305-14	24
1429	Unprecedented levels of horizontal gene transfer among spatially co-occurring Shewanella bacteria from the Baltic Sea. 2011 , 5, 131-40	48
1428	A multifaceted genomics approach allows the isolation of the rice Pia-blast resistance gene consisting of two adjacent NBS-LRR protein genes. 2011 , 66, 467-79	213
1427	Tracing protein evolution through ancestral structures of fish galectin. 2011 , 19, 711-21	13
1426	Review: Toward an integrated evolutionary understanding of the mammalian placenta. 2011 , 32 Suppl 2, S142-5	38
1425	A syncytin-like endogenous retrovirus envelope gene of the guinea pig specifically expressed in the placenta junctional zone and conserved in Caviomorpha. 2011 , 32, 885-92	24
1424	Ovalopodium desertum n. sp. and the phylogenetic relationships of Cochliopodiidae (Amoebozoa). 2011 , 162, 571-89	29
1423	Phylogenetic networks to study the origin and evolution of porcine circovirus type 2 (PCV2) in Cuba. 2011 , 151, 245-54	23
1422	Genetic characterization and evolutionary analysis of 4 Newcastle disease virus isolate full genomes from waterbirds in South China during 2003-2007. 2011 , 152, 46-54	26

1421	A comparative study on the visual adaptations of four species of moray eel. 2011 , 51, 1099-108	15
1420	CpG site degeneration triggered by the loss of functional constraint created a highly polymorphic macaque drug-metabolizing gene, CYP1A2. 2011 , 11, 283	17
1419	Signatures of positive selection in Toll-like receptor (TLR) genes in mammals. 2011, 11, 368	119
1418	Comprehensive analysis of tandem amino acid repeats from ten angiosperm genomes. 2011 , 12, 632	10
1417	Genes under positive selection in Mycobacterium tuberculosis. 2011 , 35, 319-22	12
1416	Plant Y chromosome degeneration is retarded by haploid purifying selection. 2011 , 21, 1475-9	129
1415	Molecular divergence of two orthologous scorpion toxins affecting potassium channels. 2011 , 159, 313-21	16
1414	Variation in MHC genotypes in two populations of house sparrow (Passer domesticus) with different population histories. 2011 , 1, 145-59	31
1413	The making of a new pathogen: insights from comparative population genomics of the domesticated wheat pathogen Mycosphaerella graminicola and its wild sister species. 2011 , 21, 2157-66	150
1412	On universal common ancestry, sequence similarity, and phylogenetic structure: the sins of P-values and the virtues of Bayesian evidence. 2011 , 6, 60	15
1411	Thermal energy and the rate of genetic evolution in marine fishes. 2011 , 25, 525-530	35
1410	WRKY gene family evolution in Arabidopsis thaliana. 2011 , 139, 973-83	45
1409	Multi-locus species tree of the chub genus Squalius (Leuciscinae: Cyprinidae) from western Iberia: new insights into its evolutionary history. 2011 , 139, 1009-18	11
1408	Comparative analysis of evolutionary dynamics of genes encoding leucine-rich repeat receptor-like kinase between rice and Arabidopsis. 2011 , 139, 1023-32	38
1407	Molecular evolution of a family of resistance gene analogs of nucleotide-binding site sequences in Solanum lycopersicum. 2011 , 139, 1229-40	3
1406	Molecular evolution of the membrane associated progesterone receptor in the Brachionus plicatilis (Rotifera, Monogononta) species complex. 2011 , 662, 99-106	8
1405	Reduced MHC class II diversity in island compared to mainland populations of the black-footed rock-wallaby (Petrogale lateralis lateralis). 2011 , 12, 91-103	22
1404	Molecular evolution of aminoacyl tRNA synthetase proteins in the early history of life. 2011 , 41, 621-32	35

1403	Tropomyosin is a nice marker gene for phylogenetic analysis of molluscs. 2011 , 38, 4589-93	3
1402	Comparative complete genome analysis of Indian type A foot-and-mouth disease virus field isolates. 2011 , 43, 224-33	9
1401	Evaluation of candidate F-box genes for the pollen S of gametophytic self-incompatibility in the Pyrinae (Rosaceae) on the basis of their phylogenomic context. 2011 , 7, 663-683	18
1400	In silico characterization and comparative genomic analysis of the Culex quinquefasciatus glutathione S-transferase (GST) supergene family. 2011 , 109, 1165-77	13
1399	Interkingdom protein domain fusion: the case of an antimicrobial protein in potato (Solanum tuberosum). 2011 , 297, 129-139	1
1398	A novel cationic ribonuclease with antimicrobial activity from Rana dybowskii. 2011 , 49, 369-84	8
1397	Evolutionary features and intracellular behavior of the PRTB protein. 2011, 49, 458-73	3
1396	Contrasted patterns of selection since maize domestication on duplicated genes encoding a starch pathway enzyme. 2011 , 122, 705-22	10
1395	Exploiting models of molecular evolution to efficiently direct protein engineering. 2011 , 72, 193-203	39
1394	Isolation and characterization of the CYP2D6 gene in Felidae with comparison to other mammals. 2011 , 72, 222-31	2
1393	Copia retrotransposon in the Zaprionus genus: another case of transposable element sharing with the Drosophila melanogaster subgroup. 2011 , 72, 326-38	7
1392	Co-variation among major classes of LRR-encoding genes in two pairs of plant species. 2011 , 72, 498-509	15
1391	Absence of positive selection on centromeric histones in Tetrahymena suggests unsuppressed centromere: drive in lineages lacking male meiosis. 2011 , 72, 510-20	14
1390	Positive Darwinian selection drives the evolution of the morphology-related gene, EPCAM, in particularly species-rich lineages of African cichlid fishes. 2011 , 73, 1-9	9
1389	A chimeric chromosome in the ciliate oxytricha resulting from duplication. 2011 , 73, 70-3	5
1388	An expansion of age constraints for microbial clades that lack a conventional fossil record using phylogenomic dating. 2011 , 73, 188-208	10
1387	Signatures of natural selection in a primate bitter taste receptor. 2011 , 73, 257-65	19
1386	Molecular characterization of two endothelin pathways in East African cichlid fishes. 2011 , 73, 355-68	14

1385	Structure, diversity and evolutionary patterns of expressed MHC class IIB genes in chub (Squalius cephalus), a cyprinid fish species from Europe. 2011 , 63, 167-81	13
1384	Molecular evolution of immunoglobulin superfamily genes in primates. 2011 , 63, 417-28	7
1383	Characterization of MHC class I and II genes in a subantarctic seabird, the blue petrel, Halobaena caerulea (Procellariiformes). 2011 , 63, 653-66	40
1382	Prediction of sites under adaptive evolution in flavin-containing monooxygenases: Selection pattern revisited. 2011 , 56, 1246-1255	5
1381	To be or not to be the odd one outallele-specific transcription in pentaploid dogroses (Rosa L. sect. Caninae (DC.) Ser). 2011 , 11, 37	11
1380	High levels of nucleotide diversity and fast decline of linkage disequilibrium in rye (Secale cereale L.) genes involved in frost response. 2011 , 11, 6	47
1379	Positive selection in the hemagglutinin-neuraminidase gene of Newcastle disease virus and its effect on vaccine efficacy. 2011 , 8, 150	21
1378	A late origin of the extant eukaryotic diversity: divergence time estimates using rare genomic changes. 2011 , 6, 26	46
1377	Interplay of recombination and selection in the genomes of Chlamydia trachomatis. 2011, 6, 28	57
1376	Molecular evolution of rbcL in three gymnosperm families: identifying adaptive and coevolutionary patterns. 2011 , 6, 29	16
1375	Shift in the isoelectric-point of milk proteins as a consequence of adaptive divergence between the milks of mammalian species. 2011 , 6, 40	29
1374	A rooted net of life. 2011 , 6, 45	30
1373	Positive selection on a bacterial oncoprotein associated with gastric cancer. 2011 , 3, 18	7
1372	PhyloSim - Monte Carlo simulation of sequence evolution in the R statistical computing environment. 2011 , 12, 104	36
1371	Detection of lineage-specific evolutionary changes among primate species. 2011 , 12, 274	15
1370	Detecting genomic regions associated with a disease using variability functions and Adjusted Rand Index. 2011 , 12 Suppl 9, S9	4
1369	The impact of sex-role reversal on the diversity of the major histocompatibility complex: insights from the seahorse (Hippocampus abdominalis). 2011 , 11, 121	11
1368	Adaptive molecular evolution of the Major Histocompatibility Complex genes, DRA and DQA, in the genus Equus. 2011 , 11, 128	29

1367	The mode and tempo of hepatitis C virus evolution within and among hosts. 2011, 11, 131	107
1366	Evidence for the additions of clustered interacting nodes during the evolution of protein interaction networks from network motifs. 2011 , 11, 133	13
1365	Evolution of endogenous retroviruses in the Suidae: evidence for different viral subpopulations in African and Eurasian host species. 2011 , 11, 139	9
1364	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. 2011 , 11, 142	2
1363	The evolutionary history of the SAL1 gene family in eutherian mammals. 2011 , 11, 148	18
1362	Molecular evolution of the vertebrate TLR1 gene familya complex history of gene duplication, gene conversion, positive selection and co-evolution. 2011 , 11, 149	50
1361	Testis-specific glyceraldehyde-3-phosphate dehydrogenase: origin and evolution. 2011 , 11, 160	13
1360	From Antarctica or Asia? New colonization scenario for Australian-New Guinean narrow mouth toads suggested from the findings on a mysterious genus Gastrophrynoides. 2011 , 11, 175	23
1359	Evolutionary history of Otophysi (Teleostei), a major clade of the modern freshwater fishes: Pangaean origin and Mesozoic radiation. 2011 , 11, 177	133
1358	Reproductive protein evolution in two cryptic species of marine chordate. 2011 , 11, 18	15
1357	Genetic mechanisms involved in the evolution of the cephalopod camera eye revealed by transcriptomic and developmental studies. 2011 , 11, 180	12
1356	Evidence for acquisition of virulence effectors in pathogenic chytrids. 2011 , 11, 195	40
1355	Genome-wide evidence for positive selection and recombination in Actinobacillus pleuropneumoniae. 2011 , 11, 203	26
1354	Molecular evolution of cyclin proteins in animals and fungi. 2011 , 11, 224	23
1353	Molecular adaptation in flowering and symbiotic recognition pathways: insights from patterns of polymorphism in the legume Medicago truncatula. 2011 , 11, 229	18
1352	Evolutionary patterns of two major reproduction candidate genes (Zp2 and Zp3) reveal no contribution to reproductive isolation between bovine species. 2011 , 11, 24	6
1351	Evidence for maintenance of sex determinants but not of sexual stages in red yeasts, a group of early diverged basidiomycetes. 2011 , 11, 249	27
1350	Molecular evolution under increasing transposable element burden in Drosophila: a speed limit on the evolutionary arms race. 2011 , 11, 258	25

1349	Coevolution of amino acid residues in the key photosynthetic enzyme Rubisco. 2011 , 11, 266	22
1348	Rate variation and estimation of divergence times using strict and relaxed clocks. 2011 , 11, 271	81
1347	Sex in the PAC: a hidden affair in dark septate endophytes?. 2011 , 11, 282	13
1346	A hitchhikers guide to the Galþagos: co-phylogeography of Galþagos mockingbirds and their parasites. 2011 , 11, 284	45
1345	Diversification and the rate of molecular evolution: no evidence of a link in mammals. 2011 , 11, 286	31
1344	Genomic lineages of Rhizobium etli revealed by the extent of nucleotide polymorphisms and low recombination. 2011 , 11, 305	14
1343	A Bayesian framework to estimate diversification rates and their variation through time and space. 2011 , 11, 311	73
1342	Molecular phylogeny of the higher and lower taxonomy of the Fusarium genus and differences in the evolutionary histories of multiple genes. 2011 , 11, 322	71
1341	Whole mitochondrial genome sequencing of domestic horses reveals incorporation of extensive wild horse diversity during domestication. 2011 , 11, 328	75
1340	Adaptive evolution of the matrix extracellular phosphoglycoprotein in mammals. 2011 , 11, 342	15
1339	The nonadaptive nature of the H1N1 2009 Swine Flu pandemic contrasts with the adaptive facilitation of transmission to a new host. 2011 , 11, 6	8
1338	HIV-1 infected monozygotic twins: a tale of two outcomes. 2011 , 11, 62	10
1337	Molecular evolution of a gene cluster of serine proteases expressed in the Anopheles gambiae female reproductive tract. 2011 , 11, 72	15
1336	Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. 2011 , 11, 8	61
1335	Lineage-specific late pleistocene expansion of an endemic subtropical gossamer-wing damselfly, Euphaea formosa, in Taiwan. 2011 , 11, 94	16
1334	Phylogeny and adaptive evolution of the brain-development gene microcephalin (MCPH1) in cetaceans. 2011 , 11, 98	21
1333	Venom gland transcriptomes of two elapid snakes (Bungarus multicinctus and Naja atra) and evolution of toxin genes. 2011 , 12, 1	188
1332	Genes in the terminal regions of orthopoxvirus genomes experience adaptive molecular evolution. 2011 , 12, 261	11

1331	Systematic discovery of unannotated genes in 11 yeast species using a database of orthologous genomic segments. 2011 , 12, 377		13
1330	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
1329	Genome-wide analysis of WRKY gene family in Cucumis sativus. 2011 , 12, 471		188
1328	Rigorous and thorough bioinformatic analyses of olfactory receptor promoters confirm enrichment of O/E and homeodomain binding sites but reveal no new common motifs. 2011 , 12, 561		10
1327	Distinctive mitochondrial genome of Calanoid copepod Calanus sinicus with multiple large non-coding regions and reshuffled gene order: useful molecular markers for phylogenetic and population studies. 2011 , 12, 73		27
1326	Evolution of the isoelectric point of mammalian proteins as a consequence of indels and adaptive evolution. 2011 , 79, 1635-48		12
1325	Evaluation of genetic markers for identifying isolates of the species of the genus Fusarium. 2011 , 91, 2500-4		15
1324	Increased positive selection pressure within the complementarity determining regions of the T-cell receptor Igene in New World monkeys. 2011 , 73, 1082-92		2
1323	Evolving Perceptions on the Antiquity of the Modern Avian Tree. 2011 , 306-324		17
1322	Birt Hogg-Dub[syndrome-associated FLCN mutations disrupt protein stability. 2011 , 32, 921-9		32
1321	Basic Molecular Evolution WorkshopA trans-African virtual training course: "Virtual Workshops": Is Africa ready to embrace the concept?. 2011 , 33, 243-7		1
1320	Concatenated mitochondrial DNA of the coccidian parasite Eimeria tenella. 2011 , 11, 273-8		40
1319	Unresolved direction of host transfer of Plasmodium vivax v. P. simium and P. malariae v. P. brasilianum. 2011 , 11, 209-21		56
1318	Phylogenetic analyses of mitochondrial and nuclear data in haematophagous flies support the paraphyly of the genus Stomoxys (Diptera: Muscidae). 2011 , 11, 663-70		20
1317	First insights into fern matK phylogeny. 2011 , 59, 556-66		100
1316	A comprehensive phylogeny of Neurospora reveals a link between reproductive mode and molecular evolution in fungi. 2011 , 59, 649-63		71
1315	Structural-based analysis of dihydrofolate reductase evolution. 2011 , 61, 212-30		11
1314	Selective constraints in conserved folded RNAs of drosophilid and hominid genomes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1519-29	8.3	9

1313	A pilot study of bacterial genes with disrupted ORFs reveals a surprising profusion of protein sequence recoding mediated by ribosomal frameshifting and transcriptional realignment. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3195-211	8.3	38
1312	Changes in Rubisco kinetics during the evolution of C4 photosynthesis in Flaveria (Asteraceae) are associated with positive selection on genes encoding the enzyme. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1491-503	8.3	73
1311	Genes involved in convergent evolution of eusociality in bees. 2011 , 108, 7472-7		159
1310	Measuring the evolutionary rate of protein-protein interaction. 2011 , 108, 8725-30		45
1309	Identification of novel GDNF isoforms and cis-antisense GDNFOS gene and their regulation in human middle temporal gyrus of Alzheimer disease. 2011 , 286, 45093-102		79
1308	Phylogeny and expression profile analyses of oleate- and linoleate-desaturase genes in soybean. 2011 ,		
1307	Botrytis pseudocinerea, a new cryptic species causing gray mold in French vineyards in sympatry with Botrytis cinerea. 2011 , 101, 1433-45		125
1306	Genomic differentiation between temperate and tropical Australian populations of Drosophila melanogaster. 2011 , 187, 245-60		170
1305	The breadth of antiviral activity of Apobec3DE in chimpanzees has been driven by positive selection. 2011 , 85, 11361-71		45
1304	Fast and slow implementations of relaxed-clock methods show similar patterns of accuracy in estimating divergence times. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2439-42	8.3	27
1303	What's in a likelihood? Simple models of protein evolution and the contribution of structurally viable reconstructions to the likelihood. 2011 , 60, 161-74		11
1302	Dynamics of dengue disease severity determined by the interplay between viral genetics and serotype-specific immunity. 2011 , 3, 114ra128		208
1301	Function-specific accelerations in rates of sequence evolution suggest predictable epistatic responses to reduced effective population size. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2339-49	8.3	11
1300	Patterns of codon usage bias in Silene latifolia. <i>Molecular Biology and Evolution</i> , 2011 , 28, 771-80	8.3	52
1299	Paleozoic origin of insect large dsDNA viruses. 2011 , 108, 15931-5		111
1298	"Patchy-tachy" leads to false positives for recombination. <i>Molecular Biology and Evolution</i> , 2011 , 28, 254	% -59	16
1297	Time dependency of molecular evolutionary rates? Yes and no. 2011 , 3, 1324-8		18
1296	On characterizing adaptive events unique to modern humans. 2011 , 3, 791-8		12

1295	Reverse evolution in RH1 for adaptation of cichlids to water depth in Lake Tanganyika. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1769-76	8.3	26
1294	Selection patterns on restorer-like genes reveal a conflict between nuclear and mitochondrial genomes throughout angiosperm evolution. 2011 , 108, 1723-8		190
1293	Lineage-specific variation in intensity of natural selection in mammals. <i>Molecular Biology and Evolution</i> , 2011 , 28, 383-98	8.3	31
1292	Protamine 3 shows evidence of weak, positive selection in mouse species (genus Mus)but it is not a protamine. 2011 , 84, 320-6		10
1291	Diversification at transcription factor binding sites within a species and the implications for environmental adaptation. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3331-44	8.3	5
1290	Stearoyl-acyl carrier protein desaturases are associated with floral isolation in sexually deceptive orchids. 2011 , 108, 5696-701		72
1289	The relationship between relative solvent accessibility and evolutionary rate in protein evolution. 2011 , 188, 479-88		84
1288	High sensitivity to aligner and high rate of false positives in the estimates of positive selection in the 12 Drosophila genomes. 2011 , 21, 863-74		105
1287	Evolution of cassava brown streak disease-associated viruses. 2011 , 92, 974-87		77
1286	Exploring patterns and extent of bias in estimating divergence time from mitochondrial DNA sequence data in a particular lineage: a case study of salamanders (order Caudata). <i>Molecular Biology and Evolution</i> , 2011 , 28, 2521-35	8.3	98
1285	PHAST and RPHAST: phylogenetic analysis with space/time models. 2011 , 12, 41-51		240
1284	Long-range and targeted ectopic recombination between the two homeologous chromosomes 11 and 12 in Oryza species. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3139-50	8.3	20
1283	Molecular adaptation of the chloroplast matK gene in Nymphaea tetragona, a critically rare and endangered plant of India. 2011 , 9, 193-196		6
1282	dN/dS-based methods detect positive selection linked to trade-offs between different fitness traits in the coat protein of potato virus Y. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2707-17	8.3	58
1281	The reconstructed ancestral subunit a functions as both V-ATPase isoforms Vph1p and Stv1p in Saccharomyces cerevisiae. 2011 , 22, 3176-91		20
1280	The Anolis lizard genome: an amniote genome without isochores. 2011 , 3, 974-84		37
1279	Genomic determinants of protein evolution and polymorphism in Arabidopsis. 2011 , 3, 1210-9		71
1278	Comparative vertebrate evolutionary analyses of type I collagen: potential of COL1a1 gene structure and intron variation for common bone-related diseases. <i>Molecular Biology and Evolution</i> , 2011 , 28, 533-42	8.3	40

1277	Changes in expression pattern of the teosinte branched1-like genes in the Zingiberales provide a mechanism for evolutionary shifts in symmetry across the order. 2011 , 98, 227-43		52
1276	A likelihood method for detecting trait-dependent shifts in the rate of molecular evolution. <i>Molecular Biology and Evolution</i> , 2011 , 28, 759-70	8.3	28
1275	The Dca gene involved in cold adaptation in Drosophila melanogaster arose by duplication of the ancestral regucalcin gene. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2185-95	8.3	12
1274	Directed networks reveal genomic barriers and DNA repair bypasses to lateral gene transfer among prokaryotes. 2011 , 21, 599-609		168
1273	Transcriptome analysis of sarracenia, an insectivorous plant. 2011 , 18, 253-61		25
1272	Comparative genomics of Esx genes from clinical isolates of Mycobacterium tuberculosis provides evidence for gene conversion and epitope variation. 2011 , 79, 4042-9		43
1271	Conservation and purifying selection of transcribed genes located in a rice centromere. 2011 , 23, 2821	-30	19
1270	Molecular convergence of infrared vision in snakes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 45-8	8.3	11
1269	Domestication relaxed selective constraints on the yak mitochondrial genome. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1553-6	8.3	62
1268	Extraordinary sequence divergence at Tsga8, an X-linked gene involved in mouse spermiogenesis. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1675-86	8.3	9
1267	Evolutionary constraint in flanking regions of avian genes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2481-9	8.3	5
1266	Large-scale phylogenomic analyses indicate a deep origin of primary plastids within cyanobacteria. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3019-32	8.3	85
1265	Evolutionary models accounting for layers of selection in protein-coding genes and their impact on the inference of positive selection. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3297-308	8.3	32
1264	The accuracy of species tree estimation under simulation: a comparison of methods. 2011 , 60, 126-37		190
1263	Gradual disintegration of the floral symmetry gene network is implicated in the evolution of a wind-pollination syndrome. 2011 , 108, 2343-8		51
1262	Na+-translocating membrane pyrophosphatases are widespread in the microbial world and evolutionarily precede H+-translocating pyrophosphatases. 2011 , 286, 21633-42		41
1261	Genome expansion and differential expression of amino acid transporters at the aphid/Buchnera symbiotic interface. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3113-26	8.3	43
1260	Evolutionary patterns of the mitochondrial genome in Metazoa: exploring the role of mutation and selection in mitochondrial protein coding genes. 2011 , 3, 1067-1079		109

1259	Molecular evolution of the metazoan PHD-HIF oxygen-sensing system. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1913-26	8.3	102
1258	Sequencing and analysis of plastid genome in mycoheterotrophic orchid Neottia nidus-avis. 2011 , 3, 12	96-303	91
1257	Recurrent adaptation in RNA interference genes across the Drosophila phylogeny. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1033-42	8.3	63
1256	Molecular evolution of a Y chromosome to autosome gene duplication in Drosophila. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1293-306	8.3	17
1255	Computational analysis suggests that lyssavirus glycoprotein gene plays a minor role in viral adaptation. 2011 , 2011, 143498		1
1254	Power of the likelihood ratio test for models of DNA base substitution. 2011 , 38, 2723-2737		3
1253	Nuclear-mitochondrial sequences as witnesses of past interbreeding and population diversity in the jumping bristletail Mesomachilis. <i>Molecular Biology and Evolution</i> , 2011 , 28, 195-210	8.3	21
1252	Intergenic sequence comparison of Escherichia coli isolates reveals lifestyle adaptations but not host specificity. 2011 , 77, 7620-32		52
1251	Recent and recurrent selective sweeps of the antiviral RNAi gene Argonaute-2 in three species of Drosophila. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1043-56	8.3	48
1250	Evolution of the insect yellow gene family. <i>Molecular Biology and Evolution</i> , 2011 , 28, 257-72	8.3	85
1249	Investment in rapid growth shapes the evolutionary rates of essential proteins. 2011 , 108, 20030-5		7
1248	Evolutionarily conserved surface residues constitute actin binding sites of tropomyosin. 2011 , 108, 101	50-5	60
1247	Evaluating the roles of energetic functional constraints on teleost mitochondrial-encoded protein evolution. <i>Molecular Biology and Evolution</i> , 2011 , 28, 39-44	8.3	65
1246	Evolution of a derived protein-protein interaction between HoxA11 and Foxo1a in mammals caused by changes in intramolecular regulation. 2011 , 108, E414-20		36
1245	Virulence differences in Toxoplasma mediated by amplification of a family of polymorphic pseudokinases. 2011 , 108, 9631-6		169
1244	Dynamic programming procedure for searching optimal models to estimate substitution rates based on the maximum-likelihood method. 2011 , 108, 7860-5		12
1243	Adaptive evolution of four microcephaly genes and the evolution of brain size in anthropoid primates. <i>Molecular Biology and Evolution</i> , 2011 , 28, 625-38	8.3	94
1242	Whole genome sequencing of multiple Leishmania donovani clinical isolates provides insights into population structure and mechanisms of drug resistance. 2011 , 21, 2143-56		319

1241	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. 2011 , 39, W470-4		133
1240	Identification of evolutionarily conserved non-AUG-initiated N-terminal extensions in human coding sequences. 2011 , 39, 4220-34		147
1239	Diversity and evolutionary patterns of immune genes in free-ranging Namibian leopards (Panthera pardus pardus). 2011 , 102, 653-65		11
1238	Molecular evolution of the toll-like receptor multigene family in birds. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1703-15	8.3	121
1237	Charting the host adaptation of influenza viruses. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1755-67	8.3	26
1236	The complete mitogenome of the snakehead Channa argus (Perciformes: Channoidei): genome characterization and phylogenetic implications. 2011 , 22, 120-9		23
1235	Slow protein evolutionary rates are dictated by surface-core association. 2011 , 108, 11151-6		59
1234	Fixation of deleterious mutations at critical positions in human proteins. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2687-93	8.3	8
1233	Comparative analyses of DNA methylation and sequence evolution using Nasonia genomes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3345-54	8.3	76
1232	Improved least squares topology testing and estimation. 2011 , 60, 668-75		4
1231	Approximate likelihood calculation on a phylogeny for Bayesian estimation of divergence times.	0.2	1 52
	Molecular Biology and Evolution, 2011 , 28, 2161-72	8.3	153
1230	Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection. 2011 , 21, 1686-94	0.3	74
1230	Trans genomic capture and sequencing of primate exomes reveals new targets of positive	8.3	
	Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection. 2011 , 21, 1686-94 High proportions of deleterious polymorphisms in constrained human genes. <i>Molecular Biology and</i>		74
1229	Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection. 2011 , 21, 1686-94 High proportions of deleterious polymorphisms in constrained human genes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 49-52 Progressive pseudogenization: vitamin C synthesis and its loss in bats. <i>Molecular Biology and</i>	8.3	74 6
1229	Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection. 2011, 21, 1686-94 High proportions of deleterious polymorphisms in constrained human genes. <i>Molecular Biology and Evolution</i> , 2011, 28, 49-52 Progressive pseudogenization: vitamin C synthesis and its loss in bats. <i>Molecular Biology and Evolution</i> , 2011, 28, 1025-31 A population genetics-phylogenetics approach to inferring natural selection in coding sequences.	8.3	74 6 28
1229 1228 1227	Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection. 2011, 21, 1686-94 High proportions of deleterious polymorphisms in constrained human genes. <i>Molecular Biology and Evolution</i> , 2011, 28, 49-52 Progressive pseudogenization: vitamin C synthesis and its loss in bats. <i>Molecular Biology and Evolution</i> , 2011, 28, 1025-31 A population genetics-phylogenetics approach to inferring natural selection in coding sequences. 2011, 7, e1002395 Preventing dangerous nonsense: selection for robustness to transcriptional error in human genes.	8.3	74 6 28 72

1223	PhyleasProg: a user-oriented web server for wide evolutionary analyses. 2011 , 39, W479-85		14
1222	Comparative genomics yields insights into niche adaptation of plant vascular wilt pathogens. 2011 , 7, e1002137		335
1221	Accelerated recruitment of new brain development genes into the human genome. 2011 , 9, e1001179		111
1220	Molecular evolution across the Asteraceae: micro- and macroevolutionary processes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3225-35	8.3	18
1219	Rapid genetic diversification and high fitness penalties associated with pathogenicity evolution in a plant virus. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1425-37	8.3	50
1218	A cautionary note for retrocopy identification: DNA-based duplication of intron-containing genes significantly contributes to the origination of single exon genes. 2011 , 27, 1749-53		16
1217	Accelerated and adaptive evolution of yeast sexual adhesins. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3127-37	8.3	15
1216	Detecting structural similarity of ligand interactions in the lipid metabolic system including enzymes, lipid-binding proteins and nuclear receptors. 2011 , 24, 397-403		
1215	Ancient gene duplication provided a key molecular step for anaerobic growth of Baker's yeast. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2005-17	8.3	7
1214	C(4) eudicots are not younger than C(4) monocots. 2011 , 62, 3171-81		86
1213	maxAlike: maximum likelihood-based sequence reconstruction with application to improved primer design for unknown sequences. 2011 , 27, 317-25		25
1212	Parallel evolution of a type IV secretion system in radiating lineages of the host-restricted bacterial pathogen Bartonella. 2011 , 7, e1001296		75
1211	Recent, independent and anthropogenic origins of Trypanosoma cruzi hybrids. 2011, 5, e1363		95
1210	Correlated evolution of nearby residues in Drosophilid proteins. 2011 , 7, e1001315		35
1209	Out of America to Africa or Asia: inference of dispersal histories using nuclear and plastid DNA and the S-RNase self-incompatibility locus. <i>Molecular Biology and Evolution</i> , 2011 , 28, 793-801	8.3	21
1208	Evolution of modern birds revealed by mitogenomics: timing the radiation and origin of major orders. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1927-42	8.3	183
1207	Complex evolutionary events at a tandem cluster of Arabidopsis thaliana genes resulting in a single-locus genetic incompatibility. 2011 , 7, e1002164		51
1206	Genomic transition to pathogenicity in chytrid fungi. 2011 , 7, e1002338		83

1205	Natural selection on functional modules, a genome-wide analysis. 2011 , 7, e1001093		12
1204	Interspecific sex in grass smuts and the genetic diversity of their pheromone-receptor system. 2011 , 7, e1002436		49
1203	Reshaping of global gene expression networks and sex-biased gene expression by integration of a young gene. 2012 , 31, 2798-809		36
1202	Structure and age jointly influence rates of protein evolution. 2012 , 8, e1002542		17
1201	Unleashing the genome of brassica rapa. 2012 , 3, 172		38
1200	Evolutionary Genomics of Genes Involved in Olfactory Behavior in the Drosophila melanogaster Species Group. 2012 , 8, 89-104		21
1199	Parallel duplication and partial subfunctionalization of Etatenin/armadillo during insect evolution. <i>Molecular Biology and Evolution</i> , 2012 , 29, 647-62	8.3	17
1198	Multiple mitochondrial introgression events and heteroplasmy in trypanosoma cruzi revealed by maxicircle MLST and next generation sequencing. 2012 , 6, e1584		87
1197	Parallel evolution of auditory genes for echolocation in bats and toothed whales. 2012 , 8, e1002788		69
1196	Large-scale introgression shapes the evolution of the mating-type chromosomes of the filamentous ascomycete Neurospora tetrasperma. 2012 , 8, e1002820		31
1195	Loss of the DnaK-DnaJ-GrpE chaperone system among the Aquificales. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3485-95	8.3	16
1194	Rapid functional divergence of a newly evolved polyubiquitin gene in Drosophila and its role in the trade-off between male fecundity and lifespan. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1407-16	8.3	8
1193	The voltage-gated potassium channel subfamily KQT member 4 (KCNQ4) displays parallel evolution in echolocating bats. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1441-50	8.3	37
1192	A limited role for gene duplications in the evolution of platypus venom. <i>Molecular Biology and Evolution</i> , 2012 , 29, 167-77	8.3	30
1191	Nucleoid-associated proteins affect mutation dynamics in E. coli in a growth phase-specific manner. 2012 , 8, e1002846		13
1190	Comparative genomics of the apicomplexan parasites Toxoplasma gondii and Neospora caninum: Coccidia differing in host range and transmission strategy. 2012 , 8, e1002567		154
1189	Transcriptome analysis of silver carp (Hypophthalmichthys molitrix) by paired-end RNA sequencing. 2012 , 19, 131-42		52
1188	Inference of genotype-phenotype relationships in the antigenic evolution of human influenza A (H3N2) viruses. 2012 , 8, e1002492		20

1187	Ultrafast evolution and loss of CRISPRs following a host shift in a novel wildlife pathogen, Mycoplasma gallisepticum. 2012 , 8, e1002511	95
1186	The cysteine rich necrotrophic effector SnTox1 produced by Stagonospora nodorum triggers susceptibility of wheat lines harboring Snn1. 2012 , 8, e1002467	159
1185	Molecular inferences suggest multiple host shifts of rabies viruses from bats to mesocarnivores in Arizona during 2001-2009. 2012 , 8, e1002786	117
1184	Regulatory network structure as a dominant determinant of transcription factor evolutionary rate. 2012 , 8, e1002734	5
1183	Distinct effects on diversifying selection by two mechanisms of immunity against Streptococcus pneumoniae. 2012 , 8, e1002989	38
1182	Combination of immune and viral factors distinguishes low-risk versus high-risk HIV-1 disease progression in HLA-B*5701 subjects. 2012 , 86, 9802-16	19
1181	Evolution of a membrane protein regulon in Saccharomyces. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1747-56	17
1180	Phylogeny of galactolipid synthase homologs together with their enzymatic analyses revealed a possible origin and divergence time for photosynthetic membrane biogenesis. 2012 , 19, 91-102	32
1179	Highly dynamic exon shuffling in candidate pathogen receptors what if brown algae were capable of adaptive immunity?. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1263-76	25
1178	Mitochondrial genome evolution in a single protoploid yeast species. 2012 , 2, 1103-11	38
1177	The genetic basis of pollinator adaptation in a sexually deceptive orchid. 2012, 8, e1002889	36
1176	On the Development of a Pipeline for the Automatic Detection of Positively Selected Sites. 2012 , 225-229	2
1175	A gene family derived from transposable elements during early angiosperm evolution has reproductive fitness benefits in Arabidopsis thaliana. 2012 , 8, e1002931	42
1174	LegumeIP: an integrative database for comparative genomics and transcriptomics of model legumes. 2012 , 40, D1221-9	83
1173	Phylogenomic analysis reveals dynamic evolutionary history of the Drosophila heterochromatin protein 1 (HP1) gene family. 2012 , 8, e1002729	33
1172	Recombination drives vertebrate genome contraction. 2012 , 8, e1002680	49
1171	A species-specific cluster of defensin-like genes encodes diffusible pollen tube attractants in Arabidopsis. 2012 , 10, e1001449	191
1170	Reconstruction of ancestral metabolic enzymes reveals molecular mechanisms underlying evolutionary innovation through gene duplication. 2012 , 10, e1001446	133

1169	The ligand specificity of the G-protein-coupled receptor GPR34. 2012 , 443, 841-50	21
1168	Long-term and short-term evolutionary impacts of transposable elements on Drosophila. 2012 , 192, 1411-32	36
1167	Maximum likelihood implementation of an isolation-with-migration model with three species for testing speciation with gene flow. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3131-42	44
1166	Proteome-wide discovery of evolutionary conserved sequences in disordered regions. 2012 , 5, rs1	76
1165	The genome of Prunus mume. 2012 , 3, 1318	295
1164	Trade-off between selection for dosage compensation and masculinization on the avian Z chromosome. 2012 , 192, 1433-45	57
1163	Ecological adaptation in bacteria: speciation driven by codon selection. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3669-83	16
1162	Codons support the maintenance of intrinsic DNA polymer flexibility over evolutionary timescales. 2012 , 4, 954-65	10
1161	Tracking viral evolution during a disease outbreak: the rapid and complete selective sweep of a circovirus in the endangered Echo parakeet. 2012 , 86, 5221-9	50
1160	Birth, death, and replacement of karyopherins in Drosophila. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1429-40	16
1159	Analysis of Arabidopsis genome-wide variations before and after meiosis and meiotic recombination by resequencing Landsberg erecta and all four products of a single meiosis. 2012 , 22, 508-18	89
1158	Pervasive and ongoing positive selection in the vomeronasal-1 receptor (V1R) repertoire of mouse lemurs. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3807-16	30
1157	Causes and consequences of genome expansion in fungi. 2012 , 4, 13-23	45
1156	Mutational properties of amino acid residues: implications for evolvability of phosphorylatable residues. 2012 , 367, 2584-93	29
1155	Positive selection at the ASPM gene coincides with brain size enlargements in cetaceans. 2012 , 279, 4433-40	22
1154	Sequence shortening in the rodent ancestor. 2012 , 22, 478-85	16
1153	Directional evolution of Chlamydia trachomatis towards niche-specific adaptation. 2012 , 194, 6143-53	35
1152	Genomics of adaptation and speciation in cichlid fishes: recent advances and analyses in African and Neotropical lineages. 2012 , 367, 385-94	41

1151	Birth-and-death of KLK3 and KLK2 in primates: evolution driven by reproductive biology. 2012 , 4, 1331	-8	10
1150	Developmental genetics of secretory vesicle acidification during Caenorhabditis elegans spermatogenesis. 2012 , 191, 477-91		16
1149	Evolution of the melanocortin-1 receptor (MC1R) in Boobies and Gannets (Aves, Suliformes). 2012 , 103, 322-9		11
1148	Genome-wide selection on codon usage at the population level in the fungal model organism Neurospora crassa. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1975-86	8.3	18
1147	Improving the performance of positive selection inference by filtering unreliable alignment regions. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1-5	8.3	91
1146	Assembly of an evolutionarily new pathway for pyrone biosynthesis in Arabidopsis. 2012 , 337, 960-4		68
1145	Visual pigment molecular evolution in the Trinidadian pike cichlid (Crenicichla frenata): a less colorful world for neotropical cichlids?. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3045-60	8.3	39
1144	Species-specific chitin-binding module 18 expansion in the amphibian pathogen Batrachochytrium dendrobatidis. 2012 , 3, e00150-12		33
1143	After the bottleneck: Genome-wide diversification of the Mycobacterium tuberculosis complex by mutation, recombination, and natural selection. 2012 , 22, 721-34		115
1142	Selective constraints determine the time dependency of molecular rates for human nuclear genomes. 2012 , 4, 1127-32		6
1141	DNA methylation rebalances gene dosage after mammalian gene duplications. <i>Molecular Biology and Evolution</i> , 2012 , 29, 133-44	8.3	39
1140	Efficient selection of branch-specific models of sequence evolution. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1861-74	8.3	39
1139	Comparative analysis of syntenic genes in grass genomes reveals accelerated rates of gene structure and coding sequence evolution in polyploid wheat. 2013 , 161, 252-65		87
1138	The length scale of selection in protein evolution. 2012 , 6, 16-20		
1137	SPIn: model selection for phylogenetic mixtures via linear invariants. <i>Molecular Biology and Evolution</i> , 2012 , 29, 929-37	8.3	11
1136	Evidence for compensatory evolution of ribosomal proteins in response to rapid divergence of mitochondrial rRNA. <i>Molecular Biology and Evolution</i> , 2013 , 30, 310-4	8.3	92
1135	Identification of positive selection in disease response genes within members of the Poaceae. 2012 , 7, 1667-75		6
1134	Multiple photosynthetic transitions, polyploidy, and lateral gene transfer in the grass subtribe Neurachninae. 2012 , 63, 6297-308		40

1133	Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. 2012 , 279, 3491-500		333
1132	A genome sequence resource for the aye-aye (Daubentonia madagascariensis), a nocturnal lemur from Madagascar. 2012 , 4, 126-35		48
1131	Improved harmonic mean estimator for phylogenetic model evidence. 2012 , 19, 418-38		9
1130	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. 2012 , 22, 602-10		97
1129	Sex-biased transcriptome evolution in Drosophila. 2012 , 4, 1189-200		125
1128	Genetic diversity of MHC class I loci in six non-model frogs is shaped by positive selection and gene duplication. 2012 , 109, 146-55		30
1127	Pericentromeric effects shape the patterns of divergence, retention, and expression of duplicated genes in the paleopolyploid soybean. 2012 , 24, 21-32		61
1126	Divergent evolutionary pattern of starch biosynthetic pathway genes in grasses and dicots. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3227-36	8.3	26
1125	Plasmodium cynomolgi genome sequences provide insight into Plasmodium vivax and the monkey malaria clade. 2012 , 44, 1051-5		133
1124	Fossil rhabdoviral sequences integrated into arthropod genomes: ontogeny, evolution, and potential functionality. <i>Molecular Biology and Evolution</i> , 2012 , 29, 381-90	8.3	84
1123	Genomic characterization of the Bacillus cereus sensu lato species: backdrop to the evolution of Bacillus anthracis. 2012 , 22, 1512-24		128
1122	Detecting genetic introgression: high levels of intersubspecific recombination found in Xylella fastidiosa in Brazil. 2012 , 78, 4702-14		59
1121	The plant proteome folding project: structure and positive selection in plant protein families. 2012 , 4, 360-71		13
1120	Purifying selection and molecular adaptation in the genome of Verminephrobacter, the heritable symbiotic bacteria of earthworms. 2012 , 4, 307-15		18
1119	Identification and properties of 1,119 candidate lincRNA loci in the Drosophila melanogaster genome. 2012 , 4, 427-42		165
1118	Genes involved in the evolution of herbivory by a leaf-mining, Drosophilid fly. 2012, 4, 900-16		49
1117	The rapid evolution of X-linked male-biased gene expression and the large-X effect in Drosophila yakuba, D. santomea, and their hybrids. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3873-86	8.3	47
1116	Evolutionary conservation of the PA-X open reading frame in segment 3 of influenza A virus. 2012 , 86, 12411-3		80

1115	Selective constraint on human pre-mRNA splicing by protein structural properties. 2012, 4, 966-75		9
1114	Identification of innate immunity elicitors using molecular signatures of natural selection. 2012 , 109, 4215-20		73
1113	Estimating the rate of irreversibility in protein evolution. 2012 , 4, 1213-22		29
1112	Enzyme functional evolution through improved catalysis of ancestrally nonpreferred substrates. 2012 , 109, 2966-71		69
1111	MtDNA analysis of global populations support that major population expansions began before Neolithic Time. 2012 , 2, 745		45
1110	Intense uplift of the Qinghai-Tibetan Plateau triggered rapid diversification of Phyllolobium (Leguminosae) in the Late Cenozoic. 2012 , 5, 491-499		15
1109	Pervasive indels and their evolutionary dynamics after the fish-specific genome duplication. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3005-22	8.3	29
1108	Where do phosphosites come from and where do they go after gene duplication?. 2012 , 2012, 843167		4
1107	Evolutionary analysis of heterochromatin protein compatibility by interspecies complementation in Saccharomyces. 2012 , 192, 1001-14		6
1106	GenScalpel: an application for sequence retrieval and extraction from the GenBank flatfile. 2012 , 103, 908-11		8
1105	Epstein-Barr virus isolates retain their capacity to evade T cell immunity through BNLF2a despite extensive sequence variation. 2012 , 86, 572-7		12
1104	Genome-wide analysis of syntenic gene deletion in the grasses. 2012 , 4, 265-77		111
1103	Dynamic evolution of toll-like receptor multigene families in echinoderms. 2012 , 3, 136		82
1102	Evolution of the ferritin family in vertebrates. 2012 , 4, 3		4
1101	Determinants of exon-level evolutionary rates in Arabidopsis species. 2012 , 8, 389-415		3
1100	Horizontal transfer and death of a fungal secondary metabolic gene cluster. 2012 , 4, 289-93		92
1099	Evolutionary history of LTR retrotransposon chromodomains in plants. 2012 , 2012, 874743		28
1098	Positive Selection and the Evolution of izumo Genes in Mammals. 2012 , 2012, 958164		21

1097	An ancient genomic regulatory block conserved across bilaterians and its dismantling in tetrapods by retrogene replacement. 2012 , 22, 642-55		30
1096	Multiple adaptive losses of alanine-glyoxylate aminotransferase mitochondrial targeting in fruit-eating bats. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1507-11	8.3	18
1095	PGDD: a database of gene and genome duplication in plants. 2013 , 41, D1152-8		400
1094	Roundup 2.0: enabling comparative genomics for over 1800 genomes. 2012 , 28, 715-6		34
1093	Recent acceleration of plastid sequence and structural evolution coincides with extreme mitochondrial divergence in the angiosperm genus Silene. 2012 , 4, 294-306		83
1092	Transcriptome analysis of a North American songbird, Melospiza melodia. 2012 , 19, 325-33		15
1091	RNA interference against animal viruses: how morbilliviruses generate extended diversity to escape small interfering RNA control. 2012 , 86, 786-95		9
1090	Evolutionary rate covariation reveals shared functionality and coexpression of genes. 2012 , 22, 714-20		69
1089	On the origin and evolution of thermophily: reconstruction of functional precambrian enzymes from ancestors of Bacillus. <i>Molecular Biology and Evolution</i> , 2012 , 29, 825-35	8.3	65
1088	Genome analyses of an aggressive and invasive lineage of the Irish potato famine pathogen. 2012 , 8, e1002940		2 60
1087	Genetic variability of human respiratory syncytial virus A strains circulating in Ontario: a novel genotype with a 72 nucleotide G gene duplication. 2012 , 7, e32807		205
1086	On the origins of Mendelian disease genes in man: the impact of gene duplication. <i>Molecular Biology and Evolution</i> , 2012 , 29, 61-9	8.3	35
1085	Characteristics and significance of intergenic polyadenylated RNA transcription in Arabidopsis. 2013 , 161, 210-24		18
1084	Estimating the distribution of selection coefficients from phylogenetic data using sitewise mutation-selection models. 2012 , 190, 1101-15		80
1083	Diversity of MHC class II DAB1 in the koala (Phascolarctos cinereus). 2012 , 60, 1		13
1082	Global biogeography of SAR11 marine bacteria. 2012 , 8, 595		146
1081	Comparative analysis of kabuli chickpea transcriptome with desi and wild chickpea provides a rich resource for development of functional markers. 2012 , 7, e52443		98
1080	Mitochondrial genomes and divergence times of crocodile newts: inter-islands distribution of Echinotriton andersoni and the origin of a unique repetitive sequence found in Tylototriton mt genomes. 2012 , 87, 39-51		17

1079	A comprehensive analysis of genes encoding small secreted proteins identifies candidate effectors in Melampsora larici-populina (poplar leaf rust). 2012 , 25, 279-93		109
1078	Qualitative and quantitative late blight resistance in the potato cultivar Sarpo Mira is determined by the perception of five distinct RXLR effectors. 2012 , 25, 910-9		125
1077	The NLP toxin family in Phytophthora sojae includes rapidly evolving groups that lack necrosis-inducing activity. 2012 , 25, 896-909		67
1076	Evolution of cytochrome p450 genes from the viewpoint of genome informatics. 2012 , 35, 812-7		33
1075	Gamma paleohexaploidy in the stem lineage of core eudicots: significance for MADS-box gene and species diversification. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3793-806	8.3	97
1074	Evolutionary rate and duplicability in the Arabidopsis thaliana protein-protein interaction network. 2012 , 4, 1263-74		40
1073	Molecular evolution of teleost neural isozymes. 2012 , 75, 198-213		1
1072	Positive selection on NIN, a gene involved in neurogenesis, and primate brain evolution. 2012 , 11, 903-10)	10
1071	Fast molecular evolution associated with high active metabolic rates in poison frogs. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2001-18	8.3	34
1070	Low major histocompatibility complex class I (MHC I) variation in the European bison (Bison bonasus). 2012 , 103, 349-59		16
1069	The ABO blood group is a trans-species polymorphism in primates. 2012 , 109, 18493-8		98
1068	Gene duplication and the evolution of hemoglobin isoform differentiation in birds. 2012 , 287, 37647-58		46
1067	The sunflower (Helianthus annuus L.) genome reflects a recent history of biased accumulation of transposable elements. 2012 , 72, 142-53		74
1066	Understanding phylogenetic incongruence: lessons from phyllostomid bats. 2012 , 87, 991-1024		62
1065	Evolution of an MCM complex in flies that promotes meiotic crossovers by blocking BLM helicase. 2012 , 338, 1363-5		48
1064	Synthesis of Experimental Molecular Biology and Evolutionary Biology: An Example from the World of Vision. 2012 , 62, 939-948		10
1063	Testing synchrony in historical biogeography: the case of new world primates and hystricognathi rodents. 2012 , 8, 127-37		15
1062	Mitochondrial-nuclear interactions and accelerated compensatory evolution: evidence from the primate cytochrome C oxidase complex. <i>Molecular Biology and Evolution</i> , 2012 , 29, 337-46	8.3	142

1061 Centromere retention and loss during the descent of maize from a tetraploid ancestor. 2012 , 109, 21004-9	29
1060 Genome sequences of wild and domestic bactrian camels. 2012 , 3, 1202	105
The effects of alignment error and alignment filtering on the sitewise detection of positive selection. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1125-39	125
Deep sequencing of amplicons reveals widespread intraspecific hybridization and multiple origins of polyploidy in big sagebrush (Artemisia tridentata; Asteraceae). 2012 , 99, 1962-75	39
Adaptive signals in algal Rubisco reveal a history of ancient atmospheric carbon dioxide. 2012 , 367, 483-92	72
1056 Estimating divergence times in large molecular phylogenies. 2012 , 109, 19333-8	354
1055 A comparative study of mammalian diversification pattern. 2012 , 8, 486-97	13
1054 New cis-regulatory elements in the Rht-D1b locus region of wheat. 2012 , 12, 489-500	13
Rules of engagement: molecular insights from host-virus arms races. 2012 , 46, 677-700	320
Contribution of the epigenetic mark H3K27me3 to functional divergence after whole genome duplication in Arabidopsis. 2012 , 13, R94	19
1051 Conserved rules govern genetic interaction degree across species. 2012 , 13, R57	36
1050 Epistasis as the primary factor in molecular evolution. 2012 , 490, 535-8	246
1049 Analysis of the bread wheat genome using whole-genome shotgun sequencing. 2012 , 491, 705-10	821
Divergences of MPF2-like MADS-domain proteins have an association with the evolution of the inflated calyx syndrome within Solanaceae. 2012 , 236, 1247-60	15
Population dynamics of DENV-1 genotype V in Brazil is characterized by co-circulation and strain/lineage replacement. 2012 , 157, 2061-73	35
1046 Co-expression of soybean Dicer-like genes in response to stress and development. 2012 , 12, 671-82	11
Evolutionary insights into the role of the essential centromere protein CAL1 in Drosophila. 2012 , 20, 493-504	29
Patterns of selection and polymorphism of innate immunity genes in bumblebees (Hymenoptera: Apidae). 2012 , 140, 205-17	6

1043	MHC class I variation in a natural blue tit population (Cyanistes caeruleus). 2012 , 140, 349-64	18
1042	The functional importance of sequence versus expression variability of MHC alleles in parasite resistance. 2012 , 140, 407-20	6
1041	Natural variation, functional divergence, and local adaptation of nucleotide binding site sequences in Rhododendron (Ericaceae). 2012 , 8, 879-893	4
1040	A priori and a posteriori approaches for finding genes of evolutionary interest in non-model species: osmoregulatory genes in the kidney transcriptome of the desert rodent Dipodomys spectabilis (banner-tailed kangaroo rat). 2012 , 7, 328-39	20
1039	Accelerated evolution and functional divergence of scorpion short-chain K+ channel toxins after speciation. 2012 , 163, 238-45	2
1038	Protein biophysics explains why highly abundant proteins evolve slowly. 2012 , 2, 249-56	70
1037	The genomic landscape and evolutionary resolution of antagonistic pleiotropy in yeast. 2012 , 2, 1399-410	121
1036	Evolution-guided identification of antiviral specificity determinants in the broadly acting interferon-induced innate immunity factor MxA. 2012 , 12, 598-604	104
1035	Three different anti-lipopolysaccharide factors identified from giant freshwater prawn, Macrobrachium rosenbergii. 2012 , 33, 766-74	27
1034	Evolutionary analysis of Antarctic teleost Toll-like receptor 2. 2012 , 33, 1076-85	9
1033	Four invertebrate-type lysozyme genes from triangle-shell pearl mussel (Hyriopsis cumingii). 2012 , 33, 909-15	22
1032	Molecular evolution of the neurohypophysial hormone precursors in mammals: Comparative genomics reveals novel mammalian oxytocin and vasopressin analogues. 2012 , 179, 313-8	37
1031	Genetic correlates of the evolving primate brain. 2012 , 195, 27-44	2
1030	A fine-scale chimpanzee genetic map from population sequencing. 2012 , 336, 193-8	218
1029	Contrasting patterns of evolution following whole genome versus tandem duplication events in Populus. 2012 , 22, 95-105	100
1028	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model. 2012 ,	7
1027	Ancestral capture of syncytin-Car1, a fusogenic endogenous retroviral envelope gene involved in placentation and conserved in Carnivora. 2012 , 109, E432-41	99
1026	Environmental adaptation contributes to gene polymorphism across the Arabidopsis thaliana genome. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3721-8	25

1025	Computer System for Analysis of Molecular Evolution Modes (SAMEM): analysis of molecular evolution modes at deep inner branches of the phylogenetic tree. 2011 , 11, 109-23	5
1024	A 'living fossil' eel (Anguilliformes: Protanguillidae, fam. nov.) from an undersea cave in Palau. 2012 , 279, 934-43	44
1023	The evolution of gene expression and the transcriptome-phenotype relationship. 2012 , 23, 222-9	64
1022	Adaptive evolution of the Retinoid X receptor in vertebrates. 2012 , 99, 81-9	15
1021	Involvement of AmphiREL, a Rel-like gene identified in Brachiastoma belcheri, in LPS-induced response: implication for evolution of Rel subfamily genes. 2012 , 99, 361-9	10
1020	Estimation of divergence times in cnidarian evolution based on mitochondrial protein-coding genes and the fossil record. 2012 , 62, 329-45	150
1019	Dating cryptodiran nodes: origin and diversification of the turtle superfamily Testudinoidea. 2012 , 62, 496-507	54
1018	Allopolyploid origin of highly invasive Centaurea stoebe s.l. (Asteraceae). 2012 , 62, 612-23	37
1017	Peculiar patterns of amino acid substitution and conservation in the fast evolving tunicate Oikopleura dioica. 2012 , 62, 708-17	9
1016	Opsin gene duplication and divergence in ray-finned fish. 2012 , 62, 986-1008	83
1015	Effect of genetic convergence on phylogenetic inference. 2012 , 62, 921-7	14
1014	Sexual size dimorphism predicts rates of sequence evolution of SPerm Adhesion Molecule 1 (SPAM1, also PH-20) in monkeys, but not in hominoids (apes including humans). 2012 , 63, 52-63	11
1013	Evolution and biogeography of an emerging quasispecies: diversity patterns of the fish Viral Hemorrhagic Septicemia virus (VHSv). 2012 , 63, 327-41	58
1012	Evolution of mitochondrial-encoded cytochrome oxidase subunits in endothermic fish: the importance of taxon-sampling in codon-based models. 2012 , 63, 679-84	12
1011	Three genome-based phylogeny of Cupressaceae s.l.: further evidence for the evolution of gymnosperms and Southern Hemisphere biogeography. 2012 , 64, 452-70	88
1010	New molecular markers for fungal phylogenetics: two genes for species-level systematics in the Sordariomycetes (Ascomycota). 2012 , 64, 500-12	42
1009	Monophyly, divergence times, and evolution of host plant use inferred from a revised phylogeny of the Drosophila repleta species group. 2012 , 64, 533-44	77
1008	Phylogeny, rate variation, and genome size evolution of Pelargonium (Geraniaceae). 2012 , 64, 654-70	36

1007	Structural, functional, and evolutionary analysis of the unusually large stilbene synthase gene family in grapevine. 2012 , 160, 1407-19		101
1006	Deciphering the relationship between mating system and the molecular evolution of the pheromone and receptor genes in Neurospora. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3827-42	8.3	14
1005	Rooting the eukaryotic tree with mitochondrial and bacterial proteins. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1277-89	8.3	108
1004	A gain-of-function polymorphism controlling complex traits and fitness in nature. 2012 , 337, 1081-4		132
1003	Mutations in the neverland gene turned Drosophila pachea into an obligate specialist species. 2012 , 337, 1658-61		67
1002	Parallel molecular evolution in an herbivore community. 2012 , 337, 1634-7		179
1001	Diversification of genes for carotenoid biosynthesis in aphids following an ancient transfer from a fungus. <i>Molecular Biology and Evolution</i> , 2012 , 29, 313-23	8.3	59
1000	Assessing determinants of exonic evolutionary rates in mammals. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3121-9	8.3	12
999	Exploring uncertainty in the calibration of the molecular clock. 2012 , 8, 156-9		163
998	Experimental design in phylogenetics: testing predictions from expected information. 2012 , 61, 661-74	1	11
997	The probability of correctly resolving a split as an experimental design criterion in phylogenetics. 2012 , 61, 811-21		15
996	Population genomics of Chlamydia trachomatis: insights on drift, selection, recombination, and population structure. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3933-46	8.3	74
995	Identification of novel glutathione transferases in Echinococcus granulosus. An evolutionary perspective. 2012 , 123, 208-16		8
994	Whole genome duplication of intra- and inter-chromosomes in the tomato genome. 2012 , 39, 361-8		14
993	Analysis of a naturally-occurring deletion mutant of Spodoptera frugiperda multiple nucleopolyhedrovirus reveals sf58 as a new per os infectivity factor of lepidopteran-infecting baculoviruses. 2012 , 109, 117-26		28
992	ParaAT: a parallel tool for constructing multiple protein-coding DNA alignments. 2012 , 419, 779-81		147
	Evolutionary and functional analyses of the interaction between the myeloid restriction factor		140
991	SAMHD1 and the lentiviral Vpx protein. 2012 , 11, 205-17		140

989	An unexpected loss of domains in the conservative evolution ninth complement component in a higher teleost, Miichthys miiuy. 2012 , 32, 1171-8	15
988	Immune response of four dual-CRD C-type lectins to microbial challenges in giant freshwater prawn Macrobrachium rosenbergii. 2012 , 33, 155-67	32
987	Mitochondrial genome organization and divergence in hybridizing central European waterfrogs of the Pelophylax esculentus complex (Anura, Ranidae). 2012 , 491, 71-80	18
986	Evolutionary changes of the importance of olfaction in cetaceans based on the olfactory marker protein gene. 2012 , 492, 349-53	26
985	The evolution of MHC diversity: evidence of intralocus gene conversion and recombination in a single-locus system. 2012 , 497, 52-7	20
984	Age of the last common ancestor of extant Plasmodium parasite lineages. 2012 , 502, 36-9	3
983	Small inverted repeats drive mitochondrial genome evolution in Lake Baikal sponges. 2012 , 505, 91-9	22
982	Translational selection on codon usage in the genus Aspergillus. 2012 , 506, 98-105	20
981	Computational analysis and characterization of UCE-like elements (ULEs) in plant genomes. 2012 , 22, 2455-66	23
980	Diversity at the major histocompatibility complex Class II in the platypus, Ornithorhynchus anatinus. 2012 , 103, 467-78	7
979	Nature and intensity of selection pressure on CRISPR-associated genes. 2012 , 194, 1216-25	69
978	Molecular Evidence for the Nonmonophyly of the Asian Natricid GenusXenochrophis(Serpentes, Colubroidea) as Inferred from Mitochondrial and Nuclear Genes. 2012 , 46, 263-268	3
977	Phylogenetic estimation of timescales using ancient DNA: the effects of temporal sampling scheme and uncertainty in sample ages. <i>Molecular Biology and Evolution</i> , 2013 , 30, 253-62	33
976	Evolutionary and biogeographic history of weasel-like carnivorans (Musteloidea). 2012 , 63, 745-57	110
975	Accelerated evolution and coevolution drove the evolutionary history of AGPase sub-units during angiosperm radiation. 2012 , 109, 693-708	8
974	The function and structural influence of selective relaxed constraint at functional intracellular loop3 of 5-HT(1A) serotonin-1 receptor family. 2012 , 508, 211-20	2
973	Phylogenetic and molecular evolution of the ADAM (A Disintegrin And Metalloprotease) gene family from Xenopus tropicalis, to Mus musculus, Rattus norvegicus, and Homo sapiens. 2012 , 507, 36-43	7
972	MOV10 RNA helicase is a potent inhibitor of retrotransposition in cells. 2012 , 8, e1002941	148

971	New genes expressed in human brains: implications for annotating evolving genomes. 2012, 34, 982-91	43
970	A graph-based approach for designing extensible pipelines. 2012 , 13, 163	2
969	Separating the wheat from the chaff: mitigating the effects of noise in a plastome phylogenomic data set from Pinus L. (Pinaceae). 2012 , 12, 100	82
968	Adaptive evolution of Toll-like receptor 5 in domesticated mammals. 2012 , 12, 122	36
967	Functional divergence of gene duplicates - a domain-centric view. 2012 , 12, 126	3
966	The mate recognition protein gene mediates reproductive isolation and speciation in the Brachionus plicatilis cryptic species complex. 2012 , 12, 134	12
965	Ancestral polymorphism at the major histocompatibility complex (MHCIII) in the Nesospiza bunting species complex and its sister species (Rowettia goughensis). 2012 , 12, 143	3
964	Molecular evolution of psbA gene in ferns: unraveling selective pressure and co-evolutionary pattern. 2012 , 12, 145	6
963	Multiple functionally divergent and conserved copies of alpha tubulin in bdelloid rotifers. 2012 , 12, 148	9
962	The relationship between the hierarchical position of proteins in the human signal transduction network and their rate of evolution. 2012 , 12, 192	21
961	Evolution of major histocompatibility complex class I and class II genes in the brown bear. 2012 , 12, 197	55
960	Molecular adaptation and resilience of the insect's nuclear receptor USP. 2012 , 12, 199	9
959	Complex patterns of divergence among green-sensitive (RH2a) African cichlid opsins revealed by Clade model analyses. 2012 , 12, 206	21
958	Balancing selection and genetic drift at major histocompatibility complex class II genes in isolated populations of golden snub-nosed monkey (Rhinopithecus roxellana). 2012 , 12, 207	19
957	Adaptive evolution of the chrysanthemyl diphosphate synthase gene involved in irregular monoterpene metabolism. 2012 , 12, 214	18
956	Evolutionary study of duplications of the miRNA machinery in aphids associated with striking rate acceleration and changes in expression profiles. 2012 , 12, 216	11
955	Testes-specific hemoglobins in Drosophila evolved by a combination of sub- and neofunctionalization after gene duplication. 2012 , 12, 34	8
954	Adaptive evolution and functional constraint at TLR4 during the secondary aquatic adaptation and diversification of cetaceans. 2012 , 12, 39	34

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953	Expansion and diversification of the SET domain gene family following whole-genome duplications in Populus trichocarpa. 2012 , 12, 51	36
952	Genomic characterization of the European sea bass Dicentrarchus labrax reveals the presence of a novel uncoupling protein (UCP) gene family member in the teleost fish lineage. 2012 , 12, 62	11
951	A genome-wide study of recombination rate variation in Bartonella henselae. 2012 , 12, 65	14
950	Characterization and 454 pyrosequencing of major histocompatibility complex class I genes in the great tit reveal complexity in a passerine system. 2012 , 12, 68	78
949	Slow but not low: genomic comparisons reveal slower evolutionary rate and higher dN/dS in conifers compared to angiosperms. 2012 , 12, 8	113
948	EggLib: processing, analysis and simulation tools for population genetics and genomics. 2012 , 13, 27	99
947	Comparative analysis of Mycobacterium and related Actinomycetes yields insight into the evolution of Mycobacterium tuberculosis pathogenesis. 2012 , 13, 120	53
946	Genomic characterization of the conditionally dispensable chromosome in Alternaria arborescens provides evidence for horizontal gene transfer. 2012 , 13, 171	63
945	Sequencing and comparative genomic analysis of 1227 Felis catus cDNA sequences enriched for developmental, clinical and nutritional phenotypes. 2012 , 13, 31	8
944	Comparative genomics of the classical Bordetella subspecies: the evolution and exchange of virulence-associated diversity amongst closely related pathogens. 2012 , 13, 545	82
943	Sequencing of the core MHC region of black grouse (Tetrao tetrix) and comparative genomics of the galliform MHC. 2012 , 13, 553	24
942	Sequencing of the needle transcriptome from Norway spruce (Picea abies Karst L.) reveals lower substitution rates, but similar selective constraints in gymnosperms and angiosperms. 2012 , 13, 589	49
941	Comparative genomics of bacteria in the genus Providencia isolated from wild Drosophila melanogaster. 2012 , 13, 612	22
940	Orthologous genes identified by transcriptome sequencing in the spider genus Stegodyphus. 2012 , 13, 70	31
939	Transcriptome analysis reveals the time of the fourth round of genome duplication in common carp (Cyprinus carpio). 2012 , 13, 96	87
938	Gene copy number variation and its significance in cyanobacterial phylogeny. 2012 , 12, 177	25
937	In silico evolutionary analysis of Helicobacter pylori outer membrane phospholipase A (OMPLA). 2012 , 12, 206	3
936	Identification of white campion (Silene latifolia) guaiacol O-methyltransferase involved in the biosynthesis of veratrole, a key volatile for pollinator attraction. 2012 , 12, 158	13

935	Mammalian NPC1 genes may undergo positive selection and human polymorphisms associate with type 2 diabetes. 2012 , 10, 140		14
934	Evolutionary patterns of RNA-based gene duplicates in Caenorhabditis nematodes coincide with their genomic features. 2012 , 5, 398		6
933	Genomic evidence for elevated mutation rates in highly expressed genes. 2012, 13, 1123-9		77
932	Comparative population genomics in Collinsia sister species reveals evidence for reduced effective population size, relaxed selection, and evolution of biased gene conversion with an ongoing mating system shift. 2013 , 67, 1263-78		32
931	An improved likelihood ratio test for detecting site-specific functional divergence among clades of protein-coding genes. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1297-300	8.3	90
930	Evolutionary effects of translocations in bacterial genomes. 2012 , 4, 1256-62		21
929	The draft genome of a diploid cotton Gossypium raimondii. 2012 , 44, 1098-103		673
928	Systematic position of Pinus henryi (Pinaceae) as revealed by multiple evidence. 2012 , 30, 671-679		2
927	Replacing and additive horizontal gene transfer in Streptococcus. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3309-20	8.3	23
926	Dolphin genome provides evidence for adaptive evolution of nervous system genes and a molecular rate slowdown. 2012 , 279, 3643-51		69
925	Discovering drug targets for neglected diseases using a pharmacophylogenomic cloud workflow. 2012 ,		5
924	Relative rates of evolution among the three genetic compartments of the red alga Porphyra differ from those of green plants and do not correlate with genome architecture. 2012 , 65, 339-44		39
923	References. 2012 , 138, 341-367		25
922	Functional and phylogenetic analysis of the Aspergillus ochraceoroseus aflQ (ordA) gene ortholog. 2012 , 104, 857-64		9
921	Molecular evolution of HA gene of the influenza A H1N1 pdm09 strain during the consecutive seasons 2009-2011 in Hangzhou, China: several immune-escape variants without positively selected sites. 2012 , 55, 363-6		8
920	Positive selection-guided mutational analysis revealing two key functional sites of scorpion ERG K(+) channel toxins. 2012 , 429, 111-6		2
919	Phylogenetic relationships of the Cobitoidea (Teleostei: Cypriniformes) inferred from mitochondrial and nuclear genes with analyses of gene evolution. 2012 , 508, 60-72		31
918	Codon substitution models based on residue similarity and their applications. 2012 , 509, 136-41		2

917	Species-specific size expansion and molecular evolution of the oleosins in angiosperms. 2012, 509, 247-	57	10
916	Characterization and expressional analysis of Dleu7 during Xenopus tropicalis embryogenesis. 2012 , 509, 77-84		4
915	Minority of mammalian orthologs can be regarded as physiologically closest genes. 2012 , 509, 201-5		
914	Diversity and evolution of conotoxins in Conus virgo, Conus eburneus, Conus imperialis and Conus marmoreus from the South China Sea. 2012 , 60, 982-9		28
913	First evidence of the emergence of novel putative infectious bronchitis virus genotypes in Cuba. 2012 , 93, 1046-9		9
912	Molecular and phylogenetic analysis of bovine coronavirus based on the spike glycoprotein gene. 2012 , 12, 1870-8		19
911	Sequence and analysis of the genome of the pathogenic yeast Candida orthopsilosis. 2012 , 7, e35750		47
910	The essentials of computational molecular evolution. 2012 , 855, 111-52		23
909	Selection on the protein-coding genome. 2012 , 856, 113-40		8
908	Phylogeny reconstruction in the Caesalpinieae grade (Leguminosae) based on duplicated copies of the sucrose synthase gene and plastid markers. 2012 , 65, 149-62		42
907	Marine turtle mitogenome phylogenetics and evolution. 2012 , 65, 241-50		64
906	Auxin response factor gene family in Brassica rapa: genomic organization, divergence, expression, and evolution. 2012 , 287, 765-84		45
905	Structure-function analyses of plant type III polyketide synthases. 2012 , 515, 317-35		15
904	Advances in Bioinformatics and Computational Biology. 2012,		1
903	Fish lateral line innovation: insights into the evolutionary genomic dynamics of a unique mechanosensory organ. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3887-98	8.3	10
902	Molecular phylogeny of the Entomophthoromycota. 2012 , 65, 682-94		56
901	Comparing fungal genomes: insight into functional and evolutionary processes. 2012 , 835, 531-48		7
900	The malaria parasite Plasmodium vivax exhibits greater genetic diversity than Plasmodium falciparum. 2012 , 44, 1046-50		196

899	Opsin evolution in damselfish: convergence, reversal, and parallel evolution across tuning sites. 2012 , 75, 79-91	33
898	Genomic variation in natural populations of Drosophila melanogaster. 2012 , 192, 533-98	252
897	Structural and molecular diversification of the Anguimorpha lizard mandibular venom gland system in the arboreal species Abronia graminea. 2012 , 75, 168-83	16
896	Effects of premature termination codon polymorphisms in the Drosophila pseudoobscura subclade. 2012 , 75, 141-50	5
895	Large scale of human duplicate genes divergence. 2012 , 75, 25-33	5
894	Mapping, phylogenetic and expression analysis of the RNase (RNase A) locus in cattle. 2012 , 74, 237-48	10
893	Bio.Phylo: a unified toolkit for processing, analyzing and visualizing phylogenetic trees in Biopython. 2012 , 13, 209	87
892	MHC class II DQB diversity in the Japanese black bear, Ursus thibetanus japonicus. 2012 , 12, 230	15
891	Analyses of expressed sequence tags in Neurospora reveal rapid evolution of genes associated with the early stages of sexual reproduction in fungi. 2012 , 12, 229	9
890	Molecular evolution and phylogenetics of rodent malaria parasites. 2012 , 12, 219	24
889	Protein evolution in two co-occurring types of Symbiodinium: an exploration into the genetic basis of thermal tolerance in Symbiodinium clade D. 2012 , 12, 217	83
888	The salmonid myostatin gene family: a novel model for investigating mechanisms that influence duplicate gene fate. 2012 , 12, 202	4
887	Colon cancer associated genes exhibit signatures of positive selection at functionally significant positions. 2012 , 12, 114	21
886	Deciphering the complex leaf transcriptome of the allotetraploid species Nicotiana tabacum: a phylogenomic perspective. 2012 , 13, 406	35
885	Natural selection drives rapid evolution of mouse embryonic heart enhancers. 2012 , 6 Suppl 2, S1	5
884	The evolutionary host switches of Polychromophilus: a multi-gene phylogeny of the bat malaria genus suggests a second invasion of mammals by a haemosporidian parasite. 2012 , 11, 53	30
883	Strong purifying selection in endogenous retroviruses in the saltwater crocodile (Crocodylus porosus) in the Northern Territory of Australia. 2012 , 3, 20	4
882	Rapid evolution of enormous, multichromosomal genomes in flowering plant mitochondria with exceptionally high mutation rates. 2012 , 10, e1001241	335

881	Convergent evolution of escape from hepaciviral antagonism in primates. 2012 , 10, e1001282	79
880	Armadillo 1.1: an original workflow platform for designing and conducting phylogenetic analysis and simulations. 2012 , 7, e29903	26
879	Evidence for a common toolbox based on necrotrophy in a fungal lineage spanning necrotrophs, biotrophs, endophytes, host generalists and specialists. 2012 , 7, e29943	56
878	Genome-wide identification, evolutionary expansion, and expression profile of homeodomain-leucine zipper gene family in poplar (Populus trichocarpa). 2012 , 7, e31149	60
877	Loss and gain of function in SERPINB11: an example of a gene under selection on standing variation, with implications for host-pathogen interactions. 2012 , 7, e32518	16
876	Adaptive evolution in the glucose transporter 4 gene Slc2a4 in Old World fruit bats (family: Pteropodidae). 2012 , 7, e33197	18
875	Positive and purifying selection influence the evolution of doublesex in the Anastrepha fraterculus species group. 2012 , 7, e33446	8
874	Evolutionary dynamics analysis of human metapneumovirus subtype A2: genetic evidence for its dominant epidemic. 2012 , 7, e34544	12
873	Miiuy croaker hepcidin gene and comparative analyses reveal evidence for positive selection. 2012 , 7, e35449	44
872	Whole genome sequencing and evolutionary analysis of human papillomavirus type 16 in central China. 2012 , 7, e36577	24
871	Analysis of C3 suggests three periods of positive selection events and different evolutionary patterns between fish and mammals. 2012 , 7, e37489	15
870	Is promiscuity associated with enhanced selection on MHC-DQHn mice (genus Peromyscus)?. 2012 , 7, e37562	11
869	Repertoire, genealogy and genomic organization of cruzipain and homologous genes in Trypanosoma cruzi, T. cruzi-like and other trypanosome species. 2012 , 7, e38385	28
868	Sequence comparisons of odorant receptors among tortricid moths reveal different rates of molecular evolution among family members. 2012 , 7, e38391	9
867	Differential selection on carotenoid biosynthesis genes as a function of gene position in the metabolic pathway: a study on the carrot and dicots. 2012 , 7, e38724	36
866	GLADX: an automated approach to analyze the lineage-specific loss and pseudogenization of genes. 2012 , 7, e38792	7
865	High diversity at PRDM9 in chimpanzees and bonobos. 2012 , 7, e39064	28
864	Compensatory evolution of net-charge in influenza A virus hemagglutinin. 2012 , 7, e40422	27

863	SCaMC-1Like a member of the mitochondrial carrier (MC) family preferentially expressed in testis and localized in mitochondria and chromatoid body. 2012 , 7, e40470	14
862	Molecular evolution of trehalose-6-phosphate synthase (TPS) gene family in Populus, Arabidopsis and rice. 2012 , 7, e42438	43
861	Unique features of odorant-binding proteins of the parasitoid wasp Nasonia vitripennis revealed by genome annotation and comparative analyses. 2012 , 7, e43034	48
860	Rapid intraspecific evolution of miRNA and siRNA genes in the mosquito Aedes aegypti. 2012 , 7, e44198	40
859	Coevolution in RNA molecules driven by selective constraints: evidence from 5S rRNA. 2012 , 7, e44376	9
858	Evolution of genes involved in gamete interaction: evidence for positive selection, duplications and losses in vertebrates. 2012 , 7, e44548	35
857	ASPM and the evolution of cerebral cortical size in a community of New World monkeys. 2012, 7, e44928	4
856	Two goose-type lysozymes in Mytilus galloprovincialis: possible function diversification and adaptive evolution. 2012 , 7, e45148	25
855	Pan-genomic analysis provides insights into the genomic variation and evolution of Salmonella Paratyphi A. 2012 , 7, e45346	23
854	Evolutionary reconstructions of the transferrin receptor of Caniforms supports canine parvovirus being a re-emerged and not a novel pathogen in dogs. 2012 , 8, e1002666	57
853	Targeted disruption in mice of a neural stem cell-maintaining, KRAB-Zn finger-encoding gene that has rapidly evolved in the human lineage. 2012 , 7, e47481	10
852	The roles of gene duplication, gene conversion and positive selection in rodent Esp and Mup pheromone gene families with comparison to the Abp family. 2012 , 7, e47697	11
851	Comparative mitochondrial genomics within and among yeast species of the Lachancea genus. 2012 , 7, e47834	23
850	Transcriptome sequencing and annotation for the Jamaican fruit bat (Artibeus jamaicensis). 2012 , 7, e48472	53
849	Evolutionary dynamics of the interferon-induced transmembrane gene family in vertebrates. 2012 , 7, e49265	60
848	Rapid evolution of the sequences and gene repertoires of secreted proteins in bacteria. 2012 , 7, e49403	27
847	Macroevolutionary dynamics and historical biogeography of primate diversification inferred from a species supermatrix. 2012 , 7, e49521	361
846	Arrival of Paleo-Indians to the southern cone of South America: new clues from mitogenomes. 2012 , 7, e51311	41

845	The Population Genomics of Sunflowers and Genomic Determinants of Protein Evolution Revealed by RNAseq. 2012 , 1, 575-96	30
844	Factors influencing the diversity of iron uptake systems in aquatic microorganisms. 2012, 3, 362	19
843	Primate ABO Gene is under Weak Positive Selection. 2012 , 4, 07-12	
842	STRUCTURAL AND FUNCTIONAL CONSERVATION OF S-SPECIFICITIES AMONG PYRINAE SPECIES. 2012 , 95-103	1
841	The complete mitochondrial genome sequence of the black-capped capuchin (Cebus apella). 2012 , 35, 545-52	4
840	A new skink fauna from Caribbean islands (Squamata, Mabuyidae, Mabuyinae). 2012 , 3288, 1	98
839	Insight into gene evolution within Cervidae and Bovidae through genetic variation in MHC-DQA in the black muntjac (Muntiacus crinifrons). 2012 , 11, 2888-98	1
838	Regulation of ATG6/Beclin-1 homologs by abiotic stresses and hormones in rice (Oryza sativa L.). 2012 , 11, 3676-87	18
837	Evolutionary changes in avian influenza H5N1 viruses in Thailand. 2012 , 56, 257-9	
836	Molecular evolution of the ent-kaurenoic acid oxidase gene in Oryzeae. 2012 , 35, 448-54	
835	Some problems in proving the existence of the universal common ancestor of life on Earth. 2012 , 2012, 479824	9
834	Evolution, expansion and expression of the Kunitz/BPTI gene family associated with long-term blood feeding in Ixodes Scapularis. 2012 , 12, 4	50
833	Evolution of human-specific neural SRGAP2 genes by incomplete segmental duplication. 2012 , 149, 912-22	255
832	In silico characterization and molecular evolutionary analysis of a novel superfamily of fungal effector proteins. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3371-84	61
831	Collodictyonan ancient lineage in the tree of eukaryotes. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1557-68	75
830	Evolutionary Genomics. 2012 ,	4
829	Opsin gene sequence variation across phylogenetic and population histories in Mysis (Crustacea: Mysida) does not match current light environments or visual-pigment absorbance spectra. 2012 , 21, 2176-96	8
828	Molecular phylogenetics: principles and practice. 2012 , 13, 303-14	403

827	Parallel signatures of sequence evolution among hearing genes in echolocating mammals: an emerging model of genetic convergence. 2012 , 108, 480-9	72
826	Gene turnover and differential retention in the relaxin/insulin-like gene family in primates. 2012 , 63, 768-76	13
825	Genetic evolution of the neuraminidase of influenza A (H3N2) viruses from 1968 to 2009 and its correspondence to haemagglutinin evolution. 2012 , 93, 1996-2007	44
824	The banana (Musa acuminata) genome and the evolution of monocotyledonous plants. 2012 , 488, 213-7	762
823	Extensive and continuous duplication facilitates rapid evolution and diversification of gene families. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2019-29	97
822	Evolution of increased complexity in a molecular machine. 2012 , 481, 360-4	135
821	Evolutionary diversification of Mesobuthus & corpion toxins affecting sodium channels. 2012 , 11, M111.0120.	5 4 44
820	Evidence for a convergent slowdown in primate molecular rates and its implications for the timing of early primate evolution. 2012 , 109, 6006-11	102
819	Evolution of CRISPs associated with toxicoferan-reptilian venom and mammalian reproduction. Molecular Biology and Evolution, 2012 , 29, 1807-22	75
818	Rapid coastal spread of First Americans: novel insights from South America's Southern Cone mitochondrial genomes. 2012 , 22, 811-20	126
817	Sequence divergence in the 3'-untranslated region has an effect on the subfunctionalization of duplicate genes. 2012 , 318, 531-44	4
816	Evolution of MHC class I genes in the European badger (Meles meles). 2012 , 2, 1644-62	14
815	Genome-wide and molecular evolution analysis of the Poplar KT/HAK/KUP potassium transporter gene family. 2012 , 2, 1996-2004	28
814	Incorrect handling of calibration information in divergence time inference: an example from volcanic islands. 2012 , 2, 493-500	8
813	The origins and evolution of ubiquitination sites. 2012 , 8, 1865-77	19
812	Altered patterns of fractionation and exon deletions in Brassica rapa support a two-step model of paleohexaploidy. 2012 , 190, 1563-74	129
811	Deleterious mutation accumulation in asexual Timema stick insects. <i>Molecular Biology and Evolution</i> , 2012 , 29, 401-8	52
810	Gene transfer agents: phage-like elements of genetic exchange. 2012 , 10, 472-82	254

809	A "Copernican" reassessment of the human mitochondrial DNA tree from its root. 2012 , 90, 675-84	330
808	Phylogenomic analyses support the position of turtles as the sister group of birds and crocodiles (Archosauria). 2012 , 10, 65	243
807	Fitness conferred by replaced amino acids declines with time. 2012 , 8, 825-8	18
806	Quantifying the elevation of mitochondrial DNA evolutionary substitution rates over nuclear rates in the intertidal copepod Tigriopus californicus. 2012 , 74, 310-8	26
805	Evolutionary dynamics and functional specialization of plant paralogs formed by whole and small-scale genome duplications. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3541-51	67
804	Relaxed genetic constraint is ancestral to the evolution of phenotypic plasticity. 2012 , 52, 16-30	42
803	Phylogenetic analysis of ancient DNA using BEAST. 2012 , 840, 229-41	
802	The yak genome and adaptation to life at high altitude. 2012 , 44, 946-9	472
801	Major taste loss in carnivorous mammals. 2012 , 109, 4956-61	185
800	Phylogenomic analysis of transcriptome data elucidates co-occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). 2012 , 99, 397-406	68
799	Cloning and expression analysis of an anti-lipopolysaccharide factor from giant freshwater prawn, Macrobrachium rosenbergii. 2012 , 39, 7673-80	16
798	Positive selection pressure within teleost Toll-like receptors tlr21 and tlr22 subfamilies and their response to temperature stress and microbial components in zebrafish. 2012 , 39, 8965-75	49
797	Positive selection sites in the surface genes of dengue virus: phylogenetic analysis of the interserotypic branches of the four serotypes. 2012 , 44, 408-14	6
796	Timing of butterfly parasitization of a plantEntEcale symbiosis. 2012 , 27, 437-443	5
795	Phylogenetic relationships and estimation of divergence times among Sisoridae catfishes. 2012 , 55, 312-20	7
794	Gene duplication and positive selection explains unusual physiological roles of the relaxin gene in the European rabbit. 2012 , 74, 52-60	7
793	Recombination, diversity and allele sharing of infectivity proteins between Bartonella species from rodents. 2012 , 64, 525-36	9
792	Molecular evolution of a malaria resistance gene (DARC) in primates. 2012 , 64, 497-505	10

791	Independent evolution of functional MHC class II DRB genes in New World bat species. 2012, 64, 535-47	16
790	The chimpanzee GH locus: composition, organization, and evolution. 2012 , 23, 387-98	3
789	Population dynamics and ORF3 gene evolution of porcine circovirus type 2 circulating in Korea. 2012 , 157, 799-810	8
788	Genetic variability and potential recombination events in the HC-Pro gene of sugarcane streak mosaic virus. 2012 , 157, 1371-5	19
787	Molecular cloning and evolutionary analysis of GJB6 in mammals. 2012 , 50, 213-26	1
786	Positive selection and functional divergence after melanopsin gene duplication. 2012 , 50, 235-48	7
785	Evolutionary history of copy-number-variable locus for the low-affinity FcIreceptor: mutation rate, autoimmune disease, and the legacy of helminth infection. 2012 , 90, 973-85	32
7 ⁸ 4	Divergent evolution of oxidosqualene cyclases in plants. 2012 , 193, 1022-1038	88
783	Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. 2012 , 14, 254-67	52
782	Phylogeography and bindin evolution in Arbacia, a sea urchin genus with an unusual distribution. 2012 , 21, 130-44	41
781	Evidence for genetic differentiation and variable recombination rates among Dutch populations of the opportunistic human pathogen Aspergillus fumigatus. 2012 , 21, 57-70	50
780	Analysis of polymorphism and transcription of the effector gene Avr1b in Phytophthora sojae isolates from China virulent to Rps1b. 2012 , 13, 114-22	22
779	Tunisian Potato virus Y isolates with unnecessary pathogenicity towards pepper: support for the matching allele model in eIF4E resistancepotyvirus interactions. 2012 , 61, 441-447	12
778	Striking coat colour variation in tuco-tucos (Rodentia: Ctenomyidae): a role for the melanocortin-1 receptor?. 2012 , 105, 665-680	6
777	Evolution of ASPM is associated with both increases and decreases in brain size in primates. 2012 , 66, 927-932	34
776	Adaptive evolution of the rbcL gene in Brassicaceae. 2012 , 44, 13-19	8
775	Adaptive diversity of innate immune receptor family short pentraxins in Murinae. 2012, 586, 798-803	3
774	Novel HBsAg markers tightly correlate with occult HBV infection and strongly affect HBsAg detection. 2012 , 93, 86-93	58

773	Computational model for analyzing the evolutionary patterns of the neuraminidase gene of influenza A/H1N1. 2012 , 36, 23-30	3
772	MOLECULAR PHYLOGENY AND TAXONOMY OF THE AEGAGROPILA CLADE (CLADOPHORALES, ULVOPHYCEAE), INCLUDING THE DESCRIPTION OF AEGAGROPILOPSIS GEN. NOV. AND PSEUDOCLADOPHORA GEN. NOV.(1). 2012 , 48, 808-25	26
771	No recent adaptive selection on the apyrase of Mediterranean Phlebotomus: implications for using salivary peptides to vaccinate against canine leishmaniasis. 2012 , 5, 293-305	8
770	Gene flow networks among American Aedes aegypti populations. 2012 , 5, 664-76	28
769	The Tegula tango: a coevolutionary dance of interacting, positively selected sperm and egg proteins. 2012 , 66, 1681-94	19
768	Lineage-specific variation in slow- and fast-X evolution in primates. 2012 , 66, 1751-61	14
767	Phylogeny of Leavenworthia S-alleles suggests unidirectional mating system evolution and enhanced positive selection following an ancient population bottleneck. 2012 , 66, 1849-61	17
766	Preface. 2014 , vii-viii	
765	Copyright Page. 2014 , iv-iv	
764	Foreword. 2014, v-vi	
763	Molecular survey of infectious bronchitis virus on poultry farms in Gifu Prefecture, Japan from 2021	
	to 2022 by RT-PCR with an enhanced level of detection sensitivity for the S1 gene. 2022 ,	
762	A chromosome-level genome of the booklouse, Liposcelis brunnea, provides insight into louse evolution and environmental stress adaptation. 2022 , 11,	
762 761	A chromosome-level genome of the booklouse, Liposcelis brunnea, provides insight into louse	
•	A chromosome-level genome of the booklouse, Liposcelis brunnea, provides insight into louse evolution and environmental stress adaptation. 2022 , 11, Insights into chromosomal evolution and sex determination of Pseudobagrus ussuriensis (Bagridae,	
761	A chromosome-level genome of the booklouse, Liposcelis brunnea, provides insight into louse evolution and environmental stress adaptation. 2022 , 11, Insights into chromosomal evolution and sex determination of Pseudobagrus ussuriensis (Bagridae, Siluriformes) based on a chromosome-level genome. 2022 , 29,	1
761 760	A chromosome-level genome of the booklouse, Liposcelis brunnea, provides insight into louse evolution and environmental stress adaptation. 2022, 11, Insights into chromosomal evolution and sex determination of Pseudobagrus ussuriensis (Bagridae, Siluriformes) based on a chromosome-level genome. 2022, 29, Comparative genomic analysis of Echinococcus multilocularis with other tapeworms. Assessment of phylogenetic approaches to study the timing of recombination cessation on sex	1 O
761 760 759	A chromosome-level genome of the booklouse, Liposcelis brunnea, provides insight into louse evolution and environmental stress adaptation. 2022, 11, Insights into chromosomal evolution and sex determination of Pseudobagrus ussuriensis (Bagridae, Siluriformes) based on a chromosome-level genome. 2022, 29, Comparative genomic analysis of Echinococcus multilocularis with other tapeworms. Assessment of phylogenetic approaches to study the timing of recombination cessation on sex chromosomes.	
761 760 759 758	A chromosome-level genome of the booklouse, Liposcelis brunnea, provides insight into louse evolution and environmental stress adaptation. 2022, 11, Insights into chromosomal evolution and sex determination of Pseudobagrus ussuriensis (Bagridae, Siluriformes) based on a chromosome-level genome. 2022, 29, Comparative genomic analysis of Echinococcus multilocularis with other tapeworms. Assessment of phylogenetic approaches to study the timing of recombination cessation on sex chromosomes. Evolutionary history of metazoan TMEM16 family. 2022, 107595 Testing candidate genes linked to corolla shape variation of a pollinator shift in Rhytidophyllum	O

755	A Secondary Metabolic Enzyme Functioned as an Evolutionary Seed of a Primary Metabolic Enzyme. 2022 , 39,	
754	Evolution of the Growth Hormone Gene Duplication in Passerine Birds.	
753	A chromosome-level reference genome of a Convolvulaceae species Ipomoea cairica.	О
75 ²	The genetic characterization of hemagglutinin (HA), neuraminidase (NA) and polymerase acidic (PA) genes of H3N2 influenza viruses circulated in Guangdong Province of China during 2019\(\textbf{0} 2019\).	
751	Plastid Phylogenomics and Plastomic Diversity of the Extant Lycophytes. 2022, 13, 1280	1
75°	Evolutionary Genomics of a Subdivided Species. 2022 , 39,	O
749	Comparative genomics reveals the molecular mechanism of salt adaptation for zoysiagrasses. 2022 , 22,	
748	The rattlesnake W chromosome: A GC-rich retroelement refugium with retained gene function across ancient evolutionary strata.	
747	Evolution and molecular basis of a novel allosteric property of crocodilian hemoglobin.	0
746	Genome-wide identification, characterization and expression analysis of the BMP family associated with beak-like teeth in Oplegnathus. 13,	
745	The genome of the rice planthopper egg parasitoid wasps Anagrus nilaparvatae casts light on the chemo- and mechanosensation in parasitism. 2022 , 23,	1
744	Comparative Genomics of the Waterfowl Innate Immune System. 2022 , 39,	
743	Adaptive bird-like genome miniaturization during the evolution of scallop swimming lifestyle. 2022,	
742	Molecular Mechanisms of the Convergent Adaptation of Bathypelagic and Abyssopelagic Fishes. 2022 , 14,	
741	Comparative chloroplast genome and transcriptome analysis on the ancient genus Isoetes from China. 13,	
740	Resolving marine f reshwater transitions by diatoms through a fog of gene tree discordance and hemiplasy.	0
739	Constraints on the evolution of toxin-resistant Na,K-ATPases have limited dependence on sequence divergence. 2022 , 18, e1010323	1
738	Chromosome-level Genome Assembly of the High-altitude Leopard (Panthera pardus) Sheds Light on Its Environmental Adaptation.	

737	Functional diversity and evolution of the Drosophila sperm proteome. 2022, 100281	0
736	The Type III polyketide synthase supergene family in plants: complex evolutionary history and functional divergence.	
735	Evolutionary dynamics of genome size and content during the adaptive radiation of Heliconiini butterflies.	1
734	Chromosome scale genome assemblies and annotations for Poales species Carex cristatella, Carex scoparia, Juncus effusus and Juncus inflexus.	1
733	Biochemical Evolution of a Potent Target of Mosquito Larvicide, 3-Hydroxykynurenine Transaminase. 2022 , 27, 4929	1
732	Signatures of adaptive evolution in platyrrhine primate genomes. 2022 , 119,	1
731	The sage genome provides insight into the evolutionary dynamics of diterpene biosynthesis gene cluster in plants. 2022 , 40, 111236	1
730	Rearrangement and domestication as drivers of Rosaceae mitogenome plasticity. 2022 , 20,	2
729	Divergent evolutionary trajectories shape the postmating transcriptional profiles of conspecifically and heterospecifically mated cactophilic Drosophila females. 2022 , 5,	O
728	The genome of a vestimentiferan tubeworm (Ridgeia piscesae) provides insights into its adaptation to a deep-sea environment.	
727	Divergent evolution of mitogenomics in Cetartiodactyla niche adaptation.	О
726	The interplay of DNA methyltransferases and demethylases with tuberization genes in potato (Solanum tuberosum L.) genotypes under high temperature. 13,	
725	What snakes and caecilians have in common? Molecular interaction units and the independent origins of similar morphotypes in Tetrapoda. 2022 , 289,	0
724	Microbial Populations Are Shaped by Dispersal and Recombination in a Low Biomass Subseafloor Habitat.	О
723	Whole-Genome Inter-Sex Variation in Russian Sturgeon (Acipenser gueldenstaedtii). 2022 , 23, 9469	O
722	dN/dS-H, a New Test to Distinguish Different Selection Modes in Protein Evolution and Cancer Evolution.	
721	Comparative genomics of tarakihi (Nemadactylus macropterus) and five New Zealand fish species: assembly contiguity affects the identification of genic features but not transposable elements.	
720	Comparative transcriptome and adaptive evolution analysis on the main liver and attaching liver of Pareuchiloglanis macrotrema.	

719	The chromosome-level holly (Ilex latifolia) genome reveals key enzymes in triterpenoid saponin biosynthesis and fruit color change. 13,	1
718	Comparative genomics uncovers the evolutionary history, demography, and molecular adaptations of South American canids. 2022 , 119,	O
717	Taxonomy, comparative genomics of Mullein (Verbascum, Scrophulariaceae), with implications for the evolution of Verbascum and Lamiales. 2022 , 23,	O
716	Phylogenomics revealed migration routes and adaptive radiation timing of Holarctic malaria vectors of the Maculipennis group.	О
715	Chromosome-level genome assembly and population genomic analyses provide insights into adaptive evolution of the red turpentine beetle, Dendroctonus valens. 2022 , 20,	О
714	Genomic signatures and evolutionary history of the endangered blue-crowned laughingthrush and other Garrulax species. 2022 , 20,	O
713	Cytochemical and comparative transcriptome analyses elucidate the formation and ecological adaptation of three types of pollen coat in Zingiberaceae. 2022 , 22,	
712	Complete mitochondrial genome of Pectocera sp. (Elateridae: Dendrometrinae: Oxynopterini) and its phylogenetic implications.	2
711	Genome-Wide Analysis of the NAC Family Associated with Two Paleohexaploidization Events in the Tomato. 2022 , 12, 1236	
710	A chromosome-level genome assembly of the Walking goby (Scartelaos histophorus). 9,	O
709	Rop plays conserved roles in the reproductive and digestive processes of spider mites.	
708	De Novo Whole-Genome Sequencing and Assembly of the Yellow-Throated Bunting (Emberiza elegans) Provides Insights into Its Evolutionary Adaptation. 2022 , 12, 2004	
707	Ancestral Sequence Reconstruction Identifies Structural Changes Underlying the Evolution of Ideonella sakaiensis PETase and Variants with Improved Stability and Activity.	О
706	Structural evolution of trypsinogen gene redundancy confers risk for pancreas diseases.	
705	A novel Tetrahymena thermophila sterol C-22 desaturase belongs to the Fatty Acid Hydroxylase/Desaturase superfamily. 2022 , 102397	
704	Genomic analyses of Pamir argali, Tibetan sheep, and their hybrids provide insights into chromosome evolution, phenotypic variation, and germplasm innovation. gr.276769.122	o
703	Phylogenomic Evidence for the Origin of Obligate Anaerobic Anammox Bacteria Around the Great Oxidation Event. 2022 , 39,	О
702	Phylotranscriptomic and Evolutionary Analyses of the Green Algal Order Chaetophorales (Chlorophyceae, Chlorophyta). 2022 , 13, 1389	

701	Behavioral innovation and genomic novelty are associated with the exploitation of a challenging dietary opportunity by an avivorous bat. 2022 , 104973	O
700	Enzymatic upgrading of nanochitin using an ancient lytic polysaccharide monooxygenase. 2022 , 3,	
699	Genomic health is dependent on population demographic history.	
698	Early divergence of translation initiation and elongation factors. 2022 , 31,	
697	The Neurodevelopmental Gene MSANTD2 Belongs to a Gene Family Formed by Recurrent Molecular Domestication of Harbinger Transposons at the Base of Vertebrates. 2022 , 39,	
696	The chromosome-level genome of Gypsophila paniculata reveals the molecular mechanism of floral development and ethylene insensitivity.	1
695	Relating enhancer genetic variation across mammals to complex phenotypes using machine learning.	
694	Gene fate spectrum as a reflection of local genomic properties.	
693	The Chromosome-based Genome of Paspalum vaginatum Provides New Insights into Salt-stress Adaptation.	1
692	Southern hemisphere tectonics in the Cenozoic shaped the pantropical distribution of parrots and passerines.	O
691	High-quality genomes reveal significant genetic divergence and cryptic speciation in the model organism Folsomia candida (Collembola).	О
690	Comparative Analysis of Bacillariophyceae Chloroplast Genomes Uncovers Extensive Genome Rearrangements Associated with Speciation. 2022 , 19, 10024	
689	Improved genome assembly provides new insights into the environmental adaptation of the American cockroach, Periplaneta americana.	О
688	Contrasting patterns in the early stage of SARS-CoV-2 evolution between humans and minks.	1
687	Variation of natural selection in the Amoebozoa reveals heterogeneity across the phylogeny and adaptive evolution in diverse lineages. 10,	
686	Distinct evolutionary trajectories of SARS-CoV-2-interacting proteins in bats and primates identify important host determinants of COVID-19. 2022 , 119,	1
685	Genome-Wide Characterization of Nitrogenase Reductase (nifH) Genes in the Sweet Potato [Ipomoea batatas (L.) Lam] and Its Wild Ancestors. 2022 , 13, 1428	O
684	Evolution of the odorant-binding protein gene family in Drosophila. 10,	1

683	The Complete Mitochondrial Genomes of Three Sphenomorphinae Species (Squamata: Scincidae) and the Selective Pressure Analysis on Mitochondrial Genomes of Limbless Isopachys gyldenstolpei. 2022 , 12, 2015	
682	Genomics of Secondarily Temperate Adaptation in the Only Non-Antarctic Icefish.	O
681	Genome resequencing clarifies phylogeny and reveals patterns of selection in the toxicogenomics model Pimephales promelas. 10, e13954	
680	Structural mutations of small single copy (SSC) region in the plastid genomes of five Cistanche species and inter-species identification. 2022 , 22,	O
679	The De Novo Genome Assembly of Olea europaea subsp. cuspidate, a Widely Distributed Olive Close Relative. 13,	1
678	Comparative analysis of the chloroplast and mitochondrial genomes of Saposhnikovia divaricata revealed the possible transfer of plastome repeat regions into the mitogenome. 2022 , 23,	2
677	A chromosome-level genome assembly provides insights into the environmental adaptability and outbreaks of Chlorops oryzae. 2022 , 5,	
676	Positive selection and heat-response transcriptomes reveal adaptive features of the Brassicaceae desert model, Anastatica hierochuntica.	
675	Molecular evolution of vision-related genes may contribute to marsupial photic niche adaptations. 10,	
674	Identifying climatic drivers of hybridization in Heuchereae (Saxifragaceae).	
		O
673	Genomic insights into the phylogeny and biomass-degrading enzymes of rumen ciliates.	3
673 672	Genomic insights into the phylogeny and biomass-degrading enzymes of rumen ciliates. The nearly complete assembly of Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. 2022, 100422	
	The nearly complete assembly of Cercis chinensis genome and Fabaceae phylogenomic studies	
672	The nearly complete assembly of Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. 2022 , 100422 A reference-grade genome assembly for Gossypium bickii and insights into its genome evolution	3
672 671	The nearly complete assembly of Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. 2022, 100422 A reference-grade genome assembly for Gossypium bickii and insights into its genome evolution and formation of pigment gland and gossypol. 2022, 100421	0
672 671 670	The nearly complete assembly of Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. 2022, 100422 A reference-grade genome assembly for Gossypium bickii and insights into its genome evolution and formation of pigment gland and gossypol. 2022, 100421 Eyes, Vision, and the Origins and Early Evolution of Snakes. 2022, 316-348 Insights into adaptive divergence of Japanese mantis shrimp Oratosquilla oratoria inferred from	0
672 671 670	The nearly complete assembly of Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. 2022, 100422 A reference-grade genome assembly for Gossypium bickii and insights into its genome evolution and formation of pigment gland and gossypol. 2022, 100421 Eyes, Vision, and the Origins and Early Evolution of Snakes. 2022, 316-348 Insights into adaptive divergence of Japanese mantis shrimp Oratosquilla oratoria inferred from comparative analysis of full-length transcriptomes. 9, Chromosome-level and graphic genomes provide insights into metabolism of bioactive metabolites	0

665 Neurobiological Perspectives. 2022, 269-348

664	A genomic timescale for placental mammal evolution.	O
663	A chromosome-level genome of the helmet catfish (Cranoglanis bouderius). 13,	O
662	A Long-Read Genome Assembly of a Native Mite in China Pyemotes zhonghuajia Yu, Zhang & He (Prostigmata: Pyemotidae) Reveals Gene Expansion in Toxin-Related Gene Families. 2022 , 14, 571	1
661	Genomic Insights into Genetic Diploidization in the Homosporous Fern Adiantum nelumboides. 2022 , 14,	1
660	Genomic investigation of the Chinese alligator reveals wild-extinct genetic diversity and genomic consequences of their continuous decline.	О
659	Transposons and non-coding regions drive the intrafamily differences of genome size in insects. 2022 , 25, 104873	О
658	Temperature acclimation in hot-spring snakes and the convergence of cold response. 2022 , 3, 100295	O
657	A high-quality genome of the dobsonfly Neoneuromus ignobilis reveals molecular convergences in aquatic insects. 2022 , 114, 110437	
656	Birth and death in terminal complement pathway. 2022 , 149, 174-187	
655	Evolutionary and structural analyses of the NADPH oxidase family in eukaryotes reveal an initial calcium dependency. 2022 , 56, 102436	
654	Adaptive radiation in Orinus, an endemic alpine grass of the Qinghai-Tibet Plateau, based on comparative transcriptomic analysis. 2022 , 277, 153786	O
653	Phylogeny and evolution of Cupressaceae: Updates on intergeneric relationships and new insights on ancient intergeneric hybridization. 2022 , 177, 107606	1
652	Genomic and transcriptomic analyses provide insights into valuable fatty acid biosynthesis and environmental adaptation of yellowhorn. 13,	О
651	Distinct features in fish Bouncer proteins determine sperm-egg compatibility.	0
650	Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. 2022 , 119,	1
649	Genes and sites under adaptation at the phylogenetic scale also exhibit adaptation at the population-genetic scale.	О
648	Plastome structure, phylogenomics, and divergence times of tribe Cinnamomeae (Lauraceae). 2022 , 23,	2

647	Genome-Wide Identification and Expression Patterns of the SWEET Gene Family in Bletilla striata and its Responses to Low Temperature and Oxidative Stress. 2022 , 23, 10057	O
646	Genome of Laudakia sacra Provides New Insights into High-Altitude Adaptation of Ectotherms. 2022 , 23, 10081	O
645	The necrosis- and ethylene-inducing peptide 1-like protein (NLP) gene family of the plant pathogen Corynespora cassiicola.	0
644	The genome of homosporous maidenhair fern sheds light on the euphyllophyte evolution and defences. 2021 , 8, 1024-1037	1
643	Resolution, conflict and rate shifts: insights from a densely sampled plastome phylogeny for Rhododendron (Ericaceae).	O
642	The chromosome-scale genome of the raccoon dog: Insights into its evolutionary characteristics. 2022 , 25, 105117	0
641	Genome sequencing and comparative analysis of Ficus benghalensis and Ficus religiosa species reveal evolutionary mechanisms of longevity. 2022 , 25, 105100	0
640	The genetic adaptations of Toxoptera aurantii facilitated its rapid multiple plant hosts dispersal and invasion. 2022 , 114, 110472	O
639	One-way ticket to the blue: A large-scale, dated phylogeny revealed asymmetric land-to-water transitions in acariform mites (Acari: Acariformes). 2022 , 177, 107626	O
638	Comprehensive taxon sampling and vetted fossils help clarify the time tree of shorebirds (Aves, Charadriiformes). 2022 , 177, 107620	O
637	Comparative genomics and evolutionary analysis of plant CNGCs. 2022, 7,	0
636	Testing Phylogenetic Stability with Variable Taxon Sampling. 2022 , 167-188	O
635	Dating Microbial Evolution with MCMCtree. 2022 , 3-22	0
634	Methodologies for Microbial Ancestral Sequence Reconstruction. 2022 , 283-303	O
633	Estimating the Divergence Times of Alphaproteobacteria Based on Mitochondrial Endosymbiosis and Eukaryotic Fossils. 2022 , 95-116	O
632	Chromosomal-level genome of macadamia (<i>Macadamia integrifolia</i>). 2022 , 1, 1-9	O
631	Assessing a Role of Genetic Drift for Deep-Time Evolutionary Events. 2022 , 343-359	0
630	A Computational Protocol for Dating the Evolution of Cyanobacteria. 2022 , 23-40	0

629	An Integrated Method to Reconstruct Ancient Proteins. 2022, 267-281	0
628	Genome analysis of Phrixothrix hirtus (Phengodidae) railroad worm shows the expansion of odorant-binding gene families and positive selection on morphogenesis and sex determination genes. 2023 , 850, 146917	O
627	Re-evaluating and dating myriapod diversification with phylotranscriptomics under a regime of dense taxon sampling. 2023 , 178, 107621	1
626	Chromosome-Level Genome Assembly of a Fragrant Japonica Rice Cultivar Changxianggeng 1813 Provides Insights into Genomic Variations between Fragrant and Non-Fragrant Japonica Rice. 2022 , 23, 9705	O
625	Non-synonymous to synonymous substitutions suggest that orthologs tend to keep their functions, while paralogs are a source of functional novelty. 10, e13843	О
624	Molecular archaeology of human cognitive traits. 2022 , 40, 111287	0
623	Chromosome-level Genomes Reveal the Genetic Basis of Descending Dysploidy and Sex Determination in Morus Plants. 2022 ,	0
622	A Novel Gene Controls a New Structure: PiggyBac Transposable Element-Derived 1, Unique to Mammals, Controls Mammal-Specific Neuronal Paraspeckles. 2022 , 39,	0
621	Mitogenome selection in the evolution of key ecological strategies in the ancient hexapod class Collembola. 2022 , 12,	0
620	Genome-wide identification of wheat ABC1K gene family and functional dissection of TaABC1K3 and TaABC1K6 involved in drought tolerance. 13,	O
619	Deep evaluation of the evolutionary history of the Heat Shock Factor (HSF) gene family and its expansion pattern in seed plants. 10, e13603	О
618	A chromosome-scale genome assembly of Quercus gilva: Insights into the evolution of Quercus section Cyclobalanopsis (Fagaceae). 13,	Ο
617	Evolutionary insights reveal a new role of PADI2 in transcriptional elongation.	О
616	Reduced and Nonreduced Genomes in Paraburkholderia Symbionts of Social Amoebas.	0
615	Chromosome-level assembly of Culex pipiens molestus and improved reference genome of Culex pipiens pallens (Culicidae, Diptera).	О
614	Differences in pseudogene evolution contributed to the contrasting flavors of turnip and Chiifu, two Brassica rapa subspecies. 2022 , 100427	1
613	Enterovirus 3C Protease Cleaves TRIM7 To Dampen Its Antiviral Activity.	О
612	CladeDate : Calibration information generator for divergence time estimation.	O

611	Comparative and Phylogenetic Analyses of Complete Chloroplast Genomes of Scrophularia incisa Complex (Scrophulariaceae). 2022 , 13, 1691	0
610	Comparative genomics reveals putative evidence for high-elevation adaptation in the American pika (Ochotona princeps).	O
609	Monsoon boosted radiation of the endemic East Asian carps.	О
608	Conserved non-coding sequences and de novo Mutator insertion alleles are imprinted in maize.	О
607	Divergent evolutionary trajectories of bryophytes and tracheophytes from a complex common ancestor of land plants.	4
606	Host specific sensing of coronaviruses and picornaviruses by the CARD8 inflammasome.	1
605	Impact of LTR-Retrotransposons on Genome Structure, Evolution, and Function in Curcurbitaceae Species. 2022 , 23, 10158	0
604	Utilizing Evolutionary Conservation to Detect Deleterious Mutations and Improve Genomic Prediction in Cassava.	О
603	A genome-wide search of Toll/Interleukin-1 receptor (TIR) domain-containing adapter molecule (TICAM) and their evolutionary divergence from other TIR domain containing proteins. 2022 , 17,	0
602	Comparative transcriptomics provides a new possibility to analysis Lilium germplasm resources in Midwestern China.	o
601	Comparative transcriptome analysis reveals molecular adaptations underlying distinct immunity and inverted resting posture in bats.	0
600	Transcriptomic heterochrony and completely cleistogamous flower development in the mycoheterotrophic orchid Gastrodia.	О
599	Phylogenomics and evolutionary diversification of the subfamily Polygonoideae.	0
598	Genomic patterns of divergence in the early and late steps of speciation of the deep-sea vent thermophilic worms of the genus Alvinella. 2022 , 22,	О
597	Rapid Evolution of Glycan Recognition Receptors Reveals an Axis of Host-Microbe Conflicts at Carbohydrate-Protein Interfaces.	0
596	The updated weeping forsythia genome reveals the genomic basis for the evolution and the forsythin and forsythoside A biosynthesis. 2022 ,	o
595	Comprehensive Genome-Wide Analysis of Wnt Gene Family and Expression Profiling during Limb Regeneration in Portunus trituberculatus. 2022 , 7, 258	0
594	Bat pluripotent stem cells reveal unique entanglement between host and viruses.	o

593	Long-read sequencing data reveals dynamic evolution of mitochondrial genome size and the phylogenetic utility of mitochondrial DNA in Hercules beetles (Dynastes; Scarabaeidae).	0
592	Variation in Heat Shock Protein 40kDa relates to divergence in thermotolerance among cryptic rotifer species.	Ο
591	Hybridisation has shaped a recent radiation of grass-feeding aphids.	0
590	Chromosome-level genome assembly of Amomum tsao-ko provides insights into the biosynthesis of flavor compounds.	O
589	Transcriptomic analysis of seed development in Paysonia auriculata (Brassicaceae) identifies genes involved in hydroxy fatty acid biosynthesis and seed maturation.	0
588	A variable gene family encoding nodule-specific cysteine-rich peptides in pea (Pisum sativum L.). 13,	O
587	Comparative Genome Analysis Reveals the Genomic Basis of Semi-Aquatic Adaptation in American Mink (Neovison vison). 2022 , 12, 2385	1
586	Transcriptome analysis provides insight into adaptive mechanisms of scallops under environmental stress. 9,	1
585	Using Genomes and Evolutionary Analyses to Screen for Host-Specificity and Positive Selection in the Plant Pathogen Xylella fastidiosa. 2022 , 88,	0
584	Hybridisation and chloroplast capture between distinct Themeda triandra lineages in Australia.	O
583	Draft genome assemblies of four manakins. 2022 , 9,	0
582	Unique Evolution of Antiviral Tetherin in Bats.	2
581	Optimization and deoptimization of codons in SARS-CoV-2 and the implications for vaccine development.	0
580	The genetic mechanisms underlying the convergent evolution of pollination syndromes in the Neotropical radiation of Costus L 13,	O
579	Jack of all trades: genome assembly of Wild Jack and comparative genomics of Artocarpus.	0
578	The genetic architecture of phenotypic diversity in the Betta fish (Betta splendens). 2022, 8,	1
577	Primate hemorrhagic fever-causing arteriviruses are poised for spillover to humans. 2022,	1
576	Dynamic genome evolution in a model fern. 2022 , 8, 1038-1051	4

575	Widespread convergent evolution of alpha-neurotoxin resistance in African mammals.	1
574	Phylotranscriptomics of liverworts: revisiting the backbone phylogeny and ancestral gene duplications.	o
573	Evolutionary rates of body-size-related genes and ecological factors involved in driving body size evolution of squamates. 10,	0
572	New Guinea uplift opens ecological opportunity across a continent. 2022 ,	o
571	Morphological and molecular evolution of hadal amphipod eggs provides insights into embryogenesis under high hydrostatic pressure. 10,	0
570	MAIA, Fc receptorlike 3, supersedes JUNO as IZUMO1 receptor during human fertilization. 2022 , 8,	1
569	Molecular advances to study the function, evolution and spectral tuning of arthropod visual opsins. 2022 , 377,	2
568	The extremely reduced, diverged and reconfigured plastomes of the largest mycoheterotrophic orchid lineage. 2022 , 22,	o
567	Comprehensive In Silico Analysis of RNA Silencing-Related Genes and Their Regulatory Elements in Wheat (Triticum aestivum L.). 2022 , 2022, 1-26	0
566	Evolutionary divergence of duplicated genomes in newly described allotetraploid cottons. 2022 , 119,	1
565	Phylogeny and adaptative evolution to chemosynthetic habitat in barnacle (Cirripedia: Thoracica) revealed by mitogenomes. 9,	0
564	Ambush predation and the origin of euprimates. 2022 , 8,	O
563	A seed-like proteome in oil-rich tubers.	0
562	Comparative transcriptomics of high-altitude Vulpes and their low-altitude relatives. 10,	o
561	A chromosome-level genome assembly of the Chinese cork oak (Quercus variabilis). 13,	1
560	The genome of Areca catechu provides insights into sex determination of monoecious plants.	o
559	Does IR-loss promote plastome structural variation and sequence evolution?. 13,	0
558	Chromosome-level genome assembly and functional characterization of terpene synthases provide insights into the volatile terpenoid biosynthesis of Wurfbainia villosa.	О

557	The First Chromosome-level Genome Assembly of Cheumatopsyche charites Malicky and Chantaramongkol, 1997 (Trichoptera: Hydropsychidae) Reveals How It Responds to Pollution. 2022 , 14,	0
556	Phosphorylation sites are evolutionary checkpoints against liquid-solid transition in protein condensates.	O
555	Phylogenomic Analyses of the Tenthredinoidea Support the Familial Rank of Athaliidae (Insecta, Tenthredinoidea). 2022 , 13, 858	1
554	The heterogeneity in the landscape of gene dominance in maize is accompanied by unique chromatin environments.	O
553	A genome for Cissus illustrates features underlying the evolutionary success in dry savannas.	О
552	Rapid expansion and visual specialization of learning and memory centers in Heliconiini butterflies.	O
551	Chromosome-level genome assembly and resequencing of camphor tree (Cinnamomum camphora) provides insight into phylogeny and diversification of terpenoid and triglyceride biosynthesis of Cinnamomum.	Ο
550	A chromosome-scale genome assembly of turmeric provides insights into curcumin biosynthesis and tuber formation mechanism. 13,	O
549	Distinct selection signatures during domestication and improvement in crops: a tale of two genes in mungbean.	О
548	The role of evolutionarily metastable oligomeric states in the optimization of catalytic activity.	O
547	Pan-Genome Analysis of Campylobacter: Insights on the Genomic Diversity and Virulence Profile.	О
546	Convergent genomic signatures of high-altitude adaptation among six independently evolved mammals.	O
545	FishPIE: A universal phylogenetically informative exon markers set for ray-finned fishes. 2022 , 25, 105025	О
544	Characterization of ancestral Fe/Mn superoxide dismutases indicates their cambialistic origin. 2022 , 31,	1
543	Genomic analyses of rice bean landraces reveal adaptation and yield related loci to accelerate breeding. 2022 , 13,	3
542	Adaptation and evolution of the sea anemone Alvinactis sp. to deep-sea hydrothermal vents: A comparison using transcriptomes. 2022 , 12,	Ο
541	Plastome Phylogenomics Provide Insight into the Evolution of Taxus. 2022 , 13, 1590	Ο
540	Repeated turnovers keep sex chromosomes young in willows. 2022 , 23,	1

539	Comparative Analysis of Chloroplast Genomes within Saxifraga (Saxifragaceae) Takes Insights into Their Genomic Evolution and Adaption to the High-Elevation Environment. 2022 , 13, 1673	1
538	Chromosomal-scale genome assembly of the near-extinction big-head schizothorcin (Aspiorhynchus laticeps). 2022 , 9,	O
537	Genome Assembly of the Brassicaceae Diploid Orychophragmus violaceus Reveals Complex Whole Genome Duplication and Evolution of Dihydroxy Fatty Acid Metabolism. 2022 , 100432	1
536	Organellar genome comparisons of Sargassum polycystum and S. plagiophyllum (Fucales, Phaeophyceae) with other Sargassum species. 2022 , 23,	O
535	Genomic insights into the evolutionary history and diversification of bulb traits in garlic. 2022, 23,	O
534	The genomic and bulked segregant analysis of Curcuma alismatifolia revealed its diverse bract pigmentation.	O
533	Selection-driven adaptation to the extreme Antarctic environment in the Emperor penguin.	O
532	Genomic insight into the nocturnal adaptation of the black-crowned night heron (Nycticorax nycticorax). 2022 , 23,	O
531	Novel genome sequence of Chinese cavefish (Triplophysa rosa) reveals pervasive relaxation of natural selection in cavefish genomes.	O
530	Novel trends of genome evolution in highly complex tropical sponge microbiomes. 2022, 10,	O
529	De novo genome assembly of the medicinal plant Gentiana macrophylla provides insights into the genomic evolution and biosynthesis of iridoids.	O
528	Genomic Analysis of Two Phlebotomine Sand Fly Vectors of Leishmania from the New and Old World.	O
527	Lineage-specific protein repeat expansions and contractions reveal malleable regions of immune genes.	O
526	Disentangling positive vs. relaxed selection in animal mitochondrial genomes.	O
525	The draft genome and multi-omics analyses reveal new insights into geo-herbalism properties of Citrus grandis IIomentosa[12022, 111489]	O
524	Comparative genomics of Sarcoptes scabiei provide new insights into adaptation to permanent parasitism and within-host species divergence.	1
523	A high-quality Buxus austro-yunnanensis (Buxales) genome provides new insights into karyotype evolution in early eudicots. 2022 , 20,	O
522	A chromosome-level genome assembly for Dracaena cochinchinesis reveals molecular basis of its longevity and formation of dragon blood. 2022 , 100456	O

521	The complete mitochondrial genome of the hermit crab Diogenes Edwardsii (Anomura: Diogenidae) and phylogenetic relationships within infraorder Anomura.	О
520	Investigation of mutated in colorectal cancer evolution history indicate a putative role in Th17/Treg differentiation	o
519	Genomes of Two Flying Squid Species Provide Novel Sights into Adaptations of Cephalopods to Pelagic Life. 2022 ,	0
518	The complex genome and adaptive evolution of polyploid Chinese pepper (Zanthoxylum armatum and Zanthoxylum bungeanum).	О
517	Molecular and developmental signatures of genital size macro-evolution in bugs.	О
516	An ancient respiratory system in the widespread sedimentary archaea Thermoprofundales.	О
515	The Perennial Horse Gram (Macrotyloma axillare) Genome, Phylogeny, and Selection Across the Fabaceae. 2022 , 255-279	О
514	Genome assembly of the Pendlebury Toundleaf bat, Hipposideros pendleburyi, revealed the expansion of Tc1/Mariner DNA transposons in Rhinolophoidea. 2022 , 29,	О
513	Comparative Mitogenomic Analyses and New Insights into the Phylogeny of Thamnocephalidae (Branchiopoda: Anostraca). 2022 , 13, 1765	1
512	Phylogenomics provides insights into the evolution of cactophily and host plant shifts in Drosophila. 2022 , 107653	О
511	Relationship between genome-wide and MHC class I and II genetic diversity and complementarity in a nonhuman primate. 2022 , 12,	O
510	Repeated origin of the W chromosome from the Z chromosome in Lepidoptera.	O
509	Genomic signatures of mitonuclear coevolution in mammals.	1
508	Functional Attenuation of UCP1 as the Potential Mechanism for Thickened Blubber Layer in Cetaceans.	O
507	Cross-species transmission of an ancient endogenous retrovirus and convergent co-option of its envelope gene in two mammalian orders. 2022 , 18, e1010458	О
506	The chromosome-level genome of female ginseng (Angelica sinensis) provides insights into molecular mechanisms and evolution of coumarin biosynthesis.	О
505	Weaker selection on genes with treatment-specific expression may limit plasticity evolution in Arabidopsis thaliana.	О
504	Genomic signatures associated with maintenance of genome stability and venom turnover in two parasitoid wasps. 2022 , 13,	1

503	The pangenome of the wheat pathogen Pyrenophora tritici-repentis reveals novel transposons associated with necrotrophic effectors ToxA and ToxB. 2022 , 20,	1
502	Extreme mito-nuclear discordance within Anthozoa, with notes on unique properties of their mitochondrial genomes.	O
501	Evolution and antiviral activity of a human protein of retroviral origin. 2022, 378, 422-428	2
500	Integrated global analysis in spider-flowers illuminates features underlying the evolution and maintenance of C4 photosynthesis.	O
499	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. 2022 , 20,	1
498	Characterization and evolutionary diversification of the phospholipase D gene family in mosses. 13,	O
497	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation.	0
496	The Genome of the WaspAnastatus disparisReveals Energy Metabolism Adaptations for Extreme Aggression.	O
495	The chromosome-level genome of Akebia trifoliata as an important resource to study plant evolution and environmental adaptation in the Cretaceous.	2
494	Phylogenomics reveals the evolution, biogeography, and diversification history of voles in the Hengduan Mountains. 2022 , 5,	1
493	Systematics and evolution of predatory flower flies (Diptera: Syrphidae) based on exon-capture sequencing.	1
492	The genome of single-petal jasmine (Jasminum sambac) provides insights into heat stress tolerance and aroma compound biosynthesis. 13,	O
491	Chromosome-length genome assemblies of cactophilicDrosophilailluminate links between structural and sequence evolution.	0
490	Multiple origins, one evolutionary trajectory: gradual evolution characterizes distinct lineages of allotetraploid Brachypodium.	2
489	Genomic underpinnings of convergent adaptation to high altitudes for alpine plants.	0
488	Demographic history and conservation genomics of caribou (Rangifer tarandus) in QuBec.	O
487	Museum specimens shedding light on the evolutionary history and hidden diversity of the hedgehog family Erinaceidae.	0
486	The primordial knot: the deep-rooted origin of the disulfide-rich spider venom toxins.	O

485	Prediction of a conserved pheromone receptor lineage from antennal transcriptomes of the pine sawyer genus Monochamus (Coleoptera: Cerambycidae).	0
484	Genomic Changes During the Evolution of theCoxiellaGenus Along the Parasitism-Mutualism Continuum.	O
483	Chinese fir genome and the evolution of gymnosperms.	1
482	Biogeography and eye size evolution of the ogre-faced spiders. 2022 , 12,	Ο
481	Rational and mechanistic approaches for improving biocatalyst performance. 2022 , 2, 2614-2643	Ο
480	Evaluation of Genetic Diversity and Parasite-Mediated Selection of MHC Class I Genes in Emberiza godlewskii (Passeriformes: Emberizidae). 2022 , 14, 925	Ο
479	The rugged DNA-binding sequence-fitness landscape of the LacI/GalR Family is a product of asymmetry in the operator:repressor complex.	Ο
478	Molecular Evolution of Metallothioneins of Antarctic Fish: A Physiological Adaptation to Peculiar Seawater Chemical Characteristics. 2022 , 10, 1592	1
477	Characterization and Comparative Analysis of Chloroplast Genomes in Five Uncaria Species Endemic to China. 2022 , 23, 11617	Ο
476	Chromosome-scale genome assembly provides insights into the molecular mechanisms of tissue development of Populus wilsonii. 2022 , 5,	O
475	The Chromosome-level genome of Aesculus wilsonii provides new insights into terpenoid biosynthesis and Aesculus evolution. 13,	Ο
474	Antiviral function and viral antagonism of the rapidly evolving dynein activating adapter NINL. 11,	Ο
473	Natural selection drives the evolution of mitogenomes in Acrossocheilus. 2022 , 17, e0276056	0
472	Fasulyede Tuz ve Kurakl& Stresi Altāda PIF Gen Ailesinin Genom āpāda Analizi ve Karakterizasyonu.	O
471	Chromosome-level genome assembly of the Verasper variegatus provides insights into left eye migration. 9,	0
470	Integrated phylogenomic analyses unveil reticulate evolution in Parthenocissus (Vitaceae), highlighting speciation dynamics in the Himalayan-Hengduan Mountains.	O
469	Gapless genome assembly of azalea and multi-omics investigation into divergence between two species with distinct flower color.	1
468	A conserved protein disulfide isomerase enhances plant resistance against herbivores.	O

467	Genome of the endangered Guatemalan Beaded Lizard, Heloderma charlesbogerti, reveals evolutionary relationships of squamates and declines in effective population sizes.	1
466	A contiguous de novo genome assembly of sugar beet EL10 (Beta vulgaris L.).	O
465	The Genetic Diversity and the Divergence Time in Extant Primitive Mayfly, Siphluriscus chinensis Ulmer, 1920 Using the Mitochondrial Genome. 2022 , 13, 1780	0
464	Engineering indel and substitution variants of diverse and ancient enzymes using Graphical Representation of Ancestral Sequence Predictions (GRASP). 2022 , 18, e1010633	1
463	Probing the origin of prion protein misfolding via reconstruction of ancestral proteins.	O
462	Evolution of Gene Arrangements in the Mitogenomes of Ensifera and Characterization of the Complete Mitogenome of Schizodactylus jimo. 2022 , 23, 12094	O
461	Ancestral sequence reconstruction as a tool to study the evolution of wood decaying fungi. 3,	O
460	Comprehensive Comparative Analysis and Development of Molecular Markers for Dianthus Species Based on Complete Chloroplast Genome Sequences. 2022 , 23, 12567	O
459	A Comparative Genomics Approach for Analysis of Complete Mitogenomes of Five Actinidiaceae Plants. 2022 , 13, 1827	1
458	A Chromosome-Scale Genome Assembly of Mitragyna speciosa (Kratom) and the Assessment of Its Genetic Diversity in Thailand. 2022 , 11, 1492	1
457	Diurnality shapes the visual opsin genes of colorful Neotropical frogs.	O
456	The characteristics of mRNA m6A methylomes in allopolyploid Brassica napus and its diploid progenitors.	O
455	Two closely related ureotelic fish species of the genus Alcolapia express different levels of ammonium transporters in gills.	O
454	Thirteen Dipterocarpoideae genomes provide insights into their evolution and borneol biosynthesis. 2022 , 100464	O
453	Meta-analysis of major histocompatibility complex (MHC) class IIA reveals polymorphism and positive selection in many vertebrate species.	O
452	Born with intronless ERF transcriptional factors: C4photosynthesis inherits a legacy dating back 450 million years.	O
451	Comparative genomic and transcriptomic analyses of trans-kingdom pathogen Fusarium solani species complex reveal degrees of compartmentalization. 2022 , 20,	0
450	Chromosome-level genome assembly ofTorreya grandisprovides insights into the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis.	O

449	Genome-Wide Analysis and Characterization of SABATH Gene Family in Phaseolus vulgaris Genotypes Subject to Melatonin under Drought and Salinity Stresses.	0
448	Molecular Characterization, Expression, Evolutionary Selection, and Biological Activity Analysis of CD68 Gene from Megalobrama amblycephala. 2022 , 23, 13133	1
447	The complete chloroplast genome sequences of three Broussonetia species and comparative analysis within the Moraceae. 10, e14293	1
446	Evolution of increased complexity and specificity at the dawn of form I Rubiscos. 2022, 378, 155-160	2
445	A Comparative Phylogenetic Analysis on the Chloroplast Genome in Different Reynoutria japonica Populations. 2022 , 13, 1979	0
444	The Deadly Toxin Arsenal of the Tree-Dwelling Australian Funnel-Web Spiders. 2022 , 23, 13077	O
443	Elasmobranch genome sequencing reveals evolutionary trends of vertebrate karyotype organization.	0
442	Non-triplet genetic code inEuplotesciliates is a result of neutral evolution.	Ο
441	Ontogenetic Variation in Macrocyclic and Hemicyclic Poplar Rust Fungi. 2022 , 23, 13062	Ο
440	Population genetic analyses inferred a limited genetic diversity across the pvama-1 DI domain among Plasmodium vivax isolates from Khyber Pakhtunkhwa regions of Pakistan. 2022 , 22,	Ο
439	Cistanche Species Mitogenomes Suggest Diversity and Complexity in Lamiales-Order Mitogenomes. 2022 , 13, 1791	0
438	Shared patterns of gene expression and protein evolution associated with adaptation to desert environments in rodents.	O
437	The genome sequence of Hirschfeldia incana , a new Brassicaceae model to improve photosynthetic light-use efficiency.	0
436	Unusual Dependence between Gene Expression and Negative Selection in Euplotes.	Ο
435	Phylogenomics and plastome evolution of a Brazilian mycoheterotrophic orchid, Pogoniopsis schenckii.	0
434	Evolution of the CBL and CIPK gene families in Medicago: genome-wide characterization, pervasive duplication, and expression pattern under salt and drought stress. 2022 , 22,	O
433	Chromosome-level genome assembly of the bar-headed goose (Anser indicus). 2022, 9,	0
432	Inference of gene flow between species under misspecified models.	Ο

431	Genome-wide scan for potential CD4+ T-cell vaccine candidates in Candida auris by exploiting reverse vaccinology and evolutionary information. 9,	0
430	Phylogenomics as an effective approach to untangle cross-species hybridization event: A case study in the family Nymphaeaceae. 13,	Ο
429	Mitochondrial genomic analyses provide new insights into the thissing tatp8 and adaptive evolution of Mytilidae. 2022 , 23,	1
428	The barley DIR gene family: An expanded gene family that is involved in stress responses. 13,	O
427	Whole genome resequencing and comparative genome analysis of three Puccinia striiformis f. sp. tritici pathotypes prevalent in India. 2022 , 17, e0261697	0
426	Genomic and phenotypic changes associated with alterations of migratory behavior in a songbird.	O
425	The associated evolution among the extensive RNA editing, GC-biased mutation, and PPR family expansion in the organelle genome evolution of Selaginellaceae.	0
424	Evolution of the orthopoxvirus core genome. 2023 , 323, 198975	O
423	Olfactory and gustatory receptor genes in fig wasps: Evolutionary insights from comparative studies. 2023 , 850, 146953	0
422	Natural selection pressure exerted on Bilentlmutations during the evolution of SARS-CoV-2: Evidence from codon usage and RNA structure. 2023 , 323, 198966	O
421	A partial duplication of an X-linked gene exclusive of a primate lineage (Macaca). 2023 , 851, 146997	0
420	Dissecting the genome, secretome, and effectome repertoires of Monilinia spp.: The causal agent of brown rot disease: A comparative analysis. 2023 , 195, 112120	O
419	The Soursop Genome (Annona muricata L., Annonaceae). 2022 , 149-174	O
418	Identification of sex-linked marker and candidate sex determination gene in ornamental fish, African scat (Scatophagus tetracanthus). 2023 , 563, 739023	O
417	Adaptive evolution of scn4aa in Takifugu and Tetraodon. 2022,	0
416	Mitochondrial effects on fertility and longevity in Tigriopus californicus contradict predictions of the mother's curse hypothesis. 2022 , 289,	O
415	The role of oligomerization in the optimization of cyclohexadienyl dehydratase conformational dynamics and catalytic activity.	0
414	Identification and Analysis of Stress-Associated Proteins (SAPs) Protein Family and Drought Tolerance of ZmSAP8 in Transgenic Arabidopsis. 2022 , 23, 14109	Ο

413	Investigating the eukaryotic host-like SLiMs in microbial mimitopes and their potential as novel drug targets for treating autoimmune diseases. 13,	О
412	Whole-genome assembly and annotation for the little yellow croaker (Larimichthys polyactis) provide insights into the evolution of hermaphroditism and gonochorism.	O
411	Long-read genome assemblies reveals acis-regulatory landscape associated with phenotypic divergence in two sisterSinipercafishes.	0
410	Defensive spines are associated with large geographic range but not diversification in spiny ants (Hymenoptera: Formicidae: Polyrhachis).	1
409	A high-quality chromosome-level genome assembly of Pelteobagrus vachelli provides insights into its environmental adaptation and population history. 13,	0
408	The first high-quality chromosome-level genome assembly of Phyllanthaceae (Phyllanthus cochinchinensis) provides insights into flavonoid biosynthesis. 2022 , 256,	O
407	The genome of a hadal sea cucumber reveals novel adaptive strategies to deep-sea environments. 2022 , 105545	0
406	A likely autotetraploidization event shaped the Chinese mahogany (Toona sinensis) genome. 2022 ,	O
405	Improved assembly and annotation of the sesame genome.	2
404	Positive selection-driven fixation of a hominin-specific amino acid mutation related to dephosphorylation in IRF9. 2022 , 22,	O
403	Chromosome-level genome assembly of Dongxiang wild rice (Oryza rufipogon) provides insights into resistance to disease and freezing. 13,	1
402	Whole-genome resequencing reveals complex effects of geographic-paleoclimatic interactions on diversification of Moustache toads in East Asia.	O
401	Halocynthiibacter halioticoli sp. nov., isolated from the abalone Haliotis discus hannai.	О
400	Complementary evolution of coding and noncoding sequence underlies mammalian hairlessness. 11,	1
399	Exploring clade differentiation of the Faecalibacterium prausnitzii complex. 2022, 105533	О
398	Buffering role of HSP shapes the molecular evolution of mammalian and human genomes at short and long-term scales.	O
397	Repeated out-of-Africa expansions of Helicobacter pylori driven by replacement of deleterious mutations. 2022 , 13,	Ο
396	Gut specific cardenolide resistant sodium pump primed an omnivore to feed on toxic Oleander. 2022 , 105616	O

395	Plastid phylogenomic insights into relationships, divergence, and evolution of Apiales. 2022, 256,	0
394	Molecular evolution of non-visual opsin genes across environmental, developmental, and morphological adaptations in frogs.	o
393	The Mitogenome of Sedum plumbizincicola (Crassulaceae): Insights into RNA Editing, Lateral Gene Transfer, and Phylogenetic Implications. 2022 , 11, 1661	0
392	Chromosome-level genome assembly of the Muscovy duck provides insight into fatty liver susceptibility. 2022 , 114, 110518	0
391	Plastome sequencing of South American Podocarpus species reveals low rearrangement rates despite ancient gondwanan disjunctions.	0
390	Endo-parasitoid lifestyle promotes endogenization and domestication of dsDNA viruses.	0
389	Genome-wide identification and characterization profile of phosphatidy ethanolamine-binding protein family genes in carrot. 13,	0
388	Sex-biased gene expression at single-cell resolution: Cause and consequence of sexual dimorphism.	o
387	Draft genome of six Cuban Anolis lizards and insights into genetic changes during their diversification. 2022 , 22,	1
386	Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. 2022 , 5,	1
385	Phylogenomics reveals deep relationships and diversification within phylactolaemate bryozoans. 2022 , 289,	1
384	Revisiting ancient polyploidy in leptosporangiate ferns.	0
383	De Novo Hybrid Assembly of the Salvia miltiorrhiza Mitochondrial Genome Provides the First Evidence of the Multi-Chromosomal Mitochondrial DNA Structure of Salvia Species. 2022 , 23, 14267	1
382	Evolutionary analyses of polymeric immunoglobulin receptor (pIgR) in the mammals reveals an outstanding mutation rate in the lagomorphs. 13,	O
381	Conformational epistasis impairs AlphaFold structural predictions.	0
380	Sequencing of Camelina neglecta, a diploid progenitor of the hexaploid oilseed Camelina sativa.	O
379	Ancestral Sequence Reconstruction of the Ribosomal Protein uS8 and Reduction of Amino Acid Usage to a Smaller Alphabet.	О
378	Characterization of the Chloroplast Genome Structure of Gueldenstaedtia verna (Papilionoideae) and Comparative Analyses among IRLC Species. 2022 , 13, 1942	О

377	Reaction Mechanism of Ancestral l-Lys Exidase from Caulobacter Species Studied by Biochemical, Structural, and Computational Analysis.	0
376	A Chromosome-level assembly of the Japanese eel genome, insights into gene duplication and chromosomal reorganization. 2022 , 11,	2
375	Detection of the peptidyl epitope for vaccine development against MPV. 2023, 35, 102458	O
374	Ancient origin and conserved gene function in terpene pheromone and defense evolution of stink bugs and hemipteran insects. 2023 , 152, 103879	1
373	Chromosomal-level genome and multi-omics dataset provides new insights into leaf pigmentation in Acer palmatum. 2023 , 227, 93-104	O
372	Mitogenome-based phylogenomics provides insights into the positions of the enigmatic sinensis group and the sanguinolenta group in Selaginellaceae (Lycophyte). 2023 , 179, 107673	O
371	Transcriptomic data recover a new superfamily-level phylogeny of Cucujiformia (Coleoptera, Polyphaga). 2023 , 179, 107679	O
370	Polymeric structure of the Cannabis sativa L. mitochondrial genome identified with an assembly graph model. 2023 , 853, 147081	o
369	Structural evolution of an amphibian-specific globin: A computational evolutionary biochemistry approach. 2023 , 45, 101055	0
368	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation. 2023 , 45, 101045	O
367	Discovering recent selection forces shaping the evolution of dengue viruses based on polymorphism data across geographic scales. 2022 , 8,	O
366	Chromosome-Level Genome Assembly and Multi-Omics Dataset Provide Insights into Isoflavone and Puerarin Biosynthesis in Pueraria lobata (Wild.) Ohwi. 2022 , 12, 1731	o
365	Comparative genomic analysis of five Coprinus species.	O
364	Genomic basis of the giga-chromosomes and giga-genome of tree peony Paeonia ostii. 2022 , 13,	O
363	Evolutionary Impacts of Pattern Recognition Receptor Genes on Carnivora Complex Habitat Stress Adaptation. 2022 , 12, 3331	0
362	Birth-and-death evolution of ribonuclease 9 genes in Cetartiodactyla.	o
361	African Suid Genomes Provide Insights into the Local Adaptation to Diverse African Environments. 2022 , 39,	0
360	Survivor bias drives overestimation of stability in reconstructed ancestral proteins.	O

359	A high-quality genome assembly and annotation of Quercus acutissima Carruth. 13,	О
358	Adaptive duplication and genetic diversification of protein kinase R contribute to the specificity of bat-virus interactions. 2022 , 8,	1
357	Genomic signatures of recent convergent transitions to social life in spiders. 2022, 13,	О
356	Transposable elements drive the evolution of metazoan zinc finger genes.	O
355	Widespread convergent evolution of alpha-neurotoxin resistance in African mammals. 2022, 18,	0
354	Strategy of micro-environmental adaptation to cold seep among different brittle stars colonization. 10,	O
353	The Complete Chloroplast Genome Sequence of Laportea bulbifera (Sieb. et Zucc.) Wedd. and Comparative Analysis with Its Congeneric Species. 2022 , 13, 2230	0
352	Chromosome-Level Genome Assembly of the Speckled Blue Grouper (Epinephelus cyanopodus) Provides Insight into Its Adaptive Evolution. 2022 , 11, 1810	0
351	The Fast and the Furriest: Investigating the Rate of Selection on Mammalian Toxins. 2022, 14, 842	0
350	Large-scale comparative genomics to refine the organization of the global Salmonella enterica population structure. 2022 , 8,	0
349	Plastid phylogenomics and plastome evolution in the morning glory family (Convolvulaceae). 13,	0
348	Illusion of flight? Absence, evidence and the age of winged insects.	1
347	The root-knot nematode effector MiMSP32 targets host 12-oxophytodienoate reductase 2 (OPR2) to regulate plant susceptibility.	0
346	A New Hope: A Hermaphroditic Nematode Enables Analysis of a Recent Whole Genome Duplication Event. 2022 , 14,	O
345	Comparative genomics of five Valsa species gives insights on their pathogenicity evolution.	0
344	CherryML: Scalable Maximum Likelihood Estimation of Phylogenetic Models.	O
343	Evolution and diversification of Mountain voles (Rodentia: Cricetidae). 2022, 5,	1
342	Intron-rich dinoflagellate genomes driven by Introner transposable elements of unprecedented diversity. 2022 ,	O

341	Phylogenetic Analyses of Some Key Genes Provide Information on Pollinator Attraction in Solanaceae. 2022 , 13, 2278	О
340	The chromosome-level genome assembly of goldstripe ponyfish (Karalla daura) reveals its similarity to Chinese sillago on contracted immune gene families. 9,	Ο
339	Multiple introgressions shape mitochondrial evolutionary history in Drosophila paulistorum and the Drosophila willistoni group. 2022 , 107683	0
338	Cyanobacterial Blooms Are Not a Result of Positive Selection by Freshwater Eutrophication. 2022 , 10,	1
337	Molecular Evolution of the Bactericidal/Permeability-Increasing Protein (BPIFA1) Regulating the Innate Immune Responses in Mammals. 2023 , 14, 15	1
336	Dynamic Evolution of Avian RNA Virus Sensors: Repeated Loss of RIG-I and RIPLET. 2023 , 15, 3	Ο
335	Retrieving the near-complete genome of a threatened bird from wild frozen samples.	Ο
334	Genomic data suggest parallel dental vestigialization within the xenarthran radiation.	Ο
333	Dual Domestication, Diversity, and Differential Introgression in Old World Cotton Diploids. 2022 , 14,	Ο
332	Evolution and molecular basis of a novel allosteric property of crocodilian hemoglobin. 2022,	0
331	Specific Enriched Acinetobacter in Camellia Weevil Gut Facilitate the Degradation of Tea Saponin: Inferred from Bacterial Genomic and Transcriptomic Analyses. 2022 , 10,	Ο
330	A refined characterization of large-scale genomic differences in the first complete human genome.	Ο
329	Ten Plastomes of Crassula (Crassulaceae) and Phylogenetic Implications. 2022 , 11, 1779	2
328	The genome of the king protea, Protea cynaroides.	Ο
327	Comparative analysis of mitochondrial genomes reveals marine adaptation in seagrasses. 2022, 23,	Ο
326	Stings on wings: Proteotranscriptomic and biochemical profiling of the lesser banded hornet (Vespa affinis) venom. 9,	Ο
325	De novo birth of functional microproteins in the human lineage. 2022 , 41, 111808	0
324	Genome-Wide Identification and Expression Analysis of the 14-3-3 (TFT) Gene Family in Tomato, and the Role of SlTFT4 in Salt Stress. 2022 , 11, 3491	O

323	Alternative telomere maintenance mechanism in Alligator sinensis provides insights into aging evolution. 2022 , 105850	0
322	Genome-Wide Analysis of Wheat GATA Transcription Factor Genes Reveals Their Molecular Evolutionary Characteristics and Involvement in Salt and Drought Tolerance. 2023 , 24, 27	1
321	The molecular evolution of spermatogenesis across mammals.	О
320	Impaired immune function accompanies social evolution in spiders. 2022, 18,	О
319	Evolutionary models demonstrate rapid and adaptive diversification of Australo-Papuan pythons. 2022 , 18,	O
318	The blackgrass genome reveals patterns of non-parallel evolution of polygenic herbicide resistance.	О
317	High-quality chromosome-level genome assembly of Pacific cod, Gadus macrocephalus. 9,	0
316	Pan-cancer surveys indicate cell cycle-related roles of primate-specific genes in tumors and embryonic cerebrum. 2022 , 23,	О
315	Chloroplast gene expression level is negatively correlated with evolutionary rates and selective pressure while positively with codon usage bias in Ophioglossum vulgatum L. 2022 , 22,	1
314	Genomic Legacies of Ancient Adaptation Illuminate GC-Content Evolution in Bacteria.	О
313	The ecological adaptation of the unparalleled plastome character evolution in slipper orchids. 13,	O
312	The chromosome-scale genome of Kobresia myosuroides sheds light on karyotype evolution and recent diversification of a dominant herb group on the Qinghai-Tibet Plateau.	O
311	Continent-wide phylogenomic framework reveals introgression as a driver of intra-specific diversity and enriched molecular pathways in caribou.	1
310	Convergent Genomic Signatures of High-Altitude Adaptation among Six Independently Evolved Mammals. 2022 , 12, 3572	O
309	Cylicins are a structural component of the sperm calyx being indispensable for male fertility in mice and human.	O
308	Jack of all trades: Genome assembly of Wild Jack and comparative genomics of Artocarpus. 13,	O
307	Evolutionary genetics of flipper forelimb and hindlimb loss from limb development-related genes in cetaceans. 2022 , 23,	0
306	Sequencing and description of the complete mitochondrial genome of Limatus durhamii (Diptera Culicidae). 2022 , 106805	О

305	A Novel Trichothecene Toxin Phenotype Associated with Horizontal Gene Transfer and a Change in Gene Function in Fusarium. 2023 , 15, 12	Ο
304	Molecular evolution of protein sequences and codon usage in monkeypox viruses.	Ο
303	Draft Genome of White-blotched River Stingray Provides Novel Clues for Niche Adaptation and Skeleton Formation. 2022 ,	0
302	How to survive in the world! third poplar: Insights from the genome of the highest altitude woody plant, Hippophae tibetana (Elaeagnaceae). 13,	Ο
301	Topiary: pruning the manual labor from ancestral sequence reconstruction.	1
300	Assessing the relative performance of fast molecular dating methods for phylogenomic data. 2022 , 23,	0
299	The novel compound heterozygous rare variants may impact positively selected regions of TUBGCP6, a microcephaly associated gene. 10,	О
298	Accelerated evolution of dim-light vision-related arrestin in deep-diving amniotes. 10,	Ο
297	Immunogenetic losses co-occurred with seahorse male pregnancy and mutation in tlx1 accompanied functional asplenia. 2022 , 13,	Ο
296	Evaluation of methods to detect shifts in directional selection at the genome scale.	O
295	The LEA gene family in tomato and its wild relatives: genome-wide identification, structural characterization, expression profiling, and role of SlLEA6 in drought stress. 2022 , 22,	0
294	Widespread transposon co-option in the Caenorhabditis germline regulatory network. 2022, 8,	O
293	Uncovering a 500 million year old history and evidence of pseudogenization for TLR15. 13,	0
292	Sinapis genomes provide insights into whole-genome triplication and divergence patterns within tribe Brassiceae.	0
291	Parallel evolution of opsin visual pigments in hawkmoths by tuning of spectral sensitivities during transition from a nocturnal to a diurnal ecology. 2022 , 225,	Ο
290	Whole genome analysis of clouded leopard species reveals an ancient divergence and distinct demographic histories. 2022 , 25, 105647	O
289	Chromosome-scale genome assembly of Glycyrrhiza uralensis revealed metabolic gene cluster centred specialized metabolites biosynthesis. 2022 , 29,	0
288	An improved assembly of the Cascadelhop (Humulus lupulus) genome uncovers signatures of molecular evolution and refines time of divergence estimates for the Cannabaceae family.	Ο

287	Genetic Structure and Historical Dynamics of Pinus densiflora Siebold & Dynamics Of Pinus densification & Dynamics	O
286	Actl7b-deficiency leads to mislocalization of LC8 type dynein light chains and disruption of murine spermatogenesis.	O
285	Rubbing Salt in the Wound: Molecular Evolutionary Analysis of Pain-Related Genes Reveals the Pain Adaptation of Cetaceans in Seawater. 2022 , 12, 3571	0
284	The paralogues MAGOH and MAGOHB are oncogenic factors in high-grade gliomas and safeguard the splicing of cell division and cell cycle genes.	O
283	Genomes of the cosmopolitan fruit pest Bactrocera dorsalis (Diptera: Tephritidae) reveal its global invasion history and thermal adaptation. 2022 ,	O
282	The antigen recognition portion of African buffalo class I MHC is highly polymorphic, consistent with a complex pathogen challenge environment, and the 3Iregion suggests distinct haplotype configurations.	O
281	Toll-like Receptor 3 in the Hybrid Yellow Catfish (Pelteobagrus fulvidraco? IP. vachelli?): Protein Structure, Evolution and Immune Response to Exogenous Aeromonas hydrophila and Poly (I:C) Stimuli. 2023 , 13, 288	O
2 80	Pseudo-chromosomelength genome assembly for a deep-sea eel Ilyophis brunneus sheds light on the deep-sea adaptation.	O
279	The plastid genome of twenty-two species from Ferula, Talassia, and Soranthus: comparative analysis, phylogenetic implications, and adaptive evolution. 2023 , 23,	0
278	Evolutionary dynamics of sex-biased gene expression in a young XY system: Insights from the brown alga genus Fucus.	O
277	High-quality genome of Diaphanosoma dubium provides insights into molecular basis of its broad ecological adaptation. 2023 , 106006	0
276	Na+- Clltotransporter 2 is not fish-specific and is widely found in amphibians, non-avian reptiles, and select mammals.	O
275	Chloroplast phylogenomics and the taxonomy of Saxifraga section Ciliatae (Saxifragaceae). 2023 , 13,	0
274	Similar adaptative mechanism but divergent demographic history of four sympatric desert rodents in Eurasian inland. 2023 , 6,	O
273	Pollen Coat Proteomes of Arabidopsis thaliana, Arabidopsis lyrata, and Brassica oleracea Reveal Remarkable Diversity of Small Cysteine-Rich Proteins at the Pollen-Stigma Interface. 2023 , 13, 157	0
272	Complete chloroplast genomes and comparative analysis of Ligustrum species. 2023, 13,	Ο
271	Transcriptomic analysis of seed development in Paysonia auriculata (Brassicaceae) identifies genes involved in hydroxy fatty acid biosynthesis. 13,	0
270	Adaptive Evolution of the OAS Gene Family Provides New Insights into the Antiviral Ability of Laurasiatherian Mammals. 2023 , 13, 209	1

269	Chromosome-level genome of black cutworm provides novel insights into polyphagy and seasonal migration in insects. 2023 , 21,	1
268	Chromosome-level genome assembly of a high-altitude-adapted frog (Rana kukunoris) from the Tibetan plateau provides insight into amphibian genome evolution and adaptation. 2023 , 20,	O
267	Endophytic fungi related to the ash dieback causal agent encode signatures of pathogenicity on European ash.	О
266	Genomic basis of Y-linked dwarfism in cichlids pursuing alternative reproductive tactics.	O
265	Phylogenomics reveals pervasive ancient introgression in the radiation of macaques.	О
264	Analysis of Pneumocystis Transcription Factor Evolution and Implications for Biology and Lifestyle.	O
263	Proteome-Wide Structural Computations Provide Insights into Empirical Amino Acid Substitution Matrices. 2023 , 24, 796	О
262	Demography and linked selection interact to shape the genomic landscape of codistributed woodpeckers during the Ice Age.	O
261	Adaptive evolution of hearing genes highlights multiple evolutionary paths for dolphin echolocation in different environments.	O
260	Loss of a gluconeogenic muscle enzyme contributed to adaptive metabolic traits in hummingbirds. 2023 , 379, 185-190	O
259	Multidrug resistance plasmids underlie clonal expansions and international spread of Salmonella entericaserotype 4,[5],12,i:- ST34 in Southeast Asia.	О
258	Reduced effectiveness of purifying selection on new mutations in a parthenogenic terrestrial isopod (Trichoniscus pusillus).	O
257	Investigation of the Molecular Evolution of Treg Suppression Mechanisms Indicates a Convergent Origin. 2023 , 45, 628-648	1
256	A binary interaction map between turnip mosaic virus and Arabidopsis thaliana proteomes. 2023 , 6,	O
255	The genome of the oomycete Peronosclerospora sorghi, a cosmopolitan pathogen of maize and sorghum, is inflated with dispersed pseudogenes.	О
254	Identification, Classification and Characterization of bZIP Transcription Factor Family Members in Pinus massoniana Lamb 2023 , 14, 155	O
253	Evolutionary analysis of p38 stress-activated kinases in unicellular relatives of animals suggests an ancestral function in osmotic stress. 2023 , 13,	O
252	Convergent Genomic Signatures of Cashmere Traits: Evidence for Natural and Artificial Selection. 2023 , 24, 1165	O

251	Potentially reduced fusogenicity of syncytin-2 in New World monkeys.	О
250	A chromosome-level genome assembly of radish (Raphanus sativus L.) reveals insights into genome adaptation and differential bolting regulation.	O
249	Exploring Evolutionary Relationships within Neodermata Using Putative Orthologous Groups of Proteins, with Emphasis on Peptidases. 2023 , 8, 59	0
248	Utilizing evolutionary conservation to detect deleterious mutations and improve genomic prediction in cassava. 13,	O
247	Large-scale analyses of angiosperm Flowering Locus T genes reveal duplication and functional divergence in monocots. 13,	O
246	Genetic basis underlying Lassa fever endemics in the Mano River region, West Africa. 2023 , 579, 128-136	O
245	High-quality genome sequence reveals a young polyploidization and provides insights into cellulose and lignin biosynthesis in water dropwort (Oenanthe sinensis). 2023 , 193, 116203	0
244	Mitochondrial characteristics of the powdery mildew genus Erysiphe revealed an extraordinary evolution in protein-coding genes. 2023 , 230, 123153	O
243	Role of distal sites in enzyme engineering. 2023 , 63, 108094	О
242	Prolactin and the evolution of male pregnancy. 2023 , 334, 114210	O
242	Prolactin and the evolution of male pregnancy. 2023 , 334, 114210 Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into Asymmetrical Bias and Phylogenetic Implications. 2023 , 13, 96	0
	Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into	
241	Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into Asymmetrical Bias and Phylogenetic Implications. 2023 , 13, 96 Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex	1
241 240	Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into Asymmetrical Bias and Phylogenetic Implications. 2023, 13, 96 Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. 2022, 12, The Jasmine (Jasminum sambac) Genome Provides Insight into the Biosynthesis of Flower	1 O
241 240 239	Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into Asymmetrical Bias and Phylogenetic Implications. 2023, 13, 96 Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. 2022, 12, The Jasmine (Jasminum sambac) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. 2022,	1 0
241 240 239 238	Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into Asymmetrical Bias and Phylogenetic Implications. 2023, 13, 96 Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. 2022, 12, The Jasmine (Jasminum sambac) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. 2022, Chromosome-level assembly of triploid genome of sichuan pepper (Zanthoxylum armatum). 2022, High-Quality Genomes of Pangolins: Insights into the Molecular Basis of Scale Formation and	1 0 1
241 240 239 238	Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into Asymmetrical Bias and Phylogenetic Implications. 2023, 13, 96 Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. 2022, 12, The Jasmine (Jasminum sambac) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. 2022, Chromosome-level assembly of triploid genome of sichuan pepper (Zanthoxylum armatum). 2022, High-Quality Genomes of Pangolins: Insights into the Molecular Basis of Scale Formation and Adaption to Myrmecophagous Diet. 2023, 40, Phylogenomics and systematics of Entomobryoidea (Collembola): marker design, phylogeny and	1 0 1 0

233	Variation in heat shock protein 40 kDa relates to divergence in thermotolerance among cryptic rotifer species. 2022 , 12,	o
232	Constraining Whole-Genome Duplication Events in Geological Time. 2023 , 139-154	О
231	A phylogenomic study of Iridaceae Juss. based on complete plastid genome sequences. 14,	0
230	Chromosome fusions repatterned recombination rate and facilitated reproductive isolation during Pristionchus nematode speciation.	1
229	Complete genome sequencing of nematode Aphelenchoides besseyi, an economically important pest causing rice white-tip disease. 2023 , 5,	0
228	The Impact of Multiple Sequence Alignment Error on Phylogenetic Estimation under Variable-Across-Phylogeny Substitution Models.	O
227	The molecular evolution of genes previously associated with large sizes reveals possible pathways to cetacean gigantism. 2023 , 13,	0
226	Ancient loss of catalytic selenocysteine spurred convergent adaptation in a mammalian oxidoreductase.	o
225	Dating in the Dark: Elevated Substitution Rates in Cave Cockroaches (Blattodea: Nocticolidae) Have Negative Impacts on Molecular Date Estimates.	0
224	Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. 2023 , 33, 112-128	o
223	Antibiotic hyper-resistance in a class I aminoacyl-tRNA synthetase with altered active site signature motif.	0
222	Chromosome-Level Genome Assembly of Herpetospermum pedunculosum (Cucurbitaceae). 2023 , 15,	o
221	High-quality Fagopyrum esculentum genome provides insights into the flavonoid accumulation among different tissues and self-incompatibility.	0
220	Parallel duplication and loss of aquaporin-coding genes during the But of the sealtransition as potential key drivers of animal terrestrialization.	0
219	Molecular evolution and population genetics of glutamate decarboxylase acid resistance pathway in lactic acid bacteria. 14,	0
218	Comparative Analyses Reveal the Genetic Mechanism of Ambergris Production in the Sperm Whale Based on the Chromosome-Level Genome. 2023 , 13, 361	o
217	Highly Dynamic Gene Family Evolution Suggests Changing Roles for PON Genes Within Metazoa.	0
216	Gapless Genome Assembly of Puccinia triticina Provides Insights into Chromosome Evolution in Pucciniales.	О

215	PlantTribes2: Tools for comparative gene family analysis in plant genomics. 13,	0
214	Is the Association of the Rare rs35667974 IFIH1 Gene Polymorphism With Autoimmune Diseases a Case of RNA Epigenetics?.	O
213	Genome Assembly and Comparative Analysis of the Egg Parasitoid Wasp Trichogramma dendrolimi Shed Light on the Composition and Evolution of Olfactory Receptors and Venoms. 2023 , 14, 144	0
212	Comparative gene retention analysis in barley, wild emmer, and bread wheat pangenome lines reveals factors affecting gene retention following gene duplication. 2023 , 21,	O
211	Barbel regeneration and function divergence in red-tail catfish (Hemibagrus wyckioides) based on the chromosome-level genomes and comparative transcriptomes. 2023 , 232, 123374	0
2 10	Plastid phylogenomics and molecular evolution of Thismiaceae (Dioscoreales).	O
209	Reduction, evolutionary pattern and positive selection of genes encoding formate dehydrogenase in WoodIjungdahl pathway of gastrointestinal acetogens suggests their adaptation to formate-rich habitats. 2023 , 15, 129-141	0
208	The deep-rooted origin of disulfide-rich spider venom toxins. 12,	O
207	Short structural variation fuelled CAM evolution within an explosive bromeliad radiation.	0
206	Evidence for an early green/red photocycle that precedes the diversification of GAF domain photoreceptor cyanobacteriochromes.	O
205	Identification and spatio-temporal tracking of ubiquitous phage families in the human microbiome. 1,	О
204	Retro-miRs: Novel and functional miRNAs originated from mRNA retrotransposition.	O
203	Panguiarchaeum symbiosum, a potential hyperthermophilic symbiont in the TACK superphylum. 2023 , 42, 112158	O
202	Chromosome-Level Genome Assembly of Papilio elwesi Leech, 1889 (Lepidoptera: Papilionidae). 2023 , 14, 304	O
201	Chromosome-level genome assembly provides insights into adaptive evolution of chromosome and important traits in the geckoGekko japonicus.	0
200	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. 2023 ,	O
199	Chromosome-scale genome assembly of marigold (Tagetes erecta L.): an ornamental plant and feedstock for industrial lutein production. 2023 ,	О
198	An orphan protein drove the ecological expansion of nitrogen fixation.	Ο

197	Analyses of a chromosome-scale genome assembly reveal the origin and evolution of cultivated chrysanthemum. 2023 , 14,	О
196	Adaptive evolution of the Spike protein in coronaviruses.	О
195	The genome of the pygmy right whale illuminates the evolution of rorquals. 2023, 21,	O
194	Venomous Noodles: evolution of toxins in Nemertea through positive selection and gene duplication.	O
193	The genome sequence and demographic history of Przewalskia tangutica (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau.	O
192	Actively transcribed rDNA and distal junction (DJ) sequence are involved in association of NORs with nucleoli. 2023 , 80,	O
191	Chromosome-level genome of the bean bug Megacopta cribraria in native range, provides insights into adaptation and pest management. 2023 , 237, 123989	О
190	A plastome phylogeny of Rumex (Polygonaceae) illuminates the divergent evolutionary histories of docks and sorrels. 2023 , 182, 107755	O
189	Advances in the understanding of Blattodea evolution: Insights from phylotranscriptomics and spermathecae. 2023 , 182, 107753	О
188	Seven newly sequenced chloroplast genomes from the order Watanabeales (Trebouxiophyceae, Chlorophyta): Phylogenetic and comparative analysis. 2023 , 863, 147287	O
187	Rate accelerations in plastid and mitochondrial genomes of Cyperaceae occur in the same clades. 2023 , 182, 107760	О
186	Phylogenomics reconciles molecular data with the rich fossil record on the origin of living turtles. 2023 , 183, 107773	O
185	Signatures of natural selection in tree topology shape of serially sampled viral phylogenies. 2023 , 183, 107776	0
184	All differential on the splicing front: Host alternative splicing alters the landscape of virus-host conflict. 2023 , 146, 40-56	O
183	The chromosome-level genome of double-petal phenotype jasmine (Jasminum sambac Aiton) provides insights into the biosynthesis of floral scent. 2023 ,	О
182	Reference genomes of channel catfish and blue catfish reveal multiple pericentric chromosome inversions. 2023 , 21,	O
181	Molecular evolution of the hemoglobin gene family across vertebrates.	O
180	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of Poncirus polyandra. 2023 , 115, 110617	O

179	The Populus koreana genome provides insights into the biosynthesis of plant aroma. 2023 , 197, 116453	O
178	Parallel Evolution of Sex-Linked Genes across XX/XY and ZZ/ZW Sex Chromosome Systems in the Frog Glandirana rugosa. 2023 , 14, 257	O
177	Chromosome-level genome assembly of the Colorado potato beetle, Leptinotarsa decemlineata. 2023 , 10,	O
176	Signatures of purifying selection and site-specific positive selection on the mitochondrial DNA of dromedary camels (Camelus dromedarius). 2023 , 69, 36-42	O
175	Both male and female meiosis contribute to non-Mendelian inheritance of parental chromosomes in interspecific plant hybrids (Lolium 🛘 Festuca). 2023 , 238, 624-636	O
174	Evolution of Fertilization-Related Genes Provides Insights Into Reproductive Health in Natural Ascrotal Mammals. 9,	O
173	Genomic health is dependent on long-term population demographic history. 2023, 32, 1943-1954	O
172	Chromosomal-level genome assembly of Melastoma candidum provides insights into trichome evolution. 14,	O
171	Next-generation development and application of codon model in evolution. 14,	O
170	The chromosome-level genome and key genes associated with mud-dwelling behavior and adaptations of hypoxia and noxious environments in loach (Misgurnus anguillicaudatus). 2023 , 21,	O
169	Inference of Ancient Polyploidy from Genomic Data. 2023, 3-18	O
168	Comparative genomic study of the Penicillium genus elucidates a diverse pangenome and 15 lateral gene transfer events. 2023 , 14,	O
167	Chromosome-level genomes of multicellular algal sisters to land plants illuminate signaling network evolution.	O
166	Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut (Juglans nigra). 2023 , 10,	O
165	Chromosome-Level Assembly of Flowering Cherry (Prunus campanulata) Provides Insight into Anthocyanin Accumulation. 2023 , 14, 389	0
164	Genomic identification of cotton SAC genes branded ovule and stress-related key genes in Gossypium hirsutum. 14,	O
163	A chromosome-level genome assembly of the beet armyworm Spodoptera exigua. 2023 , 115, 110571	O
162	Ancestral Sequence Reconstruction Enhances Gene Mining Efforts for Industrial Ene Reductases by Expanding Enzyme Panels with Thermostable Catalysts. 2023 , 13, 2576-2585	3

161	Phylotranscriptomics of Swertiinae (Gentianaceae) reveals that key floral traits are not phylogenetically correlated.	O
160	The seminal odorant binding protein Obp56g is required for mating plug formation and male fertility inDrosophila melanogaster.	O
159	PANAS: Pipeline and a Case Study to Obtain Synonymous and Nonsynonymous Substitution Rates in Genes of Platyhelminthes. 2023 , 90,	0
158	Complete mitochondrial genome of Thuja sutchuenensis and its implications on evolutionary analysis of complex mitogenome architecture in Cupressaceae. 2023 , 23,	O
157	Insights into the convergent evolution of fructan biosynthesis in angiosperms from the highly characteristic chicory genome. 2023 , 238, 1245-1262	0
156	Mitonuclear Interactions and the Origin of Macaque Societies. 2023, 15,	O
155	The genome of Magnolia hypoleuca provides a new insight into cold tolerance and the evolutionary position of magnoliids. 14,	0
154	Stepwise recombination suppression around the mating-type locus in an ascomycete fungus with self-fertile spores. 2023 , 19, e1010347	O
153	Expansion and loss of sperm nuclear basic protein genes in Drosophila correspond with genetic conflicts between sex chromosomes. 12,	0
152	The genome of a vestimentiferan tubeworm (Ridgeia piscesae) provides insights into its adaptation to a deep-sea environment. 2023 , 24,	O
151	Halocynthiibacter halioticoli sp. nov., isolated from the viscera of abalone Haliotis discus hannai.	0
150	Genome size evolution in grasshoppers (Orthoptera: Caelifera: Acrididae).	Ο
149	Characterization of Megabat-Favored, CA-Dependent Susceptibility to Retrovirus Infection. 2023 , 97,	0
148	A chromosome-level genome assembly of Ostrea denselamellosa provides initial insights into its evolution. 2023 , 115, 110582	O
147	Chromosome-Level Genome Assembly of the Rough-Toothed Dolphin (Steno bredanensis). 2023 , 11, 418	0
146	Parallel expansion and divergence of an adhesin family in pathogenic yeasts. 2023, 223,	O
145	Genome-Wide Identification and Expression Analysis of Calmodulin-Like Gene Family in Paspalums vaginatium Revealed Their Role in Response to Salt and Cold Stress. 2023 , 45, 1693-1711	0
144	Higher-level phylogeny and evolutionary history of nonditrysians (Lepidoptera) inferred from mitochondrial genome sequences.	O

143	De Novo Assembly and Characterization of the Transcriptome of an Omnivorous Camel Cricket (Tachycines meditationis). 2023 , 24, 4005	Ο
142	Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, Quercus dentata.	O
141	Transcriptome Identification of R2R3-MYB Gene Family Members in Pinus massoniana and PmMYB4 Response to Drought Stress. 2023 , 14, 410	1
140	Phylotranscriptomics and evolution of key genes for terpene biosynthesis in Pinaceae. 14,	O
139	How voles adapt to subterranean lifestyle: Insights from RNA-seq. 11,	O
138	Nitrogenase resurrection and the evolution of a singular enzymatic mechanism. 12,	O
137	Pangolin genomes offer key insights and resources for the world most trafficked wild mammals.	O
136	Multi-omics Investigation of Freeze Tolerance in the Amur Sleeper, an Aquatic Ectothermic Vertebrate. 2023 , 40,	O
135	Evolutionary History of thePoecilia pictaSex Chromosomes. 2023 , 15,	O
134	Draft genome of the oriental garden lizard (Calotes versicolor). 14,	O
133	De Novo Assembly and Comparative Analysis of the Complete Mitochondrial Genome of Chaenomeles speciosa (Sweet) Nakai Revealed the Existence of Two Structural Isomers. 2023 , 14, 526	O
132	The telomere-to-telomere genome of Fragaria vesca reveals the genomic evolution of Fragaria and the origin of cultivated octoploid strawberry. 2023 , 10,	O
131	Genomics of Secondarily Temperate Adaptation in the Only Non-Antarctic Icefish. 2023, 40,	O
130	Chromosome-level genome assembly of tree sparrow reveals a burst of new genes driven by segmental duplications.	O
129	Bat pluripotent stem cells reveal unusual entanglement between host and viruses. 2023 , 186, 957-974.e28	O
128	High-quality genome assemblies provide clues on the evolutionary advantage of blue peafowl over green peafowl.	O
127	Enlarged fins of Tibetan catfish provide new evidence of adaptation to high plateau.	O
126	High-quality Cymbidium mannii genome and multifaceted regulation of crassulacean acid metabolism in epiphytes. 2023 , 100564	O

125	Chloroplast genomic comparison provides insights into the evolution of seagrasses. 2023, 23,	O
124	A chromosome-level genome assembly for Erianthus fulvus provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. 2023 , 100562	O
123	Amblyopinae Mitogenomes Provide Novel Insights into the Paraphyletic Origin of Their Adaptation to Mudflat Habitats. 2023 , 24, 4362	0
122	Evolution of enzyme functionality in the flavin-containing monooxygenases. 2023 , 14,	O
121	Synteny Identifies Reliable Orthologs for Phylogenomics and Comparative Genomics of the Brassicaceae. 2023 , 15,	О
120	Ancient Rapid Radiation Explains Most Conflicts Among Gene Trees and Well-Supported Phylogenomic Trees of Nostocalean Cyanobacteria.	Ο
119	Evolution of the Growth Hormone Gene Duplication in Passerine Birds. 2023, 15,	O
118	Roadmap to the study of gene and protein phylogeny and evolution practical guide. 2023 , 18, e0279597	O
117	Identification of conserved genomic signatures specific to Bifidobacterium species colonising the human gut. 2023 , 13,	0
116	Molecular exploration of fossil eggshell uncovers hidden lineage of giant extinct bird. 2023, 14,	O
115	FREEDA: an automated computational pipeline guides experimental testing of protein innovation by detecting positive selection.	О
114	Elucidation of the GAUT gene family in eight Rosaceae species and function analysis of PbrGAUT22 in pear pollen tube growth. 2023 , 257,	О
113	Chromosome-Length Assembly of the Baikal Seal (Pusa sibirica) Genome Reveals a Historically Large Population Prior to Isolation in Lake Baikal. 2023 , 14, 619	O
112	Evolution is not Uniform Along Coding Sequences. 2023 , 40,	O
111	Chromosome-level reference genome of Tetrastigma hemsleyanum (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids.	О
110	Genomic Comparisons Reveal Selection Pressure and Functional Variation Between Nutritional Endosymbionts of Cave-Adapted and Epigean Hawaiian Planthoppers. 2023 , 15,	Ο
109	Key innovations and the diversification of Hymenoptera. 2023 , 14,	О
108	Systematic analysis and expression of Gossypium 2ODD superfamily highlight the roles of GhLDOXs responding to alkali and other abiotic stress in cotton. 2023 , 23,	Ο

107	Genome biology and evolution of mating type loci in four cereal rust fungi.	O
106	Mutational signatures in wild typeEscherichia colistrains reveal dominance of DNA polymerase errors.	O
105	Genomic analysis of Leishmania turanica strains from different regions of Central Asia. 2023 , 17, e0011145	0
104	Comparative transcriptomics reveals divergence in pathogen response gene families amongst twenty forest tree species.	O
103	Comparative Mitogenome Analyses Uncover Mitogenome Features and Phylogenetic Implications of the Parrotfishes (Perciformes: Scaridae). 2023 , 12, 410	O
102	Transcript Isoform Diversity of Ampliconic Genes on the Y Chromosome of Great Apes.	O
101	Unique gene duplications and conserved microsynteny potentially associated with resistance to wood decay in the Lauraceae. 14,	О
100	De novo assembly of a chromosome-level reference genome of the ornamental butterfly Sericinus montelus based on nanopore sequencing and Hi-C analysis. 14,	O
99	Hologenome analysis reveals independent evolution to chemosymbiosis by deep-sea bivalves. 2023 , 21,	0
98	Irreversible evolutionary loss of chitin-degrading ability in the chitinase-like protein Y m1 under positive selection in rodents. 2023 , 32,	O
97	Chromosome-level genome assembly of Phrynocephalus forsythii using third-generation DNA sequencing and Hi-C analysis. 2023 , 30,	O
96	Seagrass genomes reveal a hexaploid ancestry facilitating adaptation to the marine environment.	O
95	De novoAssembly and Comparative Analyses of Mitochondrial Genomes in Piperales. 2023, 15,	O
94	The path to flemmes fatales[Ithe evolution of toxin resistance in predatory fireflies.	O
93	Comparative Genomics of Firmicutes reveals probable adaptations for xylose fermentation in Thermoanaerobacterium saccharolyticum.	0
92	Centriole Remodeling Evolved into Centriole Degradation in Mouse Sperm.	O
91	A chromosome-scale genome sequence of sudangrass (Sorghum sudanense) highlights the genome evolution and regulation of dhurrin biosynthesis. 2023 , 136,	О
90	Co-evolution of ion channels and neurotoxins in cnidarians leads to diversification of ion channel genes.	O

89	Rhizosphere microbial community assembly and association networks strongly differ based on vegetation type at a local environment scale. 14,	0
88	Genome-Wide Identification of 2-Oxoglutarate and Fe (II)-Dependent Dioxygenase (2ODD-C) Family Genes and Expression Profiles under Different Abiotic Stresses in Camellia sinensis (L.). 2023 , 12, 1302	o
87	Molecular signature of domestication in the arboviral vectorAedes aegypti.	O
86	The origin and structural evolution ofde novogenes inDrosophila.	О
85	Mitochondrial genome evolution in the Diprionidae: Major gene rearrangement in the basal Hymenoptera.	0
84	An improved germline genome assembly for the sea lamprey Petromyzon marinus illuminates the evolution of germline-specific chromosomes. 2023 , 42, 112263	O
83	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. 2023 , 14,	0
82	Phylogeny and Evolutionary Timescale of Muscidae (Diptera: Calyptratae) Inferred from Mitochondrial Genomes. 2023 , 14, 286	O
81	Deleterious mutation load in the admixed mice population. 11,	O
80	Natural selection and convergent evolution of the HOX gene family in Carnivora. 11,	0
79	Maternal genetic history of ancient Tibetans over the past 4000 years. 2023,	О
78	Comparative genomics reveals the diversification of triterpenoid biosynthesis and origin of ocotillol-type triterpenes in Panax. 2023 , 100591	O
77	Insights into the genomic evolution and the alkali tolerance mechanisms of Agaricus sinodeliciosus by comparative genomic and transcriptomic analyses. 2023 , 9,	0
76	Polyploidization of Indotyphlops braminus, evidence from Isoform-sequencing.	O
75	Parallel evolution of fish bi-modal breathing and expansion of olfactory receptor (OR) genes: toward a universal ORs nomenclature. 2023 ,	1
74	A survey of lineage-specific genes in Triticeae reveals de novo gene evolution from genomic raw material. 2023 , 7,	O
73	Ecologically diverse island-associated lizard radiation shows idiosyncratic trait diversification shifts and homogenous speciation dynamics. 2023 , 77, 138-154	O
72	Chromosome-level de novo genome assembly of two conifer-parasitic wasps, Megastigmus duclouxiana and Megastigmus sabinae , reveals genomic imprints of adaptation to hosts.	O

71	Evolution of chemosensory and detoxification gene families across herbivorous Drosophilidae.	0
70	Retro-miRs: Novel and functional miRNAs originating from mRNA retrotransposition.	O
69	Toward novel treatment against filariasis: Insight into genome-wide co-evolutionary analysis of filarial nematodes and Wolbachia. 14,	0
68	High-Quality Chromosome-Level De Novo Assembly of the Trifolium repens.	O
67	Comparative analysis of the organelle genomes of three Rhodiola species provide insights into their structural dynamics and sequence divergences. 2023 , 23,	0
66	Genome assembly of the ectoparasitoid wasp Theocolax elegans. 2023 , 10,	O
65	Genome-wide comparative analysis between Cranoglanis bouderius and Pangasianodon hypophthalmus: Reveal the genes related to resistance to low-temperature stress.	О
64	Positive selection of neuregulin 1 (NRG-1) among three long-lived vertebrates.	О
63	Depression: an adaptive disease?.	О
62	Upregulation of ENKD1 disrupts cellular homeostasis to promote lymphoma development.	o
61	Genomic convergence underlying high-altitude adaptation in alpine plants.	О
60	Chromosome-aware phylogenomics of Assassin Bugs (Hemiptera: Reduvioidea) elucidates ancient gene conflict.	O
59	Evidence for adaptive evolution towards high magnetic sensitivity of potential magnetoreceptor in songbirds.	0
58	Phylogeny-guided genome mining of roseocin family lantibiotics to generate improved variants of roseocin. 2023 , 13,	O
57	Convergent and complementary selection shaped gains and losses of eusociality in sweat bees. 2023 , 7, 557-569	0
56	The Torreya grandis genome illuminates the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis. 2023 , 14,	O
55	Comparative Transcriptomic Analysis Reveals the Functionally Segmented Intestine in Tunicate Ascidian. 2023 , 24, 6270	О
54	Organellar genomes of giant kelp from the southern hemisphere. 2023 , 4, 78-86	О

53	Characterization of TLR1 and expression profiling of TLR signaling pathway related genes in response to Aeromonas hydrophila challenge in hybrid yellow catfish (Pelteobagrus fulvidraco? Delteobagrus fulvidraco? Delteobagrus fulvidraco? Delteobagrus fulvidraco? Delteobagrus fulvidraco?	O
52	A parasitoid serpin gene that disrupts host immunity shows adaptive evolution of alternative splicing.	O
51	MORC2 restriction factor silences HIV proviral expression.	O
50	Positive Selection and Duplication of Bat TRIM Family Proteins. 2023 , 15, 875	O
49	Genome structures resolve the early diversification of teleost fishes. 2023 , 379, 572-575	О
48	Plastome evolution in the East Asian lobelias (Lobelioideae) using phylogenomic and comparative analyses. 14,	O
47	Divergent contributions of coding and noncoding sequences to initial high-altitude adaptation in passerine birds endemic to the Qinghaillibet Plateau.	О
46	Amplicon capture phylogenomics provides new insights into the phylogeny and evolution of alpine Parnassius butterflies (Lepidoptera: Papilionidae).	O
45	Genome-Wide Analysis of the Odorant Receptor Gene Family in Solenopsis invicta, Ooceraea biroi, and Monomorium pharaonis (Hymenoptera: Formicidae). 2023 , 24, 6624	0
44	Fortuitously compatible protein surfaces primed allosteric control in cyanobacterial photoprotection.	0
44		0
	photoprotection.	
43	photoprotection. Bayesian Phylogenetic Inference of HIV Latent Lineage Ages Using Serial Sequences. High-Quality Assembly and Comparative Analysis of Actinidia latifolia and A. valvata Mitogenomes.	1
43	photoprotection. Bayesian Phylogenetic Inference of HIV Latent Lineage Ages Using Serial Sequences. High-Quality Assembly and Comparative Analysis of Actinidia latifolia and A. valvata Mitogenomes. 2023, 14, 863 In defense of Apocynaceae: inference on evolution of pyrrolizidine alkaloids from evolution of an	1 0
43 42 41	photoprotection. Bayesian Phylogenetic Inference of HIV Latent Lineage Ages Using Serial Sequences. High-Quality Assembly and Comparative Analysis of Actinidia latifolia and A. valvata Mitogenomes. 2023, 14, 863 In defense of Apocynaceae: inference on evolution of pyrrolizidine alkaloids from evolution of an enzyme in their biosynthetic pathway, homospermidine synthase. Shine: A novel strategy to extract specific, sensitive and well-conserved biomarkers from massive	1 O
43 42 41 40	photoprotection. Bayesian Phylogenetic Inference of HIV Latent Lineage Ages Using Serial Sequences. High-Quality Assembly and Comparative Analysis of Actinidia latifolia and A. valvata Mitogenomes. 2023, 14, 863 In defense of Apocynaceae: inference on evolution of pyrrolizidine alkaloids from evolution of an enzyme in their biosynthetic pathway, homospermidine synthase. Shine: A novel strategy to extract specific, sensitive and well-conserved biomarkers from massive microbial genomic datasets. 2023, 24, A high-quality chromosome-level Eutrema salsugineum genome, an extremophile plant model.	1 0 0
43 42 41 40 39	Bayesian Phylogenetic Inference of HIV Latent Lineage Ages Using Serial Sequences. High-Quality Assembly and Comparative Analysis of Actinidia latifolia and A. valvata Mitogenomes. 2023, 14, 863 In defense of Apocynaceae: inference on evolution of pyrrolizidine alkaloids from evolution of an enzyme in their biosynthetic pathway, homospermidine synthase. Shine: A novel strategy to extract specific, sensitive and well-conserved biomarkers from massive microbial genomic datasets. 2023, 24, A high-quality chromosome-level Eutrema salsugineum genome, an extremophile plant model. 2023, 24,	1 0 0

35	The terpene synthase genes of Melaleuca alternifolia (tea tree) and comparative gene family analysis among Myrtaceae essential oil crops. 2023 , 309,	O
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33	Phylogenomics revealed migration routes and adaptive radiation timing of Holarctic malaria mosquito species of the Maculipennis Group. 2023 , 21,	O
32	Mitochondrial genome of Artemisia argyi L. suggested conserved mitochondrial protein-coding genes among genera Artemisia, Tanacetum and Chrysanthemum. 2023 , 147427	O
31	Complete Genome of Rose Myrtle, Rhodomyrtus tomentosa, and Its Population Genetics in Thai Peninsula. 2023 , 12, 1582	О
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